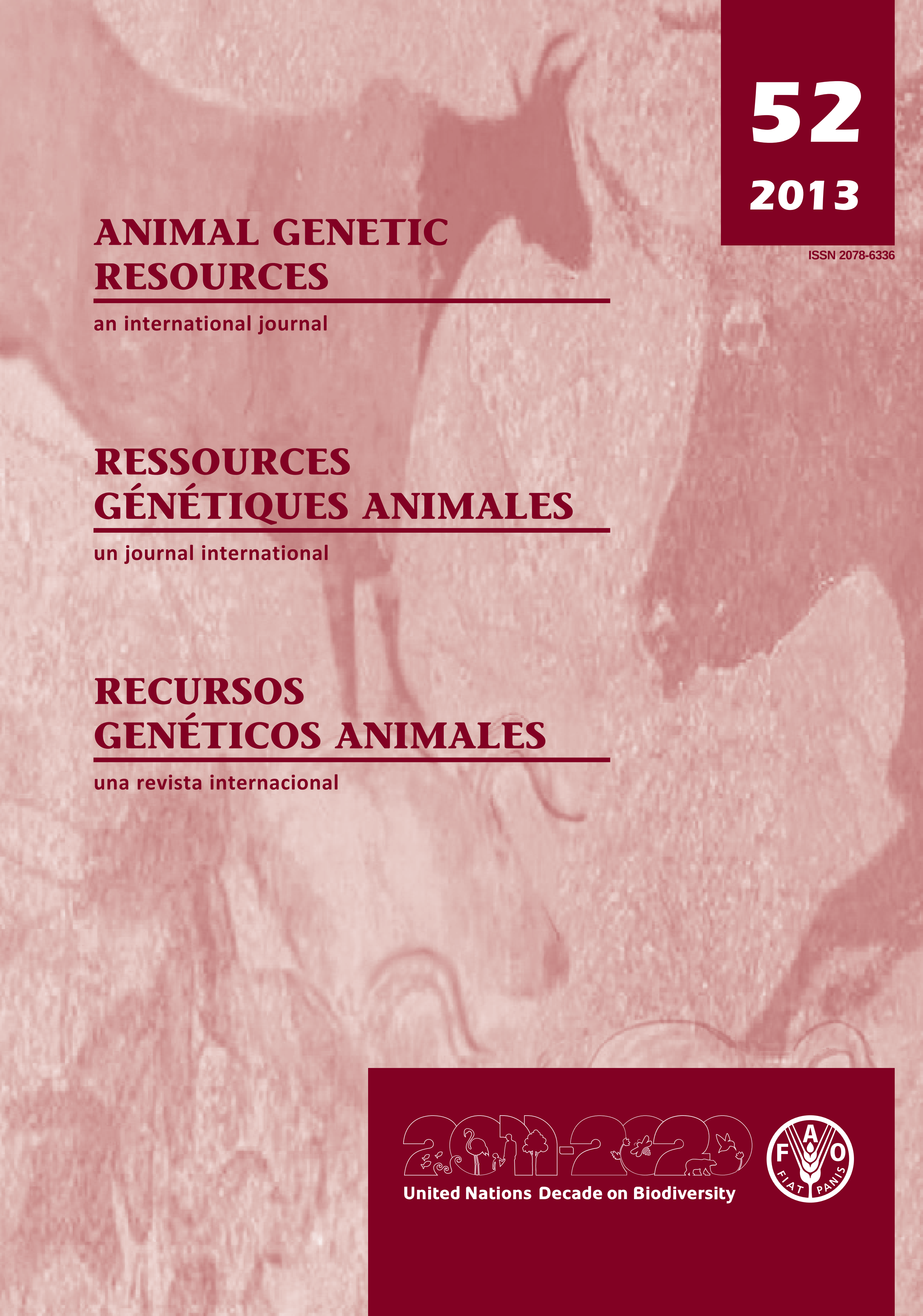

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RECURSOS GENÉTICOS ANIMALES

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Editorial

Intergovernmental meeting

The Seventh Session of the Intergovernmental Technical Working Group on Animal Genetic Resources for Food and Agriculture took place in Rome in October 2012.[1] As discussed in the editorial of volume 51, one of the main tasks facing the Working Group was to review progress made in the implementation of the Global Plan of Action for Animal Genetic Resources[2]. The Working Group welcomed the substantial progress made, but acknowledged that gaps remain to be addressed, particularly in terms of improving collaboration and the funding of activities. Detailed information can be found in the document *Synthesis progress report on the implementation of the Global Plan of Action for Animal Genetic Resources – 2012*,[3] which was prepared for the Working Group's meeting.

The information presented in the *Synthesis progress report* was also used to prepare a set of three posters:

1. Strategic priorities of the Global Plan of Action for Animal Genetic Resources[4]

(overview of the strategic priorities of the Global Plan of Action at national, regional and global levels);

2. Status of implementation of the Global Plan of Action for Animal Genetic Resources[5]

(indicators for each strategic priority at national, regional and world levels); and

3. Colour scheme expressing levels of implementation of the Global Plan of Action for Animal Genetic Resources[6]

(colour scheme used to illustrate the indicators).

The Working Group's agenda also included the preparation and timing of an update of *The State of the World's Animal Genetic Resources for Food and Agriculture*. It had been foreseen that a second report would be presented to the Commission on Genetic Resources for Food and Agriculture in 2017, 10 years after the first report was published. However, because of the heavy workload scheduled for the Commission's Sixteenth Regular Session in 2017, the Working Group was asked to consider the possibility of advancing the preparation of the second report by two years, i.e. recommending that the Commission request FAO to present the report to the Commission's Fifteenth Regular Session in 2015, which would mean having a draft ready for review by the Working Group in late 2014. The Working Group recommended that the Commission agree to this schedule. This volume of *Animal Genetic Resources* went to press before the Commission's meeting in April at which the Working Group's recommendation was to be considered.

The second report, whether presented in 2015 or later, would be regarded very much as an update of the first report, presenting the changes that have occurred during the intervening years in the status of animal genetic resources and their management, as well as the latest scientific developments in relevant fields. Reporting burdens placed on countries would be kept to a minimum and information on the state of animal genetic resources management at national level obtained via specific questionnaires rather than by requesting more elaborate country reports of the type prepared for the first report.

The Working Group's agenda also included a review of implementation of the Funding Strategy for the Implementation of the Global Plan of Action for Animal Genetic Resources (the meeting coincided with the announcement of the first set of projects chosen to receive support under the Funding Strategy);[7] the roles of small-scale livestock keepers in the conservation and sustainable use of animal genetic resources; targets and indicators for animal genetic resources; the status and trends of micro-organisms for ruminant digestion; and a review of the outcomes of the First Session of the Commission's Working Group on Access and Benefit Sharing.

Thirty years of the Commission

As well as being a potentially busy year for the international animal genetic resources community, 2013 is also the thirtieth anniversary year of the Commission. Founded in 1983 as the Commission on Plant Genetic Resources for Food and Agriculture, the Commission can look back on a long series of achievements, including the negotiation of the International Treaty on Plant Genetic Resources for Food and Agriculture and the preparation of State of the World Reports and Global Plans of Action in the plant and animal genetic resources sectors. The Commission's work has expanded from its initial focus on crops, first to animals (livestock) and later to forests, aquatic genetic resources, and invertebrates and micro-

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[1] http://www.fao.org/docrep/meeting/026/mf227e.pdf

[2] www.fao.org/docrep/010/a1404e/a1404e00.htm

[3] http://www.fao.org/docrep/meeting/026/me636e.pdf

[4] ftp://DADnet:Mobile45@ext-ftp.fao.org/ag/reserved/dad-net/GPA.pdf

[5] ftp://DADnet:Mobile45@ext-ftp.fao.org/ag/reserved/dad-net/Indicator.pdf

[6] ftp://DADnet:Mobile45@ext-ftp.fao.org/ag/reserved/dad-net/Traffic_light.pdf

[7] http://www.fao.org/ag/againfo/programmes/en/genetics/Funding_strategy.html

organisms. Links between the various sectors of genetic resources and their roles in the provision of ecosystem services are receiving ever greater attention in the Commission’s work, particularly in light of the planned preparation of a report on *The State of Biodiversity for Food and Agriculture*.

Journal archive

Readers may be interested to learn that Cambridge University Press has made all back issues of *Animal Genetic Resources* available on its web site,[8] which also features a powerful search tool.

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[8] http://journals.cambridge.org/action/displayBackIssues?jid=AGR

Animal Genetic Resources, 2013, 52, iii–iv. © Food and Agriculture Organization of the United Nations, 2013
doi:10.1017/S207863361300012X

Éditorial

Rencontre intergouvernementale

La Septième Réunion du Groupe de Travail Technique Intergouvernemental sur les Ressources Zoogénétiques pour l'Alimentation et l'Agriculture s'est tenue à Rome en Octobre 2012.[1] Comme il a été dit dans l'éditorial du volume 51, une des principales tâches que le Groupe de Travail a dû confronter a été celle d'examiner les progrès réalisés dans la mise en œuvre du Plan d'Action Mondial pour les Ressources Zoogénétiques.[2] Le Groupe de Travail a fait bon accueil au substantiel progrès réalisé, en admettant cependant qu'il existe encore des lacunes à combler, notamment en ce qui concerne l'amélioration de la collaboration et du financement des activités. Pour plus de détails, veuillez consulter le document *Synthesis progress report on the implementation of the Global Plan of Action for Animal Genetic Resources – 2012* (Rapport intérimaire de synthèse sur la mise en œuvre du Plan d'Action Mondial pour les Ressources Zoogénétiques – 2012),[3] qui a été préparé pour la réunion du Groupe de Travail.

L'information présentée dans le *Rapport intérimaire de synthèse* a aussi été utilisée pour préparer un ensemble de trois affiches :

1. *Strategic priorities of the Global Plan of Action for Animal Genetic Resources*[4] (Priorités stratégiques du Plan d'Action Mondial pour les Ressources Zoogénétiques; vue d'ensemble des priorités stratégiques du Plan d'Action Mondial aux échelles nationale, régionale et mondiale);
2. *Status of implementation of the Global Plan of Action for Animal Genetic Resources*[5] (État de mise en œuvre du Plan d'Action Mondial pour les Ressources Zoogénétiques; indicateurs pour chaque priorité stratégique aux niveaux national, régional et mondial); et
3. *Colour scheme expressing levels of implementation of the Global Plan of Action for Animal Genetic Resources*[6] (Échelle de couleur représentant les degrés de mise en œuvre du Plan d'Action Mondial pour les Ressources Zoogénétiques; échelle de couleur utilisée pour illustrer les indicateurs).

La préparation et planification d'une mise à jour de *L'État des Ressources Zoogénétiques pour l'Alimentation et l'Agriculture dans le Monde* étaient aussi à l'agenda du Groupe de Travail. Il a été prévu de présenter un deuxième rapport à la Commission des Ressources Génétiques pour l'Alimentation et l'Agriculture en 2017, dix ans après la publication du premier rapport. Toutefois, en raison de la lourde charge de travail programmée pour la Seizième Réunion Ordinaire de la Commission en 2017, il a été demandé au Groupe de Travail de prendre en considération la possibilité d'avancer la préparation du deuxième rapport de deux ans, c'est-à-dire de conseiller à la Commission qu'elle sollicite à la FAO de présenter le rapport lors de la Quinzième Réunion Ordinaire de la Commission en 2015, ce qui impliquerait qu'une ébauche serait soumise à l'examen du Groupe de Travail vers la fin de l'année 2014. Le Groupe de Travail a recommandé à la Commission d'accepter cette programmation. Ce volume de *Ressources Génétiques Animales* a été mis sous presse avant la réunion de la Commission du mois d'avril, au cours de laquelle la recommandation du Groupe de Travail devait être examinée.

Qu'il soit présenté en 2015 ou ultérieurement, le deuxième rapport constituera une mise à jour du premier rapport d'autant plus qu'il présentera les changements survenus entre-temps pour ce qui est de l'état des ressources zoogénétiques et leur gestion et les derniers développements scientifiques dans les domaines pertinents. La charge de travail que représente la rédaction des rapports pour les pays serait réduite à un minimum, l'information sur l'état de la gestion des ressources zoogénétiques à l'échelon national étant obtenue par le biais de questionnaires spécifiques plutôt qu'en demandant aux pays d'élaborer des rapports détaillés du genre de ceux préparés pour le premier rapport.

Les points suivants étaient aussi à l'agenda du Groupe de Travail: une révision de la mise en œuvre de la Stratégie de Financement pour la mise en application du Plan d'Action Mondial pour les Ressources Zoogénétiques (la rencontre a coïncidé avec l'annonce de la première série de projets sélectionnés pour recevoir le soutien de la Stratégie de Financement);[7] les rôles des petits éleveurs dans la conservation et l'utilisation durable des ressources zoogénétiques; objectifs et indicateurs pour les ressources zoogénétiques; situation et tendances en ce qui concerne les micro-organismes intervenant dans la digestion chez le ruminant; et une révision des résultats de la Première Réunion du Groupe de Travail de la Commission sur l'Accès et le Partage des Avantages.

Trente ans de la Commission

En plus d'être une année potentiellement occupée pour la communauté internationale des ressources zoogénétiques,

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[1] http://www.fao.org/docrep/meeting/027/mf227f.pdf

[2] http://www.fao.org/docrep/010/a1404f/a1404f00.htm

[3] http://www.fao.org/docrep/meeting/026/me636e.pdf

[4] ftp://DADnet:Mobile45@ext-ftp.fao.org/ag/reserved/dad-net/GPA.pdf

[5] ftp://DADnet:Mobile45@ext-ftp.fao.org/ag/reserved/dad-net/Indicator.pdf

[6] ftp://DADnet:Mobile45@ext-ftp.fao.org/ag/reserved/dad-net/Traffic_light.pdf

[7] http://www.fao.org/ag/againfo/programmes/fr/genetics/Funding_strategy.html

l'année 2013 marque le trentième anniversaire de la Commission. Fondée en 1983 sous le nom de Commission des Ressources Phytogénétiques pour l'Alimentation et l'Agriculture, la Commission peut regarder en arrière sur une longue série de réussites, parmi lesquelles la négociation du Traité International sur les Ressources Phytogénétiques pour l'Alimentation et l'Agriculture et la préparation de Rapports sur l'État Mondial et Plans d'Action Mondiaux dans les domaines des ressources phytogénétiques et zoogénétiques. Initialement focalisé sur les cultures, le travail de la Commission s'est étendu par la suite aux animaux (l'élevage), puis à la sylviculture, aux ressources génétiques aquatiques et enfin aux invertébrés et micro-organismes. L'établissement de liens entre les différents secteurs des ressources génétiques ainsi que leur rôle dans la prestation de services aux écosystèmes retiennent de plus en plus l'attention de la Commission, en particulier en vue de la préparation projetée d'un rapport sur *L'État de la Biodiversité pour l'Alimentation et l'Agriculture*.

Archives du journal

Les lecteurs seront peut-être curieux d'apprendre que tous les numéros antérieurs de *Ressources Génétiques Animales* sont disponibles sur le site web de Cambridge University Press,[8] qui est aussi équipé d'un puissant moteur de recherche.

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[8] http://journals.cambridge.org/action/displayBackIssues?jid=AGR

Animal Genetic Resources, 2013, 52, v–vi. © Food and Agriculture Organization of the United Nations, 2013
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Editorial

Encuentro intergubernamental

La Séptima Reunión del Grupo de Trabajo Técnico Intergubernamental sobre los Recursos Zoogenéticos para la Alimentación y la Agricultura se celebró en Roma en Octubre de 2012.[1] Tal y como se comentó en el editorial del volumen 51, una de las principales tareas que abordó el Grupo de Trabajo fue la revisión de los progresos alcanzados en la aplicación del Plan de Acción Mundial sobre los Recursos Zoogenéticos.[2] El Grupo de Trabajo acogió con agrado el considerable progreso realizado, pero admitió que quedan carencias por cubrir, en concreto en materia de mejora de la colaboración y del financiamiento de las actividades. El documento *Synthesis progress report on the implementation of the Global Plan of Action for Animal Genetic Resources – 2012* (Informe de síntesis de los progresos realizados en la aplicación del Plan de Acción Mundial sobre los Recursos Zoogenéticos – 2012),[3] que fue preparado para la reunión del Grupo de Trabajo, recoge una información más detallada.

La información presentada en el *Informe de síntesis de los progresos realizados* también ha sido usada para preparar un conjunto de tres pósteres:

1. *Strategic priorities of the Global Plan of Action for Animal Genetic Resources*[4] (Prioridades estratégicas del Plan de Acción Mundial sobre los Recursos Zoogenéticos; resumen general de las prioridades estratégicas del Plan de Acción Mundial a nivel nacional, regional y mundial);
2. *Status of implementation of the Global Plan of Action for Animal Genetic Resources*[5] (Estado de aplicación del Plan de Acción Mundial sobre los Recursos Zoogenéticos; indicadores para cada prioridad estratégica a nivel nacional, regional y mundial); y
3. *Colour scheme expressing levels of implementation of the Global Plan of Action for Animal Genetic Resources*[6] (Escala de color de referencia para el grado de implementación del Plan de Acción Mundial para los Recursos Zoogenéticos; escala de color usada para ilustrar los indicadores).

En la agenda del Grupo de Trabajo también se incluyeron la preparación y planificación de una actualización de *La Situación de los Recursos Zoogenéticos Mundiales para la Alimentación y la Agricultura*. Se ha previsto la presentación de un segundo informe a la Comisión de Recursos Genéticos para la Alimentación y la Agricultura en 2017, diez años después de la publicación del primer informe. No obstante, debido a la fuerte carga de trabajo programada para la Decimosexta Reunión Ordinaria de la Comisión en 2017, se ha pedido al Grupo de Trabajo que considere la posibilidad de adelantar dos años la preparación del segundo informe, es decir recomendar a la Comisión que pida a la FAO que el informe se presente en la Decimoquinta Reunión Ordinaria de la Comisión en 2015, lo cual significaría que habría que tener un borrador listo para ser revisado por el Grupo de Trabajo a finales de 2014. El Grupo de Trabajo aconsejó que la Comisión aceptara esta programación. Este volumen de *Recursos Genéticos Animales* fue llevado a la imprenta antes del encuentro de la Comisión del mes de abril, en el cual se debía considerar la recomendación del Grupo de Trabajo.

El segundo informe, ya sea presentado en 2015 o posteriormente, supondrá en gran medida una actualización del primer informe puesto que presentará los cambios acaecidos, en los años de intervalo, en el estado de los recursos zoogenéticos y en su ordenación, así como los últimos desarrollos científicos en los campos pertinentes. La carga que supone para los países la elaboración de informes sería reducida a un mínimo. Así, la información sobre la situación de la gestión de los recursos zoogenéticos a nivel nacional sería recabada a través de cuestionarios específicos en vez de solicitando a los países informes detallados como los que se prepararon para el primer informe.

La agenda del Grupo de Trabajo también contempló una revisión de la implementación de la Estrategia de Financiación para la aplicación del Plan de Acción Mundial sobre los Recursos Zoogenéticos (el encuentro coincidió con el anuncio del primer conjunto de proyectos seleccionados para ser apoyados por la Estrategia de Financiación);[7] el papel de los pequeños ganaderos en la conservación y uso sostenible de los recursos zoogenéticos; metas e indicadores para los recursos zoogenéticos; situación y tendencias respecto de los microorganismos relacionados con la digestión de los rumiantes; y una revisión de los resultados de la Primera Reunión del Grupo de Trabajo de la Comisión sobre el Acceso y la Distribución de Beneficios.

Treinta años de la Comisión

Además de ser un año potencialmente atareado para la comunidad internacional de los recursos zoogenéticos, 2013 es también el año del trigésimo aniversario de la Comisión. Fundada en 1983 como la Comisión de

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[1] http://www.fao.org/docrep/meeting/027/mf227s.pdf
[2] http://www.fao.org/docrep/010/a1404s/a1404s00.htm
[3] http://www.fao.org/docrep/meeting/026/me636e.pdf
[4] ftp://DADnet:Mobile45@ext-ftp.fao.org/ag/reserved/dad-net/GPA.pdf
[5] ftp://DADnet:Mobile45@ext-ftp.fao.org/ag/reserved/dad-net/Indicator.pdf
[6] ftp://DADnet:Mobile45@ext-ftp.fao.org/ag/reserved/dad-net/Traffic_light.pdf
[7] http://www.fao.org/ag/againfo/programmes/es/genetics/Funding_strategy.html

Recursos Fitogenéticos para la Alimentación y la Agricultura, la Comisión puede volver la vista atrás sobre una larga serie de logros, incluida la negociación del Tratado Internacional sobre los Recursos Fitogenéticos para la Alimentación y la Agricultura y la preparación de Informes sobre la Situación Mundial y Planes de Acción Mundial en los sectores de los recursos fitogenéticos y zoogenéticos. El ámbito de trabajo de la Comisión se ha ido expandiendo, desde su enfoque inicial sobre los cultivos, a los animales (la ganadería), en primer lugar, y posteriormente a la selvicultura, a los recursos genéticos acuáticos y a los invertebrados y microorganismos. La vinculación de los diferentes sectores de los recursos genéticos así como sus roles en la prestación de servicios a los ecosistemas están centrando cada vez más el trabajo de la Comisión, sobre todo en vista de la planeada preparación de un informe sobre *La Situación de la Biodiversidad para la Alimentación y la Agricultura*.

Archivo de la revista

Los lectores pueden estar interesados en saber que todos los números anteriores de *Recursos Genéticos Animales* están disponibles en la página web de Cambridge University Press,[8] la cual cuenta también con un potente motor de búsqueda.

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[8] http://journals.cambridge.org/action/displayBackIssues?jid=AGR

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Morphological traits of duck and geese breeds of West Bengal, India

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Summary

The study pertains to phenotypic characterization of some breeds of duck (common white duck and Indian runner duck), Muscovy ducks (black and white feathered and sepia feathered) besides two breeds of geese (white and brown feathered and white feathered) reared in the state of West Bengal (India). The study was conducted at five locations of the state and comprised 1395 ducks and 600 geese. The data were analysed statistically using mainly descriptive statistics, the differences in mean were analysed using Duncan's multiple range test. Both qualitative and quantitative traits were considered in the study. The qualitative traits were shank colour, bill colour, colour of the feathers, skin colour, egg shell colour, the presence or absence of beans, body carriage, bill type and colour of the eyes, while the quantitative traits included in the study were weight of the ducks and weight of the eggs. Some production traits such as numbers of eggs laid per year and dressing percentage of the drakes and ganders of each breed too have been studied. The ducks and geese are raised under semi-intensive management system and mostly depend on scavenging for their nutritional needs. This results in poor egg production and at times loss of stock because of diseases. The study regarding average egg production indicated that the Muscovy ducks and the geese have poor egg production, whereas the Indian runner followed by the common white duck are potentially the best. The ducks are important source of earnings for the small holder farmers and are raised both for meat and eggs, while the geese are reared mostly for ornamental purpose. However, the populations of the ducks are fast dwindling because of avian influenza in the region and because restocking is mostly being carried out with less adapted Khaki Campbell ducks. This happens mainly because the government farms that were responsible for providing the ducklings for restocking maintain Khaki Campbell ducks and do not have the parental stock of the native duck breeds, while restocking of the Muscovy ducks and geese are carried out by the rearers themselves. There are also no prevailing breeding programmes to conserve, select, maintain and distribute the native breeds of duck and geese. Hence, it is of earnest importance to conserve the avian genetic resources before the population dwindles further.

Keywords: *duck, geese, egg production, phenotypic characterization, West Bengal, India*

Résumé

L'étude se rapporte à la caractérisation phénotypique de quelques espèces de canard (le canard blanc commun et le canard de coureur indien), Muscovy esquive (le noir et le blanc aux plumes et sépia aux plumes) outre deux espèces d'oies (le blanc et le marron aux plumes et blancs aux plumes) a élevé dans l'état de Bengale d'ouest (l'Inde). L'étude a été dirigée à cinq emplacements de l'état et compris de 1395 canards et 600 oies. Les données ont été statistiquement analysées utilisant la statistique descriptive, les différences dans les moyens ont été analysées utiliser Duncan le test de Gamme Multiple. Traits qualitatifs et quantitatifs ont été considérés dans l'étude. Le trait qualitatif était la couleur de jambe, la couleur de facture, la couleur des plumes, la couleur de peau, pousser la couleur de coquille, la présence ou l'absence de haricots, la calèche de corps, facturent le type et la couleur des yeux, pendant que les traits quantitatifs inclus dans l'étude étaient le poids des canards et le poids des oeufs. Quelques traits de production à savoir. les nombres d'oeufs posé par an et habiller le pourcentage des canards et les jars de chaque espèce a été aussi étudié. Les canards et les oies sont élevés le système de direction en dessous à demi intensif et dépendent surtout de récupérer pour leurs besoins nutritifs. Ceci a pour résultat la production pauvre d'oeuf et à la perte de temps de du stock en raison des maladies. L'étude quant à la production d'oeuf de moyenne indique que le canard de Muscovy et les oies ont la production d'oeuf pauvre où comme le coureur indien suivi par le canard blanc commun est potentiellement le meilleur. Les canards sont la source importante de gains pour les petits agriculteurs de support et sont élevés pour la viande et les oeufs pendant que les oies sont surtout élevées pour le but décoratif. Toutefois, les populations des canards diminuent rapidement en raison de la grippe d'avian dans la région et que le regarnir est surtout exécuté avec les canards de Campbell de moins de Kaki adapté. Ceci a été principalement exécuté parce que les fermes de gouvernement qui étaient responsables de fournir les canetons pour regarnir maintiennent les canards de Campbell de Kaki et n'ont pas le stock parental des espèces de canard natales en regarnissant pour les canards de Muscovy et les oies sont exécuté par le rearers se. Il n'y a pas aussi prévaloir élève des programmes pour préserver, choisit, maintient et distribuer les espèces natales de canard et les oies. Donc; c'est d'importance sérieuse pour préserver l'avian les ressources génétiques avant que la population diminue plus ample.

Mots-clés: *canard, oies, production d'œufs, caractérisation phénotypique, le Bengale Occidental, Inde*

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Resumen
El estudio pertenece a la caracterización fenotípica de algunas castas de pato (pato blanco común y pato indio de corredor), Muscovy agacha (blanquinegro emplumado y la sepia emplumó) aparte de dos castas de gansos (blanco y marrón emplumó y blanco emplumó) crió en el estado de Bengala Occidental (India). El estudio fue realizado en cinco posiciones del estado y comprendido de 1395 patos y 600 gansos. Los datos fueron analizados utilizando estadísticamente la estadística descriptiva, las diferencias en el medio fueron analizadas utilizar prueba Múltiples de Gama de Duncan. Ambos rasgos cualitativos y cuantitativos fueron considerados en el estudio. El rasgo cualitativo fue color de zanca, color de cuenta, el color de las plumas, color de piel, incita color de esqueleto, la presencia o la ausencia de alubias, el coche del cuerpo, factura tipo y color de los ojos, mientras los rasgos cuantitativos incluidos en el estudio fueron pesos de los patos y el peso de los huevos. Algún v.gr. de rasgos de producción. números de huevos colocados por año y vestir porcentaje de los patos y gansos de cada casta también ha sido estudiado. Los patos y los gansos son levantados bajo sistema medio intensivo de gestión y dependen en su mayor parte de la barrer para sus necesidades nutricionales. Esto tiene como resultado la producción pobre de huevo y a veces pérdida de acciones debido a enfermedades. El estudio con respecto a la producción de huevo de promedio indica que el pato de Muscovy y los gansos tienen la producción pobre de huevo donde como el corredor indio seguido por el pato blanco común es potencialmente el mejor. Los patos son fuente importante de ganancias para los pequeños granjeros de poseedor y son levantados para carne y huevos mientras los gansos son criados en su mayor parte para propósito decorativo. Sin embargo, las poblaciones de los patos menguan rápidamente debido a la gripe aviar en la región y que la reabastecer es llevada a cabo en su mayor parte con patos menos adaptados de tela de uniforme Campbell. Esto fue llevado a cabo principalmente porque las granjas del gobierno que fueron responsables de proporcionar los patitos para la reabastecer mantienen que patos de tela de uniforme Campbell y no tienen las acciones paternales de las castas nativas de pato al reabastecer para los patos de Muscovy y gansos son llevados a cabo por el rearers sí mismos. No hay también prevalecer que cría programas para conservar, seleccionar, mantener y distribuir las castas nativas de pato y gansos. de ahí; es de la importancia seria de conservar los recursos genéticos aviares antes que la población mengüe adicional.

Palabras clave: *pato, gansos, producción de huevos, caracterización fenotípica, Bengala Occidental, India*

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Introduction

The state of West Bengal is situated between 21°25′24″ and 27°13′15″ N latitudes and 85°48′20″ and 89°53′04″ E longitudes. The state shares its borders with Bangladesh, Bhutan and Nepal – and four other Indian states, such as Orissa, Jharkhand, Assam and Sikkim.

The climate of the state is predominantly hot and extremely humid except for the Northern hilly district of Darjeeling. The state has the highest population density in the country and it is estimated that a total of 72 percent of the human population of the state reside in the rural areas. The residents in the rural areas depend on agriculture and allied activities for their livelihood (NABCONS 2010). Most of the farmers have small land holdings and thus small-scale poultry plays a substantial role in ensuring food security for the family besides assisting in poverty reduction. The villages in the state have water bodies that serve multiple purposes (source of water for drinking, bathing and also washing clothes and utensils) for majority of the residents. According to Besbes (2009), globally the ducks contribute 11 percent and geese 9 percent of the global poultry sector. However, in spite of the significantly high contribution of the indigenous ducks to the rural economy (especially in the coastal regions) of India, research and developmental studies on indigenous duck and geese breeds are by and large at its infancy. Tixier-Boichard, Ayalew and Jianlin (2008) suggested that characterization and inventory of poultry genetic resources are needed in countries where clearly defined poultry breeds are yet to be identified; hence properly designed scientific studies on indigenous duck and geese breeds of India need to be prioritized.

According to the reports of DAHDF (2006), the state of West Bengal has the highest duck population in India. The annual increase in duck population in West Bengal between 1997 and 2003 indicate that the annual growth rate for the native breeds/types was assessed to be 22.67 percent, while there was a reduction of 40.3 percent in the numbers of exotic duck breeds. The national trend regarding the growth of the ducks too indicated similar trend (1997–2003), while the numbers of native ducks increased by 21.35 percent, those of the exotic ones decreased by 65.87 percent during the same period DAHDF (2006). The state of West Bengal also possesses 75 percent of the total layer type duck breeds in the country; in spite of having such a large population, the average number of eggs per duck is slightly lower than those of the national average of 106 eggs per year, which may be attributed to the genotypes and management of the ducks and geese. Most of the rearers belong to economically challenged section of the society and are unable to provide much needed balanced nutrition, proper management and health services. Still the state contributed around 70 percent of the total number of duck eggs consumed in the country which may be attributed to the large duck population as mentioned earlier. The ducks are mostly seen foraging in such water bodies which may be privately owned or even communal in nature. The ducks are reared both for their meat and eggs, while geese are mostly reared for ornamental purpose although some people do consume geese meat.

However, there has since been a reduction in the number of native duck population in many districts of the West Bengal because of the outbreak of avian influenza in 2007 and again in 2008. The outbreak of this disease resulted in culling of all domesticated avian species. The restocking was later carried out by introduction of exotic duck breeds (mainly Khaki Campbell) under the guidance of the authorities of Animal Resources Development Department. The restocking has resulted in dilution of the duck genetic resources in the state in general and in the affected areas in particular.

The contribution of the ducks can be assessed by the fact that almost every rural household have a couple of them and duck eggs fetch higher price compared with those from the hens. The other reason why the native ducks are preferred over the exotic duck breeds is because their eggs fetch higher price. Traditional cuisines prepared of duck eggs and meat is considered as delicacies by the residents of the state. The eggs of the native duck breeds are preferred by the consumers for their taste, pigmentation and suitability for traditional cuisines. The eggs of the geese and that of the Muscovy ducks are seldom consumed by the rearers as the eggs are mostly used for restocking purpose.

The observation finds analogy with the observations of Halder, Ghoshal and Samanta (2007) from West Bengal and Gajendran and Karthickeyan (2009) from Tamil Nadu, India, FAO (2011). The preference of native ducks over the improved breeds and hybrids has also been reported by Jalil, Begum and Nahar (1993) and Rehman *et al.* (2009).

Materials and methods

The study was conducted in five districts of West Bengal namely Midnapur (East) (MID), 24 Parganas (South) (24 P (S)), 24 Parganas (North) (24 P (N)), Nadia (NAD) and Murshidabad (MUR) (Table 1). The three gram panchayats (local administrative bodies) were selected randomly from each district. Thereafter, villages within a gram panchayat were selected purposively keeping in mind the fact that no ducklings of exotic types were distributed in the selected villages by the local authorities in the near past. The households selected for interviews within the villages too were selected purposively keeping in mind that the owner reared only the native ducks, the houses having exotic or even seem to be cross-bred ducks were not included in the survey and the adjacent houses from where the flocks can intermingle were also not taken into consideration. This led to few numbers of household per village. The families who had recently procured native ducks from nearby markets or received them as gifts from acquaintances too were not taken into account. The percentage of different duck and geese breeds in the study vis-à-vis the total duck population as a whole in the areas studied is presented in Table 2.

The result of the study comprises both qualitative and quantitative traits of 1395 ducks and 600 geese of various breeds which were/are reared in the studied villages. The description of qualitative traits considered in this study were assessed according to the guidelines suggested by Manuel (2008). The qualitative traits studied were shank colour (white, blue and yellow), bill colour (pink white, orange, yellow, white and brown), colour of the feathers (specific colours or mixed), skin colour (white, yellow or grey), egg shell colour (white, cream or blue), the presence or absence of beans and colour of beans (white, black or dark brown), shape of bill (uniform or saddle), body carriage (horizontal, slight upright or upright) all of which were recorded through visual observation, while the quantitative traits were weight of the ducks and weight of the eggs. The age of the ducks was not considered as a parameter in the study and only adult ducks were considered for the quantitative traits. The results in Tables 3 and 4 have been presented separately for drakes and ducks and also ganders and geese because this would help the authorities to make separate selection strategies for males and females. This is also because the selection intensity for the two sexes differs; hence such information would be useful for further conservation and breeding programmes.

The rearers were interviewed using a pretested questionnaire which pertained to the prevalent duck husbandry practices in the different study areas; the questionnaire also included the questions pertaining to housing feeding, watering, disease management/treatment, marketing of the eggs and ducks, role of different family members in duck husbandry practices, breed preferences for eggs and meat purposes, average number of eggs laid by a duck, hatchability and mortality. The price of the ducks and eggs were also taken into consideration to assess the importance of the ducks among the rearers. The ducks, geese and the eggs were weighed on an electronic balance with an error margin of ±0.5 g. The dressing percentage was assessed by slaughtering the drakes and ganders followed by hot water scalding and evisceration of the gut contents including the skin. The dressing percentage was calculated according to the method suggested by Sahin and Yardimci (2009). The results were analysed statistically using SPSS v-12 for Windows (2003), the means and standard deviations (SD)/standard errors (SE) were computed using descriptive statistics, the means for the quantitative traits were compared using Duncan's Multiple Range Test and the values were considered significant at $p < 0.05$.

Results and discussions

Duck husbandry practices in the study areas

The common duck (locally known as desi/Pati hans), (Figure 1) has no definite feather colour pattern and the colour of the bill too varies from duck to duck. This

Table 1. Location of the study zones and number of ducks surveyed under each study site.

District	Name of the panchayat	Number of ducks and geese	Temperature	Latitude	Longitude	Altitude	Numbers of ducks	Reference
MID (East) 1 Mahishadal	Itamogra-2, Lakshya-1, Amritberia, Betkundu and Natshal-2	385	(07–39.0°C) highly humid	22°11′ N	87°59′E	4 m amsl	7 84 442^{a} (48.02%) 29 788^{b}	DARAH (2006a)^{a}
MUR 1. Beldanga	Andulberia-1, Begunbari, Mohula-2, Dadpur and Debkundu	382	(18–38.5°C) highly humid	23°55′60″ N	88°32′18″ E	19 m amsl	1 410 503^{a} (97.19%) 1 66 620	DARAH (2006 b)^{b}
24 P (S) 1 Joynagar. Mazilpur	Thakurchak, Baharu and Bhagabanpur	279	(10–37.5°C) highly humid	22°10′33″ N	88°25′ 4″E	2 m amsl	1 913 040^{a} (66.67%) 72 314^{b}	DARAH (2006c)^{c}
2. Basanti	Basanti town	195		22°11′21″ N	88°40′14″ E	1 m amsl	88 508^{b}	
24 P (N) 1. Jaguli	Amdanga, Kampa, Cakla and Maricha	347	(18–37.5°C) highly humid	22°55′58″ N	88°32′18″ E	10 m amsl	2 016 202^{a} (47.99%) 90 717^{b}	DARAH (2006d)^{d}
NAD 1 Haringhata	Birohi-1, Fatehpur, Mollaberia and Nagurukhra-1	407	(18–37.5°C) highly humid	22°58′ 60″ N	88°28′60″ E	10 m amsl	7 16 194^{a} (96.02%) 46 021^{b}	DARAH (2006e)^{e}
2. Chakdah	Madanpur-1, Simurali-2			23°4′60″ N	88°31′E	10 m amsl	51 694^{b}	

Note: ^{a}Number of native ducks in the district. The values in parentheses indicate the percentage of the native fowls vis-à-vis total duck population in the study area. ^{b}Estimated ducks in the panchayats studied. m amsl: meters above mean sea level; DARAH: Directorate of Animal Resources and Animal Health, Government of West Bengal.

Table 2. Number of respondents, their age, their experience in rearing ducks and average numbers of ducks per house hold selected.

District	Number of households interviewed	Sex of the respondent		Age of the respondent (years) (mean ± SD)		Average number of years rearing (years) of ducks and geese/household (mean ± SD)		Average numbers of (heads) of ducks and geese/household (mean ± SD)	
		Male	Female	Male	Female	Ducks	Geese	Ducks	Geese
MID (East)	45	8	37	32.5 ± 10.2 (22–53)	37.9 ± 7.2 (18–60)	5.6 ± 2.3 (3–9)	4.2 ± 2.6 (2–9)	5.2 ± 2.3 (2–8)	2.5 ± 1.5 (1–6)
MUR	50	12	38	34.3 ± 8.6 (18–52)	42 ± 10.4 (21–65)	6.25 ± 4.2 (2–10)	3.8 ± 1.6 (1–10)	4.5 ± 2.7 (2–7)	3.7 ± 1.2 (2–5)
24 P (S)	65	15	50	39.5 ± 11.2 (22–52)	39.5 ± 9.9 (23–63)	7.7 ± 2.1 (4–9)	5.5 ± 1.5 (2–8)	4.7 ± 2.6 (2–7)	2.4 ± 1.4 (1–4)
24 P (N)	40	6	34	37.5 ± 12.2 (19–55)	29.2 ± 16.5 (16–58)	8.7 ± 3.3 (4–12)	4.7 ± 2.4 (2–7)	7.2 ± 2.6 (3–9)	2.1 ± 0.8 (1–3)
NAD	55	10	45	33 ± 15.4 (17–52)	33.1 ± 14.3 (15–55)	8.9 ± 4.3 (3–14)	5.8 ± 1.5 (3–7)	4.7 ± 3.3 (2–9)	2.6 ± 1.3 (1–5)
Average		10	41	35.4	36.3	7.4	4.8	5.3	2.7

Note: Values in parentheses indicate the range of values.

Table 3. Percentages of different phenotypes of ducks in the study area.

Districts	Sada Pati hans		Runner		Common duck		Muscovy black and white		Muscovy sepia		Geese white and brown		Geese white		Exotics and cross-breds	
	Drake	Duck	Drake	Duck	Drake	Duck	Drake	Duck	Drake	Duck	Gander	Geese	Gander	Geese	Drake	Duck
MID (East)	16.2^{b}	22.1^{a}	0.05	0.08	45.75^{a}	40.2^{a}	3.2^{d}	4.7^{e}	0.0	0.0	8.9^{c}	9.7^{b}	11.4^{d}	12.2^{c}	14.15^{a}	11.02^{a}
MUR	19.2^{a}	20.5^{b}	0.0	0.0	41.7^{b}	39.3^{a}	6.9^{c}	9.5^{d}	1.7^{d}	1.3^{c}	10.5^{a}	11.2^{a}	12.2^{c}	13.7^{b}	7.8^{b}	4.5^{b}
24 P (S)	15.5^{b}	18.1^{c}	0.0	0.0	35.1^{c}	32.5^{c}	12.7^{a}	15.5^{a}	3.3^{c}	3.7^{b}	10.2^{a}	10.6^{a}	14.7^{a}	14.9^{a}	8.5^{b}	1.7^{c}
24 P (N)	19.1^{a}	20.2^{b}	0.0	0.0	35.2^{c}	36.6^{b}	9.9^{b}	10.5^{c}	4.1^{b}	5.3^{a}	10.7^{a}	10.9^{a}	13.9^{b}	13.8^{b}	7.1^{b}	2.7^{c}
NAD	18.5^{a}	21.0^{b}	0.0	0.0	35.9^{c}	31.5^{c}	10.2^{b}	13.2^{b}	5.5^{a}	5.7^{a}	9.3^{b}	9.8^{b}	14.1^{a}	15.9^{a}	6.5^{b}	2.9^{c}
Total average	17.7	20.4	0.05	0.08	36.8	36.0	8.6	10.7	3.7	4.0	10	10.4	13.3	14.1	8.9	4.6

^{a,b,c,d}Values with different subscripts across columns differ significantly, $P < 0.05$.

Table 4. Body weight (g ± SD) of different breeds of ducks and geese observed in the studied districts of West Bengal.

District	Common duck		Sada Pati hans		Runner		Muscovy black and white		Muscovy sepia		Geese white and brown		Geese white	
	Drake	Duck	Drake	Drake	Duck	Duck	Drake	Duck	Drake	Duck	Gander	Geese	Gander	Geese
MID (East)	1250 ± 92^{c}	1125 ± 88^{b}	1375 ± 105^{b}	1350 ± 115^{b}	1150 ± 110	1295 ± 56	2650 ± 210^{a}	1536 ± 212^{c}	–	–	3954 ± 279^{a}	3470 ± 202^{a}	3950 ± 220^{a}	3550 ± 185^{b}
N	38	32	40	46	20	22	35	30			32	35	25	30
MUR	1250 ± 80^{c}	1050 ± 75^{b}	1380 ± 98 ^{b}	1315 ± 56^{c}			2554 ± 250^{b}	1665 ± 125^{b}	1950 ± 119^{c}	1420 ± 196^{c}	3696 ± 312^{b}	3364 ± 274^{a}	3800 ± 175^{c}	3500 ± 170^{b}
N	32	32	35	40			24	32	34	30	35	37	22	29
24 P (S)	1390 ± 150^{a}	1295 ± 95^{a}	1395 ± 112^{b}	1225 ± 112^{d}			2589 ± 195^{b}	1722 ± 165^{a}	2235 ± 132^{a}	1332 ± 117^{d}	3980 ± 259^{a}	3018 ± 395^{c}	3750 ± 225^{c}	3400 ± 185^{c}
N	47	45	62	60			42	34	30	35	27	32	25	35
24 P (N)	1370 ± 95^{b}	1110 ± 105^{b}	1305 ± 125^{c}	1300 ± 110^{c}			2129 ± 207^{c}	1489 ± 175^{d}	2190 ± 127^{b}	1470 ± 106^{b}	3642 ± 396^{b}	2977 ± 222^{c}	4050 ± 175^{a}	3750 ± 220^{a}
N	39	36	25	32			27	31	15	20	29	33	28	32
NAD	1400 ± 102^{a}	1290 ± 89^{a}	1456 ± 106^{a}	1386 ± 25^{a}			1996 ± 125^{d}	1770 ± 296^{a}	2024 ± 117^{c}	1550 ± 107^{a}	3697 ± 282^{b}	3162 ± 268^{b}	3900 ± 150^{b}	3500 ± 225^{b}
N	48	43	34	37			39	32	28	32	22	27	32	33
Average	1332 ± 104	1174 ± 90	1382.2 ± 109	1315 ± 84	1150 ± 110	1295 ± 56	2383 ± 197	1636 ± 195	2109.8 ± 133	1450 ± 134	3793.8 ± 306	3198 ± 272	3890 ± 189	3540 ± 197

^{a,b,c,d}Values with different subscripts across columns differ significantly, $P < 0.05$.

Figure 1. Selling ducks at village haat.

may be because panmixia is practiced in the study areas. The feather colours may vary from dark brown to white with intermediate colours. The results from Table 2 indicate that the majority of the respondents were women. Fewer number of male respondents may be because male members leave early in the morning and return late to their home in the evenings as majority of them were associated with some form of agrarian activity, some were daily wage labours, while a few were petty businessmen and were not available at home. Although the women were involved with the husbandry practices and sales of eggs, the male members were mostly involved in the sales of adult ducks, building houses, taking the sick ducks to the veterinarians or local para veterinarians and also sale of the adult ducks. The results from Table 2 also indicate that the average age of the respondents were 35.4 years for the males and 36.3 years for the females. The study also indicated that on an average the respondents had been rearing ducks for the last 7.4 years, while that of geese were 4.8 years. This may be because the geese are primarily raised for ornamental purpose with hardly any economic importance to the rearers. It can therefore be inferred that the respondents had sufficient experience in matters related to the duck husbandry practices. The flock size vary largely on the economic status of the raisers, the study revealed that the flock size can vary from 2 to 9 ducks per household and the average flock size was assessed to be around 5.3 ducks per household. The results as obtained in this study find consonance with the observations of Halder, Ghoshal and Samanta (2007) from West Bengal, the values are well within the range reported by Hoque *et al.* (2010) from ducks, reared in coastal areas of Bangladesh.

The drake to duck ratio is usually 1 drake for 7.5 ducks, while Halder, Ghoshal and Samanta (2007) reported higher drakes to ducks ratio. The difference in ratio as observed by Halder, Ghoshal and Samanta (2007) may be attributed to the sample size and in limited study area. The less numbers of drakes as observed in this study may be because they are raised for meat and are usually sold at an early age. The study also indicates that the average flock size varied between the studied locations with the lowest number of ducks per flock observed in MUR, while the largest flock size was observed in the studied locations at 24 P (N), while the reverse was true for the geese.

The flock size for the Muscovy ducks are usually smaller and vary from 2 to 15 ducks at most averaging around 4.5 ± 2.5 ducks, the drake : duck ratio in the Muscovy ducks are more or less similar to those assessed with the common ducks, the Muscovy ducks are not reared by all members of the society and are mostly popular among the people following Islam faith and also members of lower socio-economic strata. Although the geese are reared for ornamental purpose and also for guarding the homes and the flock size varies form 1 to 6 averaging around 2.7 heads per household.

The ducks are mostly reared separately in enclosures which are adjacent to the homes of the rearers. However, the ducklings are reared mostly under bamboo baskets or under the mosquito nets. The ducklings are reared separately till they are strong enough to accompany the older flock. The observations are similar to the reports of Halder, Ghoshal and Samanta (2007) and Hoque *et al.* (2010). The ducklings are confined separately because they are unable to protect themselves from predators, while foraging with the older flocks. The common ducks are reared separately from the geese and the Muscovy ducks.

The night enclosures for the ducks are mostly (85 percent) made of locally available materials such as mud and wood/bamboo/corrugated sheet, while some of the respondents had the night shelter for their ducks prepared from mortar and bricks, the observations are in consonance with of the reports of Khanum, Chwalibog and Huque (2005) and Rehman *et al.* (2009) from Bangladesh. The doors of the enclosure are closed at night to prevent the attack from predators like wild cat and foxes. The drakes and geese are mostly allowed to forage for themselves. The ducks in lay, brooding or with ducklings are provided with additional supplements which are usually kitchen scrapes, i.e. rice leftover and rice bran which at times is mixed with the rice gruel. The ducks are also provided with molluscs and other aquatic snails occasionally, but this depends on the availability. Similar observations have also been reported by Hoque *et al.* (2001), Rehman *et al.* (2009)

and Hoque *et al.* (2010). However, the availability of the molluscs varies from location to location; in general, the quantity of molluscs is decreasing owing to the use of agrochemicals where its runoff diminishes aquatic fauna and flora and also leads to occasional poisoning of the ducks.

The feed supplements are usually provided in earthen vessels which are seldom cleaned and are the major source of infection in the flocks. Water is seldom provided to the ducks and geese and they obtain the same from ponds and water bodies, the observations are in consonance with the results of Haque, Ukil and Hossain (1993), Fouzdar, Khaleque and Alam (1999), Haque *et al.* (2003) and Halder, Ghoshal and Samanta (2007). The ducks are quite tolerant to many of the commonly prevalent diseases; however, deaths because of hepatitis, botulism, plague and cholera are quite common in the region, the duckling's being more susceptible when compared with the adults, the observations being in consonance with that of Hoque *et al.* (2010). The study also indicates that the average survivability of the ducklings vary between 40 and 80 percent averaging around 65 percent, higher mortality has been observed in the monsoon season when the temperature is hot and the relative humidity is quite high leading to various disease incidences such as cholera and dysentery. The minimum mortality has been observed to be in the spring and summer. Accidental deaths because of chills have also been reported especially during the winter months.

The eggs are mostly sold by the women to the local traders locally known as "phoreys". The women usually use the sale proceeds to procure items of daily household need, the eggs of the Muscovy ducks and that of the geese are seldom traded and are used for hatching purpose. It has also been observed that raising ducks is mostly carried out by women, the findings are in accordance with that of previous researchers (Maji, 1995; Halder, Ghoshal and Samanta, 2007; Hoque *et al.*, 2010). The price of the duck eggs is higher than those of the chickens, which might be attributed to their larger size and culinary usages. The average price of an egg as received by the rearers vary between Rs. 2.75 and 3.50 averaging around Rs. 3.25 (US \$1 = Rs 55.00 approx.), while the same is usually retailed at Rs. 6.00–7.00 per egg. The ducks are sold by the male members of the family and seldom do women participate in the sale of the ducks; however, recently, it has been observed that members of certain self-help groups (mostly women) do come to the market to sell the ducks and fowls they have raised (Figure 1).

The ducks lay their eggs early in the morning after which they are allowed to forage. The reason for poor hatchability can be because the night enclosures are mostly devoid of any proper nests and that the eggs are laid on the ground which is often wet and dirty, thereby soiling the eggs. According to the respondents, most of these soiled eggs have very poor hatchability and are hence used for table purposes or sold. The hatchability of the eggs of the common ducks varies from 50 to 75 percent, averaging around 63 percent, the higher range of the results are in consonance with the observations of Gajendran *et al.* (2005), the range value of hatchability values as obtained in the study is in consonance with the results of Ravindran, Venugopalan and Ramkrishnan (1984), Alam and Hossain (1989), Saha, Chowdhury and Hamid (1992), Islam *et al.* (2002) and Rahman *et al.* (2009). The lower value is in accordance with the observations of Chowdhury *et al.* (2004) The hatchability percentage varies from season to season, (Sastry, Thomas and Singh 1996; Das and Ali, 1999; Farooq *et al.*, 2003), The respondents reported that the hatchability was least during the months of May–August, when the temperature and humidity is the highest, similar observations were also reported by Khalequzzaman, Shah Hussain Ahmad Mahdi and Mahbur Rahman (2006).

The mortality among the ducklings are usually quite high and varies from 30 to 70 percent, which also varies from season to season and also the housing and husbandry practices, the average values as reported by the respondents was around 55 percent, while the hatchability of the Muscovy ducks vary between 45 and 75 percent averaging around 55.5 percent, the results as assessed in the study finds consonance with the observations of Banga-Mboko *et al.* (2007) from Congo, hatchability of the eggs of Muscovy ducks was reported to be the least in the summer months. The findings are in accordance with the observations of Nickolova (2005) and, Khalequzzaman, Shah Hussain Ahmad Mahdi and Mahbur Rahman (2006) who reported that the poor hatchability is a fall out of the ducks to optimize the egg temperature during brooding. The yolk of Muscovy ducks have very high fat content releasing heat in the second half of the incubation period, hence, cooling of the eggs is mandatory during that phase, which if overlooked can lead to poor hatchability. Geese, however, have slightly better hatchability ranging between 65 and 80 percent, averaging around 72.5 percent. The results presented in Table 7 indicate that the average dressing percentage did not vary significantly between the Muscovy drakes (black and white feathered), and ganders of both breeds. However, the dressing percentage of the Muscovy drakes (sepia feather) colour was $P < 0.05$ lower than those of the two breeds of ganders and Muscovy drakes (white and black feather coloured). The dressing percentage of the common ducks, sada pati hans and runner breed did not vary significantly between them but varied $P < 0.05$ with the Muscovy drakes (of both the breeds) and the ganders.

Some common breeds of ducks

The common duck

The common duck is locally known as desi/pati hans (Figure 2) has varied feather colours from almost white to black with intermediates, the colour of the shank and bill is usually slate grey and uniform. The carriage of the

Figure 2. Pati Hans or common ducks.

ducks is slightly upright, the bills are devoid of any beans. The ducklings are born with dark to yellow colour down feathers. The drakes are identified by the upward curving of feather near the back of the drake. The average body weight of the ducks and drakes as presented in Table 4 finds consonance with the observations of Rashid, Barua and Bulbul (1995) and ILRI (2004). The results from Table 4 indicate that the highest body weight was observed in the drakes and ducks reared in 24 P (S) and NAD district, while the ones reared in MUR and MID weighed the least. This may be attributed to large numbers of ponds and water bodies in these districts. As indicated by the respondents, the average age at first laying is around 180.5 ± 15.5 days; the result being in consonance with that of Hoque *et al.* (2001), Islam *et al.* (2003), Das *et al.* (2008), Gajendran and Karthickeyan (2009), Rehman *et al.* (2009). The average annual numbers of eggs (Table 5) as reported by the rearers were highest in 24 P (S), while the least numbers of eggs were reported from MUR and NAD. The average number of eggs as observed in the study finds consonance with the observations of Salam and Bulbul (1983), Haque and Ukil (1994), Haque *et al.* (2003) and Rehman *et al.* (2009). The number of eggs as obtained from the local desi duck varies with types and nutrition of the ducks, the average annual number of eggs from the desi ducks are similar to the observations of Haque *et al.* (2003), Halder, Ghoshal and Samanta (2007) and Rahman *et al.* (2009). The average weight of the eggs (Table 6) was highest in the desi ducks reared in 24 P (S), while those from NAD were the least. The average egg weight as observed is in agreement with the observations of Rithamber, Reddy and Rao (1986), Das and Hoque (2000), Khanum, Chwalibog and Huque (2005), Kabir *et al.* (2007), Das *et al.* (2008) and Rehman *et al.* (2009). The egg weight is, however, higher than those reported by Hoque *et al.* (2010), the average clutch size as reported by the rearers is around 7–10 eggs. The skin colour of these ducks varies from white to yellow. The colour of the eyes is dark. The average dressing percentage (Table 7) as observed in the study is only slightly lower than those reported by Ansary *et al.* (2008) for cross-bred ducks reared in Bangladesh.

The common white duck

The common white duck is locally known as sada pati hans (desi white duck/common white duck), (Figure 3) is characterized by white colour of the feathers and the shank and the bill are orange in colour. The body carriage is horizontal type and the bills have white coloured beans which are even observed in the ducklings. The ducklings are born with yellow down feather (Figure 4) which is

Table 5. Average (mean ± SD) number of eggs obtained from breeds of ducks and geese on an annual basis.

Districts	Desi duck	Sada Pati hans	Runner	Muscovy black and white	Muscovy sepia	Geese white and chocolate	Geese white
MID (East)	90 ± 15.5^{a}	130 ± 15.5^{b}	180 ± 20.2	37 ± 4.7^{a}	–	21.7 ± 3.6^{b}	24.5 ± 2.5^{b}
Number of respondents	22	18	5	12		15	10
MUR	62 ± 20.7^{d}	127 ± 12.6^{b}	NR	35 ± 8.9^{a}	40.3 ± 4.3^{a}	24.5 ± 2.5^{b}	22.7 ± 3.2^{c}
Number of respondents	32	14		12	5	22	20
24 P (S)	89 ± 10.4^{a}	132 ± 20.2^{b}	NR	28.5 ± 5.5^{b}	33.5 ± 2.5^{c}	27.5 ± 2.2^{a}	25.2 ± 2.7^{b}
Number of respondents	44	28		21	19	17	21
24 P (N)	85 ± 12.7^{b}	125 ± 17.2^{c}	NR	33.2 ± 5.5^{b}	41.5 ± 3.5^{a}	22.5 ± 3.5^{b}	22.9 ± 4.2^{c}
Number of respondents	22	16		14	11	13	19
NAD	74 ± 15.7^{c}	138 ± 16.5^{a}	NR	35.7 ± 3.8^{a}	36.7 ± 4.5^{b}	23.2 ± 3.2^{b}	30.5 ± 3.4^{a}
Number of respondents	21	13		12	17	14	12
Total average	80.0 ± 15	130.4 ± 16.4	180 ± 20.2	33.9 ± 5.7	36.9 ± 3.5	23.9 ± 3	25.2 ± 3.2
N	141	89	5	71	52	81	82

^{a,b,c,d}Values with different subscripts across columns differ significantly, $P < 0.05$.

Table 6. Egg weight (g ± SE) of the different ducks and geese studied.

District	Egg weight ± SE (g) and shell colour of different duck/geese types													
	Common duck (187)		Sada Pati Hans (205)		Runner 65)		Muscovy black and white (87)		Muscovy sepia (65)		Geese white and brown (87)		Geese white (79)	
	Colour	Weight	Colour	Weight	Colour	Weight	Colour	Weight	Colour	Weight	Colour	Weight	Colour	Weight
MID (East)	CLB	55 ± 4.3^{d}	CLB	67.2 ± 4.2	CLB	59.7 ± 0.8	Cream	70.5 ± 2.2^{a}	–	–	CW	77.6 ± 1.6^{a}	CW	75.2 ± 2.6^{a}
N		33		35		65		19				17		18
MUR	CLB	62.6 ± 4.5^{b}	CLB	68.5 ± 3.7	NR	NR	Cream	71.2 ± 2.1^{a}	Cream	64.3 ± 1.5^{b}	CW	78.2 ± 2.9^{a}	CW	74.5 ± 1.7^{a}
N		28		42				19		12		18		16
24 P (S)	CLB	63.7 ± 4.0^{b}	CLB	67.2 ± 3.4	NR	NR	Cream	70.6 ± 1.2^{a}	Cream	67.4 ± 1.5^{ab}	CW	75.3 ± 1.8^{b}	CW	71.4 ± 1.5^{c}
N		43		49				15		15		17		14
24 P (N)	CLB	65.4 ± 4.6^{a}	CLB	68.55 ± 1.3	NR	NR	Cream	69.1 ± 1.4^{a}	Cream	65.8 ± 1.2^{b}	CW	75.8 ± 1.6^{b}	CW	70.4 ± 2.7^{c}
N		41		34				15		17		15		15
NAD	CLB	59.7 ± 3.5^{c}	CLB	67.3 ± 2.7	NR	NR	Cream	67.8 ± 2.1^{b}	Cream	69.4 ± 1.6^{a}	CW	74.7 ± 1.3^{b}	CW	73.2 ± 1.6^{b}
N		42		45				19		21		20		16
Average		61.3 ± 4.2		67.75 ± 3.1		59.7 ± 0.8		69.8 ± 1.8		66.7 ± 1.4		76.3 ± 1.8		72.9 ± 2

^{a,b,c,d}Values with different subscripts across columns differ significantly, $P < 0.05$, CLB = Cream to bluish, CW = Cream to white.

N indicates numbers of eggs weighed.

replaced by white feather as they mature. The drakes are identified by the upward curving of feather near the back of the drake. These ducks like to move in flock and because of their characteristic white feather are easily identified. The result from Table 3 indicates that the population of the drakes was highest in MUR, while that of the duck was highest in 24 P (S). The ducks also gain good body weight and hence fetch higher price in the markets in comparison with the other duck types.

The results from Table 4 also indicates that the highest body weight among the drakes and ducks were observed in those reared in NAD, while the lowest were observed in 24 P (N) and MUR. The average body weight is higher than the values reported by Bhuiyan *et al.* (2005) and lower than those reported by ILRI (2004). The differences as observed in the study may be because the former researchers assessed the body weight at 9 weeks of age when the ducks are yet to mature and the later reported the values from farm reared ducks which were provided with balanced ration and management. It has been observed that the average age at first laying is around 135.5 ± 18.5 days; the results are lower than the values reported by Hoque *et al.* (2001) and Islam *et al.* (2003) for desi ducks of Bangladesh, but in consonance with the reports of ILRI (2004) for desi white duck of Bangladesh. The sada pati hans lay an average of 130 eggs in a year and hence are preferred by the rearers as a layer breed. The average annual numbers of eggs obtained per duck (Table 5) is higher than those of the native ducks and find similarity with the observations of Hoque *et al.* (2010), among the study areas the largest number of eggs were observed in NAD, while the least numbers of eggs were reported from the studied villages in 24 P (N). The average weight of the eggs (Table 6) find similarity with the values as reported by ILRI (2004), no differences among the studied locations were observed for the trait. The study also showed that the skin colour is yellow to white, the average dressing percentage as obtained in the study (Table 7) is lower than those reported by Ansary *et al.* (2008).

Runner

The coloured runner ducks were quite common in the study area prior to 1960s when there was a severe outbreak of duck plague and most of the ducks perished. However, ducks resembling runners with very good egg-laying potential was still reared in some villages in MID (East) district (Figure 5). The revival programme of the runner duck was initiated by Mr Sadesh Ranjan Bhowmick of Mahishadal (LIFE, 2010), a connoisseur of livestock with poultry who was able to obtain a small flock of runner type ducks in 2002 from an obscure village in MID (East) district, he collected a few drakes and ducks one of which was said to be quite old and was still laying eggs. He then went for phenotypic selection of the ducklings obtained from the mating of the collected ducks. He was successful in developing a small flock of the runner ducks which he

Table 7. Eviscerated weight and dressing percentage (mean ± SD) of drakes and ganders reared in the study zones.

Type	Numbers	Mean ± SE		Dressing (%)
		Live weight	Eviscerated carcass	
Common drake	76	1370 ± 325	620 ± 55	45.25 ± 1.3^{c}
Sada Pati hans	37	1493 ± 220	688 ± 95	46.08 ± 1.7^{c}
Runner	15	1270 ± 170	574 ± 65	45.2 ± 1.3^{c}
Muscovy (black and white feather)	41	2500 ± 330	1550 ± 34	62 ± 1.9^{a}
Muscovy (sepia)	34	2950 ± 250	1670 ± 75	56.61 ± 2.2^{b}
Gander (brown and white)	45	4400 ± 220	2650 ± 38	60.22 ± 1.3^{a}
Gander (white)	47	3717 ± 230	2207 ± 85	59.37 ± 1.4^{a}

^{a,b,c,}Values with different subscripts across columns differ significantly, $P < 0.05$.

distributed among his friends and relatives; a small flock was also gifted to Mr Gyasuudin Mondol another connoisseur at Madanpur area of NAD district; however, the flock developed by Mr Mondol was culled owing to the outbreak of avian influenza in the region in the year 2008. The feather colours of these runner ducks vary from brown to white, shank colour is orange, while the colour of the bill is slate grey in colour and, however, some ducks and drakes too have yellow coloured bill. The colour of the eyes is dark. The bill is devoid of any beans and is uniform. The body carriage is upright and the eyes are dark. The respondents reported that the egg production of the ducks ranges between 150 and 220 eggs annually averaging around 180 eggs. The average number of eggs are higher than the desi/pati hans and also the sada pati hans. Results of a study conducted in Bangladesh (Das *et al.* 2003) indicated that the body weight gain up to egg laying in runner ducks was higher than other improved duck breeds *viz*. Khaki Campbell. The average egg weight of runner ducks (Table 6) is lower than the values reported by Das *et al.* (2003), which might be attributed to the balanced nutrition provided to the ducks by the authors and also small sample size of the present study. The average clutch size as has been reported was 7–12 eggs. The average age at first egg lay was assessed to be 170.2 ± 15.5 days. The skin colour was observed to be white. The average dressing percentage of the drakes as assessed (Table 7) is lower than the values reported by Ansary *et al.* (2008).

Figure 3. Common white duck.

Muscovy ducks

In the study area, two types of Muscovy ducks have been observed, the most common was the one with black and white feather colour, while some with Sepia colour feather too have been observed, the population of the latter being much lower than the former. The Muscovy ducks are commonly known as Chine hans (Ali and Sarker, 1992; Banerjee and Banerjee, 2003) and Marie hans in some parts of 24 P (S). The body weight of the Muscovy ducks of both the types have been presented in Table 4, the sexual dimorphism is quite pronounced in the Muscovy ducks, the drakes having significantly higher body weight in comparison with the ducks, the observations are in agreement with that of Olver *et al.* (1977) and Seemann (1983). The Muscovy ducks are very poor layers and the numbers of eggs produced vary from 20 to 40 per year averaging around 28 eggs per year.

Muscovy duck (black and white feather)

This type of Muscovy ducks are characterized by black and white feathers and slate coloured shanks with some yellow markings over it, ducks with complete slate coloured shanks and flippers too are quite common, the ducklings are born with cream down with black markings

Figure 4. Ducklings of common white duck.

Figure 5. Runner ducks.

Figure 7. Black and white feathered Muscovy ducks.

the beans are quite well developed even at this stage (Figure 6). The bills of the ducks are slate grey in colour and have white beans. The caruncles being well developed in the drakes in comparison with the ducks, the red coloured caruncles extend from the bill to the eyes (Figure 7). The eyes are yellow in colour and the colour of the skin is white. The ducks have a horizontal carriage and the bill is uniform in shape. The age at sexual maturity was assessed to be 348 ± 0.5 days for the duck which coincides with the first egg laid. The Muscovies grow slowly and hence mature late. The observations are in consonance with the observations of Bhuiyan *et al.* (2005). The Muscovy ducks prefer to stay at the banks of the water bodies and seldom swim for long. They are reared for their flesh and drakes are preferred over the ducks especially because the ducks are poor layers and hence restocking can be a problem if they are slaughtered out. The result from Table 3 indicates that the highest numbers of the Muscovy ducks are reared in the studied areas of 24 P (S), while the least numbers were observed in the studied locations of MID district. The study results from Table 4 indicates that $P < 0.05$ higher body weight were observed in the drakes reared in MID, while the ducks reared in 24 P (S) and NAD had the highest body weight. Although $P < 0.05$ lower body weight were observed in the drakes and ducks reared in NAD and 24 P (N), respectively. The average body weight of both Muscovy drakes and ducks as obtained in the study (Table 4) finds consonance with the observations of Hahn *et al.* (1995) and Yakubu, Kaankuka and Ugbo (2011), the bodyweight values as reported by Omojola (2007) were, however, lower than the present findings, which might be attributed to the differences because of both genetic and non-genetic factors. The Muscovy ducks are tolerant to most of the common diseases of the ducks and hence are favoured as a source of avian meat, the findings are in consonance with the observations of Etuk *et al.* (2006). The annual egg production of the Muscovy ducks (reared under traditional management) as obtained in the present study (Table 5) indicates that the ducks reared in MID, MUR and NAD were $P < 0.05$ than those reared in other locations. The results are in agreement with the observations of Banga-Mboko *et al.* (2007). The average egg weight (Table 6) of the ducks indicate that the ducks reared in MID, MUR, 24 P (S) and 24 P (N) weighed ($P < 0.05$) higher than the other locations studied, The results related to the average egg weight finds similarity with those reported by Changkang, Ang and Guangying (1999), Nikolova, Gerzilov and Genchev (2000). However, Nikolova (2004) reported higher egg weights in white variety of Muscovy ducks. The average clutch size was reported to be 5–6 eggs with long interclutch interval. The results by Banga-Mboko *et al.* (2007) on annual numbers of clutch in Muscovy ducks of Congo indicate that the numbers are fewer than those observed in this study.

Figure 6. Ducklings of black and white feathered Muscovy ducks.

The average dressing percentage in the drakes as presented in Table 7 is lower than those reported by Etuk *et al.* (2006) and Omojola (2007) from Nigeria. This might be attributed both to genotype of the Muscovy ducks reared in both the countries and also to the husbandry methods including nutrition. Lower dressing percentage may also be a consequence of the slaughtering technique as the present dressing percentage was calculated by excluding the skin and the subcutaneous fat. The respondents have, however, reported that the meat of the Muscovy drakes, toughen with age.

The black and white feathered Muscovy ducks have been used as a parental line by the author for the development of the mule duck (Figure 8). Mule ducks are popular in many Asian countries, especially in Taiwan (Tai, Wang and Huang 1999). The feather colour of the mule duck is of mixed type, the shank and the shank is yellow with brown markings. The bill is slate grey with a yellow tip, the colour of the beans is dark brown. The skin colour too is white, eyes are yellow with horizontal body carriage and devoid of caruncles. The average slaughter weight for the male mule duck (16 weeks) was assessed to be 2775 ± 270 g, under semi-intensive system of management. The weight as obtained was significantly less than those reported by Larzul, Guy and Marie-Dominique (2004), this might be attributed to the genetic makeup of the parental stocks and also because of semi-intensive management.

Muscovy duck (Sepia colour feather)

The Sepia feathered Muscovy ducks (Figure 9) are quite rare. They are slightly smaller than the black and white feather Muscovy ducks and are characterized by the sepia feather colour and yellow colour of shank and beak. The colour of the beans is white. The skin colour is white. The body carriage is horizontal and the caruncles are rudimentary. Ducklings are khaki coloured with pink beak and yellow feet (Figure 10), the observations are in consonance with the assessment of Taibel (1961). The results from Table 3 indicate that the largest numbers of the Sepia feathered Muscovy ducks were observed in the villages of NAD district, while none was observed in the MID district. The results pertaining to the average body weight of the Sepia feather coloured is presented in Table 4, the observations indicate that the highest body weight was observed among the drakes reared in villages of 24 P (S) and ducks raised in NAD district, while the least body weight of drakes was observed in locations of MUR and NAD district, although the lowest weight was estimated in ducks reared in 24 P (S). The average body weights of ducks of this variety are within the range of values reported by Omojola (2007). However, the body weight of the mature sepia feathered variety of Muscovy duck was lower than those of the black and white feathered Muscovy ducks (Table 4). The study pertaining to the numbers of annual egg production is presented in Table 5, the results indicate that the ducks reared in MUR and 24 P (N) laid higher numbers of eggs, while the sepia feather coloured Muscovy ducks reared in 24 P (S) lay fewer number of eggs. The results from the study indicate that the average egg weight of the sepia feather coloured Muscovy ducks (Table 6) was higher in the ducks reared in NAD district. The average weight of the eggs as observed in this study finds consonance with the observations of Changkang,

Figure 9. Muscovy ducks (sepia feathered).

Figure 8. Mule duck.

Figure 10. Growers of Muscovy ducks (sepia feathered).

Ang and Guangying (1999) and Nikolova, Gerzilov and Genchev (2000). The dressing percentage of the drakes as assessed in this study (Table 7) is significantly lower than the values reported by Kazimierz *et al.* (2004), Etuk *et al.* (2006) and Omojola (2007). The low values of the dressing percentage may be attributed to both genotype and husbandry practices. It can also be attributed to the method of slaughter, as indicated earlier. The Muscovy ducks consume a lot of grass leading to the increase in size/weight of the gastrointestinal tract, thereby lowering the dressing percentage. The observations are in agreement with the reports of Siregar, Cumming and Farrell (1982), Dong and Ogle (2003) and Dang, Nguyen and Preston (2012). Moreover, in the present method of slaughter, the weight of the skin was not taken thereby lowering the dressing percentage.

Geese

There are distinctly two types of geese in the study area. The geese are known as “Raj Hans” in Bengali, which translates as King Duck, which may be because they are larger in size when compared with the other breeds of duck. One of the geese breeds observed in the study area has white and brown feathers, while the other breed is white feathered without any markings. The respondents have reported mating between the two geese. The geese are mostly reared for ornamental purpose; however, some respondents reported that the meat is also consumed in the 24 P (S) and also in MUR. The geese breeds are devoid of knob (on the forehead) and dewlap. The geese lay very few eggs, the results of which are presented in Table 5. The less egg production in geese as observed in the present study may be attributed to the breed, nutrition and most of all the high temperature and humidity prevailing in the region. According to Petersen, Chima and Horst (1976) and Kohne and Jones (1975) high temperature and humidity lowers the egg weight and also egg production in geese.

White with brown feathers

These geese are characterized by white and the brown coloured feathers. The brown coloured feathers are seen originating from the back of the skull following the neck and to the back, where they intermingle with the white feathers (Figure 11). There is also intermediate white and brown feather, which extends till the thigh, which is followed by white feathers which extends up to the shank. The throat, breast and the abdomen feathers are white. The bill is brown and the shanks yellow. The bills are devoid of any beans and the eyes are dark coloured and the body carriage is slightly upright. The bill is uniform and the skin colour is white… There is a dearth of scientific research on geese breeds in India which may be because they have almost no commercial use when compared with other domestic fowls. The results from Table 3 indicates that the population of the ganders were highest in MUR and 24 P (S), while the population of the geese were ($P < 0.05$) higher in the villages of MUR, 24 P (N) and 24 P (S). The observations in Table 4 indicate that the average body weight of the gander was highest in MID and 24 P (S), while the geese reared in MID and MUR weighed the highest. In contrary, the lowest body weight of the geese was reported from the studied locations of 24 P (S) and 24 P (N). The average body weight of the geese with white and brown feathers as assessed in the study is within the range body weight values of local Turkish geese as reported by Ergul and Pingel (2003) and Sahin and Yardimci (2009). The average number of eggs obtained from the white and brown feathered geese as presented in Table 5 was highest in MUR and 24 P (S). The results from Table 6 indicate that the highest egg weight was assessed in the geese reared in MID and MUR. The results from Table 7 indicate that the dressing percentage is lower than those reported by Betu″l and Zehra (2009). The lower values of dressing percentage may be attributed to both genotype and husbandry practices prevalent in the study areas. The lower dressing percentage as obtained in the study may also be attributed to the slaughtering technique, a larger portion of the live weight being the skin weight, weight of the feet, feather and fat, the observations being in agreement with those of Fortin *et al.* (1983) and also Stevenson (1985).

Figure 11. Geese (white and brown feathered).

White feathered geese

The white feathered geese are characterized by orange shank and bill, the bill is uniform with no beans. The neck is long, the males at times have a very small knob on their heads (Figure 12). The skin colour is white and the body has a slight upright carriage. The eyes are dark coloured. The results of the survey indicated that the age at first egg lay varied between 275 and 350 days of age averaging at 303 ± 45 days. These geese are reared for ornamental purpose but are very good in guarding the premises; however, they can be quite noisy at times. The result from Table 3 is indicative that the geese are reared in large numbers in NAD and 24 P (S), while they are rarely seen in MID district. The results from Table 4

Figure 12. Geese (white feathered).

indicate that the body weight at maturity was highest in the gander reared in MID and 24 P (N) ducks reared in 24 P (N) weighed the highest. The average body weight of the geese assessed in this study is in agreement with the values reported by Sahin and Yardimci (2009). However, the values are lower than those reported by Larzul *et al.* (2000) from France, Wężyk *et al.* (2003) and Murawska and Bochno (2008) in white feathered geese from Poland. The average egg production as presented in Table 5 indicates that the egg production among the geese reared in NAD is the highest, while those reared in MUR laid the least number of eggs. The results pertaining to the average number of eggs is presented in Table 5, the results as obtained in this study is in consonance with the observations of Wang *et al.* (2009). The average egg weight as observed in the study is presented in Table 6 of the geese reared in MID and MUR had the highest egg weight. The average dressing percentage (Table 7) is significantly lower than the values reported by Larzul *et al.* (2000) and Murawska and Bochno (2008).

Conservation of genetic resources

There was an outbreak of avian influenza in West Bengal in the winter months of 2007 and again in the year 2008 (Patil 2010). As per the standard protocol, all domestic avian species in the affected panchayats were culled in all the affected districts. The restocking of the ducks are being carried out by introduction of Khaki Campbell ducks, SA PPLPP (2009) and Anonymous (2011), while the geese and Muscovy population has dwindled significantly as there are no replacement stock for them. The restocking with Khaki Campbell ducks is leading to serious losses of indigenous domestic avian genetic resources in the region and hence immediate steps are needed to prevent any further loss of genetic resources and steps are needed to be carried out to conserve the indigenous duck genetic resources in the state. This can be carried out by incorporating the native duck and geese breeds in breeding and selection programmes in the days to come.

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Signature of artificial selection and ecological landscape on morphological structures of Ethiopian village chickens

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Summary

Village chickens have been kept for millennia under patronage of smallholder farmers. Our study was intended at dissecting the signature of artificial selection and ecological variation on morphological structures of Ethiopian village chickens. This report was based on visual traits of 798 chickens and a concise one-to-one interview of 399 farmers for their preferences on chicken morphology. Significant population-specific differences in morphological counts were commonly found for rare morphological variants. Most of them were frequently seen in Jarso chickens, while some of them unique to Jarso chickens. This might be explained by the effect of location-specific evolutionary forces and differences in their breeding histories. The high within population variation in the frequency of morphological counts was observed among these panmictic chicken populations largely evolved under uncontrolled mating. Single comb was not (less) preferred by majority of the farmers (93.8 percent); it was thus present at a low frequency (26.7 percent). Farmers have shown high preference for yellow shank (42.3 percent), which was then frequently observed (61.1 percent). The reported reasons for morphological likeness were visual appeal, market demand and cultural and religious values. The absence of significant variation in preferences for chicken morphology among communities between the two study sites was attributed to their multifunctional needs.

Keywords: *village chickens, morphological structure, Mendelian inheritance, farmers' preference, ecological variation*

Résumé

Les poules des zones rurales ont été maintenues depuis des milliers d'années sous les auspices des petits éleveurs. Notre étude a cherché à démêler les effets distinctifs que la sélection artificielle et la variation écologique ont eus sur la morphologie des poules des zones rurales éthiopiennes. Ce rapport s'est basé sur des traits visuels de 798 poules et sur une enquête concise, faite de façon individuelle, à 399 éleveurs auprès de leurs préférences en question de morphologie des poules. Des différences significatives, propres aux populations, ont généralement été décelées pour les mesures morphologiques chez des variantes morphologiques rares. La plupart d'entre elles ont été fréquemment observées chez les poules Jarso alors que certaines sont uniques aux poules Jarso. Ceci peut être expliqué par l'effet de forces évolutives propres à l'emplacement et par des différences historiques dans les pratiques d'élevage. Une grande variabilité intra-populationnelle a été observée pour la fréquence des mesures morphologiques parmi les populations panmictiques de poules qui, dans l'ensemble, ont évolué suivant des accouplements non contrôlés. La crête simple n'a pas été celle préférée par la plupart des éleveurs (93,8 pour cent); c'est ainsi qu'elle est présente à faible fréquence (26,7 pour cent). Les éleveurs ont montré une préférence prononcée pour les tarses jaunes (42,3 pour cent), qui sont fréquemment observés (61,1 pour cent). Les raisons signalées pour la ressemblance morphologique ont été l'attrait visuel, la demande du marché et les valeurs culturelles et religieuses. L'absence de variation significative, entre les communautés des deux lieux étudiés, pour les préférences sur la morphologie des poules a été attribuée à leurs besoins multifonctionnels.

Mots-clés: *poules des zones rurales, structure morphologique, hérédité Mendélienne, préférences des éleveurs, variation écologique*

Resumen

Las gallinas de las poblaciones rurales han sido conservadas durante milenios bajo el auspicio de los pequeños ganaderos. Nuestro estudio ha pretendido desentrañar el efecto distintivo que la selección artificial y la variación ecológica han tenido sobre la morfología de las gallinas de las áreas rurales etíopes. Este informe se basó en rasgos visuales de 798 gallinas y en una breve entrevista individual a 399 ganaderos sobre sus preferencias en torno a la morfología de las gallinas. De forma generalizada, se encontraron diferencias significativas, específicas de las poblaciones, para las medidas morfológicas en variantes morfológicas escasas. Por lo general, la mayoría fueron observadas en gallinas Jarso mientras que algunas fueron exclusivas de las gallinas Jarso. Esto se podría explicar por el

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efecto de fuerzas evolutivas específicas de la ubicación y por diferencias en sus respectivos procesos históricos de cría. Se observó una elevada variabilidad intrapoblacional en la frecuencia de las medidas morfológicas entre estas poblaciones panmícticas de gallinas que han evolucionado, en gran parte, siguiendo apareamientos indiscriminados. La mayoría de los ganaderos (93,8 por ciento) manifestaron que la cresta sencilla no era su preferida; por ello apareció en una baja frecuencia (26,7 por ciento). Los ganaderos mostraron una marcada preferencia por los tarsos amarillos (42,3 por ciento), que eran observados frecuentemente (61,1 por ciento). Las razones indicadas para la similitud morfológica fueron el atractivo visual, la demanda del mercado y los valores culturales y religiosos. La ausencia de variación significativa, entre las comunidades de los dos emplazamientos estudiados, para las preferencias acerca de la morfología de las gallinas se atribuyó a sus necesidades multifuncionales.

Palabras clave: *gallinas de zonas rurales, estructura morfológica, herencia Mendeliana, preferencias de los ganaderos, variación ecológica*

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Introduction

Village chickens have been kept for millennia under traditional management practices of smallholder farmers; therefore they are adapted to a wide range of ecological settings. They are characterized by non-descript and hypervariable phenotypic landscape (Orheruata, Adegite and Okpeku, 2006; Halima *et al.*, 2007; Dana *et al.*, 2010a; Egahi *et al.*, 2010; Melesse and Negesse, 2011). They show striking morphological variations in plumage colour and pattern, comb shape, earlobe colour, shank colour, etc. (Orheruata, Adegite and Okpeku, 2006).

Studies conducted in the early twentieth century confirmed a Mendelian mode of inheritance pattern in these visual traits (e.g. Bateson, 1909; Punnett, 1923). It has been substantiated that single comb (the wild type) is recessive to all comb types; except the comb-less variant. The causative genetic variants for some of these morphological traits were mapped to their respective genomic regions (e.g. Dorshorst, Okimoto and Ashwell, 2010; Wragg *et al.*, 2012). Segregation of these traits in village chickens has been influenced by a long lasting practice of uncontrolled breeding and this has provided a unique and powerful resource for genetic mapping (Wragg *et al.*, 2012). Moreover, this genetic structure provides an opportunity to study the effect of artificial selection and ecological landscape on the morphological structure of domestic fowl.

The origin and status of this diversity, however, remains largely unknown and the influence of natural and/or artificial selection on morphological diversity of village chickens has not been sufficiently studied. However, it is strongly believed that the multipurpose function of village chickens has played its own role in shaping this phenotypic diversity. This is indeed true, because, such diversity is important for them to survive in resource-limited production systems with hostile environmental settings. This high phenotypic diversity has been partly induced by the act of uncontrolled breeding. This represents the main difference observed between village chickens and their commercial and fancy counterparts that have been selected for decades to produce phenotypically standardized populations.

Genetic improvement of village chickens for production traits is exceptionally rare (Dessie *et al.*, 2011). However, there is some sort of selection on visual traits even by smallholder farmers who keep chickens not only for their direct use values such as egg and meat production but also to satisfy their visual appeal and to meet their cultural and religious needs (Dessie and Ogle, 2001; Dana *et al.*, 2010a; Melesse and Negesse, 2011). To meet their personal preferences, individuals and/or communities commonly have their own preference rankings for visual traits. However, showing an inclined type of preference towards some variants of morphology is not uncommon. This type of selective breeding practice has been used to maintain and increase the frequencies of particular phenotype(s) for the preferred traits (Bartels, 2003). Smallholder farmers usually have broad breeding objectives to fulfil their versatile needs (Dana *et al.*, 2010b; Moges, Mellesse and Dessie, 2010) through keeping flocks of diverse phenotypes. This study was intended at dissecting village chickens' morphological structures and to elicit farmers' preferences for visual traits.

Materials and methods

The study sites

The study sites include Horro district (37°01′E to 37°12′E longitudes and 9°55′N to 9°77′N latitudes, recorded for the study villages only) from Western Ethiopia and Jarso district (42°10′E to 42°16′E longitudes and 9°25′N to 9°41′N latitudes) from Eastern Ethiopia. These two study sites are ~870 km apart and are known by their noticeable differences in farming systems and ecological landscapes. Horro district is characterized by a sub-humid type of agro-ecological zone and food self-sufficiency. According to Horro District Office of Agriculture's unpublished data, the average annual rainfall is 1 685 mm (ranging from 1 300 to 1 800 mm) and average annual temperature is 19 °C (from 14 to 24 °C). Majority of the inhabitants are Christians (~98 percent) and the agricultural (rural) population accounted for 88 percent of the district's human population. It consists of 21 rural villages. It is typically characterized by a cereal dominated crop livestock mixed farming system. Livestock and livestock products are among the main sources of on-farm incomes. The major types of crops grown are maize, teff (*Eragrostis tef*), noug (*Guizotia abyssinica*), wheat, barley, faba bean and peas. The livestock species kept by farmers in descending number of counts include cattle, sheep, chickens, goats, horses and donkey. The major soil types are redzinas, haplic and luvic phaeozems.

Similarly, unpublished data obtained from Jarso District Office of Agriculture show that Jarso district is characterized as a semi-arid agro-ecological zone and food deficient. The average annual rainfall is 700 mm (from 600 to 900 mm) and the average temperature is 21 °C (from 14 to 24 °C). Unlike Horro district, nearly all the inhabitants are Muslim (99 percent). It has 18 rural villages. It is characterized by undulating and degraded landscape. Majority of the farmers earn their living from khat (*Catha edulis*) and Irish and sweet potatoe production, and petty trading. Livestock species reared by farmers in descending number of counts are chickens, cattle, sheep, goats, donkeys, camels and a few feral horses. The main soil types include lithosols, vertic luvisols, eutric regosols, vertic cambisols and eutric fluvisols.

The study populations

According to the respective district agriculture offices, the total number of chickens found in Horro and Jarso were 38 776 and 62 829, respectively. Both chicken populations subsist on scavenging and mating is uncontrolled and in most instances random.

Sampling methods

The study sites were selected based on their wide variations in socio-economic and agro-ecological settings. A reconnaissance tour was made in both districts to identify sampling units (villages). A pilot study was conducted to gain hands on experience on sampling and data collection practices. Villages that are found nearby town centres were excluded from sampling to keep at minimum the influence of urban affiliated farming systems on a typical rural village-based chicken management system. Only farmers that keep indigenous chickens were visited. From each district two market sheds were selected and each market shed was represented by two villages. Accordingly, we sampled eight villages with four from each district. Equal numbers of households were visited in each village, market shed and district. The data were collected twice in 2011 (from April to June and from October to November).

Twenty-five households were sampled from each village during each field visit and two adult chickens over ~6 months of age were sampled from each household. Sampled chickens were snapshot and scored for unique morphological variants. Households and chickens were selected from the list of farmers in a village and from a family flock, respectively, using random table numbers. This was done when more than two adult birds met our selection criteria. However, when flock size was small, two adult chickens were directly sampled. In the absence of a cock, two hens were sampled. Using this strategy, we sampled 798 chickens (400 in Horro and 398 in Jarso district) from 399 households (200 from Horro and 199 from Jarso district).

Data sources

Multiple photographs of each chicken were taken from lateral, front and dorsal sides besides the details of the head and leg regions. Morphologies were scored in the field by direct physical observation and by looking at individual photographs. Owing to the rudimentary and ambiguous nature of hens' comb, we analysed this trait for cocks only. Moreover, chicken owners were briefly interviewed for their preferences for comb shape and shank colour, and to state their reasons for preferences they have made. Earlobe has no equivalent local name and farmers do not value of this trait while selecting their breeding stocks. Therefore, variation in earlobe colour in the study sites could be under the influence of breeding history and natural selection.

Data management and analysis

Dependent variables were analysed using the nonparametric Chi-square test in R (R Core Team, 2012). Logistic regression analysis in SPSS (2007) was used to analyse binomial type response variables (Equation 1).

$$L_i = \mathrm{In}\left[\frac{p_i}{1-p_i}\right], \qquad (1)$$

where p_i is the probability of the presence of a phenotype, $1-p_i$ the probability for the absence of a phenotype and L_i the natural log of odds ratio. This model used district as a classifying variable.

Cramer's V (Equation 2) as estimated using SPSS (2007) was used to test possible association between three pigmentation traits (earlobe colour, shank colour and beak colour) and the association between district and four morphological traits (crest, earlobe colour, shank colour and beak colour).

$$V = \sqrt{\frac{\chi^2}{n(k-1)}}, \qquad (2)$$

where V is Cramer's V, n the total number of observations and k the number of studied traits.

Correspondence analysis (CA) was used to visualize the discriminating power of earlobe colour, shank colour, beak colour and crest variants using CA Package (Nenadić and Greenacre, 2007) as implemented in R (R Core Team, 2012).

Equation (3) was used to analyse the effect of three explanatory variables on live weight of the sampled chickens using SPSS (2007):

$$y = \mu + A + B + C + A^*B + A^*C + B^*C + e, \qquad (3)$$

where y is the live weight of a chicken, μ the common mean, A, B and C representing sex, location and sampling slot, respectively, and e the residual term.

Results

Counts of sampled chickens

We sampled 160 cocks and 240 hens from Horro district (cock to hen ratio of 1:1.5) and 121 cocks and 277 hens (1:2.29) from Jarso district, though our sampling strategy favoured sampling of more number of hens. This difference in the ratios was because of frequent absence of cocks in flocks sampled from Jarso ($\chi^2_1 = 5.22$; $P = 0.022$). Sampling less number of cocks than hens is not unusual in village chickens, because in most instances cocks are the ones that are slaughtered for religious and/or cultural ceremonies, to welcome guests and to meet family's dietary protein need. Moreover, cocks are sold out more frequently to cover incidental expenses.

Comb-shape variants

We observed seven types of comb shapes (single, buttercup, duplex, pea, rose, strawberry and walnut) across the two districts (Table 1 and Figure 1a–e). The proportions of different types were significantly different ($\chi^2_7 = 802.07$; $P < 0.001$). However, we left a few ambiguous comb shapes unclassified ($n = 3$). In Horro, cocks' comb shapes were limited to rose and single types, whereas other comb types, though rare, were observed in Jarso cocks. Mutant comb types were more common than the single comb as of the wild-type, i.e. 73.3 percent ($n = 206$) versus 26.7 percent ($n = 75$) ($\chi^2_1 = 61.07$; $P < 0.001$). Single comb was found in 28 of Horro and 47 of Jarso cocks ($\chi^2_1 = 11.76$; $P = 0.001$). The logistic regression analysis also shows that the chance of finding single-combed cocks in Horro district is less likely by the order of 66 percent.

Comb-shape preferences

Farmers have a dichotomous type of classification and preference for comb-shape variants. This preference has been made between single and the rest of comb types. This shows that farmers do not care so much the details of morphological differences observed among mutant comb types. We found that 98 percent of Horro and 89.5 percent of Jarso farmers preferred to have non-single combed chickens ($\chi^2_1 = 0.39$; $P = 0.535$). Preferences of comb shapes were dictated by reasons described in Table 2.

Ear tuft and variants of other Mendelian traits

Rudimentary types of ear tufts were observed in all sampled chickens despite slight variations in their size and appearance. However, multiple spur, polydactyl, heterodactyl, syndactyly and bantam chickens were not found. Only one naked neck chicken (not picked up by random sampling) was found in Horro district. The absence of naked neck birds might be associated with high elevation of the study districts (higher than ~2 000 m above sea level for all sampled villages). Farmers also showed no preference for the naked neck phenotype. Their main reasons were lack of visual appeal (58.0 percent); unfamiliarity (41.0 percent) and low market demand (12.4 percent). Farmers also considered that naked neck chickens are affected by cold weather and rain (3.8 percent) and they are more vulnerable to predators (1.9 percent).

Table 1. Observed count differences in cocks' comb variants within and between districts.

Comb types	Horro	Jarso	Total	χ^2
	***N* (%)**	***N* (%)**	***N* (%)**	
Rose	130 (81.3)	49 (40.5)	179 (63.7)	17.96***
Single (wild)	28 (17.5)	47 (38.8)	75 (26.7)	11.76**
Pea	0 (0.0)	9 (7.4)	9 (3.2)	11.90**
Walnut	0 (0.0)	6 (5.0)	6 (2.1)	7.93*
Strawberry	0 (0.0)	5 (4.1)	5 (1.8)	6.61*
Butter cup	0 (0.0)	3 (2.5)	3 (1.1)	3.97*
Duplex	0 (0.0)	1 (0.8)	1 (0.4)	1.32^{ns}
Unclassified	2 (1.3)	1 (0.8)	3 (1.1)	0.12^{ns}
χ^2	171.65***	193.91***	795.93***	

^{ns}Not significant; *$P < 0.05$; **$P < 0.01$; ***$P < 0.001$.

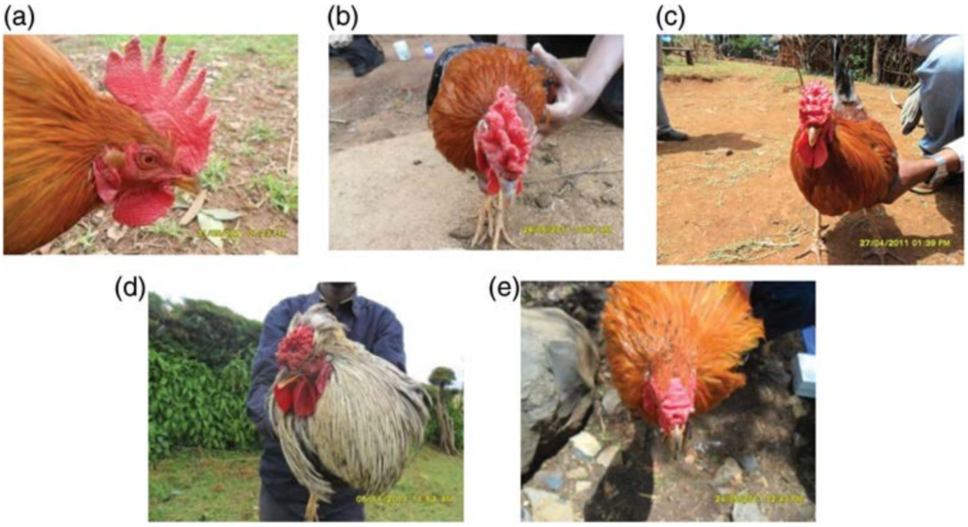

Figure 1. Comb types: (a) single, (b) pea, (c) rose, (d) strawberry and (e) walnut.

Table 2. Stated reasons for comb type preferences of farmers.

Stated reasons	Horro	Jarso	Overall	χ^2
	N (%)	N (%)	N (%)	
Aesthetic value	82 (32.4)	81 (35.2)	163 (33.8)	0.28^{ns}
Market demand	140 (55.3)	122 (53.0)	262 (54.2)	0.12^{ns}
Religious and cultural value	15 (5.9)	4 (1.7)	19 (3.9)	5.38*
Better growth rate	16 (6.3)	23 (10.0)	39 (8.1)	2.02^{ns}
χ^2	170.79***	152.43***	321.10***	

^{ns}Not significant; *$P < 0.05$; **$P < 0.01$; ***$P < 0.001$.

Tufted crest

Tufted crest (Figure 2) was commonly observed in hens ($n = 106$, 83.5 percent) than cocks ($n = 21$, 16.5 percent) ($\chi_1^2 = 55.82$, $P < 0.001$). This is a typical characteristic feature of sex-influenced traits. Logistic regression analysis also shows that the likelihood of being crestless in cocks is more likely by 77.3 percent than in hens. Moreover, the chance of finding crested chickens in Horro district was ~10.5 times more likely than in Jarso district. The proportion of crested phenotype recorded for both districts was 16.1 percent (127/791) and this shows the abundance of crestless chickens ($\chi_1^2 = 364.56$, $P < 0.001$). In Horro district, 111 crested chickens (27.9 percent, 111/398) were sampled, whereas there were 16 (4.1 percent, 16/393) only in Jarso district ($\chi_1^2 = 69.87$, $P < 0.001$).

Figure 2. Crest: (a) crested hen and (b) crestless hen.

Earlobe colour

The village chickens display high diversity in earlobe colouration (Figure 3a–d). For example, we found red and pink earlobes that are mingled or peppered with varying proportions of white and yellow colours. This made the classification of earlobe colours into distinct phenotypic classes challenging. Therefore, we grouped them into broader phenotypic classes by pooling closely related ones to a single slot (Table 3).

Beak colour

Usually the two horny mandibles of chickens' beak display variations in their colour. The lower mandible is usually brighter than the upper one and this creates a mosaic appearance. This might be because of continuous exposure of the upper part of the beak to direct sunlight besides the differential act of location-specific biochemical processes. Observed beak colour phenotypes are presented in Table 4 and are displayed in Figure 4a–c.

Shank colour

The commonest shank colours were yellow and white, whereas the rare variants included slate blue, green,

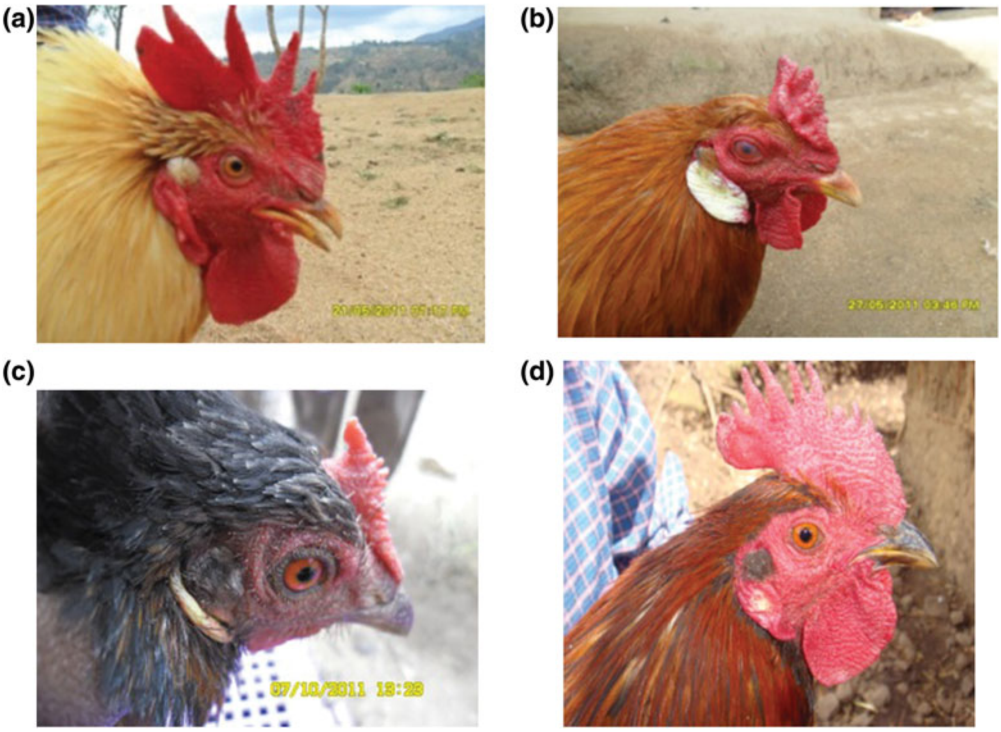

Figure 3. Earlobe colour: (a) red, (b) white, (c) yellow and purple and (d) white-spotted red.

Table 3. Earlobe colour variants of the chicken populations.

Earlobe colour	Horro	Jarso	Total	χ^2
	N (%)	*N* (%)	*N* (%)	
Dark brown	1 (0.3)	0 (0.0)	1 (0.1)	0.97^{ns}
Pink	78 (19.9)	41 (10.8)	119 (15.5)	10.29**
Pink and white	63 (16.1)	75 (19.8)	138 (17.9)	1.49^{ns}
Pink and yellow	0 (0.0)	6 (1.6)	6 (0.8)	ND
Red	159 (40.7)	120 (31.7)	279 (36.3)	4.21*
Red and white	81 (20.7)	123 (32.5)	204 (26.5)	10.13**
White	6 (1.5)	11 (2.9)	17 (2.2)	1.65^{ns}
Yellow	3 (0.8)	2 (0.5)	5 (0.7)	0.17^{ns}
χ^2	359.86***	307.11***	822.81***	

^{ns}Not significant; *$P < 0.05$; **$P < 0.01$; ***$P < 0.001$; ND, not done.

Table 4. Beak colour variants observed in the chicken populations.

Beak colour	Horro	Jarso	Total	χ^2
	N (%)	*N* (%)	*N* (%)	
Yellow	153 (39.1)	145 (38.4)	298 (38.8)	0.03^{ns}
White	2 (0.5)	5 (1.3)	7 (0.9)	1.39^{ns}
Brownish yellow	176 (45.0)	103 (27.2)	279 (36.3)	16.72***
Brown	37 (9.5)	71 (18.8)	108 (14.0)	11.89**
Black	23 (5.9)	54 (14.3)	77 (10.0)	13.55**
χ^2	328.78***	146.02***	429.23***	

^{ns}Not significant; **$P < 0.01$; ***$P < 0.001$.

Figure 4. Beak colour: (a) brownish yellow, (b) yellow and (c) black.

black and brown (Table 5 and Figure 5a–e). Out of 14 mottled shanks observed, 13 of these were found in Jarso district ($\chi_1^2 = 10.70$, $P = 0.001$). Dark shanks (black, slate blue and willow green) were also relatively more frequent in Jarso than Horro district ($\chi_1^2 = 47.90$, $P < 0.001$).

Preference of shank colour

Farmers were asked to rank their favourite shank colour namely white, yellow or black (slate blue) using a pre-coded checklist; however, a few farmers mentioned red shank as an additional variant. This represents a deep yellow shank that has vertical streaks of light pink bands. Farmers showed highly skewed preferences towards yellow shank (Table 6).

Feathered shank and spur

Lightly feathered shank (ptilopody, Figure 6) was rarely found, and only 2.1 percent (17/798) of all the sampled chickens had this phenotype ($\chi_1^2 = 731.44$, $P < 0.001$). This included seven from Horro district (1.8 percent, 7/400, $\chi_1^2 = 372.\ 49$, $P < 0.001$) and 10 from Jarso district (2.5 percent, 10/398, $\chi_1^2 = 359.0\ 1$, $P < 0.001$). However, difference in the proportions of ptilopody between the two districts was not significant ($\chi_1^2 = 0.54$, $P = 0.461$). A well grown spur was observed in cocks whereas it was rudimentary in most of the sampled hens (data not shown). Length of spur is usually influenced by age of the bird, the older the bird, the longer the spur.

Correspondence analysis of qualitative traits

The summary function of CA analysis (Nenadić and Greenacre, 2007) showed that the three (the original variables (four morphological traits) minus one) principal inertias (eigenvalues) accounted for 56.54, 24.96 and 18.5 percent of the total variance (the corresponding values were 0.029, 0.013 and 0.009, respectively). Most of the study birds

Table 5. Observed phenotypes of shank colour.

Shank colour	**Horro**	**Jarso**	**Total**	χ^2
	***N* (%)**	***N* (%)**	***N* (%)**	
Yellow	279 (71.5)	190 (50.4)	469 (61.1)	14.01 **
White	93 (23.8)	91 (24.1)	184 (24.0)	0.01^{ns}
Black	7 (1.8)	23 (6.1)	30 (3.9)	9.09*
Slate blue	4 (1.0)	37 (9.8)	41 (5.3)	27.70***
Green	6 (1.5)	23 (6.1)	29 (3.9)	10.55**
Mottled	1 (0.3)	13 (3.4)	14 (1.8)	10.70**
χ^2	942.18***	370.64***	1 246.83***	

^{ns}Not significant; *$P < 0.05$; **$P < 0.01$;***$P < 0.001$.

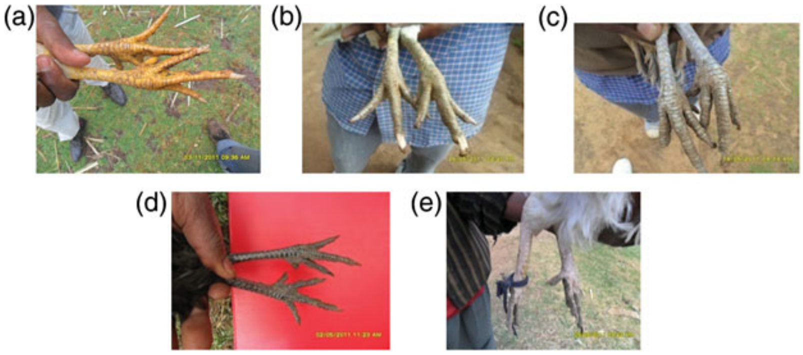

Figure 5. Shank colour: (a) yellow, (b) green, (c) slate blue, (d) black and (e) white.

Table 6. Preferences of farmers to shank colour types.

Shank colour	Horro	Jarso	Overall	χ^2
	N (%)	N (%)	N (%)	
Yellow	80 (39.4)	88 (45.4)	168 (42.3)	0.83^{ns}
White	57 (28.1)	44 (22.7)	101 (25.4)	1.14^{ns}
Black/slate blue	31 (15.3)	36 (18.6)	67 (16.9)	0.63^{ns}
Red	35 (17.2)	26 (13.7)	61 (15.4)	0.95^{ns}
χ^2	30.20***	46.25***	72.87***	

^{ns}Not significant; ***$P < 0.001$.

were tightly clustered (Figure 7). Variations of earlobe colour, shank colour, beak colour and crest explained 39.4, 20.2, 23.3 and 17.1 percent of the total inertia, respectively (with inertia values of 0.020, 0.010, 0.012 and 0.009, respectively). This shows that despite its binary nature, crest variation contributed to a substantial part of the total variance. Only a few outlier birds showed higher inertia whereas for most of the sampled birds, individual difference for traits considered was found to be weak (Figure 8). All the four traits showed coordinates of different signs (direction of the arrows) and this indicated the presence of weak correlation among them.

Relationship between qualitative traits

Cramer's V test revealed that the three morphological traits, which were characterized by different colour variants showed low but statistically significant relationships, i.e. earlobe versus shank colour (0.230, $P < 0.001$); earlobe versus beak colour (0.122, $P = 0.003$) and beak colour versus shank colour (0.266, $P < 0.001$). Cramer's V analysis also showed statistically significant association between district and variants of crest (0.324, $P < 0.001$), earlobe colour (0.230, $P < 0.001$), shank colour (0.331, $P < 0.001$) and beak colour (0.320, $P < 0.001$).

Live weight

District and sex showed significant effects on the live weight of sampled chickens (Table 7) ($P < 0.001$), however, sampling slot did not affect the live weight ($P = 0.483$). The interaction effect between location and sex ($P = 0.017$) and location and sampling slot were significant ($P < 0.001$), however, the interaction between sex and sampling slot was not visible ($P = 0.396$). We found an R^2 value of 32.41 percent from the fitted model. This showed that the remaining variation in live weight was explained by hidden environmental factors and an individual and/or population-based genetic differences.

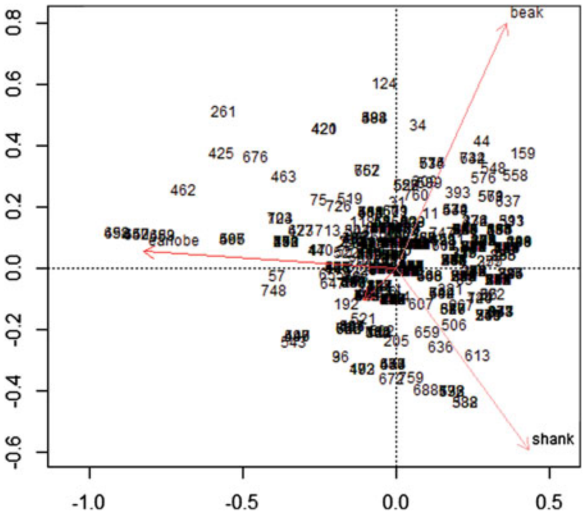

Figure 7. A CA plot obtained from earlobe, shank and beak colours and crest variants of sampled chickens. Serial numbers 1–391 and 392–769, respectively, represent Horro and Jarso chickens.

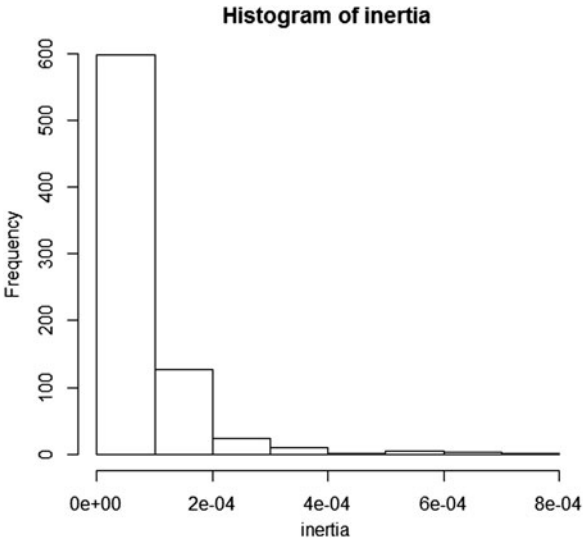

Figure 8. Frequency distribution of eigenvalues (inertias) explained by individual birds.

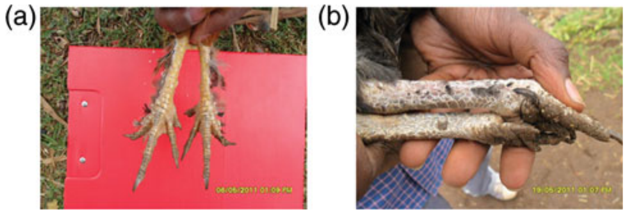

Figure 6. Feathered shanks.

Table 7. Least square means (LSM ± S.E) for live weight (kg) of the chicken populations.

Classifying variable	Horro district	Jarso district
Sex		
Cock	1.63 ± 0.021^a	1.45 ± 0.024^b
Hen	1.24 ± 0.017^a	1.16 ± 0.017^b
Sampling slot		
First	1.39 ± 0.019^a	1.35 ± 0.020^a
Second	1.49 ± 0.019^a	1.27 ± 0.021^b

Superscripts that appeared with different alphabets across row show statistically significant difference at $P < 0.01$.

Discussion

Morphology refers to the outward appearance of an organism and it can be used to group members of a population into sub-groups. Morphological variations (Figure 9) have been a subject of thorough studies owing to its importance in evolutionary biology and socio-economic life of subsistence farmers. For example, the interviewed farmers showed highly skewed preferences for particular kinds of birds than others, which substantiate its importance.

Variants of comb shape

Rareness of single comb (26.7 percent) found in our study is inconsistent with the report of Melesse and Negesse (2011) for southern Ethiopian chickens (55.0 percent). Moreover, high proportion of single comb was reported for Shelleng and Song (96.45 percent, Apuno, Mbap and Ibrahim, 2011), Dekina (51 percent, Daikwo, Okpe and Ocheja, 2011) and Edo State chickens (92 percent, Orheruata, Adegite and Okpeku, 2006) from Nigeria, and for Desi chickens of Bangladesh (97 percent, Bhuiyan, Bhuiyan and Deb, 2005). This commonness might be associated with special importance of this phenotype to adapt to warm climates and possibly because of variations in culture and religion. For example, the southern Ethiopia region is dominated by Protestant Christians (55.5 percent, FDREPCC, 2008) and the dogma of this religion is strictly against sacrificial offerings and associated practices. Hence people living in this part of Ethiopia are most likely not worried about comb type. High demand for mutant-type comb shapes observed elsewhere in Ethiopia (Dessie and Ogle, 2001; Dana *et al.*, 2010a; Moges, Mellesse and Dessie, 2010) is of limited importance in this region. However, in line with our findings, Dana *et al.* (2010a) reported a low averaged proportion of single comb phenotype in five indigenous chicken populations (13 percent). Similarly, Dong Xuan *et al.* (2006) reported a low frequency of single comb in Dong Tao chickens in Vietnam (10 percent). We found that single comb was relatively more common in Jarso (38.8 percent) than Horro chickens (17.5 percent). This is because Jarso is almost entirely inhabited by Muslims who hardly sacrifice chickens for cultural and/or ritual purposes. This traditional practice otherwise requires sacrifice of non-single combed chickens in the context of Ethiopian tradition (Moges, Mellesse and Dessie, 2010).

Figure 9. The non-descript scavenging chicken and their natural habitat: (a) Horro chickens and (b) Jarso chickens.

Dong Xuan *et al.* (2006) reported pea comb as the commonest variant (90 percent) in Vietnamese Dong Tao chickens. Similarly, Dana *et al.* (2010a) reported pea comb as a common variant in Horro chickens, however, we hardly found this phenotype in the same population. Halima *et al.* (2007) also reported pea comb as a common variant in northwestern Ethiopia chickens. In line with our findings, rareness of pea comb was reported in Beninese chickens (Youssao *et al.*, 2010). The presence of v-shaped comb was reported in 13.4 percent of northwestern Ethiopian chickens (Halima *et al.*, 2007), however, it was rarely seen in this study. We found rose comb as the commonest variant and this partly agrees with Melesse and Negesse (2011) who reported rose comb as the second most common variant. However, all these findings should be treated with caution owing to inconsistencies in the definition of comb types.

Farmers' preference for comb shape

Mutant comb types are mostly preferred by farmers and consumers in Ethiopia. For example, 81.1 percent of farmers in northwestern Ethiopia showed preference to mutant-type combs, which is comparable with our findings (Moges, Mellesse and Dessie, 2010). Sizable proportion of farmers (36.4 percent) also included cultural and religious values in their breeding objectives (Moges, Mellesse and Dessie, 2010) and this has also been reflected in our findings on comb type and shank colour preferences. A quarter of the interviewed farmers in central highlands of Ethiopia also used chickens for sacrificial and healing purposes (Dessie and Ogle, 2001). This indicates the special importance of morphological traits in fulfilling cultural and religious needs. This is common because plumage colour and pattern, sex, comb shape and age have been used as the main criteria to slaughter chickens (cocks) for cultural and religious ceremonies (Dessie and Ogle, 2001). Variation in different combinations of these traits in turn determines market demand and price. Most likely inclusion of morphological traits as selection criteria has been driven by such demand (Muchadeyi *et al.*, 2009; Dana *et al.*, 2010b; Moges, Mellesse and Dessie, 2010).

Muchadeyi *et al.* (2009) noted that in some instances chickens were culled based on their comb shape and plumage colour. This shows the influence of artificial selection on morphological structure of village chickens. Systematic culling of single-combed chickens through sale and ordinary consumptive slaughter is common in Ethiopia. Elsewhere in Ethiopia this has been practiced for centuries to reduce the frequency of this phenotype in a breeding flock. Owing to its homozygous recessive expression pattern, sizable reduction in allelic frequency can be easily achieved through continuous culling.

Through the continuous practices of skewed selection for Mendelian traits such as comb shapes, farmers indirectly affect metric traits influenced by pleiotropic effect of loci controlling the expression of Mendelian traits. For example, the homozygous rose is known to reduce fertility (Crawford and Smyth, 1964) and pea comb is noted to reduce tissue mass (see Wright *et al.*, 2009 for a review). Significant phenotypic correlations observed between some morphological traits indicates the influence of farmers' selection for a trait on the associated traits. This can be also seen from ecological adaptation perspectives. For example, in elevated highland areas that experience temperate-like weather, chickens having mutant comb types that are characterized by reduced surface area might be better adapted owing to reduction in heat loss (see Wright *et al.*, 2009 for pea comb).

Crested versus crest-less chickens

The rareness of crest reported in Nigerian (17.03 percent, Egahi *et al.*, 2010) and Ugandan chickens (12 percent, Ssewannyana *et al.*, 2008) are in line with our findings. Dana *et al.* (2010a) also reported an average proportion of 34 percent of crested chickens (ranging from 1 to 75 percent) for five chicken populations in Ethiopia, particularly 33 percent for Horro chickens, which is comparable with our findings for the same population (27.9 percent). However, Halima *et al.* (2007) reported a higher proportion of crested chickens (48.8 percent) in northwestern Ethiopia. The frequency of this trait showed variation among geographical locations. For example, it was rare in south and southwestern Ethiopia compared with northwestern and western Ethiopia (Dana *et al.*, 2010a). This variation has been also observed between our populations. Wang *et al.* (2012) noted a voluminous crest in cocks than in hens, however, a completely different situation has been observed in this study. For example, we observed a low proportion of cocks showing the rudimentary form of this phenotype.

Variants of earlobe colour

In line with our findings: earlobe, comb and wattle colours are commonly red in fancy chickens (Wragg *et al.*, 2012). We observed earlobe colours different from the only single-coloured types reported for southern Ethiopian chickens (Melesse and Negesse, 2011). Red and pink earlobes mingled or peppered with varying proportion of white colour were present in both study districts. In agreement with our findings, some Kenyan indigenous chicken populations were characterized by intermingled red and white earlobe colours (Kingori, Wachira and Tuitoek, 2010). The proportion of white earlobe colour that we found (2.2 percent) is much lower than the one observed in Beninese Forest type (60.8 percent) and Savannah-type chickens (45.1 percent) (Youssao *et al.*, 2010), Nigerian chickens (73.21 percent, Egahi *et al.*, 2010) and Ugandan chickens (48 percent, Ssewannyana *et al.*, 2008). White earlobe is a characteristic feature of chickens of the Mediterranean region (FAO, 2010). Comparable with our findings, Orheruata, Adegite and Okpeku (2006) from Edo State in Nigeria reported red earlobe colour as the commonest one (60 percent), however, reasonably higher proportion of white earlobe (39 percent) was also observed in this population. Red earlobe was once reported as the second most frequent one (47 percent) in Ugandan chickens (Ssewannyana *et al.*, 2008). Vij, Tantia and Vijh (2006) reported brown earlobe as the commonest variant in Punjab brown chickens, however, we found only a single bird (0.1 percent) showing this phenotype. Earlobe was prominently seen in all the sampled chickens, however, it was not clearly visible in the majority (64 percent) of Ugandan chickens (Ssewannyana *et al.*, 2008). Despite controversies over the inheritance pattern of this trait (Warren, 1928), polygenic and sex-linked patterns have been reported (Warren, 1928; Wragg *et al.*, 2012).

Variants of beak colour

Unlike our study populations that had been dominated by brownish yellow beaks, Kenyan indigenous chickens usually have black and dark grey beaks (Kingori, Wachira and Tuitoek, 2010). Beak colour in Punjab brown chickens of India is yellow, however, its upper part turns black as the chicken ages (Vij, Tantia and Vijh, 2006). A comparable type of mosaic beak colour was observed in this study.

Variants of shank colour

We found yellow as the commonest shank colour type (61.1 percent). This is comparable with reports of Halima *et al.* (2007, 64.4 percent), Dana *et al.* (2010a, 60 percent) and Melesse and Negesse (2011, 52.5 percent) from Ethiopia; Daikwo, Okpe and Ocheja (2011) for Dekina chickens in Nigeria (40.5 percent) and Ssewannyana *et al.* (2008) for Ugandan chickens (42 percent). Moreover, Bhuiyan, Bhuiyan and Deb (2005) and Orheruata, Adegite and Okpeku (2006) reported yellow shank as the second most frequent phenotype for Bangladeshi Desi chickens (32 percent) and for Nigerian chickens (30 percent). However, all these findings are inconsistent with Youssao *et al.* (2010) who reported the presence of this phenotype in only 5 percent of Beninese chickens. White shank colour is the second common phenotype in our findings (24.0 percent), and this is comparable with Ugandan chickens (20 percent, Ssewannyana *et al.*, 2008) and Bangladesh Desi chickens (29 percent, Bhuiyan, Bhuiyan and Deb, 2005). However, white shank was the commonest phenotype in Nigerian chickens (41 percent, Orheruata, Adegite and Okpeku, 2006) and the second commonest type in Beninese chickens (40.1 percent, Youssao *et al.*, 2010). Unlike our report, reasonably high proportions of dark shanks were reported for a number of village chicken populations in developing countries. These include black shank at 39 percent in Bangladeshi Desi chickens (Bhuiyan, Bhuiyan and Deb, 2005); 42.2 or 29 percent in Nigerian chickens (Orheruata, Adegite and Okpeku, 2006; Egahi *et al.* 2010) and 21 percent in Ugandan chickens (Ssewannyana *et al.*, 2008). Slate blue shank is among the rare variants in our populations. This phenotype is, however, the commonest one in Beninese chickens (43.3 percent, Youssao *et al.*, 2010). Moreover, dark shank colour is a typical characteristic feature of the red jungle fowl (for reviews, see Brisbin and Peterson, 2007 and the references therein). Green shank was rarely seen (3.9 percent) in this study and a comparable proportion (0.5 percent) was reported for Ugandan chickens (Ssewannyana *et al.*, 2008). However, Halima *et al.* (2007) reported a higher proportion of green-shanked chickens (12 percent) from northwestern Ethiopia. Rareness of green shank is not surprising, because it is unfavourably correlated with viability (see McGibbon, 1979 and the references therein). Uniquely, Apuno, Mbap and Ibrahim (2011) have reported the highest proportion of pink shank (38.8 percent) in Nigerian chickens.

Lightly feathered shank

We sampled 2.1 percent chickens that have feathered shank and this low frequency is invariably confirmed by the report of Melesse and Negesse (2011) (2 percent) and Halima *et al.* (2007) (2.5 percent) from Ethiopia, and in the work of Ssewannyana *et al.* (2008) on Ugandan chickens (4 percent).

Colours of combs and wattle

In line with our findings (data not shown), almost all combs and wattles of indigenous chickens in Kenya were red, except a few variants spotted with white and black colours (Kingori, Wachira and Tuitoek, 2010). However, we have not found any spotted phenotypes. It is biologically important to study the colour of these two phenotypes because their colours are usually used as indicators of chickens' health and egg laying status (Hume, 2011). Moreover, Navara, Anderson and Edwards (2012) reported a positive correlation between brightness of comb and sperm viability.

The influence of ecological variation and artificial selection

Unlike quantitative traits, environment has little effect on traits that show Mendelian mode of inheritance. However, we found that even qualitative traits that were not under the influence of direct artificial selection were significantly different between the two chicken populations (e.g. some variants of shank, earlobe and beak colours). This might indicate the influence of ecological variation and their breeding history. Moreover, four of the morphological traits (crest, earlobe colour, shank colour and beak colour) showed statistically significant association with district and this shows the influence of ecological landscape on morphological traits. Although the preference of farmers for comb shape and shank colour was not significantly different between study sites, differences in culture and religion possibly have contributed especially to variation in single comb proportions between the two chicken populations. The intra population low frequency of single comb and high frequency of yellow shank possibly indicates the influence of artificial selection. However, as a weak selection pattern of farmers is intended at keeping chickens displaying different phenotypes to meet their multiple needs, a clear-cut morphological difference is not found among village chicken populations.

Proposed reasons for observed morphological differences

Except tufted crest, all other mutations were mostly seen in Jarso chickens. This might be because of the difference in breeding history between these two chicken populations. There are historical and archaeological evidences for earlier settlement of people in northern Ethiopia (e.g. D'Andrea *et al.*, 2011) and perhaps human settlement in eastern Ethiopia where Jarso district is located had been initiated closer to this historical time point (Betemariam, 2011). The degraded landscape also indicates a longer history of agriculture in Jarso area. On the other hand, elderly farmers in Horro recalled the very recent (~40 years back) presence of intact dense forest cover in the area, which have now, been cleared for agricultural activities and human settlement. We also noticed that Horro still has patches of dense natural forest cover and the district's land use pattern data has also confirmed an extant cover of ~42.6 percent natural forest. Jarso is closer to the outlet for an ancient trade route between Ethiopia and the Middle East through Red Sea coast – one of the presumed route for the introduction of domestic chickens from their centres of domestications (Blench and Macdonald, 2000). This indicates that domestic chickens might have arrived and the foundation stock most likely founded earlier in Jarso than Horro.

Variation in live weight between two chicken populations

The average live weight of the sampled chickens was 1.54 ± 0.016 kg for cocks and 1.20 ± 0.012 kg for hens and this is comparable with the findings of Melesse and Negesse (2011) (cocks = 1 427 ± 18 g and hens = 1 144 ± 18 g) and Dana *et al.* (2010a) (cocks = 1 612 g and hens = 1 266 g) from Ethiopia, and Daikwo, Okpe and Ocheja (2011) (cocks = 1.32 ± 0.02 kg and hens = 1.05 ± 0.01 kg) for Dekina chickens from Nigeria. However, the average body weight reported by Youssao *et al.* (2010) for Savannah and Forest chickens in Benin (1 177 g for cock and 965 g for hen) and Halima *et al.* (2007) from Ethiopia (1 259.6 and 847 g for cocks and hens, respectively) are lower than our findings. Higher live weights were reported from Uganda (2.1 kg for cock and 1.4 kg for hen) (Ssewannyana *et al.*, 2008) and for Punjab brown chickens from India (2.15 ± 0.94 kg for cocks and 1.57 ± 0.04 kg for hens) (Vij, Tantia and Vijh, 2006). The live weight of the well-defined and large-framed Dong Tao chickens from Vietnam (3.6 kg for cock and 2.6 kg for hen, Dong Xuan *et al.*, 2006) is, however, higher than the average live weight of non-descript village chickens commonly reported in literatures. Olawunmi, Salako and Afuwape (2008) reported an average weight of 1.01 kg for cocks and 0.92 kg for hens in Yoruba chickens, whereas they reported 1.79 and 1.46 kg for Fulani chickens, indicating the presence of wide variation even among chicken populations sampled from the same country. We also found significant differences in live weight of the two chicken populations (Table 7). Variation in chickens live weight, however, needs to be treated with caution. Live weight may vary because of inaccuracies of weighing scales, individual differences in measuring accuracy, age of the bird and season of the year at which the chicken is weighed (during seasons of relatively better feed supply most likely chickens have higher live weight). Moreover, genetic and other environmental (stochastic) factors possibly affect the live weight of village chickens.

Conclusion

Most of the rare morphological variants found in our study were present in Jarso chickens (except crest), which shows the high phenotypic diversity of Jarso chickens. This indicates that Jarso chickens might have descended from earlier founding chicken population. This is possible because phenotypic diversity is positively correlated with the length of breeding history and inversely related to geographical distance from the centre of domestication (Jarso is closer to the presumed centre of domestication for domestic fowl). Owing to its ancient inhabitation, stochastic factors and evolutionary forces might have had longer time to provoke and modulate germline mutations in Jarso chickens. Moreover, owing to the influence of a long history of artificial selection, Jarso chickens most likely have had better chance to accumulate some of the rare variants observed. Difference in their ancestral genetic background (genetic structure of the founder population) and variation in ecological landscape might have contributed to the observed differences. The lower relative diversity observed in most of the morphological traits in Horro chickens on the other side might be the consequence of the very recent introduction of chickens following the short history of human settlement. The relative abundance of crested chickens in Horro district, however, might be associated with high frequency of crested alleles in the founder population.

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Population history and genetic variability of the American Shire horse

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Summary

The American Shire horse breed is currently listed in “critical condition”, the most serious threat category assigned by the American Livestock Breeds Conservancy. Despite concern for the breed’s future, however, a thorough genetic analysis of the breed has not been conducted to date. Pedigree data from 85 671 Shire horses born between 1806 and 2011 were used to determine current and historical genetic variability in the Shire horse since the first imported animals arrived from the United Kingdom to the United States. From this larger dataset, a reference population of 1 152 animals representing the most current generation was defined. Effective population size was 330.5, with 832 total founders and high pedigree completeness (98.2 percent) to five generations. Effective number of founders, ancestors and genomes were 104.5, 28.6 and 13.9, respectively. Average inbreeding coefficient was 2.4 percent from complete pedigree data and 1.3 percent when the most recent five generations were considered. Demographic analysis also revealed a population bottleneck in the 1950s. The ten most influential male and female ancestors contributed 48.5 percent and 11.6 percent, respectively, to the reference population, and only three foundation sires are responsible for 95.6 percent of all sire lines in the current generation. Although current assessment of genetic variability indicates a relatively healthy population, the small number of breeding animals, low birth rates and steady rise in inbreeding coefficients mark the American Shire as an at-risk breed for which conservation strategies should be considered.

Keywords: *inbreeding, pedigree analysis, genetic diversity, breed conservation, horse*

Résumé

La race de cheval Shire Américain est actuellement répertoriée comme race en état critique, celle-ci étant la catégorie dans laquelle l’Association Américaine pour la Conservation des Races de Bétail classe les races les plus menacées. Néanmoins, malgré l’intérêt porté au futur de la race, une étude génétique exhaustive n’a pas encore été menée. Les données généalogiques de 85 671 chevaux Shire nés entre 1806 et 2011 ont été utilisées pour déterminer la variabilité génétique actuelle et historique de la race équine Shire depuis l’arrivée aux États-Unis des premiers animaux importés du Royaume-Uni. À partir de cette base de données, une population de référence de 1152 animaux a été créée pour représenter la génération la plus actuelle. La taille effective de la population a été de 330,5, avec 832 fondateurs au total et une généalogie assez complète (98,2 pour cent) jusqu’à cinq générations. Le nombre effectif de fondateurs, d’ancêtres et de génomes a été de 104,5, 28,6 et 13,9, respectivement. Le coefficient moyen de consanguinité a été de 2,4 pour cent pour l’ensemble de la généalogie et de 1,3 pour cent pour les cinq générations les plus récentes. L’analyse démographique a aussi révélé un goulot d’étranglement génétique dans la population dans les années 50 du XXème siècle. Les dix ancêtres mâles et femelles les plus influents ont apporté, respectivement, le 48,5 et 11,6 pour cent de la population de référence, et seulement trois étalons fondateurs sont responsables du 95,6 pour cent de toutes les lignées paternelles de la génération actuelle. Bien que la présente évaluation de la variabilité génétique laisse entrevoir que la population est relativement saine, le petit nombre d’animaux reproducteurs, les faibles taux de naissances et l’augmentation continue des coefficients de consanguinité situent la race équine Shire Américain dans un état de risque, comme quoi des stratégies de conservation devraient être prises en considération.

Mots-clés: *consanguinité, analyse généalogique, diversité génétique, conservation des races, cheval*

Resumen

La raza equina Shire Americano está actualmente catalogada como raza en situación crítica. La Asociación Americana para la Conservación de las Razas de Ganado clasifica así a las razas que se hallan más amenazadas. Pese al interés puesto en el futuro de la raza, no se ha llevado todavía a cabo un análisis genético exhaustivo de la raza. Se usaron los datos genealógicos de 85 671 caballos Shire, nacidos entre 1806 y 2011, para determinar la variabilidad genética actual e histórica del caballo Shire desde la llegada a Estados Unidos de los primeros animales importados del Reino Unido. A partir de esta base de datos, se definió una población de referencia más pequeña (1 152 animales) como representación de la generación más actual. El tamaño efectivo de la población fue de 330,5, con 832 fundadores totales y una alta compleción del pedigrí (98,2 por ciento) hasta cinco generaciones. El número efectivo de fundadores, de ancestros y de genomas fue de 104,5, 28,6 y 13,9, respectivamente. El coeficiente medio de endogamia fue del 2,4 por ciento para datos genealógicos completos y de 1,3 por ciento cuando se consideraron las cinco generaciones más recientes. El análisis demográfico también sacó a la luz un cuello de botella en la población en los años 50 del siglo XX. Los diez ancestros machos y hembras más

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influyentes aportaron, respectivamente, el 48,5 por ciento y el 11,6 por ciento de la población de referencia, y sólo tres machos fundadores son responsables del 95,6 por ciento de todas las líneas paternas de la generación actual. Si bien la presente evaluación de la variabilidad genética indica que la población está relativamente sana, el pequeño número de animales reproductores, las bajas tasas de natalidad y el continuo aumento de los coeficientes de consanguinidad hacen que el caballo Shire Americano se encuentre en una situación de riesgo y que se deban considerar estrategias para su conservación.

Palabras clave: *endogamia, análisis de genealogía, diversidad genética, conservación de razas, caballo*

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Introduction

The Shire (Figure 1) is known as the largest of all horse breeds, standing up to 2 m (19.2 hands) tall at the shoulder (ALBC, 2012a). Originating in England, the breed descends from “The Great Horse”, a heavy horse developed for medieval warfare. Later bred as a general-purpose agricultural and urban draught horse, the average Shire horse weighs about 910 kg and can pull a 4 500 kg load.

Shire horses played a key role in early American history. In the early nineteenth century, 80 percent of Americans lived on farms. Draft horses were in high demand, replacing oxen in terms of agricultural efficiency and general draught power. To satisfy demand for quality heavy horses, agents were sent to France, the Netherlands and the United Kingdom to purchase pedigreed stock (Moore-Colyer, 2000). Shire horses were first introduced to the United States in the mid-1800s, and the American Shire Horse Association (ASHA) was established in 1885 to oversee registration of animals, genetic preservation and breed promotion. The registry has been active continuously except for the period between 1955 and 1961, when most breeding activity ceased and the Shire horse nearly became extinct in the United States. Although some Shires are still used as agricultural or urban work horses or in promotional hitches for breweries and other commercial businesses, the widespread mechanization of the early twentieth century and subsequent urbanization of rural farmland has resulted in a worldwide drop in Shire numbers and a shift to more recreational uses for the breed. Today, the American Livestock Breeds Conservancy has assigned the American Shire horse “critical” status, its most serious threat category reserved for populations with less than 200 new registrations annually in the United States, and an estimated global population of less than 2 000 animals (ALBC, 2012b).

Despite concern for the breed’s future in the United States, however, no assessment of population history or genetic variability has been completed to date. Such data are critical to allow for determination of breed conservation strategies and metrics of success once genetic management programmes are implemented. Therefore, the objective of this study was to evaluate current and historic levels and inbreeding, population demographics, and the number and contributions of ancestors and founders to the American Shire horse population.

Materials and methods

Pedigree information was obtained from the World Wide Shire Studbook (www.shirestudbook.com), an online database created in a joint effort between the AHSA, the Canadian Shire Horse Association, and the Shire Horse Society, the Shire horse organization for the United Kingdom. Animal ($n = 86$ 494) data included sire, dam, animal registration number, birth date and gender. After edits and corrections, the dataset included 85 767 horses born between 1806 and 2011 registered in the American and/or English studbooks. From this dataset, a reference population including only American horses of the most current generation (2003–2011) was defined ($n = 1$ 142). Pedigrees of these animals were traced as far back as possible ($n = 4$ 718 ancestors), with founders defined as animals with both parents unknown.

Population descriptive statistics were calculated using SAS/STAT software version 9.2 (SAS Inst., Cary, NC). Pedigree completeness, complete generation equivalents, length and number of generation intervals, inbreeding coefficients, effective population size and effective number of founders, ancestors and founder genomes were calculated using PEDIG software (Boichard, 2002) as previously described by Bhatnagar, East and Splan (2011). Total and marginal contributions of ancestors were also calculated for influential males and females. Finally, contributions of founder males to contemporary sire lines were determined by tracing the paternal lineages of all animals at 10-year intervals from 1922 to 2011.

Results

Generation intervals were calculated for stallion–daughter, stallion–son, mare–daughter and mare–son pathways (Boichard, 2002). Values were not significantly different among pathways (range 8.27–9.04) and the average generation interval was determined to be 8.65 years. This value was used to determine which years to include in the reference population (i.e. 2003–2011), representing the most current generation of American Shire horses.

Estimates of genetic variability depend largely on the amount of available pedigree information, which may be measured via pedigree completeness. Within the total Shire horse population, pedigree completeness peaks at

Figure 1. Shire horses working on an agricultural plot in Ohio. Photo by Emily Cullison. Used with permission.

90 percent in the first generation and then steadily decreases as more generations are included (Figure 2). In contrast, pedigree completeness for the reference population remains near 100 percent for five generations before it begins to decline. Maximal pedigree depth extended to 19 generations in contemporary animals. The average complete generation equivalent for the reference population was 9.12, and was 8.22 for the total population.

Demographic data for American-registered horses are shown in Figure 3. Animal numbers rose in the late 1930s before falling to less than five registered animals born per year between 1952 and 1957. Recovery was slow but animal numbers increased linearly between 1970 and 2000, and peaked in 2004 with more than 175 registered and domestically bred foals born that year. Figure 4 illustrates the number of Shire horses in the reference population database by year of birth, sex and percent imported stock, and indicates that the majority of horses in the pedigrees of the reference population were imported. Only after 1990 does the percentage of imported horses drop below 50 percent.

Average inbreeding coefficients were 2.4 percent considering all available generations, and 1.3 percent when only

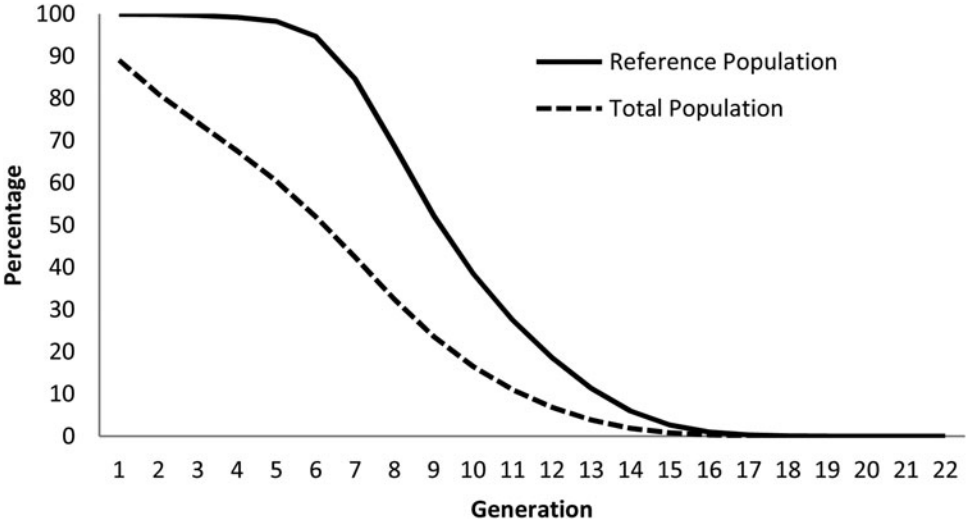

Figure 2. Average percent of pedigree completeness for the total and reference populations.

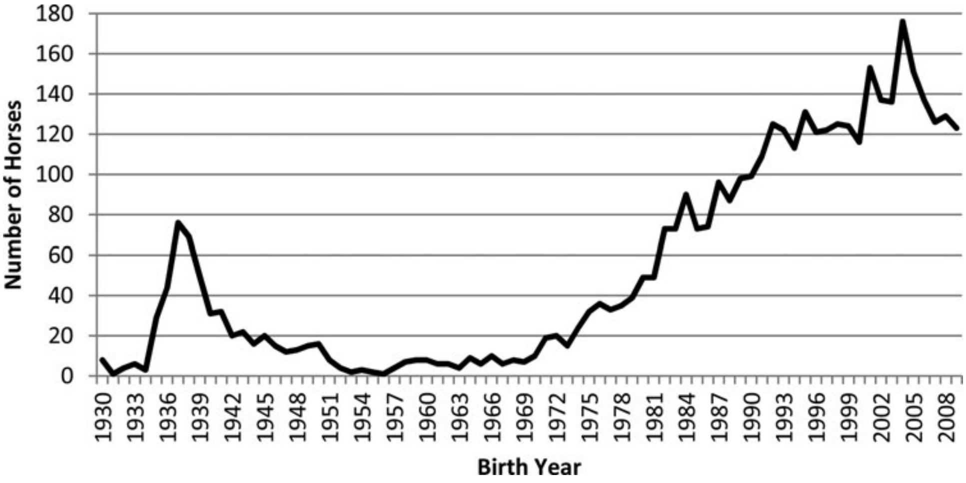

Figure 3. Number of domestically bred horses appearing in the American Shire Horse studbook, by birth year.

the most recent five generations were considered (Figure 5). With the reference population, representing the most recent generation, average inbreeding was 4.0 percent. Non-zero inbreeding coefficients were found for 71.7 percent of horses. Considering all pedigree information, inbreeding levels remained under 1 percent until the bottleneck of the 1950s, and have risen steadily afterward. Despite a short lag period, a lower value, but a very similar trend, is seen when only the last five generations are used, with identical peaks and troughs from 1992-on.

Table 1 summarizes results from pedigree analysis of the Shire horse reference population. The ten most influential male and female ancestors, along with their respective marginal and total contributions to the reference population, and number of progeny, are shown in Table 2. Together, the top ten stallions accounted for nearly half (48.5 percent) of the male influence on modern day pedigrees, while the top ten mares accounted for only an 11.6 percent contribution. Investigation into paternal lineages revealed only six sire lines present in the current

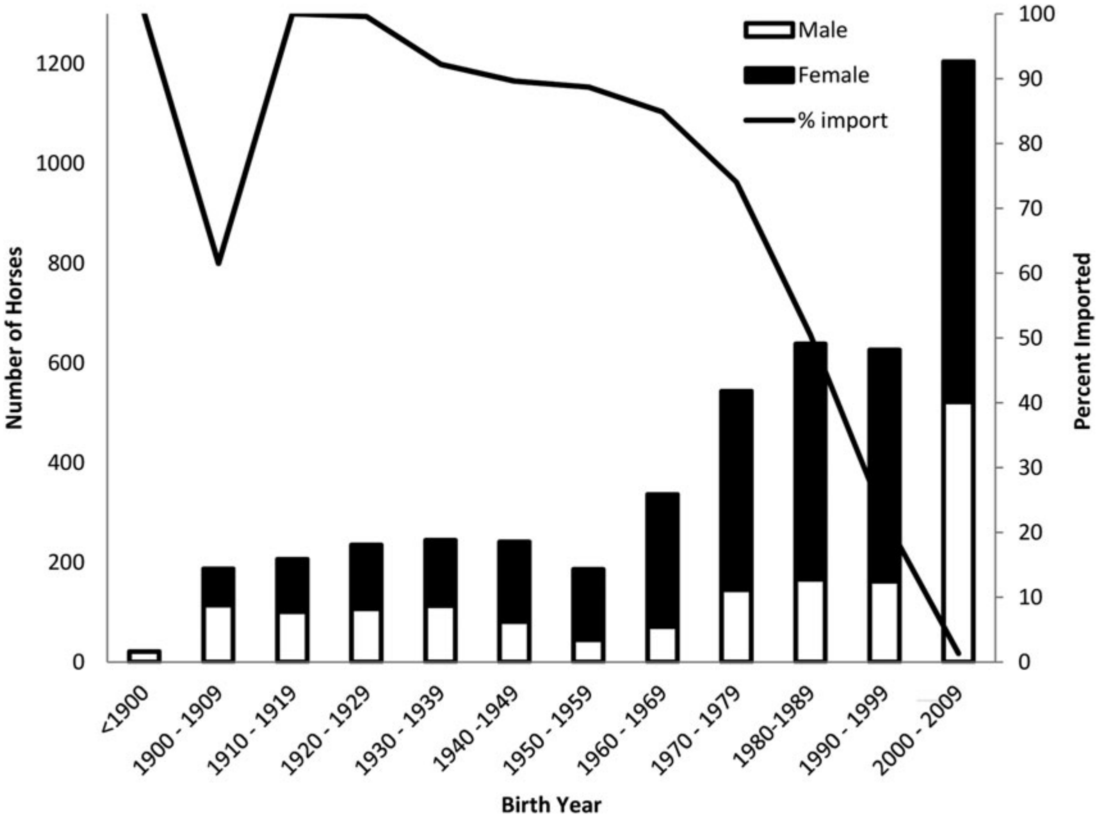

Figure 4. Number of Shire horses in reference population database by year of birth, sex and percent imported stock.

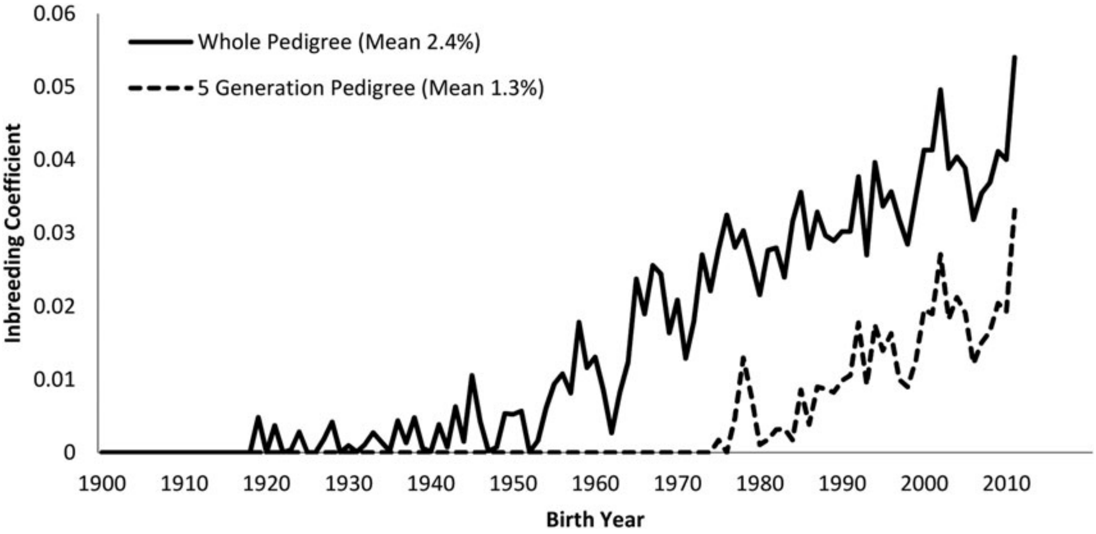

Figure 5. Average inbreeding coefficients by year of birth when tracing five generations or when using the entire available pedigree of the reference population.

generation, with 96 percent of horses tracing to just three foundation sires (Figure 6).

Discussion

Population demographics reported here are consistent with the widely accepted history of the breed as it developed in the United States (ASHA, 2012). Most early foundation stock was imported between 1880 and 1918. After World War I, imports for Shires and other draft horses dropped drastically. Despite an initial rise in domestically bred horses in the 1930s, numbers fell through the 1940s and 1950s, as increasing mechanization reduced the usage of heavy horses in agricultural and urban sectors. In 1955, it is reported that there were less than 50 Shire horses in the entire United States (ASHA, 2012). During this time, the registry became inactive, reopening six years later in 1961. After this bottleneck event, numbers rose steadily during the last three decades of the twentieth century before reaching a peak in 2004. The percentage of imported horses contributing to the reference population dataset, which represents all domestically born animals in the most current generation as well as their ancestors, remained high until the 1970s.

Table 1. Summary of pedigree analysis for the American Shire horse reference population.

Parameter	
Average inbreeding coefficient, whole pedigree, %	2.4
Average inbreeding coefficient, five-generation pedigree, %	1.3
Reference population size, *n*	1 152
Effective population size, *n*	303.5
Total founders, *n*	832
Effective founders, *n*	104.5
Effective ancestors, *n*	28.6
Effective genomes, *n*	13.9
Ancestors explaining 50% of gene pool, *n*	11
Ancestors explaining 75% of gene pool, *n*	31
Ancestors explaining 80% of gene pool, *n*	39
Ancestors explaining 90% of gene pool, *n*	50
Gene pool explained by 100 ancestors, %	94.8

Measures of genetic variability based on studbook records rely heavily on pedigree completeness. Lack of complete pedigree information can result in underestimation of inbreeding coefficients and incorrect assignment of influence to founders and ancestors (MacCluer *et al.*, 1983; Teegan, Edel and Thaller, 2008). Pedigree completeness among the American Shire breed was similar to that found in other horse populations (Aberle, Wrede and Distl, 2004; Valera *et al.*, 2005; Hamann and Distl, 2008; Olsen *et al.*, 2010; Bhatnagar, East and Splan, 2011). The average complete generation equivalent found for the American Shire horse population (8.22) is similar to that reported for Andalusian horses (8.26; Valera *et al.*, 2005) and German Hanoverian horses (8.34; Hamann and Distl, 2008), but much lower than values described for the Lipizzan horse (15.22; Zechner *et al.*, 2002). Generation interval for the Shire horse was similar to the 10-year span that has been reported for many horse breeds (Moureaux *et al.*, 1996; Bhatnagar, East and Splan, 2011; Schurink, Arts and Ducro, 2012; Vicente, Carolino and Gama, 2012). Longer generation intervals are often present in breeds with an extensive evaluation or a breeding approval process, while shorter generation intervals may be seen in populations with the heavy use of artificial insemination.

The mean coefficient of inbreeding remained low until the bottleneck of the mid-1950s, and then began to rise. The clear lag and parallel rate in increase of inbreeding coefficients based on five-generation pedigrees indicates that higher levels of inbreeding have occurred in recent generations. This is consistent with the marked rise in animal numbers and steep drop in the number of imported horses

Table 2. Total and marginal genetic contribution (percent) for the most influential ten male and female ancestors in the American Shire horse reference population.

Ancestor	Birth year	Total contribution	Marginal	
			Contribution	No. of progeny
Stallion				
His Excellency	1941	11.76	11.76	19
Crossfields Supreme	1959	6.15	6.15	37
Newton Fields Ambassador	1945	5.49	5.49	13
Ratby Majestic	1950	5.10	5.10	12
Hainton Warrant	1964	5.59	4.19	36
Grange Wood Clifford What's Wanted	1948	4.19	4.19	10
Hillmoor Enterprise	1970	4.57	3.14	36
Alneland Delegate	1959	3.13	3.13	26
Snelson Magnus	1990	4.08	2.98	17
Alneland Masterpiece	1966	3.13	2.35	10
Mare				
Carr House Flower	1939	2.66	2.10	4
Princess Anne	1950	2.04	1.99	3
Wingerworth Sunset	1960	1.88	1.41	2
Dawn	1965	1.11	0.85	3
Tannis Camrose	1949	0.85	0.85	2
Quixhill Bess	1953	0.94	0.84	1
Tanatside Grey Lady	1954	0.82	0.82	5
Culcliffe Nickel Coin	1950	1.29	0.78	4
Boothay Princess	1955	1.05	0.71	2
Trusley Brooktulip	1963	1.72	0.65	2
Edingale Lady in White	1971	1.45	0.63	1

within the last 30 years. Although the mean inbreeding level for the reference population is fairly low (3.4 percent), more than 15 percent of animals have an inbreeding coefficient greater than 10 percent, with some as high as 33 percent. The similar rates of ascent in inbreeding between full- and five-generation pedigrees also indicate there have been no recent practices implemented to curb inbreeding in the population. Recent analysis of the Norwegian Fjord horse in North America, a breed with similar population structure and inbreeding levels, revealed that introgression of foreign stock and registry mandates prohibiting parent–offspring and sibling-to-sibling matings, resulted in a drop and stabilization of inbreeding levels within the modern-day population (Bhatnagar, East and Splan, 2011).

Inbreeding levels in the English or American Shire horse have not been previously reported in the literature, but values for the American Shire horse calculated in this study were comparable to those reported for similarly sized populations of draught-bred horses, such as the North American Norwegian Fjord Horse (4.3 percent; Bhatnagar, East and Splan, 2011), the Swiss Franches-Montagnes (6.0 percent; Poncet *et al.*, 2006) and the Austrian Noriker (5.0 percent; Druml, Baumung and Sölkner, 2009). Higher inbreeding levels are reported for closed populations with deeper populations (e.g. 12.5 percent for the thoroughbred; Cunningham *et al.*, 2001 and 8.6–14.4 percent for the Lipizzan; Zechner *et al.*, 2002) and/or smaller effective population sizes (e.g. 36.9 percent for the Sorraia; Luis, Cothran and Oom, 2007). Lower average inbreeding coefficients are calculated for breeds that continually allow introgression of new genes from outside populations (e.g. 1.4 percent for the Hanoverian; Hamann and Distl, 2008).

Effective population size was 28.7 percent of the total reference population, indicating unequal representation of the breeding stock during breed formation. The effective number of founders, which is equivalent to the number of equally contributing founders expected to produce the same genetic diversity as the population under study, is a measure of loss of genetic variability from unequal founder contributions. In the Shire horse reference population, the total number of founders was 832, while the effective number of founders was 104.5 or 12.6 percent of total founders. This is similar to that reported for the French Arabian Horse (135; Moureaux *et al.*, 1996), Noriker draft horses (117.2; Druml, Baumung and Sölkner, 2009) and North American Norwegian Fjord horse (96; Bhatnagar, East and Splan, 2011), but smaller than that calculated for Selle Francais horses (333; Moureaux *et al.*, 1996) and larger than published values for the Andalusian (39.6; Valera *et al.*, 2005), the Spanish Arabian horse (38.6; Cervantes *et al.*, 2008) and the Thoroughbred (28; Cunningham *et al.*, 2001). The effective number of ancestors was 28.6, similar to that reported for North American Norwegian Fjord (30; Bhatnagar, East and Splan, 2011) and Noriker draught (29.3; Druml, Baumung and Sölkner, 2009) and Lipizzan horses (26.2; Zechner *et al.*, 2002). The high ratio of f_e/f_a (3.7) reveals disproportionate use of some breeding animals, presumably stallions, resulting in loss of genetic diversity relative to that expected under random mating conditions. This is consistent with the high marginal and total contributions for several of the influential stallions in the breed (e.g. His Excellency) and the known bottleneck that occurred during the mid-1950s. This ratio was higher than that reported for several breeds of similar pedigree structure and inbreeding levels (Druml, Baumung and Sölkner, 2009; Bhatnagar, East and Splan, 2011).

Within the American population of Shire horses, only six sirelines are present in the current generation. Of these lines, three foundation stallions account for 95.6 percent of the modern day paternal lineages. Champion's Clansman (*ca.* 1900) represents the highest contribution

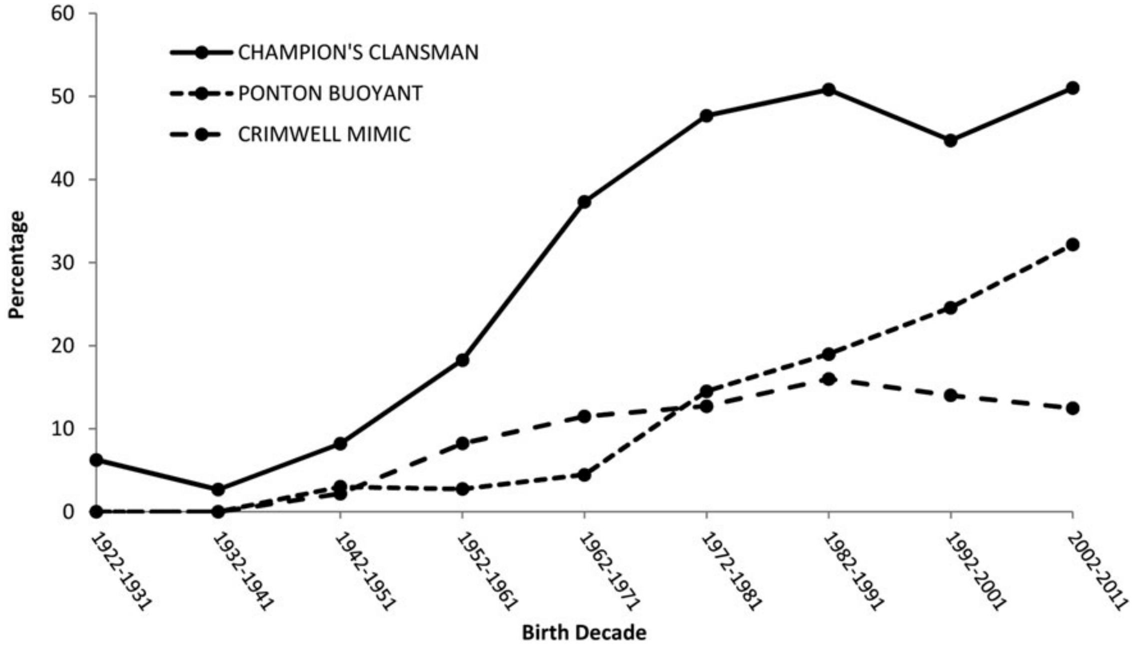

Figure 6. Contributions of top three male founders to paternal lineages, representing 96 percent of modern-day sirelines.

at 51 percent, while Ponton Buoyant (1939) and Crimwell Mimic (1936) contribute 32.2 percent and 12.5 percent, respectively. In most well-established breeds, a small number of sirelines can be found, with one sireline representing the majority of pedigrees (Cunningham *et al.*, 2001; Cervantes *et al.*, 2008). In modern-day thoroughbreds, with pedigree records tracing to the mid-1600s, only three sirelines remain, with 95 percent of all horses tracing to one Y-chromosome source (Cunningham *et al.*, 2001). In a more recent analysis of the Lusitano horse, nine paternal lineages were identified in the current generation, with two sires contributing to 95 percent of these sirelines (Cervantes *et al.*, 2008).

Conclusions

Current measures of genetic variability for the American Shire horse indicate that although the breed is not in immediate danger, conservation strategies should be developed and implemented to prevent further loss of genetic diversity. Small effective population size, unequal contributions of founders, low effective numbers of founders and ancestors, and a high ratio of the two parameters provides evidence that the breed has undergone loss of genetic variability over time beyond that expected from a random genetic drift. In addition, an increase in the number of foals born annually and the subsequent reduction in the use of an imported breeding stock have fuelled a linear rise in inbreeding coefficients in recent years. Thus, while current levels of inbreeding are not particularly high compared with several other closed breed populations, there is valid concern for reduction of genetic variability in future generations. The registry may wish to consider prohibiting mating of close relatives or incentives for breeders who utilize the breeding stock from less popular strains. In addition, steps may be taken to help educate breeders in methods that will minimize inbreeding and help maintain a broad genetic base for the breed. Careful and deliberate intervention, along with vigilant evaluation of conservation strategies, will allow the American Shire horse to maintain a genetically vibrant population.

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Morphological characterization of indigenous sheep in Southern Regional State, Ethiopia

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Summary

Information on morphological characteristics is a prerequisite to sustainable breed improvement, utilization and conservation. The present study was initiated to describe the physical and morphological characteristics of indigenous sheep reared in Sidama-Gedeo, Kembata Tembaro-Hadiya, Gurage-Silte, Gamogofa and Wolaita zones of Southern Regional State of Ethiopia. Data on the assessment of qualitative characters and linear body measurements were obtained from a total of 3966 sheep that were drawn from 928 households. The results indicated that the most common tail form in the Sidama-Gedeo, Kembata Tembaro-Hadiya, Gurage-Silte and Wolaita sheep was of long fat type ending with a straight tip, whereas that of Gamogofa sheep was long thin tail ending with a curve tip. Hair coat colour pattern was mainly plain followed by patchy. The common hair of sheep in all studied zones was short and smooth. Sheep from Sidama-Gedeo, Kembata Tembaro-Hadiya and Gurage-Silte were devoid of wattle and ruff. Rams of Gurage-Silte and Wolaita had higher ($P < 0.05$) body weight values than those of other locations. Ewes of Sidama-Gedeo and Wolaita had relatively high ($P < 0.05$) body weight, whereas those of Gurage-Silte, Gamogofa and Wolaita had significantly high chest girth values. Gurage-Silte and Gamogofa rams had large ($P < 0.05$) chest girth values. The height at withers was high ($P < 0.05$) for both sexes in Sidama-Gedeo, Kembata Tembaro-Hadiya and Wolaita sheep. The highest body length was obtained from Wolaita rams, followed by Gamogofa and Kembata Tembaro-Hadiya rams, whereas the lowest body length was obtained from Gurage-Silte rams. Ewes of Sidama-Gedeo had higher ($P < 0.05$) body length values than those of other zones. The dendrogram indicated a close association among the sheep of Kembata Tembaro-Hadiya, Gurage-Silte and Sidama-Gedeo. However, sheep in Wolaita and Gamogofa were more distantly associated with those of the three zones. It can be concluded that the sheep in the study zones may possess unique adaptive features useful in designing sustainable sheep improvement strategies. However, a molecular-based genetic assessment of the population structure found in the study region might be given due consideration.

Keywords: *phenotypic characterization, qualitative character, linear body measurement, indigenous sheep, Southern Regional State of Ethiopia*

Resumen

Disponer de información sobre los caracteres morfológicos es un prerrequisito para la mejora, utilización y conservación sostenible de las razas. El presente estudio se inició con el fin de describir las características físicas y morfológicas del ganado ovino autóctono criado en las zonas de Sidama-Gedeo, Kembata Tembaro-Hadiya, Gurage-Silte, Gamo-Gofa y Wolayta en la Región Pueblos del Sur de Etiopía. Para la determinación de los caracteres cualitativos y de las medidas corporales lineales, se recogieron datos de un total de 3966 animales procedentes de 928 hogares. Los resultados indicaron que la forma más común de cola en las ovejas de las zonas de Sidama-Gedeo, Kembata Tembaro-Hadiya, Gurage-Silte y Wolayta fue una cola larga de tipo graso terminada en una punta recta mientras que la forma de cola más común en las ovejas de Gamo-Gofa fue una cola larga y estrecha terminada en una punta curva. El patrón de color del pelaje fue principalmente uniforme seguido de patrones moteados. En todas las zonas estudiadas, el pelo de las ovejas fue comúnmente corto y liso. Las ovejas de Sidama-Gedeo, Kembata Tembaro-Hadiya y Gurage-Silte estuvieron desprovistas de mamellas y de melena en el cuello. Los carneros de Gurage-Silte y Wolayta tuvieron un peso corporal mayor ($P < 0.05$) que los de otras zonas. Las ovejas de Sidama-Gedeo y Wolayta tuvieron un peso corporal comparativamente mayor ($P < 0.05$) mientras que las de Gurage-Silte, Gamo-Gofa y Wolayta presentaron una mayor circunferencia pectoral. Los carneros de Gurage-Silte y Gamo-Gofa tuvieron unos valores de circunferencia pectoral elevados ($P < 0.05$). La altura a la cruz fue mayor ($P < 0.05$) para ambos sexos en el ganado de Sidama-Gedeo, Kembata Tembaro-Hadiya y Wolayta. La mayor longitud corporal se obtuvo en los carneros Wolayta, seguidos por los de Gamo-Gofa y Kembata Tembaro-Hadiya, mientras que la menor fue la de los carneros de Gurage-Silte. Las ovejas de Sidama-Gedeo tuvieron mayores ($P < 0.05$) longitudes corporales que las de otras zonas. El dendograma indicó una vinculación cercana entre las ovejas de Kembata Tembaro-Hadiya, Gurage-Silte y Sidama-Gedeo. No obstante, la vinculación de las ovejas de estas tres zonas con las ovejas de Wolayta y Gamo-Gofa fue más lejana. Se puede concluir que las ovejas de las zonas de estudio podrían poseer rasgos adaptativos únicos, útiles para el diseño de estrategias sostenibles de mejora del ganado

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ovino. Sin embargo, se debe considerar detenidamente una evaluación genética, con base molecular, de la estructura poblacional encontrada en el área de estudio.

Palabras clave: *caracterización fenotípica, carácter cualitativo, medida corporal lineal, ganado ovino autóctono, Región de los Pueblos del Sur de Etiopía*

Résumé

Disposer d'information sur les caractéristiques morphologiques est un prérequis pour l'amélioration, l'utilisation et la conservation durables des races. La présente étude a été entamée dans le but de décrire les caractéristiques physiques et morphologiques des ovins indigènes élevés dans les zones de Sidama-Gedeo, Kembata Tembaro-Hadiya, Gurage-Silte, Gamu-Gofa et Wolayta dans la Région des Peuples du Sud en Éthiopie. Les données utilisées pour la détermination des caractères qualitatifs et les mesures corporelles linéaires furent obtenues sur un total de 3966 moutons provenant de 928 ménages. Les résultats ont indiqué que la forme la plus commune de queue chez les moutons des zones de Sidama-Gedeo, Kembata Tembaro-Hadiya, Gurage-Silte et Wolayta a été une queue longue et grasse terminant en une pointe droite alors que la queue des moutons du Gamu-Gofa a été une queue longue et fine terminant en une pointe courbe. Le patron des couleurs du pelage a été principalement uniforme suivi de dessins tachetés. Dans toutes les zones d'étude, le pelage des moutons a été généralement court et lisse. Les moutons de Sidama-Gedeo, Kembata Tembaro-Hadiya et Gurage-Silte n'ont présenté ni de pendeloques ni de crinière sur le cou. Les béliers de Gurage-Silte et Wolayta ont eu un poids corporel plus élevé ($P < 0.05$) que ceux d'autres zones. Les brebis de Sidama-Gedeo et Wolayta ont eu un poids corporel relativement élevé ($P < 0.05$) alors que celles de Gurage-Silte, Gamu-Gofa et Wolayta ont présenté une plus grande circonférence pectorale. Les béliers de Gurage-Silte et Gamu-Gofa ont eu des valeurs de circonférence pectorale élevées ($P < 0.05$). Pour les deux sexes, la hauteur au garrot a été élevée ($P < 0.05$) chez les moutons de Sidama-Gedeo, Kembata Tembaro-Hadiya et Wolayta. La plus grande longitude corporelle a été reportée chez les béliers Wolayta, suivis par les béliers de Gamu-Gofa et Kembata Tembaro-Hadiya, alors que la plus courte a été celle des béliers de Gurage-Silte. Les brebis de Sidama-Gedeo ont présenté des valeurs de longitude corporelle plus élevées ($P < 0.05$) que celles des autres zones. Le dendrogramme a indiqué un lien étroit entre les moutons de Kembata Tembaro-Hadiya, Gurage-Silte et Sidama-Gedeo. Toutefois, le lien entre les ovins de ces trois zones et ceux de Wolayta et Gamu-Gofa a été plus faible. Il peut être conclu que les ovins des zones d'étude semblent posséder des caractéristiques adaptatives uniques, utiles à la conception de stratégies durables d'amélioration des ovins. Cependant, une évaluation génétique, à base moléculaire, de la structure de la population trouvée dans la zone d'étude reste à être prise en considération.

Mots-clés: *caractérisation phénotypique, caractère qualitatif, mesure corporelle linéaire, ovins indigènes, Région des Peuples du Sud d'Éthiopie*

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Introduction

Adapted indigenous animal genetic resources provide sustainable options to smallholder livestock production in developing countries. However, about a third of the recorded animal genetic resources globally are at high risk of loss (FAO, 2007), whereas the genetic potential of these livestock populations for further improvement remains largely unknown. There is therefore an urgent need to characterize these genetic resources, to quantify differentiation and to examine relationships between existing breeds in order to design rational breeding programme for conservation and sustainable utilization.

Ethiopia is believed to be one of the major gateways for domestic sheep migration from Asia into Africa (Devendra and McLeroy, 1982). With 25.5 million sheep (CSA, 2011) and 14 traditional populations (Gizaw *et al.,* 2007, 2008), there are highly diversified indigenous sheep types which are parallel to the diversity in ecology (Galal, 1983), ethnic communities and production systems in the country. The livestock in general and sheep in particular are valuable genetic resources adapted to the harsh climatic conditions of the country, resistant and/or tolerant to a wide range of parasites and diseases and have the ability to efficiently utilize limited feed resources (Galal, 1983; Tibbo, 2006; Gizaw *et al.,* 2007). They support regular income in both tangible and/or intangible manners to a large human population through the sale of live animals and skins (Abebe, Kannan and Goetsch, 2010). They are also considered as living bank against the various environmental calamities (crop failure, drought and flooding) and have socio-cultural values for diverse traditional communities (Edea *et al.,* 2010). The most important traits of sheep for livestock keepers in most tropical countries including Ethiopia are body size and conformation, fertility and prolificacy, survivability and early maturity.

Sheep types in Ethiopia as observed by Gizaw (2008) are highly affiliated to specific ethnic communities. Several traditional sheep types are reared by and named after specific communities. Sheep reared by a community may be isolated from other types because of isolation of communities or traditional cultural barriers. Some communities attach special cultural values to their sheep and exclude the use of breeding stock from other populations, resulting in cultural barrier to gene flow (Gizaw *et al.,* 2007).

Information on morphological characteristics is a prerequisite to sustainable breed improvement, utilization and conservation (FAO, 2012). This is also a prelude to community-based breeding strategies which warrant that the breeds have to be well studied beforehand, and traits, which make them unique, be characterized both at phenotypic and genetic levels. The identification and proper use of local sheep types will further contribute to improved food security of the developing countries by reducing the pressure on the environment and provide a long term and sustainable source of income and thereby arresting migration of human population to the urban areas.

Recent studies indicated that the current population/genetic structure in Ethiopian sheep is strongly associated with historical patterns of sheep migration, geographic isolation and interbreeding, whereas morphological diversity follows ecological patterns (Gizaw *et al.,* 2007). Southern Nations and Nationalities Regional State of Ethiopia with its approximately 4.5 million sheep population (CSA, 2011) and its great variation in climate and topography as well as multi-ethnic diversity, represents a good reservoir of sheep genotypes.

Information available on Ethiopian sheep types is not only scarce but also limited to already known specific sheep types involving on-station managed flocks with major emphasis on body weight and related measurements. Previous physical and morphological studies were also limited in their scope as they were concentrated only on a few commonly recognized indigenous sheep types such as Horro, Menz, Afar and Bonga and/or are based on few animals (Galal, 1983; Awgichew, 2000; Abegaz *et al.,* 2002; Lemma, 2002; Getachew *et al.,* 2010; Edea *et al.,* 2010), which hardly represent the sheep types found in the whole country in general and in Southern Nations and Nationalities Regional State of Ethiopia in particular. A more comprehensive morphological and molecular characterization study was conducted by Gizaw *et al.* (2007, 2008) using 14 sheep populations that were traditionally recognized, phenotypically distinct, and/or geographically/ecologically isolated populations. However, except for the Adilo and Bonga sheep types, the sheep populations from the Southern Nations and Nationalities Regional State of Ethiopia were grossly unrepresented in this particular study. Moreover, very few sheep samples consisting of only ewe populations were used for the quantification of qualitative characters and quantitative morphometrical traits (Gizaw *et al.,* 2008). The present study was thus initiated to bridge the gap left behind from the previous studies and thus describes the physical and morphological characteristics of indigenous sheep types found in eight administrative zones of Southern Nations and Nationalities Regional State of Ethiopia.

Materials and methods

Description of the study areas and sampling procedure

Contrary to previous studies undertaken by various scholars, in the current study we did not target sheep types traditionally recognized by ethnic and/or geographic nomenclatures, rather we included all sheep types from randomly selected districts of densely populated major administrative zones of the Region. The study was conducted from December 2010 to July 2011 in eight administrative zones of Southern Nations, Nationalities and Peoples Regional State of Ethiopia. Among the eight administrative zones, Sidama and Gedeo, Kembata Tembaro and Hadiya as well as Gurage and Silte were clustered into three and described as Sidama-Gedeo (SIG), Kembata Tembaro-Hadiya (KTH) and Gurage-Silte (GUS) zones, respectively. The clustering was based on their closeness in geographical terrain and similarity in social and cultural values of the human population. The other two administrative zones namely Wolaita (WOL) and Gamogofa (GAG) were not clustered together because of the differences in size and diversity of the environment and the vegetation.

Stepwise purposive selection procedure was carried out in the study area where the districts and the Kebeles (villages) were purposively selected based on the available sheep population in each study zone. This was followed by identification of the households which owned at least four sheep and had prior experience in sheep husbandry. Among the identified households, 180–200 of them were then randomly selected from each zone to obtain the qualitative and quantitative sample data. All the sheep in the sampled households were included in the current study. Information on pertinent environmental variables and sheep types of the studied zones and districts is presented in Table 1.

Data collection procedures

Morphological characterization

Data on the assessment of qualitative characters and quantitative morphometrical traits were obtained from a total of 3966 sheep that were drawn from 928 households. For the assessment of quantitative morphometrical traits, only those aged one year and above were considered for the purpose of uniformed comparison. The FAO (2012) qualitative and quantitative sheep breed descriptor list was followed to characterize the sheep types phenotypically and morphologically.

Qualitative characters: Data on coat colour pattern, coat colour type, hair coat type, tail type, tail form, head profile, ear form, presence and absence of wattle, horn, ruff, and horn shape were observed and recorded for rams and ewes separately.

Quantitative morphometrical characters: They were obtained by a measuring tape calibrated in centimetres

Table 1. Environmental variables and sheep populations of the study locations.

Clustered zones	Districts	Studied sheep number	Altitude (m asl)	Latitude (°N)	Longitude (°E)	Annual avg. max. temp. (°C)	Annual avg. min. temp. (°C)	Annual rainfall (mm)	Total sheep population in the area
Sidama-Gedeo	Hula	237	2809	6.40–6.75	38.46–38.78	19.1	6.2	1425	81 922
	Melga	200	2195	5.14–7.89	35.92–37.14	24.7	11.7	1200	17 441
	Gedeb	222	2245	5.20–6.30	34.4–36.3	21.0	17.0	1443	39 160
	Bule	210	2817	5.80–6.50	32.5–34.0	18.0	10.0	1433	41 400
Kembata Tembaro-Hadiya	Doyogena	199	2629	7.27–7.42	37.88–38.05	20.7	12.1	958	11 220
	Tembaro	198	2116	7.18–7.36	37.35–37.61	25.9	14.0	1012	11 498
	Lemu	199	2306	7.42–7.75	37.80–38.07	23.1	10.8	1137	28 312
	Misha	196	2598	7.51–7.88	37.66–37.92	22.6	9.9	1691	35 271
Gurage-Silte	Enemur-Ener	210	2097	7.80–7.91	37.68–37.80	22.0	19.5	1247	37 303
	Geta	210	2993	7.87–7.96	37.81–37.95	16.0	13.0	984	31 776
	Silte	210	1996	7.99–8.10	37.96–38.10	25.2	10.6	1058	46 788
	Merab Azernet	210	2889	7.43–7.66	37.86–37.90	17.0	14.0	1200	52 756
Gamogofa	Chencha	184	2631	6.13–6.41	37.46–37.65	22.5	12.6	1321	43 562
	Dita	184	2566	6.12–6.39	37.36–37.55	22.5	10.1	1450	44 872
	Bonke	184	2329	5.65–6.19	37.05–37.42	21.2	9.9	1990	128 509
	Gezegofa	184	1600	6.21–6.57	36.67–36.94	25.0	15.1	1500	12 568
Wolaita	Boloso Sore	184	1752	7.98–7.18	37.62–37.83	22.5	17.6	1449	26 928
	Damot Gale	184	2043	6.89–7.11	37.75–37.99	25.1	13.6	1175	25 739
	Sodo Zuria	184	1854	6.72–6.99	37.59–37.86	25.6	14.6	1321	23 457
	Humbo	184	1618	6.50–6.81	37.57–38.04	25.0	17.6	1150	17 520

Source: NMA (2012).

(cm) after restraining and holding the animals in an unforced position. All measurements were taken by the same personnel in each zone while sheep were in an up-right plane during measurement. The following linear body measurements were taken: chest girth, height at withers, shoulder width, pelvic width, body length, ear length, head length, horn length, tail length and circumference, scrotum circumference, canon length and canon circumference. The morphometrical measurements were taken using self devised equipments and according to the methods suggested by Macjowski and Zieba (1982). Body weight was measured using suspended spring balance with 50 kg capacity with ±100 g error margin (for heavier animals) and 25 kg capacity with ±50 g error margin (for lighter ones). The age of animals was estimated using dentition method as suggested by Charray, Humbert and Leif (1992).

Data analysis

Preliminary data analysis such as homogeneity test, normality test and screening of outliers was employed before conducting the main data analysis. Discrete measurements on the form and appearance of the investigated animals were analysed using the frequency procedure of chi-square test.

Body weight and quantitative linear body measurements were analysed using the generalized linear model procedures (SPSS, 2003). Administrative zones were fitted as fixed independent variables, whereas body weight and linear body measurements were fitted as dependent variables. Means were separated using Duncan's multiple range test procedure and values were considered significant at $P < 0.05$. Hierarchical cluster analysis was conducted and dendrogram constructed based on Euclidean distances between populations derived from morphological variables using the unweighted pair-group method to describe morphological clustering pattern of the investigated sheep types. The major quantitative morphometrical variables included in the hierarchical cluster analysis were body weight, chest girth, body length, height at withers, pelvic width and shoulder length of the rams and ewes, in which the data for individual traits were pooled for both sexes within each of the studied zones.

Results

Qualitative characters

The results relating to the qualitative characters in all sheep raised in the five administrative zones are presented in Tables 2–4. Data presented in Table 2 indicate combined results of the major qualitative characters of both sexes. Plain coat colour pattern was observed in all zones with sheep in KTH having significantly ($P < 0.05$) higher proportions than those of SIG, GUS and WOL (Table 2). The sheep in GAG were characterized by having significantly ($P < 0.05$) larger numbers with patchy coat colour pattern than those found in other zones.

As shown in Table 2 and Figure 1a, the brown coat colour with brown dominant type was commonly observed among the sheep reared in SIG. The word 'dominance' indicates that besides the colours mentioned there were patches or spotting of other colours. The most common hair coat colour in KTH sheep was brown dominant followed by white dominant (Figure 1b). The dominant hair coat colour of sheep in GAG was black (33 percent) followed by red (25 percent) (Figure 1c). The red hair coat colour predominates (31 percent) in sheep of WOL (Figure 1d). The commonly observed hair coat colour of sheep in GUS was primarily white followed by red and brown dominant (Figure 1e).

Most of (80 percent and above) the sheep in SIG, GUS, GAG and WOL were characterized by possessing short and smooth hair. The hair of most KTH sheep (62 percent) was short and smooth, whereas the rest was long and coarse. As shown in Figures 1a, b, d and e, the most common tail type and form in SIG, KTH, GUS and WOL sheep were of long fat type ending with a straight tip. However, the tail type of sheep in GAG was dominantly long and thin ending with curve tip form (Figure 1c).

The values of some qualitative characters observed in ewes are presented in Table 3. Proportionately the ewes in SIG, KTH and WOL had higher numbers of straight head profiles, whereas those with concave head profile were observed in large numbers in GAG and GUS. The convex type of head profile predominated only in GUS. In ewes, semi pendulous and horizontal ear forms were the most commonly observed type across the zones. However, about 42 percent ewes in SIG were observed with rudimentary ear form. Most of the ewes in SIG, KTH and GUS were devoid of wattles, whereas the reverse was observed in GAG and WOL (Figure 1a–e). Ruff was grossly absent in most of the zones. Over 60 percent of sheep in GUS and GAG were horned, whereas the polled ewes outnumbered the horned ones in SIG. However, similar proportions of horned and polled ewes were observed in KTH and WOL. Rudimentary horn shapes predominated in SIG and KTH, whereas straight and curved types were mostly observed in GUS.

The average values of some qualitative characters observed in rams are presented in Table 4. About 90 percent of male sheep in KTH and WOL were observed with straight head profile followed by SIG (71 percent) and GAG (67 percent), whereas those with concave profile were predominantly found in GUS (87 percent). High proportions of ear forms oriented horizontally were observed in GUS followed by WOL. The rams with semi-pendulous ear form were mostly observed in KTH (98 percent) followed by GAG, whereas short and rudimentary ear forms were mostly observed in those raised in SIG. Large proportions of rams (over 96 percent) in all zones were devoid of wattles except those in WOL. Ruff was mostly absent in SIG,

Table 2. Percentage values for some phenotypic qualitative traits observed in sheep populations ($N = 3966$).

Traits	SIG ($n = 868$)	KTH ($n = 792$)	GUS ($n = 835$)	GAG ($n = 735$)	WOL ($n = 736$)
Colour pattern					
Plain	55^{b} (477)	75.5^{a} (598)	36^{c} (298)	1^{d} (5)	59^{b} (428)
Patchy	44^{b} (383)	14.5^{d} (115)	44^{b} (367)	99^{a} (730)	29^{c} (217)
Spotted	1^{d} (8)	10^{c} (79)	20^{a} (170)	NR	13^{b} (91)
Colour type					
White	5^{c} (44)	5.3^{c} (42)	14^{b} (116)	11^{b} (79)	20^{a} (149)
Black	10^{b} (91)	5^{c} (38)	7^{b} (56)	33^{a} (240)	5.4^{c} (40)
Red	NR	12.2^{c} (97)	10^{d} (86)	25.0^{b} (183)	31^{a} (227)
Brown	27^{a} (233)	12^{b} (94)	1.1^{e} (10)	9^{c} (66)	7.2^{d} (53)
Fawn	10^{b} (91)	NR	2.5^{a} (21)	NR	NR
Grey	2.6^{c} (23)	NR	1^{d} (9)	4.2^{b} (41)	9.1^{a} (67)
Roan	NR	NR	3^{a} (26)	NR	0.2^{b} (1)
White dominant	2.3^{d} (20)	19^{a} (150)	16.2^{b} (135)	5.5^{c} (41)	1.0^{e} (6)
Black dominant	17^{a} (147)	NR	16^{a} (133)	4.2^{b} (31)	1.5^{c} (11)
Brown dominant	25^{b} (215)	31.1^{a} (247)	8.5^{c} (71)	2.4^{d} (18)	2^{d} (12)
Fawn dominant	0.5^{b} (4)	NR	1.7^{a} (15)	NR	NR
Red dominant	NR	2.1^{b} (17)	16^{a} (132)	2.2^{b} (15)	19^{a} (140)
Roan dominant	NR	7.9^{a} (63)	2^{b} (14)	2^{b} (14)	2^{b} (15)
Others	NR	5.5^{a} (44)	1.3 (11)	1 (7)	2^{b} (15)
Hair type					
Short and smooth	80^{b} (697)	62^{c} (490)	91^{a} (763)	96.5^{a} (710)	81^{b} (596)
Long and coarse	NR	38^{a} (302)	9^{c} (72)	3.5^{d} (25)	19^{b} (140)
Short and coarse	20 (171)	NR	NR	NR	NR
Tail type					
Short fat	15^{b} (34)	23^{a} (184)	NR	3.2^{c} (24)	2.0^{c} (17)
Long fat	78^{b} (678)	53^{c} (423)	100^{a} (835)	11^{d} (79)	80^{b} (589)
Short thin	0.25^{c} (2)	13^{a} (102)	NR	17^{a} (124)	2.0^{b} (16)
Long thin	2^{d} (19)	10.5^{c} (83)	NR	69^{a} (508)	16^{b} (114)
Docked	16 (135)	NR	NR	NR	NR
Tail form					
Curved tip	16.0^{b} (141)	7^{b} (54)	NR	90^{a} (659)	4.4^{b} (33)
Straight tip	68^{b} (590)	93^{a} (738)	100^{a} (835)	5.0^{c} (38)	95.5^{a} (703)
Blunt	0.2^{b} (2)	NR	NR	5.0^{a} (38)	NR
Docked	15.5 (135)	NR	NR	NR	NR

^{a,b,c,d,e} Indicated values among rows for traits significantly differ at $\chi^2 < 0.05$.

Values in parenthesis indicate number of observations.

NR = not reported; SIG = Sidama-Gedeo; KTH = Kembata Tembaro-Hadiya; GUS = Gurage-Silte; GAG = Gamogofa; WOL = Wolaita.

KTH and GUS. Horn was present in most of the rams across all studied zones with variable proportions ranging from 64 percent to 92 percent. However, about 36 percent of male sheep in GAG were polled. About 61 and 39 percent of the rams in SIG had rudimentary and straight horn shapes, respectively. Most of the rams in KTH and GUS had a curving horn shapes with either upward or downward orientations.

Quantitative morphometrical characters

Rams

As presented in Table 5, significantly ($P < 0.05$) high body weight values were found in rams from GUS and WOL. The chest girth of rams from GUS and GAG was significantly ($P < 0.05$) higher than those from other zones where similar values were observed. The height at withers was similar among rams in SIG, KTH, GUS and WOL, but significantly ($P < 0.05$) higher than those in GAG. Rams in KTH, GAG and WOL had similar body length values being significantly ($P < 0.05$) higher than those in SIG and GUS. Rams reared in SIG, KTH and WOL had significantly ($P < 0.05$) higher pelvic width values than those in GAG and GUS (Table 5). There was also significant ($P < 0.05$) difference between zones for shoulder width in rams, the highest value being observed in those from GAG but the lowest from sheep KTH.

The values of cannon length indicated significant ($P < 0.05$) differences among the populations in which rams in SIG, KTH and WOL had higher values than those in GAG and GUS. Although the canon circumference did not differ significantly among zones, it was the highest in rams from GUS and GAG, whereas similar values were observed among other zones.

Similar values in head length were observed in rams reared in KTH, GUS, GAG and WOL being significantly ($P < 0.05$) higher than those in SIG. Moreover, there were significant variations in head width in which rams reared in SIG, KTH, GUS and GAG had significantly ($P < 0.05$) higher values than those in WOL.

The tail and ear length values were similar among rams reared in SIG, KTH, GUS and WOL and they were significantly ($P < 0.05$) higher than those observed in SIG. The

Table 3. Percentage values for some phenotypic qualitative characters observed in ewes ($N = 2557$).

Characters	SIG ($n = 610$)	KTH ($n = 573$)	GUS ($n = 555$)	GAG ($n = 185$)	WOL ($n = 634$)
Head profile					
Straight	90^{b} (551)	98.4^{a} (564)	5^{d} (28)	28^{c} (53)	96^{a} (596)
Concave	NR	NR	56^{b} (312)	72^{a} (132)	3.4^{c} (21)
Convex	10^{b} (59)	1.6^{c} (9)	39^{a} (215)	0	2.7^{c} (17)
Ear form					
Erect	NR	NR	NR	17^{a} (32)	3.4^{b} (21)
Horizontal	11^{c} (65)	NR	82^{a} (454)	63^{b} (116)	64^{b} (398)
Semi Pendulous	47.5^{b} (290)	99^{a} (566)	18^{d} (101)	20^{d} (37)	34^{c} (210)
Rudimentary	42^{a} (255)	1^{b} (7)	NR	NR	1^{b} (5)
Wattle					
Present	12^{c} (73)	2.4^{d} (14)	3^{d} (15)	64^{b} (118)	92^{a} (567)
Absent	88^{b} (537)	97.5^{a} (559)	97^{a} (540)	36^{c} (67)	11^{d} (67)
Ruff					
Present	NR	NR	0.3 (2)	NR	NR
Absent	100 (610)	100 (573)	99.7 (553)	NR	NR
Horn					
Present	42.4^{c} (259)	52.5^{b} (301)	62^{a} (344)	64^{a} (119)	52^{b} (322)
Absent	57.6^{a} (351)	47.5^{a} (272)	38^{b} (211)	36^{b} (66)	51^{a} (312)
Horn shape					
Straight	11.5^{b} (30)	15^{b} (48)	34^{a} (119)	NR	NR
Curving upward	NR	29.8^{b} (91)	44^{a} (150)	NR	NR
Curving downward	NR	2.2^{b} (6)	22^{a} (75)	NR	NR
Rudimentary	88.5^{a} (229)	53^{b} (160)	NR	NR	NR

^{a,b,c,d,e} Indicated values among rows for traits significantly differ at $\chi^2 < 0.05$.
Values in parenthesis indicate number of observations.
NR = Not reported; SIG = Sidama-Gedeo; KTH = Kembata Tembaro-Hadiya; GUS = Gurage-Silte; GAG = Gamogofa; WOL = Wolaita.

tail circumference values were the highest in rams from GUS and the lowest in rams from GAG. However, these values were similar among those rams reared in SIG and KTH. The highest horn length values were observed in rams reared in GUS but the lowest in those from SIG. The scrotal circumference in rams from SIG, GUS and

Table 4. Percentage values of some qualitative characters in rams ($N = 1409$).

Characters	SIG ($n = 258$)	KTH ($n = 219$)	GUS ($n = 280$)	GAG ($n = 550$)	WOL ($n = 102$)
Head profile					
Straight	71^{b} (183)	92.3^{a} (202)	0.7^{c} (2)	67^{b} (369)	94^{a} (96)
Concave	NR	NR	87^{a} (244)	33^{b} (181)	5.0^{c} (5)
Convex	29^{a} (75)	7.7^{c} (17)	12^{b} (34)	NR	1^{d} (1)
Ear form					
Erect	NR	NR	NR	16^{a} (90)	0.7^{b} (1)
Horizontal	18^{d} (46)	NR	81^{a} (228)	48^{c} (262)	74^{b} (76)
Semi Pendulous	20^{d} (53)	98.2^{a} (215)	19^{d} (52)	36^{b} (198)	24.5^{c} (25)
Rudimentary	24^{a} (62)	1.8^{b} (4)	NR	NR	NR
Short and inclined	37 (97)	NR	NR	NR	NR
Wattle					
Present	NR	3.1^{b} (7)	2.5^{b} (7)	3^{b} (16)	93^{a} (95)
Absent	100^{a} (258)	96.9^{a} (212)	97.5^{a} (273)	97^{a} (534)	1^{b} (7)
Ruff					
Present	4^{c} (10)	9.6^{b} (21)	13.6^{a} (38)	NR	NR
Absent	96^{a} (248)	90^{a} (198)	86^{b} (242)	NR	NR
Horn					
Present	89^{a} (229)	90^{a} (197)	95^{a} (267)	64^{b} (353)	92^{a} (94)
Absent	11^{b} (29)	10^{b} (22)	5^{d} (13)	36^{a} (197)	8^{c} (8)
Horn shape					
Straight	39^{a} (89)	14^{b} (27)	6^{c} (17)	NR	NR
Curving upward	NR	42 (83)	49 (130)	NR	NR
Curving downward	NR	30^{b} (59)	42^{a} (113)	NR	NR
Rudimentary	61^{a} (140)	14^{b} (28)	3^{c} (7)	NR	NR

^{a,b,c,d,e} Indicated values among rows for traits significantly differ at $\chi^2 < 0.05$.
Values in parenthesis indicate number of observations.
NR = not reported; SIG = Sidama-Gedeo; KTH = Kembata Tembaro-Hadiya; GUS = Gurage-Silte; GAG = Gamogofa; WOL = Wolaita.

Figure 1. Variations in some qualitative traits of indigenous sheep populations found in southern Regional State of Ethiopia. (a) = Sidama-Gedeo female sheep, polled; (b) = Kembata Tembaro-Hadiya male sheep, horned; (c) = Gamogofa female sheep, polled; (d) = Wolaita female sheep, polled; (e, f) = Gurage-Silte sheep flocks, horned.

WOL was significantly ($P < 0.05$) higher than those from other zones.

Ewes

As shown in Table 6, the body weight was significantly ($P < 0.05$) heavier in ewes from SIG and WOL than those from KTH, GUS and GAG, where similar values were recorded. The chest girth values of ewes in GUS, GAG and WOL were similar, but significantly ($P < 0.05$) higher than those in SIG and KTH. Ewes from SIG, KTH and WOL had significantly ($P < 0.05$) higher height at wither values than those from other zones. The highest body length value was obtained from ewes reared in SIG and it was significantly ($P < 0.05$) higher than those in KTH, GAG and WOL which had similar values. The lowest body length was obtained from ewes reared in GUS. In general, male and female sheep in GUS had the lowest body length values.

Ewes in SIG, KTH and WOL had a significantly ($P < 0.05$) high pelvic width value as compared with other zones. The lowest pelvic width value was obtained in ewes reared in GUS. The shoulder width values in ewes from SIG and GAG were significantly ($P < 0.05$) higher than those from KTH, GUS and WOL which exhibited similar values.

The canon length was comparable among ewes in SIG, KTH and WOL, being significantly ($P < 0.05$) higher than those in GUS and GAG which showed similar values. The canon circumference and head length values did not indicate significant difference in ewes reared across all zones.

Ewes from SIG, KTH, GUS and GAG had significantly ($P < 0.05$) higher head width values than those from WOL. The tail length was significantly ($P < 0.05$) higher in ewes raised in GUS and WOL than those in other zones. The values for the tail circumference were significantly ($P < 0.05$) higher in ewes from SIG and GUS than

Table 5. Average values of quantitative morphometrical traits of rams (means ± SD, cm; $N = 1076$).

Morphometrical traits	SIG ($n = 240$)	KTH ($n = 200$)	GUS ($n = 273$)	GAG ($n = 283$)	WOL ($n = 80$)	Overall mean
Body weight (kg)	27.6 ± 2.3^{b}	27.5 ± 6.0^{b}	30.8 ± 4.5^{a}	28.0 ± 4.0^{b}	32.0 ± 5.3^{a}	29.2
Chest girth	72.1 ± 5.4^{b}	71.5 ± 5.7^{b}	76.8 ± 4.6^{a}	75.9 ± 5.6^{a}	73.1 ± 1.5^{b}	74.1
Height at withers	65.5 ± 4.8^{a}	65.8 ± 6.3^{a}	65.7 ± 3.5^{a}	57.1 ± 4.3^{b}	65.4 ± 1.2^{a}	64.0
Body Length	64.0 ± 5.1^{b}	65.8 ± 5.5^{a}	48.6 ± 3.8^{c}	66.4 ± 3.2^{a}	68.8 ± 0.8^{a}	63.0
Pelvic width	16.5 ± 1.1^{a}	15.6 ± 1.9^{a}	11.1 ± 1.7^{c}	14.0 ± 0.9^{b}	15.5 ± 1.1^{a}	14.6
Shoulder width	15.6 ± 1.6^{a}	13.9 ± 1.6^{b}	15.4 ± 1.9^{a}	16.8 ± 1.1^{a}	14.8 ± 0.5^{b}	15.4
Cannon length	14.3 ± 1.6^{a}	14.4 ± 1.7^{a}	12.3 ± 1.5^{b}	13.0 ± 0.6^{b}	14.3 ± 0.5^{a}	14.0
Canon circumference	7.10 ± 0.9	7.30 ± 0.8	8.10 ± 0.7	7.91 ± 0.6	7.10 ± 0.5	7.52
Head width	10.1 ± 1.9^{a}	11.6 ± 1.1^{a}	10.4 ± 1.2^{a}	9.71 ± 0.6^{a}	8.20 ± 0.4^{b}	10.0
Head length	16.1 ± 0.6^{b}	17.0 ± 1.1^{a}	17.6 ± 1.3^{a}	17.0 ± 1.2^{a}	17.7 ± 0.6^{a}	17.1
Tail length	34.8 ± 7.1^{a}	36.0 ± 7.3^{a}	34.5 ± 4.2^{a}	27.9 ± 2.6^{b}	34.6 ± 4.2^{a}	33.5
Tail circumference	25.1 ± 4.6^{a}	25.4 ± 5.0^{a}	26.4 ± 5.4^{a}	16.4 ± 1.5^{b}	19.9 ± 1.3^{b}	22.6
Ear length	10.0 ± 0.8^{a}	10.8 ± 1.3^{a}	11.2 ± 1.5^{a}	8.41 ± 0.7^{b}	10.5 ± 0.5^{a}	10.2
Horn length	10.6 ± 6.1^{c}	20.1 ± 8.5^{a}	22.3 ± 9.4^{a}	12.8 ± 4.9^{bc}	15.8 ± 3.7^{b}	16.3
Scrotum circumference	25.7 ± 1.2^{a}	17.6 ± 4.4^{b}	22.2 ± 5.2^{a}	19.7 ± 3.4^{b}	22.5 ± 3.2^{a}	21.5

^{a,b,c} Means across rows between zones with different superscript letters are significantly ($P < 0.05$) different.
SIG = Sidama-Gedeo; KTH = Kembata, Tembaro-Hadiya; GUS = Gurage-Silte; GAG = Gamogofa; WOL = Wolaita.

those from KTH, GAG and WOL which had similar values. Significantly ($P < 0.05$) high ear length values were observed in ewes from KTH, GUS and WOL as compared with those from SIG and GAG. The study further indicated that the horn length was significantly ($P < 0.05$) higher in the ewe population raised in GUS, GAG and WOL than those in SIG and KTH.

The dendrogram of Figure 2 indicated a close relationship among the sheep reared in KTH, GUS and SIG. However, the sheep in WOL and GAG were distantly associated with those in other three zones.

Discussion

Qualitative characters

This study describes the morphology and phenotypes of sheep found in eight administrative zones of Southern Regional State of Ethiopia. It was proposed by Gizaw *et al.* (2007) to categorize the Adilo sheep of Southern Regional State of Ethiopia with Arsi-Bale sheep. However, Adilo has been long known as a hot spot of sheep market place where livestock from various parts of the region collected, traded and dispatched to different regions of the country; hence it does not necessarily represent a single district of the study region. The dendrogram in the current study clearly indicated that the WOL sheep greatly differentiated from sheep in other zones. Although not obvious, the GAG sheep were also segregated from those closely related sheep found in KTH, GUS and SIG which share geographic proximity and similarities in ecology and communities who own the sheep, thus allowing gene flow among populations.

It is apparent that coat colour patterns can vary between the head, neck, trunk and limbs. In both sexes, the predominant coat colour patterns were plain and patchy with similar proportions of appearance. This is consistent with the reports of Edea *et al.* (2010) and Tibbo and Ginbar (2004) for Bonga and Horro sheep types of Ethiopia.

Table 6. Average values of quantitative morphometrical traits of ewes (means ± SD, cm; $N = 2047$).

Morphometrical traits	SIG ($n = 345$)	KTH ($n = 534$)	GUS ($n = 411$)	GAG ($n = 370$)	WOL ($n = 387$)	Overall mean
Body weight (kg)	27.2 ± 3.2^{a}	25.8 ± 4.2^{b}	25.4 ± 4.0^{b}	25.5 ± 5.1^{b}	27.4 ± 5.0^{a}	26.3
Chest girth	63.5 ± 1.8^{c}	69.5 ± 3.8^{b}	70.5 ± 5.0^{a}	73.0 ± 6.3^{a}	70.1 ± 5.0^{a}	69.4
Height at withers	64.8 ± 1.0^{a}	63.3 ± 3.3^{a}	61.0 ± 3.3^{b}	57.0 ± 4.0^{c}	63.5 ± 3.3^{a}	62.0
Body Length	68.4 ± 1.0^{a}	64.3 ± 5.1^{b}	46.5 ± 3.1^{c}	64.3 ± 4.7^{b}	63.7 ± 4.2^{b}	61.4
Pelvic width	16.1 ± 1.1^{a}	15.9 ± 1.1^{a}	10.8 ± 1.0^{c}	14.8 ± 2.0^{b}	15.5 ± 1.2^{a}	15.0
Shoulder width	16.0 ± 1.1^{a}	13.2 ± 1.3^{b}	14.0 ± 1.0^{b}	16.0 ± 2.1^{a}	13.0 ± 1.6^{b}	14.4
Canon length	14.0 ± 0.4^{a}	14.3 ± 1.5^{a}	12.3 ± 0.5^{b}	13.2 ± 0.5^{b}	14.8 ± 1.0^{a}	13.7
Canon circumference	6.91 ± 0.4	6.70 ± 0.5	7.8 ± 0.50	6.50 ± 1.0	6.53 ± 0.6	6.89
Head width	10.0 ± 0.3^{a}	11.0 ± 1.0^{a}	10.1 ± 0.0^{a}	9.21 ± 1.3^{a}	7.50 ± 1.3^{b}	9.57
Head length	16.1 ± 0.5	17.0 ± 0.7	17.0 ± 1.0	16.5 ± 1.3	17.9 ± 1.1	16.9
Tail length	27.0 ± 12^{b}	26.5 ± 5.7^{b}	31.5 ± 3.0^{a}	23.4 ± 7.2^{c}	34.6 ± 3.6^{a}	28.6
Tail circumference	17.5 ± 2.8^{a}	13.5 ± 3.3^{b}	18.0 ± 2.0^{a}	14.5 ± 6.5^{b}	13.1 ± 3.4^{b}	15.1
Ear length	10.2 ± 0.6^{b}	11.2 ± 1.0^{a}	11.2 ± 0.7^{a}	9.21 ± 2.0^{c}	11.0 ± 1.1^{a}	10.5
Horn length	7.25 ± 2.2^{b}	6.79 ± 3.7^{b}	8.70 ± 2.3^{a}	10.0 ± 7.5^{a}	8.03 ± 5.0^{a}	8.15

^{a,b,c} Means across rows between zones with different superscript letters are significantly ($P<0.05$) different.
SIG = Sidama-Gedeo; KTH = Kembata, Tembaro-Hadiya; GUS = Gurage-Silte; GAG = Gamogofa; WOL = Wolaita.

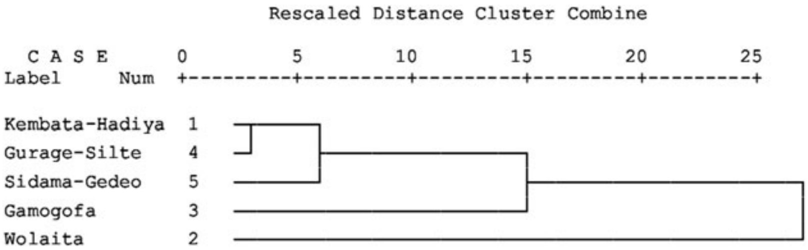

Figure 2. Unweighted pair group method with arithmetic averaging dendrogram based on between population Euclidean distances derived from morphological variables.

In both sexes, the proportion of sheep having red and brown coat colour was greater than that of other coat colours. The results are in good agreement with the findings of Galal (1983) for Menz sheep as well as Tibbo *et al.* (2004) and Edea *et al.* (2010) for Horro and Bonga sheep. The higher proportion of animals with red coat colour could be a reflection of strong selection for animals manifesting red colour to meet the preference of market demand. Most of the sheep studied were characterized by short and smooth hair. According to the findings of Gizaw *et al.* (2008), the Adilo sheep were reported to be short-haired, whereas the Arsi-Bale, Bonga and Afar sheep were characterized by hairy fibre hair.

Sheep in SIG, KTH, GUS and WOL had a characteristic long fat tail with a straight tip. These findings are in good agreement with the work of Gizaw *et al.* (2008) for Adilo and Arsi-Bale, Getachew *et al.* (2010) for Horro and Menz and Edea *et al.* (2010) for Bonga sheep. In other studies conducted by Tibbo *et al.* (2004) and Getachew *et al.* (2010), the Menz sheep had a characteristic short fat tail, which was curved upward at the tip. However, GAG sheep were characterized by a long thin tail ending with a slight curve tip. These findings are contrary to the results of Gizaw *et al.* (2008), who reported Adilo sheep as having a long fat tail. The reason for this discrepancy could be explained by the small sample numbers assessed in the previous studies and also the fact that Adilo is basically a trading place where there are possibilities of genetic admixture among sheep populations coming from the neighbouring regions.

The presence of wattle is comparatively low in rams but high in ewes. These findings are consistent with the reports of Tibbo and Ginbar (2004). It was observed that ruff was absent in both ewes and rams. This is in agreement with the reports of Edea *et al.* (2010) for Bonga and Horro sheep. In agreement with the findings of Getachew *et al.* (2010), most sheep of both sexes in all zones were characterized by the presence of horns. In contrary, both the rams and ewes among the Bonga sheep were reported to be polled (Gizaw *et al.,* 2008; Edea *et al.,* 2010).

Quantitative morphometrical traits

The body weight values of the ewes as obtained from the present study were higher than those reported by Abebe, Kannan and Goetsch (2010) and Tafa, Melaku and Peters (2010) for yearling Arsi-Bale sheep and Banerjee, Kefelew and Sintayehu (2010) for yearling and ewes aged above 2 years. However, the values were lower than those of other sheep types of Ethiopian origin reported by Galal (1983) for Horro and Menz. The body weight of sheep from GUS and WOL was comparable to that of Bonga sheep, but higher than Horro sheep (Edea *et al.,* 2010). However, the body weight in the SIG and KTH sheep were in agreement with that of Horro sheep. The observed differences in body weight might be caused by the age of animals, sheep type and management and/or production environments in which the animals were kept. Generally, live weight of male sheep from GUS and WOL meets the recommended live export body weight of 30 kg at yearling age (Tibbo, 2006). In agreement with the works of Tibbo *et al.* (2004), rams were consistently heavier and larger in body size than ewes.

Figures for height at withers, chest girth and body length in ewes observed in this study were comparable to those reported by Abegaz (2007) for Gumuz sheep and Lemma (2002) for central highland and north-western highland sheep. The height at withers of ewes was similar to those reported by Baffour-Awuah *et al.* (2000) from Ghana, Afolayan, Adeyinka and Lakpini (2006) for Yankasa sheep of Nigeria, Traoré *et al.* (2008) for Burkina Faso sheep, Abegaz, Hegde & Taye (2011) for Gumuz ewes and Tibbo *et al.* (2004) for Horro and Menz ewes of Ethiopia. However, these values in the present study were lower than those reported by Galal (1983) for Horro sheep, Taye *et al.* (2010) for Washera sheep and Lemma (2002) for Western highland sheep of Ethiopia, but higher than the Abergelle sheep reared in Tigray region of Ethiopia (Seare *et al.,* 2007). The height at withers of GAG, WOL and KTH sheep was comparable with that of Horro and Bonga sheep under on-station management (Edea *et al.,* 2010). Getachew *et al.* (2010) also reported similar values for Menz and Afar sheep studied under their habitant production environments.

The results in the present study pertaining to rams raised in different zones indicate that the height at wither values find similarities with the observations of Lemma (2002), Taye *et al.* (2010) and Seare *et al.* (2007). However, higher values for this trait have been reported by Abdel-Moneim (2009) for Egyptian rams.

The overall chest girth values of ewes obtained from the current study are comparable to those reported by Tibbo *et al.* (2004) for mature female Menz and Horro sheep. However, chest girth values reported by Getachew *et al.* (2010) for Menz and Afar sheep were lower than those observed in the current study. These variations might be explained by the fact that Menz sheep are characterized by long fleece with coarse wool type having small body size which are known to be more adapted to cold environments (Gizaw *et al.,* 2008; Getachew *et al.,* 2010). Similarly, the Afar sheep have been also characterized by small body size and are more suitable to extreme arid and hot environment (Getachew *et al.,* 2010).

The overall body length values of ewe populations in the current study are consistent with the findings of Tibbo *et al.* (2004) for Menz and Horro sheep and Getachew *et al.* (2010) for Afar sheep. The values related to body length of ewes in the present study are also comparable to those of Traoré *et al.* (2008), Taye *et al.* (2010) and Abegaz, Hegde & Taye (2011). The body length of the Horro adult ewes as reported by Gizaw *et al.* (2008) was comparable to that of ewes reared in SIG.

The result for pelvic width in the present study finds similarity with that of Taye *et al.* (2010) for the Washera ewes of Ethiopia. Tibbo *et al.* (2004) reported pelvic width values ranging from 15.9 to 16.9 cm for 2-year-old Menz and Horro ewes, which are in good agreement with current findings of both sexes. However, the pelvic width values observed in the ewes of GUS and GAG were lower than those of the Washera sheep reported by Taye *et al.* (2010). Similarly, higher pelvic width values (17.9–20.7 cm) were reported for Menz and Afar sheep (Getachew *et al.,* 2010). These variations might be associated with the age, sheep type and sex of investigated sheep types in the present and previous investigations.

The average head width values for rams and ewes in studied locations are lower than those reported by Handiwirawan, Noor, and Sumantri (2011) for Indonesian sheep breeds. The overall tail length of sheep obtained from the current study was higher than reported for Afar and Menz sheep (Getachew *et al.,* 2010) but comparable to that of Horro sheep (Awgichew, 2000) as well as Adilo and Arsi-Bale female sheep (Gizaw *et al.,* 2008). The tail length and circumference of rams were generally higher than ewes, which were possibly associated with body size variations. The tail circumference observed in ewes was comparable to those reported for Menz and Horro sheep (Awgichew, 2000) but higher than those of both sexes of Menz and Afar sheep under field conditions (Getachew *et al.,* 2010).

The ear length values of rams find similarity with the observations of Taye *et al.* (2010) and Abegaz, Hegde and Taye (2011). As observed by Traoré *et al.* (2008), ear length of ewes of Burkina Faso was lower than those obtained from the present study. Similarly, lower values for ear length have been reported by Taye *et al.* (2010) for Washera sheep of both sexes, but the ear length values of the Sudan-Sahel ewes of Burkina Faso sheep reported by Traoré *et al.* (2008) were comparable with those of the present findings. The ear length values in the present study were longer than those reported for Abergelle ewes (Seare *et al.,* 2007).

The scrotal circumferences as obtained from rams raised in SIG were comparable to that reported by Edea *et al.* (2010) for Horro sheep, whereas sheep in GUS and WOL had similar values to that of the Bonga rams. The overall values of scrotal circumference were generally comparable to those reported by Getachew *et al.* (2010) for the rams of Menz, but lower than that of Afar sheep under their production environments. A scrotal circumference is an indirect measure of ram fertility and used to asses breeding soundness of ram with a high heritability (Söderquist and Hulten, 2006).

Conclusions

The present study was initiated to describe the qualitative characters and quantitative morphometrical traits of indigenous sheep types reared in Southern Nations and Nationalities Regional State of Ethiopia. This study revealed the presence of high variability in the observed qualitative and quantitative morphometrical characteristics among the sheep studied in all administrative zones. It is thus concluded that the indigenous sheep in these zones may possess unique adaptive features that are useful in designing sustainable sheep improvement programmes in the region. Moreover, the sheep from the Gamogofa and Wolaita showed some distinctive features that were not observed in other sheep. It is thus recommended to assess the population structure of these indigenous sheep using molecular tools.

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Multivariate analyses of morphological traits in Algerian goats, Sétif, north-eastern Algeria

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Summary
A total of 700 adult female goats from Sétif area (Algeria), were investigated for eight qualitative morphological traits and 17 body measurements. Sampling included three environmental areas: Northern, Central and Southern area. Coefficients of variation ranged from 10.9 percent to 34.7 percent, showing high heterogeneity. Canonical analyses showed that differences in body measurements between the three area-populations were large and significant in all traits ($P < 0.001$). The shortest Mahalanobis distance was found between North-Center populations (2.8), while that between Center (4.0) and (8.6) between North-South populations were the largest. Discriminant analysis showed that most goat-populations were classified into their environmental-area, North (73.0 percent), Center (66.8 percent) and South (79.3 percent) with a few misclassified individuals. Correspondence analysis indicated no large differences between the goat populations; they were more homogeneous for qualitative traits. This information will constitute the basis for further characterization and develop conservation strategies for Algerian goat populations

Keywords: *Algeria, goats, body measurements, canonical analysis, characterization, correspondence analysis, discrimination, multivariate analysis, qualitative traits*

Résumé
La caractérisation de 700 chèvres adultes a été réalisée dans la région de Sétif (Algérie). L'échantillonnage a concerné trois sites environnementaux: Nord, Centre et Sud. Selon les résultats obtenus, les coefficients de variation ont varié de 10,9% à 34,7%, inférant ainsi une large hétérogénéité. L'analyse canonique a fait ressortir de larges et significatives ($P < 0.001$) différences pour les mesures corporelles. Les distances de Mahalanobis, ont été aussi significatives entre les trois zones. Pour ce qui est l'analyse discriminante, la plus-part des individus ont été classés dans leur zone d'origine, avec un très faible nombre d'individus mal classé. L'analyse des correspondances, au contraire, a démontré une grande homogénéité intra-zone pour les variables qualitatives.

Mots-clés: *Algérie, chèvres, mesures corporelles, analyse canonique, caractérisation, analyse des correspondances, discrimination, analyse multivariée, variables qualitatives*

Resumen
En un total de 700 cabras adultas de la provincia de Sétif (Argelia), se estudiaron ocho caracteres morfológicos cualitativos y diecisiete medidas corporales. El muestreo se realizó en tres ambientes: zonas Norte, Centro y Sur. Los coeficientes de variación oscilaron entre un 10,9% y un 34,7%, mostrando una elevada heterogeneidad. Mediante análisis canónico se observó que existían amplias diferencias significativas ($P < 0,001$), entre las poblaciones de las tres áreas, para todas las medidas corporales. La menor distancia de Mahalanobis se dio entre las poblaciones Norte y Centro (2,8), mientras que las distancias entre las poblaciones Centro y Sur (4,0) y Norte y Sur (8,6) fueron mayores. El análisis discriminante clasificó a la mayoría de las poblaciones caprinas en sus respectivas áreas ambientales, Norte (73,0%), Centro (66,8%) y Sur (79,3%) con escasos individuos catalogados equivocadamente. El análisis de correspondencias no arrojó grandes diferencias entre las poblaciones de cabras, que fueron más homogéneas para los caracteres cualitativos. Esta información va a servir de base para futuras caracterizaciones y para el desarrollo de estrategias de conservación en las poblaciones caprinas argelinas.

Palabras clave: *Argelia, cabras, medidas corporales, análisis canónico, caracterización, análisis de correspondencias, análisis discriminante, análisis multivariante, caracteres cualitativos*

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Introduction

In Algeria, there are approximately 3 million goats that are a source of income for about 800 000 small farmers. Goats constitute a tradition in Algeria. They are found in small numbers (4 or 5) or with sheep in the same flock. In Algeria, there are no defined breeds as such, but they are considered as populations according to the area. They present many advantages to farmers which are: ability to tolerate harsh climates, good recovery capacity from drought, suitability to poor systems because of small size and ability

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to thrive on poor quality diets, low milk production and animals for sale. The mating system is based on exchange of males from one farmer to another. No breeding programmes have been implemented to improve productivity of small ruminants. Small ruminants are bred extensively (Dekhili and Aggoun, 2007). In Algeria, information on goat resources is scarce, which does not contribute to the characterization of different local genetic types. To improve animal productivity or to maintain genetic diversity which allows farmers to select or to sell more animals or to create new breeds, a solid strategy is needed to identify and understand the productivity of these populations in their regions. However, before that, an adequate phenotypic and genetic characterization is needed. The first step of the characterization of Algerian local genetic resources is to assess variation in morphological traits (Delgado *et al.*, 2001). Many authors have suggested use of multifactorial analysis for morphological traits in order to assess phenotypic variation within and between goat populations (Traoré *et al.*, 2008a, b; Yakubu *et al.*, 2010; Legaz *et al.*, 2011; Yakubu, 2011). The main objectives of this study are to identify any distinct goat populations and to describe their external characteristics (qualitative and quantitative) within the Algerian production environment (Sétif).

Materials and methods

Environmental areas and goat populations

The high plateaux of Sétif are divided naturally into three environmental areas according to climate conditions, altitude, type of soil and vegetation:

Northern area: is located between 1 500 to 2 000 m of altitude, with an annual rainfall of ≤700 mm, with low temperatures varying from −5 to 20 °C and grassy, bushy and shrubby vegetation, usually quite sparse, with ligneous species. Soils are black, hygroscopic and mainly of clay;

Central area: is located between 900 to 1 200 m of altitude, with annual rainfall of ≤400 mm. Temperatures are varying from −1 to 25 °C. Vegetation is mainly based on fallow ground or stubble of cereals. Soils are more silty with brown colour;

Southern area: is at 800 m of altitude with annual rainfall of ≤250 mm. Vegetation steppe is quite sparse, with ligneous species: *Stippa tenacissima and Artemesia herba-alba*. Soils are more of limestone, with white colour and salty. Temperatures are varying from −1 to 27 °C (ONM, 2010).

The three environmental areas described above are habitats of the goat populations concerned with this investigation, which is the first in both Sétif region and in Algeria. Each area is divided into districts: four districts for Northern area, three districts for Southern area and five for Central area.

Data collection

During the summer of 2010, sampling was carried out on a total of 14 flocks, selected at random, located in three different areas in eastern Algeria. A total of 660 non-pregnant adult female goats from 3- to 4-years old, were included in this investigation and were distributed as follows: 101 for North, 405 for Centre and 154 individuals for South. All goats were scored for 17 body measurements (quantitative) concerning width size and dimensions of animals. These are influences and may depend on numerous genes and are economically important. The second type of data are nine coded qualitative discrete traits, such as colour or categorical (presence or absence). Body measurements or quantitative traits were carried out by three technicians using Lydthin stick, tape measure and Vernier calipers. Animals were put on a flat floor and held by the farmers. The 17 body measurements obtained were: head length (hl), ear length (el), neck length (nl), body length (bl), trunk length (trl), pelvis length (pl), hip width (hw), ischion width (iw), chest size (cs), chest depth (cd), chest width (cw), height at withers (htw), height at back (hb), height at sacrum (hs), side depth (sd), hair length (hrl) and tail length (tl). The eight qualitative traits scored are as follows: head colour (hc), ear position (ep), profile position (pp), coat colour (cc), presence of goatee (gp), presence of pendants (pdp), colour of legs (lc) and udder development (ud).

The data collection was done as follows: qualitative and quantitative traits were collected simultaneously in the field and were reported on files or cards. Individual files were prepared before starting characterization. Hence, the data were collected on the conditions in which animals are bred. Once the data were collected, they were reported on Excel file to be analysed later. Questionnaires were elaborated as well, to collect information about production environment, mating, feeding, selection and other activities.

Statistical analyses

Statistical analyses were carried out using the SAS/STAT package (1999). Basic statistics for body measurements and qualitative traits were obtained using PROC UNIVARIATE and PROC FREQUENCY, respectively. The influence of the environmental area on the 17 body traits measured was assessed using the PROC MIXED, fitting a model including as effects the area (with three levels: North, Centre and South) and districts as a random effect nested within the area to account for non-independency of sampling in each district. Least square means and their standard errors were obtained for each body trait by area level. Duncan's multiple-range test was performed on all area means of body measurement traits using PROC GLM. Stepwise discriminant procedure was applied using PROC STEPDISC to determine which

Table 1. Overall arithmetic mean (cm) with their standard error (SE), coefficient of variation (CV), least square means (cm) and their standard error (SE) for each area analysed for each of the seven body measurements.

Traits	Overall-means (cm) ± SE	CV	Northern-area LSM(cm) ± SE	Central-area LSM(cm) ± SE	Southern-area LSM(cm) ± SE
Bl	94.5 ± 0.6	14.5	$93.5^{a} \pm 0.6$	$97.1^{b} \pm 0.7$	$86.8^{c} \pm 0.3$
Cd	32.1 ± 0.2	14	$33.4^{a} \pm 0.4$	$32.7^{a} \pm 0.2$	$29.1^{b} \pm 0.4$
Cs	74.9 ± 0.4	11.6	$77.2^{a} \pm 0.9$	$76.7^{a} \pm 0.4$	$67.5^{b} \pm 0.8$
Cw	24.2 ± 0.2	22.2	$26.9^{a} \pm 0.5$	$23.9^{b} \pm 0.2$	$22.7^{c} \pm 0.5$
El	18.5 ± 0.3	19.7	$17.6^{a} \pm 0.3$	$19.3^{b} \pm 0.2$	$16.9^{a} \pm 0.3$
Hb	68.4 ± 0.4	10.9	$71.6^{a} \pm 0.7$	$70.2^{a} \pm 0.3$	$60.3^{b} \pm 0.6$
Hl	18.7 ± 0.1	12.5	$20.0^{a} \pm 0.3$	$19.3^{a} \pm 0.1$	$15.6^{b} \pm 0.2$
Hrl	10.1 ± 0.2	34.7	$11.7^{a} \pm 0.3$	$10.0^{b} \pm 0.1$	$8.8^{c} \pm 0.3$
Hs	68.3 ± 0.4	11.2	$71.2^{a} \pm 0.8$	$69.9^{a} \pm 0.3$	$60.8^{b} \pm 0.7$
Htw	66.9 ± 0.4	11.4	$70.2^{a} \pm 0.8$	$68.4^{b} \pm 0.4$	$59.5^{c} \pm 0.7$
Hw	15.7 ± 0.1	14.4	$17.7^{a} \pm 0.2$	$15.6^{b} \pm 0.1$	$14.2^{c} \pm 0.2$
Iw	13.5 ± 0.1	16.9	$14.9^{a} \pm 0.2$	$13.5^{b} \pm 0.1$	$12.1^{c} \pm 0.2$
Nl	37.4 ± 0.3	17.2	$39.2^{a} \pm 0.7$	$38.8^{b} \pm 0.3$	$31.6^{c} \pm 0.6$
Pl	20.5 ± 0.2	17.9	$21.5^{a} \pm 0.3$	$20.8^{a} \pm 0.1$	$18.6^{b} \pm 0.3$
Sd	38.1 ± 0.3	14.6	$40.2^{a} \pm 0.5$	$39.1^{a} \pm 0.2$	$33.3^{b} \pm 0.5$
Tl	18.4 ± 0.2	23.9	$21.7^{a} \pm 0.4$	$18.5^{b} \pm 0.2$	$15.5^{c} \pm 0.4$
Trl	62.4 ± 0.4	14.9	$67.0^{a} \pm 0.9$	$63.8^{b} \pm 0.4$	$54.7^{c} \pm 0.8$

Traits: Bl, body length; Cd, chest depth; Cs, chest size; Cw, chest width; El, ear length; Hb, height at back; Hl, head length; Hrl, hair length; Hs, height at sacrum; Htw, height at withers; Hw, hip width; Lw, ischion width; Nl, neck length; Pl, pelvis length; Sd, side depth; Tl, tail length; Trl, trunk length. $^{a-c}$Different superscript indicate significant difference ($P < 0.05$).

morphological traits have more discriminant power than others. The CANDISC procedure was used to perform canonical analysis to derive canonical functions, linear combinations of the quantitative variables that summarize variation between areas and compute between areas Mahalanobis distance matrix. The ability of the computed canonical function to assign each individual goat to its sampling area was calculated as the percent of correct assignment using DISCRIM procedure. The association between the qualitative traits was assessed via correspondence analysis using the PROC CORRESP of SAS. When necessary for descriptive purposes, canonical variables and correspondence analysis dimensions were plotted using Microsoft Excel.

Table 2. Frequency of each class level of qualitative traits scored in Sétif area goats (and percentage for each qualitative trait in brackets).

Traits	Class level	Northern area	Central area	Southern area	Overall frequency (%)
Hc	Black	20(22.5)	23(6.2)	3(2.6)	46(8.0)
	White	14(15.7)	93(25.1)	3(2.6)	110(19.1)
	Spotted in black	55(61.7)	254(68.7)	110(94.8)	419(72.7)
Ud	Developed	65(73.3)	319(86.2)	105(90.5)	489(85.0)
	Non-developed	24(26.9)	51(13.8)	11(9.5)	86(15.0)
Ep	Vertical	9(10.1)	59(15.9)	–	68(11.8)
	Horizontal	24(26.9)	105(28.4)	28(24.1)	157(27.3)
	Dropping	56(62.9)	206(55.7)	88(75.8)	350(60.9)
Pp	Right	87(97.8)	346(93.5)	85(73.3)	518(90.1)
	Arched	2(2.3)	24(6.5)	31(26.7)	57(9.9)
Cc	White	4(15.7)	102(27.6)	10(8.6)	126(21.9)
	Black	34(38.2)	80(21.6)	56(48.3)	170(29.6)
	Spotted in brown	41(46.1)	188(50.8)	50(43.1)	279(48.5)
Gp	Absent	19(21.4)	65(17.6)	13(11.2)	97(16.9)
	Present	70(78.7)	305(82.4)	103(88.8)	498(83.1)
Pdp	Absent	84(94.4)	341(92.1)	109(93.9)	534(92.9)
	Present	5(5.6)	29(72.8)	7(6.0)	41(7.1)
Lc	White	38(47.7)	220(59.5)	58(50.0)	316(55.0)
	Black	25(28.1)	43(11.6)	32(27.6)	100(17.4)
	Spotted in black	36(29.2)	107(28.9)	26(22.4)	159(27.7)

X^2 test showed that incidence of all analysed traits varied significantly among environmental areas ($P < 0.05$).

[1] Traits: c, coat colour; Ep, ear position; Hc, head colour; Gp, presence of goatee; Lc, legs colour; Pdp, presence of pendant; Pp, profile position; Ud, udder development.

Table 3. Summary of stepwise selection of traits.

Step	Variables entered	Partial R^2	F-value	$P > F$	Wilk's Lambda	$P <$ Lambda	Average Squared Canonical Correlation	$P >$ ASCC
1	Hl	0.3035	124.6	***	0.6965	***	0.152	***
2	Hw	0.0938	29.55	***	0.6312	***	0.198	***
3	Bl	0.0977	30.85	***	0.5695	***	0.240	***
4	Hb	0.0879	27.43	***	0.5194	***	0.270	***
5	El	0.0727	22.27	***	0.4817	***	0.296	***
6	Cw	0.0513	15.34	***	0.4569	***	0.314	***
7	Tl	0.0446	13.2	***	0.4366	***	0.328	***
8	Trl	0.0176	5.06	***	0.4289	***	0.333	***
9	Sd	0.0141	4.03	**	0.4228	***	0.337	***

***$P < 0.005$; **$P < 0.01$.

Traits: Bl, body length; Cw, chest width; El, ear length; Hb, height at back; Hl, head length; Hw, hip width; Tl, tail length; Trl, trunk length; Sd, side depth.

Results and discussion

Continuous traits

Least square means for the body measures analysed by environmental area are given in Table 1. Overall, the Northern area had the highest values ($P < 0.05$) for 15 traits or 88 percent. These traits were mainly related to length (6), width (3), height (3), depth (2) and size (1). The Central area had the highest values for all traits compared with the South goats. This indicates that the North goats are different than the two other types of goats located in the Centre and in the South; as, the Centre ones are different from the South ones, as well. Goat populations are exhibiting different phenotypes according to the area. These morphological differences shown by univariate analysis constitute an indication of the inherent genetic constitution of each goat population. The presented coefficient of variation (Table 1) varied from 10.94 percent to 34.67 percent. Therefore, a large variation is shown in the body measures.

Qualitative traits

Incidence in percentage of each level of the eight qualitative traits recorded for all individuals and for each environmental area (Table 2), suggests that goats are mainly spotted black in head (72.7 percent), with drooping ears (60.9 percent), right pp (90.1 percent), gp (83.1 percent), absence of pendants (92.9 percent), with white legs colour (58.0 percent) and developed udder (85.0 percent). cc varied from one area to another. Black and spotted in brown (38.2 percent, 46.1 percent) in North and 48.28 and 43.1 percent in South; Spotted in brown, white and black (50.8 percent −27.6 percent −21.6 percent) for the Central area.

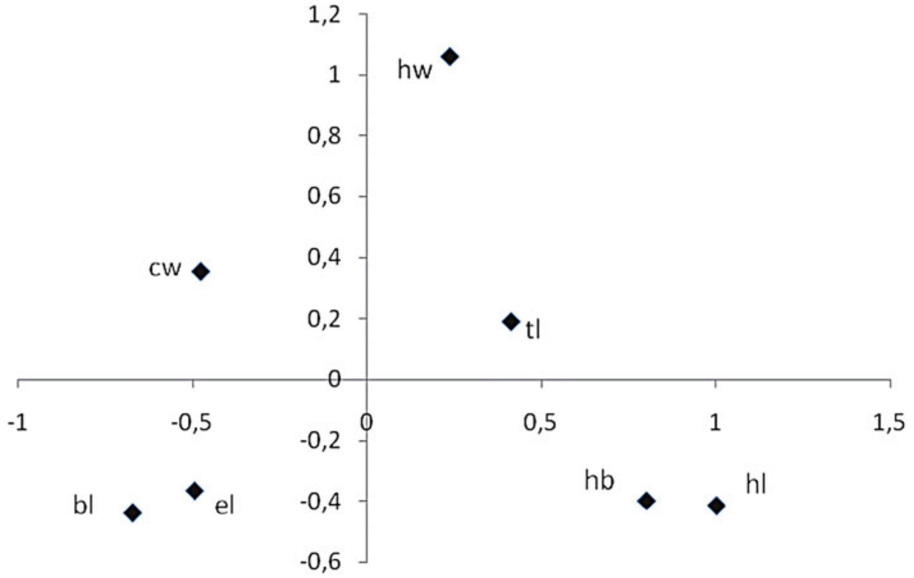

Figure 1. Bi-dimensional plot illustrating the association between body measures in Sétif goat assessed via canonical analysis. Traits: HW, hip width; CW, chest width; TL, tail length; BL, body length; EL, ear length; HB, height at back; HL, head length.

Multivariate analyses

Results of the stepwise discriminant analysis are presented in Table 3. Nine of the seventeen measured variables were found to be significant ($P < 0.01–0.005$). However, hl followed by hw, bl, hb, el, cw and tl had more discriminant power than the others as shown by their higher R^2 and F-values. Then, the other traits (trl-sd) were removed from the final model. This suggests that taking these seven traits (hl, hw, bl, hb, el, cw and tl) would be more important in differentiating goats between areas. The canonical analysis identified two statistically significant ($P < 0.005$) canonical variables (CAN1 and CAN2). CAN1 and CAN2 accounted for 76 and 24 percent of the total variation, respectively. Figure 1 shows a bi-dimensional plot illustrating the relationship between body measurement on the x-axis, hl, hb and tl are well separated from the other linear traits. Although on the y-axis, hw is well separated from the other traits. The between environmental areas Mahalanobis distance matrix is given in Table 4. All pairwise distances were highly significant ($P < 0.005$). Therefore, a large variation is shown in the body measures. The largest distance was found between the Northern and the Southern areas (8.6), and 4.0 between the Centre and the South, while between the North and the Centre it was 2.8. The hypotheses that area's means are equal in the populations analysed were tested using Wilk's Lambda. This had a significant value ($P < 0.005$) of 0.43656191 ($F = 41.52$: degree of freedom = 14) showing clearly, that differences found between areas were statistically different from zero. Phenotypic differences are present among populations, which are separated by geographical locations.

Adaptive divergence in morphological traits was higher between North goat-populations and South ones, and lower between North and Centre goat-populations. This indicates that the genetic exchange, through males, that has been used over time might have lowered the genetic distance between North and Centre and between Centre and South, which has been facilitated by geographic proximity. The values computed for CAN1 and CAN2 for each individual were plotted by environmental areas (Figure 2). All individuals, within the area, are spread and more or less clustered on the right of the X-axis. In this respect, the discriminant analysis carried out gave more information (Table 5). Most of the individuals within the area were classified into their source population (North: 73.0 percent; Centre: 66.8 percent; South: 79.3 percent).

Table 4. Mahalanobis distance between goat populations sampled in each environmental area identified in Sétif.

Area	Central	Southern
Northern	2.8***	8.6***
Southern	4.04***	

***$P < 0.005$.

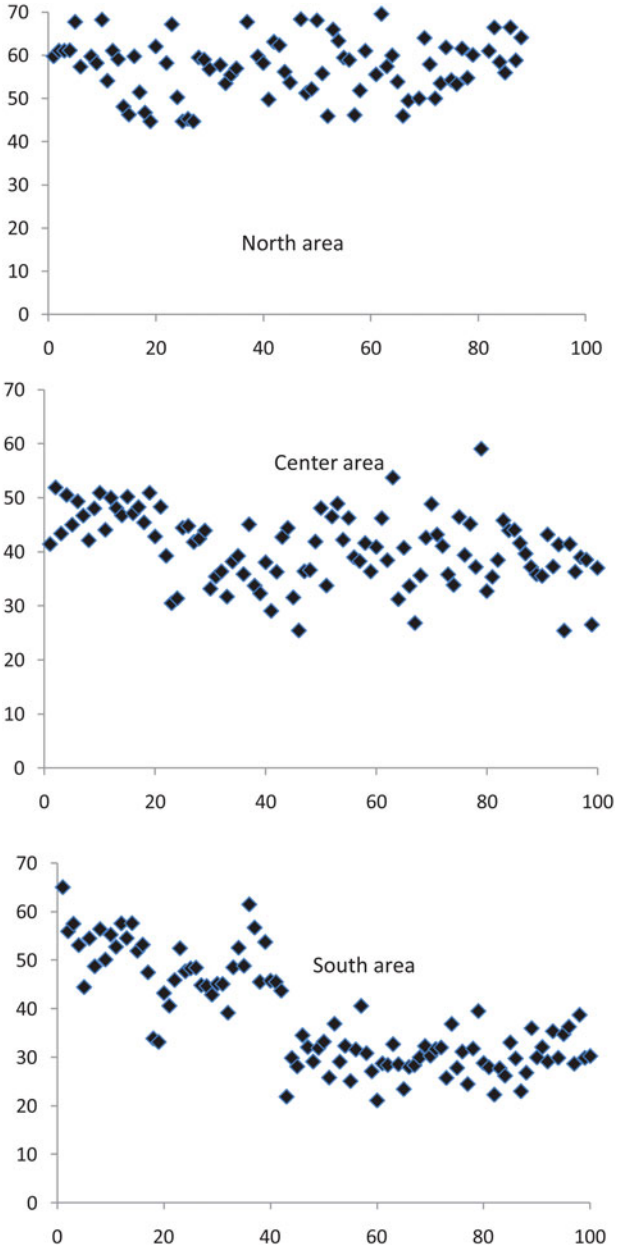

Figure 2. Bi-dimensional representation of the canonical traits associated with individuals sampled in each of the environmental areas of Sétif. Traits: HW, hip width; CW, chest width; TL, tail length; BL, body length; EL, ear length; HB, height at back; HL, head length.

Table 5. Percentage of classification into environmental area for Setif goat individual sampled, according to the environmental area of sampling, using morphological structural traits and discriminant analysis.

Area	Northern	Central	Southern
Northern	73.03	21.35	5.62
Central	18.38	66.76	14.86
Southern	5.17	15.52	79.31
Total	24.17	49.39	26.43

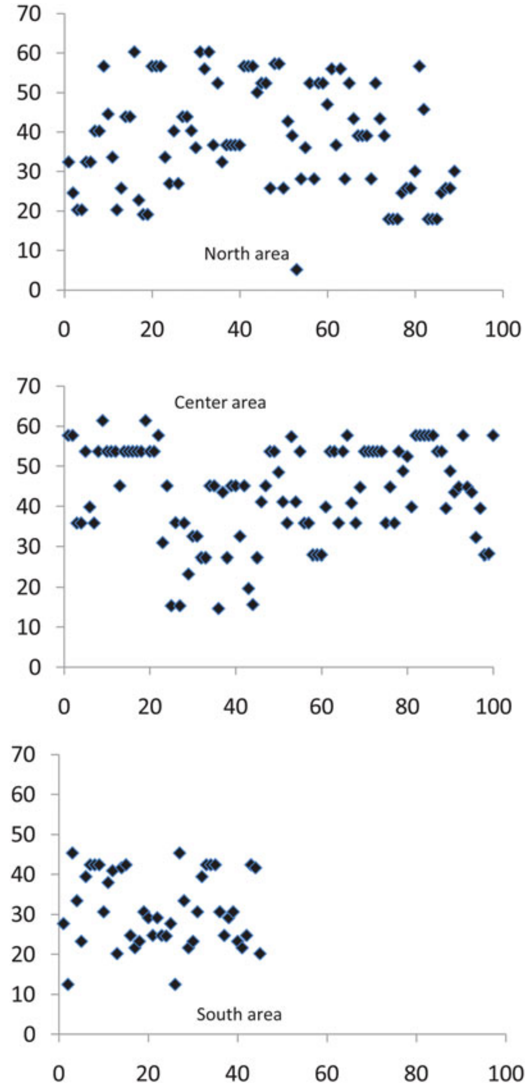

Figure 3. Bi-dimensional representation of the individuals sampled in each of the environmental areas of Sétif via correspondence analysis for 8 qualitative traits.

A small part of the individuals was “erroneously” cross classified. This indicates that each area-goat population has its own genetic constitution, which might be because of the lack of correction for age within population. Correspondence analysis carried out on the eight qualitative traits recorded showed that four of them (hc, ep, cc and lc) explained 75.0 percent of the inertia. Therefore, the analysis was re-run using only these four traits where Figure 3 shows the values computed for the two identified dimensions for each environmental area. The first and second dimensions identified explained, respectively, 56.5 and 43.5 percent of the total variation. The scenario identified for each environmental area was almost similar to that previously reported for the body measures, except for the South where the individuals were more clustered in the left. Although, North and Centre individuals are more spread in the X-axis rather than those of the South where they are more clustered to the left of the X-axis. As was declared earlier, there are no real differences between individuals within area in the qualitative traits (Table 2). Animal genetic resources are a part of biological diversity and are important in any development programme. Between breed diversity is considered as an important criterion to be considered when ordering priorities for conservation of breeds. As we know, phenotypes are an expression of genetic characteristics under environmental conditions; therefore, phenotypic variance is influenced by genetic variance and environmental one. To understand the phenotypic description under Algerian conditions would help, indeed, for an accurate comparison with other goat populations from the North to the South of the country. Further characterization using genetic analyses is helpful and necessary. The presented results showed significant morphological variation among all three goat populations in the three areas. This intra-area homogeneity found could be because of the environmental conditions in which goat populations are bred. This might indicate a certain relationship between phenotypic constitution intra area, adding to this the combination of the same set of genes and geographical differences.

Conclusion

A significant morphological variation was found among the three goat populations of Sétif, mainly because of geographical differences and mating procedure. It can be considered that there are three geographical goat populations, where each type has its own particularities. They exhibit large phenotypic diversity. They are bred at low selection intensity, and might be subject to high natural selection pressure; pedigrees are not known and genetic structure is mainly influenced by migrations drift and natural selection. This investigation showed that hl, hw, body length, hb, el, cw, tl and sd were the most discriminating variables to separate the three goat populations between areas. These results would aid further characterization, management and improvement of the Algerian small ruminant. However, more solid characterizations using protein and microsatellite markers are needed as complements.

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Microsatellite-based genetic evaluation of Ghumusar goats of Orissa, India

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Summary

Ghumusar is an inadequately studied goat population of western region of Ganjam district of Orissa state. Sporadic information is available on its morphological traits but no information is found on its genetic variability. Therefore, an attempt was made to measure the genetic diversity in Ghumusar goat population using 25 microsatellite markers. Genomic DNA isolated from blood samples drawn at random from 50 individuals were utilized for this study. The average number of observed allele was 9.80 and the effective average number of allele was 4.28. The polymorphic information contents ranged from 0.53 to 0.91. The average observed and expected heterozygosity was 0.73 and 0.71, respectively. The values of Nei's gene diversity in Ghumusar goat population ranged from 0.11 to 0.87 with a mean of 0.69. The overall Fis value was observed to be 0.002, which is not significantly different from zero; hence indicating no global deficit of heterozygotes. Under sign test, expected number of loci with heterozygosity excess (Hee) was 14.88, 14.79 and 14.74 for the infinite allele model (IAM), stepwise mutation model (SMM) and two-phased model (TPM) of mutation, respectively. The observed number of loci with heterozygotic excess (He) was 14, 8 and 2 under these three models, respectively. Under all the three models, He was less than Hee and this deviation was significant under SMM and TPM models. There was no serious genetic reduction in effective population size as indicated by L-shaped curve in Ghumusar goat population.

Keywords: *microsatellite markers, polymorphism, genetic diversity, Ghumusar goat*

Résumé

Les chèvres Ghumusar constituent une population caprine de l'ouest du district de Ganjam, dans l'état d'Orissa, à peine étudiée. On ne dispose que de l'information sporadique sur ses traits morphologiques sans qu'il ait été trouvé de l'information sur sa variabilité génétique. C'est ainsi que l'on a cherché à mesurer la diversité génétique chez la population des chèvres Ghumusar au moyen de 25 marqueurs microsatellites. Pour mener cette étude, l'ADN génomique isolé dans les échantillons de sang prélevés sur 50 individus choisis au hasard a été utilisé. Le nombre moyen d'allèles observés a été de 9,80 alors que le nombre moyen effectif a été de 4,28. Les contenus d'information polymorphique ont varié entre 0,53 et 0,91. L'hétérozygotie moyenne observée et attendue a été respectivement de 0,73 et 0,71. Les valeurs de la diversité génétique de Nei ont varié de 0,11 à 0,87, avec une moyenne de 0,69, au sein de la population de chèvres Ghumusar. Il a été observé que la valeur globale pour le paramètre F_{IS} était de 0,002, ce qui n'est pas statistiquement différent de zéro et indique donc une absence de déficit en hétérozygotes. Pour ce qui est du test des signes, le nombre attendu de loci avec excès d'hétérozygotie (Ha) a été respectivement de 14,88, 14,79 et 14,74 pour le modèle d'allèles infinis, le modèle de mutation par étape et le modèle de mutation en deux phases. Le nombre de loci observé avec excès d'hétérozygotie (Ho) a été de 14, 8 et 2 pour ces trois modèles, respectivement. Pour les trois modèles, Ho a été plus bas que Ha et cette déviation a été significative dans le cas des modèles à mutation par étape et à mutation en deux phases. Comme indiqué sur la courbe en forme de L, il n'y a pas eu de réduction génétique sévère dans la taille effective de la population des chèvres Ghumusar.

Mots-clés: *marqueurs microsatellites, polymorphisme, diversité génétique, chèvre Ghumusar*

Resumen

Las cabras Ghumusar constituyen una población caprina del oeste del distrito de Ganjam en el estado de Orissa escasamente estudiada. Se dispone de información esporádica sobre sus rasgos morfológicos pero no se encuentra ninguna información sobre su variabilidad genética. Es por ello que se ha intentado medir la diversidad genética en la población de cabras Ghumusar usando 25 marcadores microsatélites. Para este estudio se utilizó el ADN genómico aislado en las muestras de sangre de 50 individuos seleccionados aleatoriamente. El número medio de alelos observados fue de 9,80 mientras que el número medio efectivo ascendió a 4,28. Los contenidos de información polimórfica variaron entre 0,53 y 0,91. La heterocigosis media observada y esperada fue respectivamente de 0,73 y 0,71. Los valores de diversidad genética de Nei en la población caprina Ghumusar oscilaron entre 0,11 y 0,87 con una media de 0,69. Se observó que el valor global para el estadístico F_{IS} era de 0,002, el cual no difiere significativamente de cero con lo que esto indica que globalmente no hubo déficit de heterocigotos. En el caso de la prueba de signos, el número esperado de loci con exceso de heterocigosis fue de 14,88, 14,79 y 14,74 para el modelo de alelos infinitos, el modelo de mutación por pasos y el modelo de mutación en dos fases,

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respectivamente. El número de loci con exceso de heterocigosis observado fue, respectivamente, de 14, 8 y 2 para estos tres modelos. Bajo los tres modelos, el número observado de loci con exceso de heterocigosis fue menor que el esperado y esta desviación fue significativa bajo los modelos de mutación por pasos y de mutación en dos fases. Tal y como indica la curva en forma de L, no se ha dado una reducción genética grave en el tamaño efectivo de población para las cabras Ghumusar.

Palabras clave: *marcadores microsatélites, polimorfismo, diversidad genética, cabra Ghumusar*

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Introduction

Ghumusar goats form a local goat population of Orissa, which is found in the western part of Ganjam district, i.e. Bhanjanagar and its adjoining areas of Ghumusar tehsil of Orissa. The Ghumusar goats are known for good meat quality, early maturity and high prolificacy (Patro *et al.*, 2007). The body size is bigger than that of Black Bengal, but smaller than Ganjam goats, the two well-known meat breeds of goat found in Orissa. The Ghumusar goats had higher body weights at birth compared with Bengal-type goats. Their overall mean of body weights at birth, 3, 6, 9 and 12 months of age are 1.75 ± 0.02, 7.14 ± 0.04, 10.18 ± 0.03, 13.01 ± 0.03 and 17.05 ± 0.03 kg, respectively (Patro *et al.*, 2007). These goats have lower first kidding age compared with Ganjam goats, but closer to that of Black Bengal goats (Rao *et al.*, 2002). Twins are very common (62.5 percent), whereas triplets are not very common (8.0 percent). Limited information is available on the phenotype and performance of these goats, but no information on genetic diversity occurring within the Ghumusar goat population. Knowledge of genetic variability existing in a population is of utmost importance to frame any breeding programme for the propagation and genetic improvement of a breed. Therefore, an attempt has been made to know the within-population genetic variability occurring in Ghumusar goat population. The results of this study can be exploited for planning the breeding strategies to propagate and genetically improve this goat population.

Materials and methods

DNA isolation and polymerase chain reaction (PCR) amplification

Blood samples were collected from randomly selected 50 animals distributed in the breeding tract. Care was taken that the sampled animals do not have the common parentage. Genomic DNA was isolated following the standard phenol/chloroform protocol (Sambrook, Fritsch and Maniatis 1989). A battery of 25 microsatellite markers given in Table 1 was used for genetic diversity assessment of Ghumusar goat population. PCR was carried out using the standardized parameters following the touchdown-PCR protocol used by us for the amplification of genomic DNA (Verma *et al.*, 2007a, b; Dixit *et al.*, 2010). In brief, amplification for each primer was performed in a 10 µl final reaction volume containing 50 ng of genomic DNA, 10 pmol of each primer, 10 mM dNTPs, 0.5 µl Taq polymerase and 10X buffer. The amplification was carried out for 35 cycles with initial denaturation at 95 °C for 10 min, second denaturation at 95 °C for 30 s, annealing with different temperatures up to 1 min, extension for 45 s at 72 °C and final extension for 7 min at 72 °C. The amplified products were checked by electrophoresis on 2% (w/v) agarose gel. After ensuring the amplification, the PCR products were run on an automated DNA sequencer.

Genotyping

The PCR products were mixed in a ratio of 1:1.5:2:2 of FAM (blue), VIC (green), NED (yellow) and PET (red) labelled primers, respectively. The multiplexed mixture (0.5 µl) was combined with 0.3 µl of Liz 500 as internal lane standard (Applied Biosystems, USA) and 9.20 µl of Hi-Di Formamide per sample. The resulting mixture was denatured by incubation for 5 min at 95 °C and sequenced on automated DNA sequencer. The electropherogram drawn through GeneScan was used to extract sizing details of DNA fragment using Gene Mapper software (version 3.0).

Statistical analysis

Different measures of within-breed genetic variations, namely total number of alleles, allele frequencies, effective number of alleles (Ne), observed heterozygosity (Ho), expected heterozygosity (He), were estimated using the POPGENE software package (Yeh *et al.*, 1999).

Polymorphism information content (PIC) for each locus was calculated according to Botstein *et al.* (1980). The within-population inbreeding estimate (Fis) at each microsatellite locus was estimated using the FSTAT version 2.9.3.2 computer program (Goudet, 2002). Gene diversity that measures the average expected heterozygosity at each locus was also estimated by the same software.

To detect whether the Ghumusar goat population has experienced a reduction in the effective population size (genetic bottleneck), two different approaches were followed. In the first approach, based on heterozygosity excess (Hee), two different tests, namely a “sign test”

Table 1. Number of alleles, heterozygosity, PIC, inbreeding estimates and genetic diversity in Ghumusar goat population.

Locus	Na	Ne	Ho	He	PIC	Fis	Gene diversity
ILSTS005	5.00	2.26	0.75**	0.56	0.65	−0.33	0.84
ILSTS030	10.00	6.03	0.72**	0.84	0.89	0.14	0.27
ILSTS033	13.00	5.80	0.81	0.83	0.88	0.23	0.41
ILSTS065	13.00	4.67	0.79	0.79	0.87	−0.00	0.87
ILSTS087	13.00	8.54	0.93*	0.89	0.91	−0.04	0.79
ETH225	5.00	1.69	0.46*	0.41	0.64	−0.11	0.82
ILSTS058	10.00	5.77	0.92*	0.83	0.87	−0.10	0.11
ILSTS059	13.00	5.50	0.94*	0.82	0.89	−0.14	0.82
OarAE129	11.00	6.27	0.84*	0.85	0.87	0.00	0.80
OarHH64	16.00	4.16	0.87*	0.76	0.84	−0.13	0.77
RM4	7.00	4.75	0.97*	0.79	0.79	−0.22	0.75
ILSTS082	18.00	4.78	0.75	0.80	0.89	0.05	0.75
ILSTS034	4.00	2.09	0.81***	0.52	0.53	−0.56	0.87
ILSTS019	9.00	4.21	0.83	0.77	0.83	−0.08	0.79
ILSTS008	14.00	5.50	0.58	0.83	0.88	0.29	0.76
ILSTS022	7.00	3.01	0.90***	0.67	0.72	−0.33	0.82
OMHC1	12.00	3.38	0.72	0.71	0.79	−0.01	0.84
OarJMP29	4.00	1.43	0.13	0.30	0.58	0.54	0.58
OarFCB48	8.00	2.90	1.00	0.66	0.64	−0.51	0.76
OarFCB304	20.00	7.92	0.76	0.88	0.91	0.13	0.85
RM088	8.00	3.60	1.00	0.73	0.74	−0.37	0.11
ILSTS002	8.00	4.37	0.91*	0.78	0.81	−0.17	0.77
ILSTS029	9.00	3.29	0.86*	0.70	0.73	−0.23	0.65
ILSTS044	3.00	1.28	0.00	0.22	0.53	1.00	0.71
ILSTS049	7.00	3.37	0.00	0.74	0.85	1.00	0.80
Mean	9.80	4.28	0.73	0.71	0.78	0.002	0.69

Na, observed no. of alleles; Ne, effective no. of alleles; Ho, observed heterozygosity; He, expected heterozygosity; PIC, polymorphic information contents; Fis, within population inbreeding.
$^*P < 0.05$, $^{**}P < 0.01$, $^{***}P < 0.001$.

and a "Wilcoxon sign-rank test", were employed under different models of microsatellite evolution like, the infinite allele model (IAM), stepwise mutation model (SMM) and two-phased model (TPM) of mutation. The second approach was the graphical representation of the mode-shift indicator proposed by Luikart and Cornuet (1998). These two approaches were conducted using Bottleneck v1.2.02 software (http://www.ensam.inra.fr/URLB; Cornuet and Luikart (1996)).

Results and discussion

Phenotypic attributes

The Ghumusari goats are medium-sized goats, coat colour is predominantly black and brown, but animal with white and brown sports are also seen (Figure 1). The hair is short and lustrous. Face is straight and forehead is prominent. Both the sexes are horned. Horns are long, flat, directed upward and backward. Ears are medium in size and kept straight or horizontal.

Microsatellite markers

The precision of microsatellite-based genetic variability depends on the type and number of markers and the polymorphism they can detect at the loci (Barker, 1994). Therefore, the suitability of markers was studied by knowing the number of alleles at different loci and PICs. In the present investigation, the markers used are neutral and are widely distributed in the genome, their chromosomal locations are given somewhere else (Verma *et al.*, 2007a). Most of the microsatellites of this battery have been used to study the genetic variability in other Indian goat breeds such as Marwari (Kumar *et al.*, 2005), Attapaddy (Aggarwal *et al.*, 2007), Sirohi (Verma *et al.*, 2007a), Kutchi (Dixit *et al.*, 2008), Gohilwadi (Kumar *et al.*, 2009), Southern Indian goat breeds (Dixit *et al.*,

Figure 1. Colour variants of Ghumusar goats.

2010), Changthangi (Mishra *et al.*, 2010) and Konkan Kanyal (Mishra *et al.*, 2012). All the microsatellite markers were amplified successfully in Ghumusar goats also.

Genetic variability

The locus-wise number of alleles, heterozygosity and polymorphic information contents for all microsatellite markers used in the present study are presented in Table 1. A total of 247 alleles were observed for the 25 microsatellite loci. The observed number of alleles per locus ranged from 3.00 (ILSTS044) to 20.00 (OarFCB304) with a mean of 9.80 alleles per locus, whereas Ne ranged from 1.28 (ILSTS044) to 8.54 (ILSTS087) with a mean of 4.28. It has been suggested by Barker (1994) that locus with at least four alleles should be considered for diversity analysis. In the present study, majority of the markers (except ILSTS044) exhibited more than four alleles. Higher number of alleles for most of the loci indicated that all the markers were appropriate to study the genetic diversity. This is supported by the higher range of PIC values, which ranged from 0.53 (ILSTS34) to 0.91. All of the 25 microsatellite loci had PIC values greater than 0.5 indicating their high degree of informativeness for population genetic studies (Botstein *et al.*, 1980). The mean observed number of allele estimated in Ghumusar goat population was higher than that of Jakhrana goat breed (Verma *et al.*, 2007b) and Marwari goat breed (Kumar *et al.*, 2005). However, higher values were reported by Mishra *et al.* (2010) in Changthangi goats, Verma *et al.* (2007a) in Sirohi goats and Kumar *et al.* (2009) in Gohilwadi goats.

The Ho ranged from 0.00 (ILSTS044, ILSTS049) to 1.00 (RM088) with mean 0.73, while the expected ranged from 0.22 (ILSTS044) to 0.89 (ILSTS087) with mean 0.71 (Table 1). The Hos differed from expected values positively or negatively at most of the loci. The heterozygote deficiency was observed at about 36% loci. At 13 loci (ILSTS005, ILSTS087, ILSTS059, OarHH64, RM4, ILSTS034, ILSTS019, ILSTS022, OarFCB48, RM088, ILSTS002 and ILSTS029) the Ho was more than the expected values indicating an excess of heterozygotes, but the mean Ho was not significantly different from the expected one. The deviation of heterozygosity from the expected values may be due to the selection for/against heterozygotes, null alleles, population subdivision owing to the genetic drift however, pinpointing the exact reason is difficult. The high genetic diversity was also observed in northern Indian goat breeds by many workers (Kumar *et al.*, 2005, 2009; Verma *et al.*, 2007a, b; Dixit *et al.*, 2008, 2011; Rout *et al.*, 2008; Mishra *et al.*, 2010, 2012). Similar observation was made in Chinese goats (Li *et al.*, 2008), Spanish and Egyptian goats (Serrano *et al.*, 2009) and Italian goats (Muema *et al.*, 2009). The values of Nei's gene diversity in Ghumusar goat population was lowest (0.11) for ILSTS058 and RM088 and highest (0.87) for ILSTS065 and ILSTS034 with mean 0.69.

Fis is an estimate of variation within population that measures the homozygosity or reduction in heterozygosity in an individual that occurs because of non-random mating within population. Among negative values, Fis ranged from −0.56 (ILSTS034) to −0.01 (OMHC1), whereas positive values ranged from 0.05 (ILSTS082) to 1.00 (ILSTS044, ILSTS049). The positive value indicates within-population inbreeding directly or indirectly resulting in the increase in homozygosity and reduction in heterozygosity. The negative Fis indicated the excess of heterozygotes. The overall Fis value was observed to be 0.002, which showed the marginal global deficit of heterozygotes.

The Ghumusar goat population was evaluated for mutation-drift equilibrium to detect the occurrence of genetic bottleneck (reduction in effective population size) in the recent past. Three different tests were performed to detect the Hee/deficiency under the assumption of three different mutation models namely IAM, SMM and TPM, and the values for different estimates are given in Table 2. Under sign test, expected number of loci with Hee was 14.88, 14.79 and 14.74 for IAM, SMM and TPM, respectively. The observed number of loci with heterozygotic excess (He) was 14, 8 and 2 under these three models, respectively. Under all the models He was less than Hee. This difference was significant under SMM and TPM and thus, the null hypothesis of mutation-drift equilibrium is rejected except for IAM. Under standardized difference test, the statistics T2 is equal to 0.449, −4.357 and −2.347 for IAM, TPM and SMM, respectively. All the values are significantly lower than 1.645, the tabulated value of normal distribution, therefore, accepting the hypothesis of mutation-drift equilibrium (absence of bottleneck) in the population. The negative value of T2 indicated that the expansion in population size

Table 2. Mutation drift equilibrium, He/deficiency under different mutation models in Ghumusar goats.

Test	Item	Models		
		IAM	TPM	SMM
Sign test	Number of loci with excess heterozygosity (He)	14	17	23
	Number of loci with expected heterozygosity excess (Hee)	14.88	14.79	14.74
Standardized test	T-2	0.449	−4.357	−12.304
Wilcoxon test	Probability (one tail for H excess)	0.22092	0.9915	1.0000
	Probability (two tail for H excess)	0.44184	0.01051	0.0000

IAM, infinite allele model, TPM, two-phase model; SMM, stepwise mutation model.

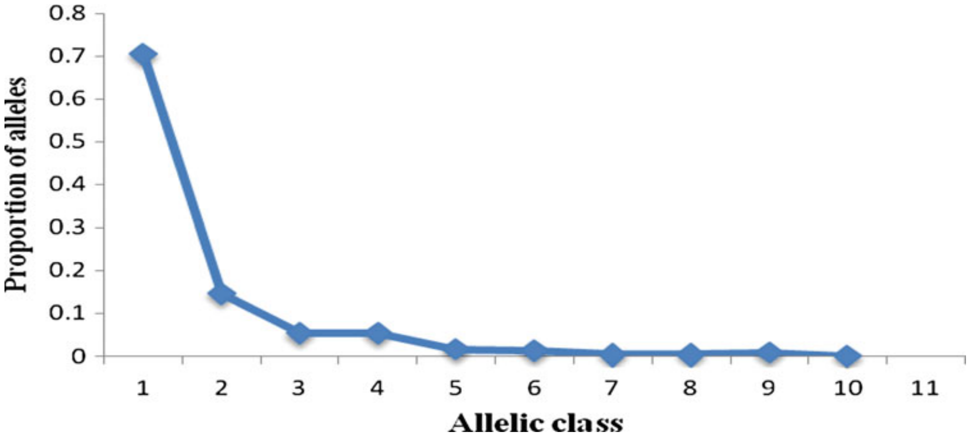

Figure 2. L-shaped distribution of allele frequencies in Ghumusar goat population.

may be because of immigration of some private (unique) alleles in population. Similar results were obtained with Wilcoxon sign-rank test that gave probability values of 0.2209, 0.9915 and 1.0000. All the values are significantly higher than 0.05 and again supports the acceptance of null hypothesis. Another test that can be utilized to test the bottleneck is the mode shift that is a qualitative graphical test of Luikart and Cornuet (1998). The method utilizes allelic classes and proportion of alleles occurring in Ghumusar goat population. The curve obtained (Figure 2) showed a normal L-shaped distribution of allele frequencies without any mode shift indicating the absence of any genetic bottleneck in the recent past. The shift mode test can detect the bottleneck up to 40–80 generations, while the quantitative test of Cornuet and Luikart (1996) can detect bottleneck up to 250 generations.

Conclusion

The study thus presents valuable insight into the existing genetic variability in Ghumusar goat population. All the microsatellite markers amplified satisfactorily and exhibited allelic polymorphism. Therefore, high genetic diversity was found in Ghumusar goat population as measured by the high values of polymorphic information content per locus and by heterozygosity in the population that indicated the presence of genetic variability. Substantial genetic diversity and polymorphism observed across the loci in Ghumusar goat population could be exploited for designing the appropriate breeding strategies for the propagation and improvement of these goats.

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Morphological characterization of the Azikheli buffalo in Pakistan

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Summary

This study aims to characterize Azikheli, an undocumented buffalo breed, in its home tract (Khwazakhela, Swat, Pakistan) under traditional farming conditions. For this purpose, 108 buffalo cows and 27 bulls were randomly selected. Mean, standard error, Student's *t* test and Chi-square test were used for various comparisons. The results show that the majority of animals have a brown coat colour. Cows have significantly higher heart girths, longer horns, longer necks and wider faces at the level of the eyes than bulls, whereas bulls have significantly longer bodies, longer ears, thicker horns, thicker necks and larger hooves than cows. Horns are flat laterally, directed backwards and then slightly upwards without twisting, leading to a sickle to semi-sickle appearance. Owing to its small body size and brown coat colour, the breed is well adapted to mountain slope grazing and thrives well away from swamps. Its adaptation to mountainous ecosystems warrants its *in situ* conservation.

Keywords: *phenotypic, morphometric, characteristics, Azikheli buffalo breed, Pakistan*

Résumé

Cette étude cherche à caractériser la race de buffle non documentée Azikheli dans son territoire d'origine (Khwazakhela, Swat, Pakistan) sous les conditions d'élevage traditionnelles. Pour ce faire, 108 bufflonnes et 27 mâles ont été sélectionnés au hasard. La moyenne, l'erreur type, le test de Student et le test du Khi-carré ont été utilisés pour faire plusieurs comparaisons. Les résultats montrent que la plupart des animaux ont un pelage brun. Les vaches ont, significativement, une circonférence thoracique plus grande, des cornes et des cous plus longs et une face plus large au niveau des yeux, par rapport aux mâles. Par contre, les mâles ont, significativement, des oreilles et des corps plus longs, des cornes et des cous plus gros et des onglons plus grands que ceux des bufflonnes. Les cornes partent horizontalement vers les côtés puis se dirigent vers l'arrière et finalement montent sans se tordre, ce qui fait que les cornes aient l'aspect d'une faucille ou demi-faucille. En raison de sa petite taille corporelle et de la couleur brune de son pelage, la race est bien adaptée au pâturage sur les flancs des montagnes et se développe bien en dehors des zones marécageuses. Son adaptation aux écosystèmes montagneux garantit sa conservation *in-situ*.

Mots-clés: *caractéristiques phénotypiques et morphométriques, race de buffle Azikheli, Pakistan*

Resumen

Este estudio pretende caracterizar el ganado Azikheli, una raza de búfalos no documentada, en su área de origen (Khwazakhela, Swat, Pakistán) y bajo condiciones de cría tradicionales. Con este fin, se seleccionaron aleatoriamente 108 búfalas y 27 machos. Se usaron la media, el error estándar, la prueba t de Student y la prueba Chi-cuadrado para realizar múltiples comparaciones. Los resultados muestran que la mayoría de los animales presentan una capa de color marrón. Las vacas tienen, significativamente, mayores circunferencias torácicas, cuernos y cuellos más largos y la cara más ancha a la altura de los ojos, en comparación con los toros. Sin embargo, los toros tienen, significativamente, cuerpos y orejas más largos, cuernos y cuellos más gruesos y pezuñas más grandes que las vacas. Los cuernos parten de forma horizontal hacia los lados para a continuación dirigirse hacia atrás y después ligeramente hacia arriba sin retorcerse, con lo que adquieren un aspecto de hoz o semi-hoz. Debido a su pequeño tamaño corporal y al color pardo de su capa, la raza está bien adaptada al pastoreo en las laderas de montaña y se desarrolla bien fuera de las zonas pantanosas. Su adaptación a ecosistemas montañosos garantiza su conservación *in-situ*.

Palabras clave: *características fenotípicas y morfométricas, raza de búfalos Azikheli, Pakistán*

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Figure 1. Map of the study area.

Introduction

Indigenous livestock breeds are known for their hardiness, disease resistance, survival on little inputs and adaptability to variable environments (Köhler-Rollefson *et al.*, 2009). Such breeds are therefore believed to be more economically efficient than other breeds when raised in their home tract (Ayalew *et al.*, 2003). Many indigenous livestock breeds are, however, on the verge of extinction because of their gradual dilution, as driven by market demands and inappropriate use of new breeding technology (Köhler-Rollefson *et al.*, 2009). Limited awareness of the adaptive characteristics of indigenous livestock breeds owing to a lack of proper scientific documentation is one of the key reasons for such dilution (Hassen *et al.*, 2007; Köhler-Rollefson *et al.*, 2009).

There are quite a number of indigenous livestock breeds that still need to be scientifically documented and characterized to enable their conservation (Bhatia & Arora, 2005). To make the conservation of indigenous breeds a reality and ensure sustainable use of their genetic diversity, it is particularly desirable that their phenotypic characteristics and performance be evaluated in their home tracts and under traditional management conditions (Zarate, 1996). Identification of specific breed attributes can also contribute to better use of these genetic resources by farmers (Mwacharo *et al.*, 2006).

In Pakistan, the most thoroughly studied indigenous buffalo breeds are Nili-Ravi and Kundi, though 37 percent of the buffalo population has been categorized as non-descript (Khan *et al.*, 2007). These non-descript breeds also include Azikheli, which is known for its adaptation to the mountain environment (Khan *et al.*, 2011). The present investigation is thus designed to study the morphological (physical and morphometric) characteristics of Azikheli in its home tract under traditional management conditions.

Materials and methods

Home tract and study area

The Azikheli is named after its original home tract known as Azikhel (Khwazakhela union council). Khwazakhela, which covers an approximate area of 124 km^2 and is one of several tributary valleys of the Swat River, has been chosen as the study area for this investigation (Figure 1). Khwazakhela has a mean temperature ranging from −2°C to 33°C and an average annual rainfall of 1400 to 1500 mm (Khan & Atta-ur Rahman, 2010).

The broader home tract of the breed includes the watershed of the Swat River (Swat district) and the Panjkora River (Lower and Upper Dir districts), as well as the Shangla, Buner, Batagram, Manshera and Malakand districts, and covers approximately 20 000 km^2 and has an elevation range from 516 to 3 314 m a.s.l. Pockets of the breed can also be found in the districts of Mardan, Charsadda, Nowshera and Sawabi as a result of buffalo transhumance that prevails in some farming communities.

Sampling pattern

Khwazakhela union council includes seven main villages. Three villages were randomly selected: Tikdarai, Tetabat and Bar Shamak (Figure 1). The number of cows (with at least one parturition) and bulls (aged 3 years or more, and which are used for breeding purposes) randomly selected from these villages is presented in Table 1. For the cows, measurements were made within 2–3 months

Table 1. Sampling pattern.

Name of village	Total number of households	Number of adult cows			Number of adult bulls	
		Total	With at least one parturition	Randomly selected	Total	Randomly selected
Tikdharai	248	992	252	36	22	9
Tetabat	218	872	220	36	18	9
Bar Shamak	211	844	214	36	16	9
Total	677	2 708	686	108	56	27

after parturition by using measuring tape according to Food and Agriculture Organization (1986).

Physical characteristics (colour of the body coat, forehead, eyelashes, eyes, horns, muzzle, forelegs, hind legs and hooves) were recorded for each selected animal, and measurements were taken for the heart girth (body circumference immediately posterior to the front leg), body length (distance from shoulder point to pin bone), height at withers (the vertical distance from the ground level to the highest point of withers) and at hip bone (the vertical distance from the ground level to the hipbone), width of head (between horns and between eyes), ear length (distance from the tip of the ear to the base of the ear), ear width (at the widest part of ear), face length (the distance between the head pol and muzzle), horn length (the distance from the tip of the horn to the base of the horn both along greater and smaller curvatures), horn circumference (at base, middle region and below tip), neck length (the distance from at the junction with shoulder to at the junction with head) and circumference (at the midway from the junction with shoulder and junction with head), loin length (distance from withers to last rib), chine (distance from last rib to hipbone), rump length (distance from hip to pin bone) and width (distance between the lateral surfaces of the tuber coxae), height of front leg below the knee (vertical distance from knee to the ground level), height of hind leg below hock (vertical distance from hock to the ground level), height of pastern (vertical distance from pastern to ground level) and circumference of hoof and length of tail (distance from the tail drop to the tip of the tail).

Figure 2. Azikheli cow.

Statistical analysis

Chi-square tests of independence were used to compare the physical characteristics of bulls and cows. Mean, standard error and Student's *t* test were calculated for morphometric measurements of both sexes.

Table 2. Physical characteristics of Azikheli.

Body part	Colour pattern (%)	Cow, *n* = 108	Bull, *n* = 27	Chi-square value	*P*-value
Coat	Brown	62.04	59.26	$\chi^2_{(3)} = 0.32$	>0.05
	Black	22.22	22.22		
	Black and white	11.11	14.82		
	White	04.63	03.70		
Forehead	Completely white	61.11	55.56	$\chi^2_{(2)} = 2.93$	>0.05
	White-spotted	29.63	29.63		
	White extended to nose bridge	09.26	14.81		
Eyelashes	White	50.00	44.44	$\chi^2_{(3)} = 0.45$	>0.05
	Black	27.78	29.64		
	Brown	17.59	22.22		
	Reddish with black tinge	04.63	03.70		
Eyes	Shiny blue	80.00	76.00	$\chi^2_{(1)} = 0.45$	>0.05
	Black	20.00	24.00		
Horns	Completely brown	34.26	29.63	$\chi^2_{(3)} = 0.54$	>0.05
	Black	51.85	51.85		
	Brown with black tips	09.26	11.11		
	Black with brown tips	04.63	07.41		
Muzzle	White	55.55	51.85	$\chi^2_{(3)} = 0.17$	>0.05
	Black	15.74	18.53		
	Black and white	14.81	14.81		
	Black-pigmented to whitish-pigmented	13.90	14.81		
Forelegs	White below knee	75.00	70.37	$\chi^2_{(2)} = 0.96$	>0.05
	Completely white	10.19	07.41		
	Black and white	14.81	22.22		
Hind legs	White below hock	65.74	59.26	$\chi^2_{(2)} = 0.41$	>0.05
	Completely white	14.82	18.52		
	Black and white	19.44	22.22		
Hoof	Brown	60.19	55.55	$\chi^2_{(2)} = 0.22$	>0.05
	Black	37.04	40.75		
	Brown with black striation	2.77	03.70		

Figure 3. Azikheli bull.

Table 3. Mean values (± SEM) of morphometric measurements (cm) of Azikheli.

Variables	Cow	Bull
Heart girth	191.36 ± 1.26	177.68 ± 3.76***
Body length	140.39 ± 0.94	147.89 ± 2.60***
Height at withers	131.35 ± 0.57	130.01 ± 0.78$^{\text{NS}}$
Height at hip bone	123.41 ± 0.41	124.08 ± 0.67$^{\text{NS}}$
Width of head between horns	22.74 ± 0.27	22.15 ± 0.47$^{\text{NS}}$
Width of head between eyes	20.37 ± 0.13	19.43 ± 0.32***
Ear length	21.39 ± 0.18	22.80 ± 0.23$^{\text{NS}}$
Ear width	16.46 ± 0.12	16.86 ± 0.21$^{\text{NS}}$
Face length	52.45 ± 0.2	52.67 ± 0.55$^{\text{NS}}$
Horn length along greater curvature	42.52 ± 1.02	35.7 ± 1.36***
Horn length along smaller curvature	27.55 ± 0.82	21.62 ± 0.68***
Horn circumference at base	22.60 ± 0.22	25.12 ± 0.41***
Horn circumference in middle region	20.13 ± 0.22	20.83 ± 0.31$^{\text{NS}}$
Horn circumference below tip	7.63 ± 0.13	7.13 ± 0.21$^{\text{NS}}$
Neck length	42.57 ± 0.37	40.50 ± 0.57*
Neck circumference	89.60 ± 0.61	97.32 ± 1.81***
Loin length	35.97 ± 0.36	34.55 ± 0.55$^{\text{NS}}$
Chine	45.95 ± 0.54	46.76 ± 0.80$^{\text{NS}}$
Rump length	41.45 ± 0.31	42.03 ± 0.39$^{\text{NS}}$
Rump width	51.03 ± 0.37	50.43 ± 0.59$^{\text{NS}}$
Height of front leg below knee	30.34 ± 0.25	31.34 ± 0.43$^{\text{NS}}$
Height of hind leg below hock	46.27 ± 0.32	47.51 ± 0.38$^{\text{NS}}$
Height of pastern	5.92 ± 0.11	5.65 ± 0.14$^{\text{NS}}$
Hoof circumference	51.26 ± 0.38	53.53 ± 1.00*
Tail length	71.39 ± 1.04	67.38 ± 1.58$^{\text{NS}}$

NS, non-significant.
*$P < 0.05$, ***$P < 0.01$.

Results

Physical characteristics

No significant differences were observed between cows and bulls (Table 2). Figures 2 and 3 show examples of the Azikheli cow and bull, respectively.

Morphometric characteristics

Table 3 shows that Azikheli cows have a significantly larger heart girth, wider forehead, longer horns and longer neck than bulls. On the other hand, bulls have a significantly longer body, thicker horns and neck, and larger hooves than cows. Horns are flat laterally, and directed backwards and slightly upwards without twisting. The upward curve is variable and gives the horn a sickle or semi-sickle appearance. This is a specific characteristic of the Azikheli breed.

Discussion

Buffaloes show a variety of coat colours, with most riverine buffaloes being black to ashy grey (Soysal *et al.*, 2007), while the coat colour of swamp buffaloes ranges from grey to completely black, with very few having a white coat (Miao *et al.*, 2010). The common buffalo breeds of Pakistan are predominantly black (Khan *et al.*, 2005) with only occasional occurrence of brown coats (8 percent) in Nili-Ravi and Kundi buffalo (Maqsood, 1980). A dark coat causes heat intolerance because it absorbs a great deal of solar radiation and this is one of the reasons why dark-coated breeds wallow in swamps (Marai & Haeeb, 2010). The dominant brown coat colour (62.04 percent) in Azikheli seems to be an adaptation to the mountainous environment, where swamps are not available.

The farmers of the area prefer *Sra Chargai* (a brown coat colour with a completely white forehead) to *Sra Tikai* (a brown coat colour with a white spot on forehead).

The non-significant difference between the colour patterns of various body parts of the Azikheli cow and bull may be due to the prevalence of natural selective forces over social preferences in determining coat colour in bovines (Seo *et al.*, 2007).

Information on morphological characteristics is helpful in ensuring effective management and conservation of animal

Table 4. Comparison of morphometric measurements (cm) of Azikheli and Nili-Ravi.

Characteristics	Azikheli		Nili-Ravi[a,b]	
	Cow	Bull	Cow	Bull
Heart girth	191.36 ± 1.26	177.68 ± 3.76	215–225	225–226
Body length	140.39 ± 0.94	147.89 ± 2.60	145–149	159–165
Height at withers	131.35 ± 0.57	130.01 ± 0.78	125–135	135–137

[a] Khan, Younas & Hanjra (1982), Ranjhan & Pathak (1993), Borghese & Moioli (2005).
[b] Values for morphometric measurements of Nili-Ravi are in ranges.

genetic resources with a view to obtaining phenotypically pure local genetic resources for future selection and breed improvement strategies (Yakubu *et al.*, 2010). Berthouly *et al.* (2009) recorded heart girth, body length, height at withers, neck circumference, ear length and thorax depth as appropriate variables to differentiate the local Vietnamese swamp buffalo population from other buffalo breeds. For Pakistani buffalo breeds, such information is limited to heart girth, body length and height at withers, hence comparative measurements shown in Table 4 are limited to these three parameters.

Comparison of these parameters between the two breeds reveals that the body size of Azikheli is smaller than that of Nili-Ravi, a breed that is well adapted to life in the plains. Owing to their low maintenance requirements (Ibrahim & Brannang, 2001), smaller animals are considered less susceptible to fodder shortages (Hall, 1998) and are able to move more easily and rapidly on mountain slopes (Ouma *et al.*, 2004). As the Azikheli is native to mountain valleys with high seasonal fluctuations in the availability of feed resources, its smaller body size can be interpreted as an adaptive trait to fodder fluctuations, as well as to grazing in mountain terrain and transhumance. Sexual size dimorphism has been observed in the present study, with a longer body of the bull, whereas the cow has a large heart girth size and wider head at the eyes.

Conclusion

Given its small body size and brown coat colour, it appears that the breed is well adapted to mountain slope grazing and variable availability of feed resources. Differentiating characteristics of the Azikheli include the dominant brown coat colour and the sickle-shaped horns. In view of climate change and the likelihood of an increase in the frequency of extreme weather events in mountain regions in particular, livestock breeds like the Azikheli could prove to be a valuable resource for mountain dwellers in terms of adaptation to such weather extremes. The morphometric characteristics described here provide a basic description of the breed, but studies on genotypic characteristics and plans for *in situ* participatory conservation of the Azikheli are suggested measures to secure its appropriate conservation.

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On-farm phenotypic characterization of indigenous cattle populations of Gamo Goffa zone, Southern Ethiopia

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Summary
An exploratory survey of local cattle populations of Gamo Goffa Zone in south-western Ethiopia was conducted between April 2011 and May 2012 to identify and phenotypically characterize cattle populations. Ten focus group discussions with key informants as well as phenotypic data from sample mature animals were used to generate data, including quantitative trait data from 560 animals and qualitative trait data from 867 animals. Findings from focus group discussions revealed that, even if local cattle are found widely distributed throughout the study area, they are not known by any common name or breed type. Results from analysis of variance (ANOVA) on continuous variables showed significant ($P < 0.0001$) differences between sites. Tukey's multiple mean comparison test showed that each quantitative traits were significant ($P < 0.0001$) for sites. Chi-square test was also significant ($P < 0.0001$) for most of the categorical variables per sites. Based on a discriminant analysis, sample populations were classified into their respective sites with overall hitting rate was 63.15 percent for females and 74.89 percent for males. Canonical discriminant (CANDISC) analysis showed quantitative traits and Mahalanobis' distances between sites were significant ($P < 0.0001$). The stepwise discriminant (STEPDISC) analysis for both populations showed that most variables had significant ($P < 0.0001$) power in explaining phenotypic variation. These information from focus group discussions and phenotypic variation analyses led to identification of two cattle populations that deemed to be distinct breed types (Gamo highland and lowland). Thus, indigenous cattle population of the study area was not homogenous on their phenotypic features, and further genetic characterization should be done to confirm their genetic distinctiveness.

Keywords: *phenotypic characterization, indigenous cattle populations, Gamo Goffa Zone, Southern Ethiopia*

Résumé
D'avril 2011 à mai 2012, une étude prospective des populations bovines locales de la région du Gamu-Gofa dans le sud-ouest de l'Éthiopie a été menée pour identifier et caractériser phénotypiquement les populations bovines. Dix groupes focaux de discussion, munis d'informateurs clés ainsi que de données phénotypiques provenant des animaux adultes de l'échantillon, ont été utilisés pour générer l'information, y comprises des données quantitatives de 560 animaux et des données qualitatives de 867 animaux. Les conclusions des groupes focaux de discussion ont révélé que, bien que les bovins locaux fussent largement distribués dans l'aire d'étude, le bétail n'était connu ni par un nom commun ni par un type racial. Les résultats de l'analyse ANOVA des variables continues ont montré des différences significatives ($P < 0{,}0001$) entre les localisations. Pour chacune des variables quantitatives, le test de Tukey de comparaisons multiples a décelé des différences significatives ($P < 0{,}0001$) entre les localisations. Le test chi-carré a aussi été significatif ($P < 0{,}0001$), pour ce qui est de l'effet de la localisation, pour la plupart des variables catégorielles. D'après l'analyse discriminante, les populations échantillonnées ont été classées dans leurs respectifs emplacements avec un taux global de réussites de 63,15 pour cent pour les femelles et de 74,89 pour cent pour les mâles. L'analyse discriminante canonique a retrouvé des différences significatives ($P < 0{,}0001$) entre localisations pour les variables quantitatives et les distances de Mahalanobis. Pour les deux populations, l'analyse discriminante pas à pas "stepwise" a montré que la plupart des variables a contribué de façon significative ($P < 0{,}0001$) à expliquer la variation phénotypique. L'information des groupes focaux de discussion et les analyses de la variation phénotypique ont conduit à identifier les deux populations bovines considérées comme étant deux types raciaux différents (terres hautes et terres basses du Gamo). Ainsi, les caractéristiques phénotypiques de la population bovine indigène de l'aire d'étude n'ont pas été homogènes, la caractérisation génétique serait donc à poursuivre afin de confirmer les différences génétiques.

Mots-clés: *caractérisation phénotypique, populations bovines indigènes, région du Gamu-Gofa, Sud d'Éthiopie*

Resumen
Entre abril de 2011 y mayo de 2012 se realizó un estudio prospectivo de las poblaciones de ganado bovino local de la región de Gamo-Gofa en el suroeste de Etiopía con el fin de identificar y caracterizar fenotípicamente las poblaciones bovinas. Se usaron diez grupos focales de discusión, provistos con informadores clave así como con datos fenotípicos muestreados en animales adultos, para generar información, incluyendo datos de variables cuantitativas de 560 animales y datos de variables cualitativas de 867 animales. Las conclusiones de los grupos focales de discusión revelaron que, si bien el ganado bovino local estaba ampliamente distribuido por el área de

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estudio, el ganado no era conocido por ningún nombre común ni tipo racial. Los resultados del análisis ANOVA de las variables continuas mostraron diferencias significativas ($P < 0{,}0001$) entre emplazamientos. Para cada una de las variables cuantitativas, la prueba de comparación múltiple de Tukey mostró que hubo diferencias significativas ($P < 0{,}0001$) entre emplazamientos. La prueba Chi-cuadrado también fue significativa ($P < 0{,}0001$) entre emplazamientos para la mayoría de las variables categóricas. En base al análisis discriminante, las poblaciones muestrales fueron clasificadas en sus respectivos emplazamientos con una tasa global de aciertos de 63,15 por ciento para las hembras y 74,89 por ciento para los machos. El análisis discriminante canónico mostró que las variables cuantitativas y las distancias de Mahalanobis eran significativamente ($P < 0{,}0001$) distintas entre emplazamientos. Para ambas poblaciones, el análisis discriminante por pasos "stepwise" mostró que la mayoría de las variables contribuyeron de forma significativa ($P < 0{,}0001$) a explicar la variación fenotípica. La información de los grupos focales de discusión y los análisis de la variación fenotípica llevaron a la identificación de dos poblaciones bovinas que fueron consideradas como dos tipos raciales distintos (tierras altas y tierras bajas de Gamo). Así, la población bovina autóctona del área de estudio no fue homogénea en sus rasgos fenotípicos, con lo que se debería proseguir con la caracterización genética para confirmar sus diferencias genéticas.

Palabras clave: *caracterización fenotípica, poblaciones bovinas autóctonas, región de Gamo-Gofa, Sur de Etiopía*

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Introduction

Ethiopia is believed to have the largest livestock population in Africa. Results of the latest livestock population census showed about 53.4 million heads of cattle (CSA, 2010/11), without including cattle populations of three zones of Afar and six zones of Somali Regions. The majority (99.26 percent) of the cattle population are local breeds, which are found in rural areas under subsistence mode of farming. Cross-bred and pure exotic cattle accounted for about 0.64 and 0.1 percent, respectively (CSA, 2010/11).

Apart from the large cattle population widely distributed throughout the country, the multiple production and service functions of cattle are crucial in the livelihoods of farmers and pastoralists. They serve as sources of milk, meat, hide, draft power and manure as well as contribute to nutrient recycling at the farm level (Getachew and Gashaw, 2001). Moreover, at the level of the national economy, the livestock sector contributes 26 percent of the agricultural gross domestic product (GDP) and 12 percent to the national GDP (CSA, 2008/09).

Based on the available information as summarized in Domestic Animal Genetic Resources Information System (DAGRIS) database (DAGRIS, 2011) there are 33 recognized indigenous cattle breeds in Ethiopia. Lately some more breed types have been identified and reported, such as the Wegera, Dembia and Mahibere-silassie breeds in the north-west (Wuletaw, 2004), Abergalle and Irob cattle breeds in the north (Zerabruk and Vangen, 2005), Gojjam Highland zebu and Fogera breeds in the central highlands (Getachew, 2006) and Wollo Highland, Raya Sanga and Afar Sanga in the north-east (Tadesse, 2005). However, only a small number of recognized cattle breed types have a fair description of their physical appearance, indications of their level of production, reproduction and genetic attributes (Ayalew *et al.*, 2004). Owing to lack of specific information, cattle of the present study area are generally referred to in the existing literature as Goffa zebu or Goffa Dwarf (Epstein, 1971; Payne and Hodges, 1997; Rege and Tawah, 1999). This does not reflect the current phenotypic diversity of the cattle populations in the Gamo Goffa zone of south-western Ethiopia.

Phenotypic as well as genetic characterization of indigenous livestock genetic resources provides the basis for any livestock development intervention. Clearly, sustainable utilization of local breeds is the best means of conserving these genetic resources. The first essential step towards sustainable utilization of these resources is to identify the major breed types, establish their population size as well as their geographical distribution and describe their typical qualitative and quantitative phenotypic traits (Negussie and Ayalew, 2002). On that basis, the present study was conducted to survey local cattle types in the Gamo Goffa zone to test the general hypothesis that the local cattle populations of this zone are phenotypically homogenous.

Materials and methods

Description of study area

This study was conducted in Gamo Goffa zone of south-western Ethiopia. Gamo Goffa zone is one of 13 zones of the Southern Nations, Nationalities and Peoples Regional State (SNNPRS) and consists of 15 rural districts and two town administrations. It is situated near the centre of the region around 5°57″–6°71″N latitude and 36°37″–37°98″E longitude. Its general elevation ranges from 600 to 3500 m asl; it receives 600–1600 mm rainfall per annum and annual temperature ranges from 10°C to 34°C (Gamo Goffa zone ARDD, 2010). Agro-ecological features of each study sites are presented in Table 1 below.

The topography of the zone is characterized by undulating landscapes that favour the existence of different climatic zones. The total human population of the zone was

Table 1. Description of the study sites.

Districts/sites	Altitude (m)	Temperature (°C)	Rainfall (mm)	Agro-ecology
Bonke	631–3400	10.8–24.5	841–1600	Highland (majority)
Chencha	1001–3500	10.5–22.5	1201–1600	Highland
Boreda	1400–2600	10.2–27.5	850–1500	Highland
Arbaminch Zuria	600–1500	12–32.6	801–1350	Lowland
Mirab Abaya	650–1600	12.633.5	600–1300	Lowland

reported as about 1.6 million (CSA, 2008/09) with a population density of 80 inhabitants per km^2.

The farming practices are mainly mixed crop–livestock systems, with crops being more dominant in the higher altitude areas and livestock being more significant in lowland areas. According to CSA (2010/11), the estimated livestock population and beehives of Gamo Goffa zone were 1 438 752 cattle, 800 704 sheep, 336 941 goats, 128 054 equines, 1 050 744 chickens and 60 996 beehives.

Study population

Indigenous cattle populations in the Gamo Goffa zone and households keeping cattle constitute the study population.

Sample size and sampling method

To define the sampling frame, available background information on the existence of phenotypically unique cattle populations in Gamo Goffa zone was surveyed through single rapid exploratory field visits to the study area coupled with focus group discussions and review of available secondary information. Based on that information, 15 rural districts of the study zone were categorized into three groups matching three presumably distinct cattle population types. These were cattle populations of highlands, mid altitude areas and the lowland area. Three sample districts (Bonke, Chencha and Boreda) from highlands and two districts (Arba-Minch-Zuria and Mirab-Abaya) from lowlands were selected for actual data collection. Cattle populations of the mid-altitude areas did not show distinct features that make them different from those of the highland and lowland areas, and instead appeared to have intermediate features of other two types. Therefore, samples were not taken from mid-altitude districts. Five study districts were selected purposively taking into account the dominant agro-ecological zone of the districts, local knowledge on cattle population types and size of the cattle population.

Linear body measurements were taken from 560 mature animals that were randomly selected from herds of representative households. Data on qualitative body form and shape were taken from a total of 867 animals (Table 2). The target number of sample cattle for a study site was 50–100 adult cows and about 30 bulls (FAO, 2012). Local cattle populations from similar agro-ecology were considered as similar in their phenotypic features, which were later verified by outcomes of focus group discussions. In order to base the phenotypic characterization on the mature body size of sample populations, morphometric measurements were taken from animals of at least 3 years of known age, or those with all their milk teeth erupted (i.e. full mouth). Elders, village leaders and individuals with extensive knowledge on unique history of existing cattle populations were selected in consultation with local agricultural extension workers for focus group discussions.

Data collection methods

Focus group discussion

Preliminary field visits were made after gathering secondary data from local livestock extension staff about the type and distribution of indigenous cattle types in the study area. Then key informant focus group discussions were held with representatives of farmer groups, extension staff and the district administration officers. A total of ten focus group discussions were held – two per site, each having 8–12 farmers plus a representative of the extension staff. The researcher facilitated the discussion at all sites. The main points for discussion included indigenous knowledge about history of origin and introduction of existing cattle types, distinctive features of the cattle types as well as their desirable and undesirable characteristics, utility and status of the existing cattle populations and other information related to indigenous cattle.

Observations and linear body measurements

Majority of both quantitative and qualitative variables recorded in this study were adapted from the standard cattle breed descriptor list of FAO (2012). In addition, FAO (1984, 1986) cattle breed descriptor lists that were extensively reviewed and applied in Ethiopia (Wuletaw,

Table 2. Sample sizes by study site.

Sites	Quantitative traits		Qualitative traits		Focus group discussions held
	Male	Female	Male	Female	
Bonke	34	76	60	100	2
Chencha	37	88	55	115	2
Boreda	36	70	59	120	2
Arbaminch Zuria	36	76	65	120	2
Mirab-Abaya	42	65	59	114	2
Total	185	375	298	569	10

2004; Tadesse, 2005; Taye, 2005) were considered and a final list of variables was developed.

Depending on FAO (2012) guideline and identified cattle population type, their distribution in the study area, 185 mature adult males (both intact and castrated) and 375 heifers and cows were randomly selected for morphometric measurements. Therefore, a total of 569 female and 298 male cattle were sampled for recording their qualitative traits. A total of 16 qualitative traits were observed: coat colour pattern, coat colour type, facial profile, muzzle colour, presence of horn, horn shape, horn orientation, ear shape, ear orientation, rump profile, facial profile, hump shape, hump location, naval flap size, udder size and teat size. Similarly, 15 quantitative traits were measured in different age categories of adult animals. Quantitative traits considered include: body length, height at wither, heart girth, neck length, ear length, tail length, horn length, pelvic width, hump length, hock circumference, canon bone circumference, dewlap width, preputial sheath width, muzzle circumference and navel flap length. Measurements were taken from each trait using textile tape measurement in centimetre unit. Heart girth was measured in the early morning before the animals were taken to grazing and watering areas.

Data management and statistical analysis

All data were entered, cleaned and managed using MS Excel© worksheet. Box plots, scatter plots and tests of normality were done to check normality of quantitative variables prior to taking data to analysis.

Information compiled from focus group discussions was summarized and synthesized to describe the origin, distribution, major characteristics and status of the respective cattle populations.

Qualitative data collected were subjected to the frequency procedure of SAS (2002) version 9.0. Chi-square tests were employed to test for the difference between the factors of interest between sites. The pair-wise comparisons for each of the categorical variables across sites based on *P*-value were derived from Bonferroni's correction (Petrie and Watson, 1999).

The importance of each quantitative variable in explaining phenotypic differences between sample cattle populations of the five sites was examined using the generalized linear model (GLM) of SAS (2002). The generated site least squares means of each of the variable were then compared using Tukey's test of multiple comparison (Klockars, Hancock and McAweeney, 1995). Considering known physiological differences among female and male animals in the measured quantitative variables, data were analysed separately for the two sex groups. The following model was used for analysing quantitative phenotypic variation between the female sample populations by considering site and parity as fixed main effects:

$$Y_{ijk} = \mu + S_i + P_j + e_{ijk},$$

where Y_{ijk} is the observed value of the linear body measurements, μ is the overall mean, S_i is the fixed effect of site i ($i = 1\ldots5$), P_j is the fixed effect of parity j ($j = 1\ldots3$), where parity was categorized as 0–2 = 1, 3–4 = 2 and >4 = 3, and e_{ijk} is the residual error.

Similarly, taking site and age class as fixed main effects, the following model was used to analyse quantitative data from males:

$$Y_{ijk} = \mu + S_i + A_j + e_{ijk},$$

where Y_{ijk} is the observed value of the linear body measurements, S_i is the fixed effect of site i ($i = 1\ldots5$), A_j is the fixed effect of age class j ($j = 1\ldots3$), where age in years was categorized as 3–5 = 1, >5–7 = 2 and >7 years = 3, and e_{ijk} is the residual error.

All interaction effects for both models were not statistically significant and so dropped from the final model.

Discriminant analysis was used on quantitative variables to classify the sampled populations into homogenous groups on the basis of the measured variables (Afifi and Clark, 1996; SAS, 2002). For canonical discriminant analysis (CANDISC), Mahalanobis' distance was used to check distance between measured populations. The stepwise discriminant (STEPDISC) analysis was employed to identify variables for their relative importance in discriminating between identified groups (SAS, 2002). Non-parametric discriminant analysis was performed to check importance of categorical variable in classifying the sample populations into homogenous groups.

Discriminant analysis models used to derive classification function for the female and male sample populations, respectively, are shown below:

$$\begin{aligned}\mathrm{SF}_i = {} & C_i + w_i\mathrm{BL} + w_i\mathrm{CBC} + w_i\mathrm{TL} + w_i\mathrm{HW} + w_i\mathrm{DW} \\ & + w_i\mathrm{EL} + w_i\mathrm{HG} + w_i\mathrm{HL} + w_i\mathrm{MC} + w_i\mathrm{NPL} + w_i\mathrm{PW} \\ & + w_i\mathrm{HC} + w_i\mathrm{HP} + w_i\mathrm{AB}, \\ \mathrm{SM}_i = {} & C_i + w_i\mathrm{BL} + w_i\mathrm{CBC} + w_i\mathrm{TL} + w_i\mathrm{DW} + w_i\mathrm{EL} \\ & + w_i\mathrm{HG} + w_i\mathrm{HL} + w_i\mathrm{HP} + w_i\mathrm{MC} + w_i\mathrm{PSW} \\ & + w_i\mathrm{PW} + w_i\mathrm{HW} + w_i\mathrm{AB} + w_i\mathrm{HC},\end{aligned}$$

where subscript 'i' denotes the respective group, C_i is a constant for the ith group, w_i is the weight of the corresponding variable in the computation of the classification score for the ith group, SF_i is the resultant classification score in female population, SM_i is the classification score in male population, BL is the body length, CBC is the canon bone circumference, DW is the dewlap width, EL is the ear length, HG is the heart girth, HL is the horn length, HP is the hump length, HC is the hock circumference, MC is the muzzle circumference, NL is the navel length, PW is the pelvic width, HW is the wither height, PSW is the preputial sheath width, AB is the neck length and TL is the tail length.

Table 3. Least square means ± SE of quantitative body measurements (cm) for all sites by sex.

Dependant variable	Male ($N = 186$)	Female ($N = 375$)	Sex
Body length	120.27 ± 0.67	108.76 ± 0.47	$P < 0.0001$
Dewlap width	19.85 ± 0.09	16.34 ± 0.18	$P < 0.0001$
Ear length	18.68 ± 0.14	18.06 ± 0.09	$P = 0.0004$
Heart girth	149.27 ± 0.81	141.27 ± 0.52	$P < 0.0001$
Horn length	17.86 ± 0.53	15.98 ± 0.32	$P = 0.0013$
Cannon bone circumference	14.01 ± 0.12	13.45 ± 0.07	$P < 0.0001$
Hump length	18.28 ± 0.25	12.60 ± 0.14	$P < 0.0001$
Hock circumference	29.43 ± 0.17	28.35 ± 0.12	$P < 0.0001$
Neck length	38.35 ± 0.21	36.01 ± 0.13	$P < 0.0001$
Pelvic width	37.06 ± 0.17	33.63 ± 0.14	$P < 0.0001$
Mouth circumference	39.00 ± 0.20	37.30 ± 0.12	$P < 0.0001$
Tail length	76.26 ± 0.39	72.35 ± 0.27	$P < 0.0001$
Wither height	110.58 ± 0.57	102.10 ± 0.42	$P < 0.0001$

Results and discussion

Quantitative variation

All the quantitative dependent variables were significantly ($P < 0.05$) affected by sex of the animal (Table 3), confirming the widely held notion that male and female populations have markedly different body form as measured in the quantitative variables. As a result, analyses of variance (ANOVAs) on quantitative variables were performed separately for the two sexes.

ANOVA of quantitative traits in the male sample population

The overall phenotypic variation in all qualitative traits was highly significantly ($P < 0.0001$) affected by site and age class of the animals (Table 4). Since no interaction was found statistically significant, only main effects were considered. The highest (82.4 percent) rate of determination (R^2) values was calculated for body length and the smallest value for dewlap width (27.35 percent). In male sample populations, coefficients of variability ranged from 3.29 for body length to 31.84 percent for horn length.

Table 4. Level of significance of main effects for quantitative variables and their associated R^2 values for the male sample population.

Dependant variable	Mean values	Site	Age class	R^2	CV
Body length	120.27	$P < 0.0001$	$P < 0.0001$	82.4	3.29
Dewlap width	19.31	$P < 0.0001$	$P = 0.0020$	27.35	16.50
Ear length	18.68	$P < 0.0001$	$P < 0.0001$	39.5	8.79
Heart girth	149.27	$P < 0.0001$	$P < 0.0001$	64.40	4.60
Horn length	17.86	$P < 0.0001$	$P < 0.0001$	42.94	31.84
Canon bone circumference	14.01	$P < 0.0001$	$P < 0.0001$	30.80	10.10
Hump length	18.28	$P < 0.0001$	$P < 0.0001$	69.50	10.98
Hock circumference	29.42	$P < 0.0001$	$P < 0.0001$	63.52	5.04
Neck length	38.35	$P < 0.0001$	$P < 0.0001$	63.64	4.69
Sheath length	8.24	$P < 0.0001$	$P < 0.0001$	67.23	19.88
Pelvic width	37.01	$P < 0.0001$	$P < 0.0001$	65.03	4.06
Mouth circumference	39.00	$P < 0.0001$	$P < 0.0001$	44.26	5.50
Tail length	76.26	$P < 0.0001$	$P < 0.0001$	50.56	5.09
Wither height	110.58	$P < 0.0001$	$P < 0.0001$	41.84	5.56

Pair-wise comparisons of the least squares means of variables between sites (Table 5) revealed that male sample populations from Mirab-Abaya and Arbaminch-Zuria districts had the largest measurement values for all variables than from Bonke, Chencha and Boreda districts. This shows that cattle populations sampled from lowland sites were larger in their linear measurements than highland ones. As presented in Table 5, samples from Chencha followed by sample populations from Boreda and Bonke had significantly lower least squares means for most of quantitative variables.

ANOVA in quantitative traits in the female sample population

The ANOVA showed that site and parity had highly significant ($P < 0.0001$) effect on the total variation of all quantitative traits for female sample populations (Table 6). R^2 values ranged from 23.4 to 57.1 percent for hump length and heart girth, respectively. Coefficient

Table 5. Least squares means and pair wise comparisons between sites of linear body measurements (cm) for male population by sites.

Dependant variable	Bonke	Chencha	Boreda	A/Zuria	M/Abaya
Body length	115.26^{c}	115.03^{c}	115.13^{c}	125.30^{b}	130.64^{a}
Dewlap width	18.36^{b}	17.80^{b}	18.27^{b}	20.31^{a}	21.45^{a}
Ear length	17.63^{b}	18.24^{b}	19.49^{a}	17.94^{b}	19.85^{a}
Heart girth	145.32^{b}	140.55^{c}	143.79^{cb}	156.92^{a}	159.85^{a}
Horn length	15.64^{c}	15.14^{c}	13.80^{c}	19.49^{b}	24.74^{a}
Canon bone circumference	13.52^{c}	13.48^{c}	13.59^{c}	15.23^{a}	14.45^{b}
Hump length	17.17^{b}	15.75^{c}	16.08^{cb}	20.75^{a}	21.19^{a}
Hock circumference	28.20^{b}	28.21^{b}	27.83^{b}	30.86^{a}	31.62^{a}
Neck length	37.32^{c}	36.51^{cd}	36.27^{d}	41.17^{a}	40.19^{b}
Sheath length	6.57^{c}	7.02^{c}	6.11^{c}	9.97^{b}	11.02^{a}
Pelvic width	36.20^{c}	35.62^{c}	35.88^{c}	38.11^{b}	39.12^{a}
Mouth circumference	38.82^{c}	37.62^{c}	38.82^{c}	39.61^{b}	41.26^{a}
Tail length	74.73^{c}	73.13^{c}	74.11^{c}	78.08^{b}	80.52^{a}
Wither height	109.50^{bc}	108.05^{c}	109.02^{bc}	112.22^{b}	113.62^{a}

^{a,b,bc,c,cb,cd,d} Least squares means with different superscripts within the same row are significantly ($P < 0.05$) different.

Table 6. Level of significance of main effects for each of the variables and associated R^2 (%) values for the female sample population.

Dependant variable	Mean	Site	Parity	R^2 (%)	CV
Body length	108.79	$P < 0.0001$	$P < 0.0001$	40.6	6.57
Dewlap width	16.35	$P < 0.0001$	$P < 0.0001$	32.7	18.73
Ear length	18.06	$P < 0.0001$	$P < 0.0001$	26.5	9.18
Heart girth	141.30	$P < 0.0001$	$P < 0.0001$	57.1	4.83
Horn length	15.94	$P < 0.0001$	$P < 0.0001$	34.2	32.46
Canon bone circumference	13.45	$P < 0.0001$	$P < 0.0001$	26.2	9.81
Hump length	12.60	$P < 0.0001$	$P < 0.0001$	23.4	19.77
Hock circumference	12.35	$P < 0.0001$	$P < 0.0001$	45.5	6.38
Neck length	36.02	$P < 0.0001$	$P < 0.0001$	40.6	5.59
Pelvic width	33.63	$P < 0.0001$	$P < 0.0001$	27.3	7.19
Mouth circumference	37.28	$P < 0.0001$	$P < 0.0001$	42.0	4.92
Tail length	72.37	$P < 0.0001$	$P < 0.0001$	30.0	6.21
Navel flap length	3.00	$P < 0.0001$	$P < 0.0001$	33.0	28.6
Wither height	102.13	$P < 0.0001$	$P < 0.0001$	42.0	6.14

of variability of female sample population explained by the model ranged from 4.92 percent for mouth circumference to 32.46 percent for horn length, respectively.

Pair-wise comparisons between sites (Table 7) showed significant ($P < 0.0001$) differences for all the quantitative traits. The highest least squares means for all measurements were recorded for sample cattle populations of Mirab-Abaya and Arbaminch-Zuria. As was observed on the male sample populations, relatively small measurements were observed for sample cattle populations at Bonke, Chencha and Boreda districts.

Qualitative variations

The chi-square tests for colour type, horn orientation, ear orientation, dewlap size and rump size were highly significant, compared with those for facial profile, colour pattern and hump shape. All other variables were not significant ($P > 0.05$). Associations of categorical variables with sites were much variable and ranged from 0.124 to 0.526 for hump location and dewlap size, respectively, using Phi coefficient; 0.123 for hump location, 0.462 for coat colour type using contingency coefficient, 0.115 for body condition score and 0.465 for dewlap size using Cramer's V (Table 8).

Table 8. Chi-square tests and levels of association of sites with the categorical variables.

Variable	*P*-value	Phi coefficient	Contingency coefficient	Cramer's V
Coat colour Pattern	$P = 0.040$	0.233	0.227	0.165
Coat colour type	$P < 0.0001$	0.521	0.462	0.261
Muzzle colour	$P = 0.210$	0.191	0.187	0.135
Horn presence	$P = 0.341$	0.174	0.171	0.123
Horn shape	$P = 0.073$	0.288	0.298	0.277
Horn orientation	$P < 0.0001$	0.399	0.371	0.199
Ear shape	$P = 0.109$	0.159	0.157	0.159
Ear orientation	$P < 0.0001$	0.462	0.420	0.327
Hump shape	$P = 0.038$	0.234	0.228	0.165
Hump location	$P = 0.334$	0.124	0.123	0.123
Facial profile	$P = 0.005$	0.225	0.219	0.225
Dewlap size	$P < 0.0001$	0.526	0.372	0.465
Rump size	$P < 0.0001$	0.329	0.313	0.233
Condition score	$P = 0.461$	0.199	0.195	0.115

As presented in Table 8, variables other than colour pattern, muzzle colour, horn shape, hump shape, dewlap size, navel flap size and udder size did not make significant contributions in distinctly separating sample populations. Pair-wise comparisons made using the Bonferroni's correction grouped sample populations from Bonke, Chencha and Boreda into similar group and those from

Table 7. Least square means and pair wise comparisons between sites of body measurements (cm) for female population.

Dependant variable	Bonke	Chencha	Boreda	A/Zuria	M/Abaya
Body length	105.47^{c}	105.00^{c}	108.92^{b}	115.83^{a}	115.00^{a}
Dewlap width	14.79^{c}	14.98^{c}	16.65^{b}	17.98^{a}	20.37^{a}
Ear length	17.31^{b}	17.95^{b}	18.82^{a}	18.88^{a}	19.24^{a}
Heart girth	136.10^{b}	136.74^{b}	135.73^{b}	150.65^{a}	153.80^{a}
Horn length	13.35^{c}	14.88^{b}	15.13^{b}	19.97^{a}	20.73^{a}
Cannon bone circumference	13.00^{d}	13.48^{c}	13.61^{cb}	14.43^{a}	13.98^{b}
Hump length	10.86^{c}	12.38^{b}	13.55^{a}	13.83^{a}	13.28^{a}
Hock circumference	27.36^{c}	27.39^{c}	27.96^{b}	30.30^{a}	30.62^{a}
Neck length	35.94^{b}	34.19^{cb}	34.88^{c}	37.95^{a}	38.21^{a}
Navel flap length	2.11^{c}	2.56^{b}	2.39^{b}	4.57^{a}	5.56^{a}
Pelvic width	32.75^{d}	32.76^{d}	33.69^{c}	34.51^{b}	35.80^{a}
Mouth circumference	37.32^{c}	37.17^{c}	37.03^{c}	38.42^{b}	39.82^{a}
Tail length	69.68^{d}	71.44^{c}	72.85^{b}	75.60^{a}	74.94^{a}
Wither height	99.68^{c}	98.27^{c}	103.33^{b}	108.62^{a}	107.76^{a}

^{a,b,c,cb,d}Least squares means with different superscripts within the same row are significantly ($P < 0.05$) different.

Table 9. Pair-wise comparisons of discrete variables using the Bonferroni's correction.

Variable	Bonke	Chencha	Boreda	M/ Abaya	A/ Zuria
Coat colour pattern	a	a	a	b	b
Coat colour type	a	a	a	a	a
Muzzle colour	a	a	a	b	b
Horn presence	a	a	a	a	a
Horn shape	a	a	a	b	a
Horn orientation	a	a	a	a	a
Ear shape	a	a	a	a	a
Ear orientation	a	a	a	a	a
Hump shape	a	a	a	b	b
Hump location	a	a	a	a	a
Facial profile	a	a	a	a	a
Dewlap size	a	a	a	b	b
Rump size	a	a	a	a	a
Nave l flap size	a	a	a	b	b
Udder size	a	a	a	b	b
Teat size	a	a	a	a	a

Sites with same letter on the same row are not significantly different at ($P < 0.05$).

Arbaminch Zuria and Mirab Abaya into another category (Table 9).

Multivariate analysis

Discriminant analysis

The correct classification for female sample population into their site group ranged from 43.18 to 81.43 percent (Table 10). The overall average error count estimate was 36.85 percent for all observations and 63.15 percent of the samples were correctly classified. This higher error rates, for instance in Chencha and Arbaminch Zuria populations, indicate lower homogeneity of cattle populations in these samples and perhaps greater admixtures with adjacent cattle population types. For instance, populations from highland sites (Bonke, Chencha and Boreda) shared high number of cross-classifications with each other; this was also true for Arbaminch-Zuria and Mirab-Abaya. This also confirms that populations from these sites were phenotypically more closely related to each other.

In the case of males, the correct classifications ranged from 69.44 to 80.95 percent (Table 11). The overall percentage correctly classified for male sample populations was 74.89 percent. The highest correct classification percentage was observed for Mirab-Abaya in contrast to the least for samples from Arbaminch-Zuria district.

The overall correct classification rate (hit ratio) of 74.89 percent for males was higher than 63.15 percent for females. The first five quantitative variables that contributed more to group discrimination for female sample populations were muzzle circumference, neck length, navel flap length, heart girth and pelvic width. Ear length, hump length and tail length had least power in explaining variation between female populations across sites. For the male sample populations, the most significant discriminating quantitative variables were pelvic width, neck length, hump length, preputial sheath width and hock circumference.

Canonical discriminant analysis

The pair-wise squared Mahalanobis' distances between sites for female sample populations were highly significant ($P < 0.0001$). This shows that female populations from each site have distinct and measurable group differences from other sampled populations. The shortest distance (3.77) was measured between Bonke and Chencha sites and the longest distance (22.74) was measured between M/Abaya

Table 10. Number of observations and percent classified (below) in different sites for female sample population using discriminant analysis.

From site	A/Zuria	Bonke	Boreda	Chencha	M/Abaya	Total
A/Zuria	42 (55.26)	4 (5.26)	9 (11.84)	4 (5.26)	17 (22.37)	76 (100)
Bonke	1 (1.32)	53 (69.74)	11 (14.47)	11 (14.47)	0 (0.00)	76 (100)
Boreda	0 (0.00)	3 (4.29)	57 (81.43)	10 (14.29)	0 (0.00)	70 (100)
Chencha	3 (3.41)	27 (30.68)	20 (22.73)	38 (43.18)	0 (0.00)	88 (100)
M/Abaya	11 (16.92)	3 (4.62)	2 (3.08)	6 (9.23)	43 (66.15)	65 (100)

Table 11. Number of observations and percent classified (below) in different sites for male sample population using discriminant analysis.

From site	Bonke	M/Abaya	Chencha	A/Zuria	Boreda	Total
Bonke	24 (70.59)	0 (0.00)	4 (11.76)	1 (2.94)	5 (14.71)	34 (100)
M/Abaya	1 (2.38)	34 (80.95)	2 (4.76)	5 (11.90)	0 (0.00)	42 (100)
Chencha	5 (13.51)	0 (0.00)	28 (75.68)	0 (0.00)	4 (10.81)	37 (100)
A/Zuria	5 (13.89)	3 (8.33)	2 (5.56)	25 (69.44)	1 (2.78)	36 (100)
Boreda	2 (5.56)	0 (0.00)	6 (16.67)	0 (0.00)	28 (77.78)	36 (100)

Table 12. Squared Mahalanobis' distance between sites for the female sample populations.

From site	A/Zuria	Bonke	Boreda	Chencha	M/Abaya
A/Zuria	+++				
Bonke	18.79	+++			
Boreda	16.09	9.97	+++		
Chencha	16.68	3.77	5.77	+++	
M/Abaya	4.90	20.42	22.74	20.20	+++

Table 14. Squared Mahalanobis distance between sites for the male sample populations.

From site	A/Zuria	Bonke	Boreda	Chencha	M/Abaya
A/Zuria	+++				
Bonke	11.92	+++	+++	+++	+++
Boreda	20.86	4.75	3.53	18.23	
Chencha	13.34	3.10	25.45		
M/Abaya	8.96	20.17			

and Boreda sites (Table 12). This indicates that sample populations from Bonke and Chencha, and perhaps Boreda as well, were not much different in the group quantitative features under consideration. The same is true in group differences between Arbaminch-Zuria and Mirab Abaya.

The univariate statistic testing the hypothesis that class means are equal shows that each variable is a highly significant ($P < 0.0001$) contributor to the total variation. The multivariate statistics for differences between the sites was also significant ($P < 0.0001$) in all of the four multivariate tests (Wilks' lambda, Pillai's trace, Hotelling–Lawley trace and Roy's greatest root for female sample population; Table 13). Wilks' lambda, the ratio of within-group variability to total variability on the discriminator variables, is an inverse measure of the importance of the discriminant functions. The Wilks' lambda test for the female sample populations was 0.223 (Table 13). This shows that most (77.77 percent) of the variability in the discriminator variables was because of differences between populations rather than variation within populations.

The procedure for canonical discriminant analysis extracted four canonical variates for female sample populations, of which the first two canonical variates (can1 and can2) accounted for about 89.01 percent of the total variation (Table 13). The rest two canonical variates account for only 10.09 percent of the total variance. The plot of the first two canonical variates (can1 and can2) shows that can1 best separated female sample populations of the two sites (Arbaminch-Zuria and Mirab-Abaya, lowland types), from the other three sites (highland types). The second canonical variate further separated sample populations at Bonke from those at Boreda, with those at Chencha falling in between the two. Based on these results, the CANDISC procedure of SAS (2002) classified female sample populations into two distinct populations – highland and lowland types.

In the case of male sample populations, the squared Mahalanobis' distance between the sites was slightly higher than it was for female populations. The shortest distance (3.10) was observed between Bonke and Chencha sites and the longest distance was between Boreda and Mirab-Abaya sites with a value of 25.45 standard units (Table 14). The distances expressed here between sample populations are due to distinct phenotypic differences between populations for quantitative traits. Both univariate and multivariate tests generated from canonical discriminant analysis confirmed the existence of highly significant differences between male sample populations between highland sites (Bonke, Chencha and Boreda) and lowland sites (Arbaminch-zuria and Mirab-Abaya).

Four canonical variates were also extracted from canonical discriminant analysis on the male sample populations as was the case for female populations. The first two canonical variates (can1 and can2) altogether explained 90.24 percent of the total variation, with the remaining two accounting for only 9.76 percent of the total variation (Table 15). Based on the coefficients of the first canonical discriminant function (can 1), two clear groups of cattle populations of the study area emerged: highland types (Bonke, Chencha and Boreda) and lowland types (Arbaminch-Zuria and Mirab-Abaya).

The plot of the first two canonical variates showed to some extent similar pattern with those of female populations. In contrast with female populations, the first canonical variate

Table 13. Multivariate statistics and *F* approximations for female population.

Statistic				Value	*F* value	Num DF	Den DF	*Pr* > *F*
Wilks' lambda				**0.2236**	11.67	56	1390.8	$P < 0.0001$
Pillai's trace				1.1141	9.93	56	1440	$P < 0.0001$
Hotelling–Lawley trace				2.1608	13.72	56	1075.4	$P < 0.0001$
Roy's greatest root				1.4854	38.20	14	360	$P < 0.0001$
Eigen value		Proportion	Cum.	Ratio	*F* value	Num DF	Den DF	*Pr* > *F*
1	1.48	0.68	0.68	0.22	11.67	56	1390.8	$P < 0.0001$
2	0.43	0.20	**0.8901**	0.5557	5.97	39	1060.9	$P < 0.0001$
3	0.1348	0.0624	0.9525	0.7991	3.55	24	718	$P < 0.0001$
4	0.1027	0.0475	1.0000	0.9069	3.36	11	360	$P = 0.0002$

Table 15. Multivariate statistics and *F* approximations of male population.

Statistic				Value	*F* value	Num D	Den D	*Pr* > *F*
Wilks' lambda				**0.088**	10.05	56	651.77	$P<0.0001$
Pillai's trace				1.567	7.82	56	680	$P<0.0001$
Hotelling–Lawley trace				4.431	13.11	56	495.5	$P<0.0001$
Roy's greatest root				3.177	38.58	14	170	$P<0.0001$
Eigenvalue		Proportion	Cum.	Ratio	*F* value	Num DF	Den DF	*Pr* > *F*
1	3.1770	0.7169	0.71	0.088	10.05	56	651.77	$P<0.0001$
2	0.8222	0.1855	**0.9024**	0.371	5.08	39	498.23	$P<0.0001$
3	0.2259	0.0510	0.95	0.676	3.04	24	338	$P<0.0001$
4	0.2064	0.0466	1.00	0.828	3.19	11	170	$P=0.0006$

(can1) separated sample population of Arbaminch-Zuria and Mirab-Abaya from the other three sites that appeared bundled together. The second canonical variate (can2) further differentiated male sample populations of Bonke and Arbaminch-Zuria from Bonke and Mirab-Abaya, again Chencha appearing as an intermediate. These discriminations are in fact stronger than the outcomes based on the female samples.

Stepwise discriminant analysis

All 14 quantitative variables for both sexes were separately subjected to the STEPDISC procedure of SAS (2002) and 13 variables for females and 12 variables for males were identified as best discriminating variables on Stepwise selection summary. Wilks' lambda test shows that all the traits considered were highly significant ($P<0.0001$) contributors to discrimination of the total population into separate groups. The variables with the highest discriminating powers on the male population were sheath width, ear length, neck length, muzzle circumference, horn length, wither height, body length, canon bone circumference, hock circumference, pelvic width, heart girth and hump length (Table 16). Dewlap width and tail length did not have significant discriminating powers on the male population and were removed.

Similarly, best variables that discriminated the sample female population were heart girth, hump length, neck length, wither height and pelvic width (Table 17). Hump length was weak in separating female sample population and was removed.

Non-parametric discriminant analysis

The overall hit rate obtained from non-parametric discriminant classification was 93.6 percent (Table 18). This indicates that categorical variables are also important in classifying the populations in phenotypically distinct groups. Wuletaw (2004) reported similarly lower error rate of 2 percent, in contrast to 47.5 percent and 22.8 percent by Getachew (2006) and Tadesse (2005), respectively for similar categorical variables.

Description of the identified cattle types

Results from focus group discussions, field observations on discrete phenotypic features and univariate as well as multivariate analyses revealed that there are two major cattle types/strains identified in the study area. These are termed as Gamo highland and Gamo lowland populations taking into account their phenotypic differences as well as their geographic distribution. Both have well-developed

Table 16. Stepwise selection summary table for male populations.

Step	Entered	Partial R^2	*F*value	*Pr* > *F*	Wilks' Lambda	*Pr* < lambda	Average Squared canonical correlation	ASCC
1	PSW	0.53	51.75	$P<0.0001$	0.46	$P<0.0001$	0.13	$P<0.0001$
2	Ear length	0.22	13.09	$P<0.0001$	0.35	$P<0.0001$	0.18	$P<0.0001$
3	Neck length	0.26	15.83	$P<0.0001$	0.26	$P<0.0001$	0.23	$P<0.0001$
4	Muzzle Circ.	0.13	6.89	$P<0.0001$	0.22	$P<0.0001$	0.26	$P<0.0001$
5	Horn length	0.11	5.68	$P=0.0003$	0.20	$P<0.0001$	0.28	$P<0.0001$
6	HW	0.10	5.12	$P=0.0006$	0.18	$P<0.0001$	0.29	$P<0.0001$
7	Body length	0.22	12.36	$P<0.0001$	0.14	$P<0.0001$	0.32	$P<0.0001$
8	CBC	0.12	6.04	$P<0.0001$	0.12	$P<0.0001$	0.34	$P<0.0001$
9	Hock Circ.	0.09	4.36	$P=0.0022$	0.11	$P<0.0001$	0.34	$P<0.0001$
10	Pelvic width	0.07	3.64	$P=0.0071$	0.10	$P<0.0001$	0.36	$P<0.0001$
11	Heart girth	0.06	2.81	$P=0.0271$	0.09	$P<0.0001$	0.37	$P<0.0001$
12	Hump length	0.04	1.89	$P=0.1147$	0.09	$P<0.0001$	0.38	$P<0.0001$

Note: PSW = perputial sheath width; CBC = canon bone circumference; HW = height at withers; Circ. = circumference.

Table 17. Stepwise selection summary table for female populations.

Step	Entered	Partial R^2	*F* value	$Pr > F$	Wilks' lambda	$Pr <$ lambda	Average Squared canonical correlation	ASCC
1	Heart girth	0.5095	96.07	$P < 0.0001$	0.49	$P < 0.0001$	0.12	$P < 0.0001$
2	Hump length	0.1323	14.06	$P < 0.0001$	0.42	$P < 0.0001$	0.15	$P < 0.0001$
3	Neck length	0.0821	8.23	$P < 0.0001$	0.39	$P < 0.0001$	0.18	$P < 0.0001$
4	HW	0.1001	10.21	$P < 0.0001$	0.35	$P < 0.0001$	0.19	$P < 0.0001$
5	Pelvic width	0.0762	7.55	$P < 0.0001$	0.32	$P < 0.0001$	0.21	$P < 0.0001$
6	Ear length	0.0598	5.80	$P = 0.0002$	0.30	$P < 0.0001$	0.22	$P < 0.0001$
7	Horn length	0.0489	4.68	$P = 0.0011$	0.29	$P < 0.0001$	0.23	$P < 0.0001$
8	NPL	0.0479	4.57	$P = 0.0013$	0.27	$P < 0.0001$	0.24	$P < 0.0001$
9	Body length	0.0442	4.19	$P = 0.0025$	0.26	$P < 0.0001$	0.25	$P < 0.0001$
10	CBC	0.0473	4.48	$P = 0.0015$	0.25	$P < 0.0001$	0.25	$P < 0.0001$
11	Muzzle circ.	0.0430	4.04	$P = 0.0032$	0.24	$P < 0.0001$	0.26	$P < 0.0001$
12	Tail length	0.0297	2.74	$P = 0.0285$	0.23	$P < 0.0001$	0.27	$P < 0.0001$
13	Hock circ.	0.0257	2.36	$P = 0.0528$	0.22	$P < 0.0001$	0.27	$P < 0.0001$

Note: NPL = navel flap length; CBC = canon bone circumference; HW = height at withers; Circ. = circumference.

Table 18. Number of observations and percent classified (below in the bracket) into site using non-parametric discriminant for both sample populations.

From site	Bonke	M/Abaya	Chencha	A/Zuria	Boreda	Total
Bonke	152 (95.00)	5 (3.13)	3 (1.88)	0 (0.00)	0 (0.00)	160 (100)
M/Abaya	18 (10.59)	148 (87.06)	4 (2.35)	0 (0.00)	0 (0.00)	170 (100)
Chencha	16 (8.94)	8 (4.47)	155 (86.59)	0 (0.00)	0 (0.00)	179 (100)
A/Zuria	0 (0.00)	0 (0.00)	0 (0.00)	178 (99.44)	1 (0.56)	179 (100)
Boreda	0 (0.00)	0 (0.00)	0 (0.00)	0 (0.00)	178 (100)	178 (100)

humps and express zebu characteristics and hence both could be considered to be zebu-type cattle.

Gamo highland sub-population

These cattle were known by their high adaptability behaviour to highland production environment which is characterized by a cold climatic condition, long wet season, undulated topographic feature and high altitude above 2500 m asl. Crop residue, natural vegetation and *Enset* were major sources of feedstuffs. Animals are housed together with humans. They are multi-purpose animals and kept mainly for milk, manure, cash, traction and meat.

Key informants explained that highland cattle types are not known by general name in the community. However, owners give local names depending on coat colour type. However, some owners give traditional names to identify their animals from the herd. No clear origin information was available and farmers believe that they may have evolved from adjacent highland areas through local marketing channels. They are also well adapted to highland districts of the zone and other neighbouring areas.

Their physical distinctness is explained by small compact body size, mainly small dewlap size, small erect and thoracic hump, straight and lateral oriented ear, and proportionate head with mainly straight facial profile. Few animals were recorded with concave facial profiles. Major horn orientation recorded was upward and some had tips pointing lateral. Muzzle colour almost not pigmented and a few were found with black pigmentation. Tails were medium and reach hock bone. Spotted/pied mixture of black with other colours (red, grey and white) was common. Rump shape is mainly sloping and some are flat and roofy. Females have small to medium udder size; mainly small navel flap. Medium teat size for female animals and medium sheath size for male animals was recorded.

According to local sources, the total indigenous cattle population of all highland districts is estimated to be about 723 thousand heads. The population size is reportedly declining. Diminishing grazing land, poor extension service and poor breeding activities (indiscriminate cross breeding with Holstein bulls and traditional selection focused on high production) were suggested to have contributed to the reduction in population size (Figures 1 and 2).

Gamo lowland sub-population

This type of cattle adapts to the hotter climatic conditions of lower altitude areas with long dry season and mainly plain topography. Some of these areas are infested with tsetse flies. The altitude is below 1500 m. The dominant production system is livestock–crop mixed, and communal grazing on natural bushy pastures is common. These cattle are not known by any local name. It was suggested in the

Figure 1. Breeding cow from Bonke site.

focus group discussions that these cattle may be either related to or originated from lowland pastoral areas of Borana and South Omo.

Major production functions of the cattle include milk, draft and meat. Their roles in generating cash and meeting social obligations are also recognized. The current total estimated population of lowland cattle is 437 000, and this is known to be declining. Prevalence of various diseases and heavy parasitic infestations, expansion of crop farming at the expense of pastures, seasonal feed scarcity and lack of genetic improvement programme of existing local cattle are the major constraints identified.

Peculiar characteristics of this zebu type of cattle are mainly plain coat colour and with some being pied and spotted. Majority are plain dark/light red and fawn colour. Red and white mixtures were dominant and rarely white and black spotted were observed. Hump is located mainly at thoracic position and mostly dropping for adult males. However, there were also some cattle with cervico-thoracic hump. They were medium to large in body size with well-developed dewlap, medium neck length, wide muzzle circumference mostly with no pigmentation. Tails are long and thin, and pelvic bone is wide. In addition, majority of female animals were identified by their medium navel flap length and large, squarely arranged medium teat size and well-developed medium-sized udder. They are medium to long horned. About 92.5 percent were horned with curve shape and oriented upward. Ears are long, straight edged (81.0 percent) and laterally oriented (72.6 percent). Sample pictures from lowland cattle subpopulation are presented in Figures 3 to 5.

Figure 2. Breeding bull from Boreda site.

Figure 3. Breeding bull from Arba-Minch Zuria district.

Figure 4. Adult male animal from Mirab-Abaya district.

Figure 5. Breeding female herd from Arba-Minch Zuria district.

Conclusions

ANOVA on continuous variables showed significant ($P < 0.0001$) differences between sites, both for females and males populations. Chi-square tests for categorical variables between sites showed highly significant ($P < 0.0001$) differences between sites for most of the variables. Based on results of the discriminant analysis, sample populations were classified into two – highland and lowland cattle populations, which were corroborated by results of the canonical discriminant analysis. Results of the stepwise discriminant analysis also confirmed the distinct aggregate phenotypic differences between highland- and lowland-type cattle populations. These statistical results confirmed outcomes of the focus group discussions in which consensus was built on clear differences in body form and size between cattle populations of the highland and lowland areas of Gamo Goffa Zone.

Based on these results, the hypothesis that the local cattle populations of Gamo Goffa zone are phenotypically homogenous is rejected. Therefore, the highland- and lowland-type of cattle are significantly different in their phenotypic characteristics that merit further in-depth phenotypic and genetic studies not only to investigate their breed identity but also to lay out the basis for sustainable utilization and improvement of this indigenous genetic resource.

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Morphological characterization of Achai cattle in sedentary and transhumant systems in Pakistan

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Summary

Achai is an as yet undocumented but well-adapted cattle breed of the Hindu Kush Mountains of northern Pakistan, which is reared under sedentary farming system (SFS) and transhumant farming system (TFS). This paper compares the morphological (physical and morphometric) characteristics of this cattle breed under both farming systems to know the effect of these styles of management. Data were collected from 108 adult females and 108 males in SFS and 108 females and 36 males in TFS on physical characteristics (colour of the coat, horns, eyelashes, muzzle, hoof, switch) and morphometric measurements – i.e. heart girth, body length, height at withers, height at hipbone, face length, horn length, horn circumference, ear (length and width), neck length, dewlap length, chine length, loin length, rump (length and width), length below knee, hoof circumference, tail and switch length. Results showed that farming systems significantly affect most of the morphological characteristics of both sexes, particularly the morphometric measurements with tall and leggy conformation for TFS cows and bulls. This indicates an adaptation to long distance transhumance and mountain terrain grazing. It can be concluded that the Achai has the potential to adapt to the requirements of specific farming systems. There is hence a need for the conservation of its adaptive traits in both farming systems.

Keywords: *Achai cattle, morphological characterization, sedentary farming system, transhumant farming system*

Resumen

Pese a ser una raza bovina muy bien adaptada a las condiciones montañosas del macizo Hindu Kush en el norte de Pakistán, el ganado Achai sigue siendo un gran desconocido a día de hoy. La raza Achai es criada bajo un sistema ganadero estante (SGE) y un sistema ganadero trashumante (SGT). Este artículo compara las características morfológicas (físicas y morfométricas) de esta raza bovina bajo ambos sistemas ganaderos para conocer el efecto de estos tipos de manejo. Los datos fueron recogidos en 108 hembras adultas y 108 machos del SGE y en 108 hembras y 36 machos del SGT. Se tomaron datos de características físicas (color de la capa, de los cuernos, de las pestañas, del hocico, de las pezuñas y de la punta de la cola) y medidas morfométricas (perímetro torácico, longitud corporal, altura a la cruz, altura a la grupa, longitud de la cara, longitud y circunferencia de los cuernos, longitud y anchura de las orejas, longitud del cuello, longitud de la papada, longitud del tronco, longitud de los lomos, longitud y anchura de la grupa, longitud bajo las rodillas, circunferencia de las pezuñas, longitud de la cola y del mechón de pelo final). Los resultados mostraron que el sistema ganadero afecta significativamente a la mayoría de las características morfológicas de ambos sexos, en especial a las medidas morfométricas. Así, vacas y toros del SGT son animales altos con patas largas. Esta conformación refleja una adaptación a trashumancias de larga distancia y a un pastoreo en terrenos montañosos. Se puede concluir que el ganado Achai tiene potencial de adaptación a las necesidades de sistemas ganaderos específicos. Existe por tanto la necesidad de conservar los rasgos adaptativos de ambos sistemas de explotación.

Palabras clave: *ganado bovino Achai, caracterización morfológica, sistema ganadero estante, sistema ganadero trashumante*

Résumé

Bien qu’elle soit une race bovine bien adaptée aux conditions montagneuses de la chaîne Hindu Kush du nord du Pakistan, la race Achai demeure encore de nos jours assez inconnue. Ces animaux sont élevés selon un système d’élevage sédentaire (SES) et un système d’élevage transhumant (SET). Cet article compare les caractéristiques morphologiques (physiques et morphométriques) de cette race bovine élevée selon les deux systèmes d’exploitation pour connaître l’effet de ces pratiques d’élevage. Les données ont été prélevées sur 108 femelles adultes et 108 mâles en SES et 108 femelles et 36 mâles en SET. Les suivantes caractéristiques physiques ont été évaluées: couleur de la robe, des cornes, des cils, du museau, des sabots et de la mèche de la queue, et les suivantes mesures morphométriques ont été prises: périmètre thoracique, longueur du corps, hauteur au garrot, hauteur à la croupe, longueur de la tête, longueur et circonférence des cornes, longueur et largeur des oreilles, longueur du cou, longueur du fanon, longueur du tronc, longueur de l’échine, longueur et largeur de la croupe, longueur sous le genou, circonférence des sabots, longueur de la

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queue et de la mèche finale. Les résultats ont montré que les systèmes d'élevage affectent de façon significative la plupart des caractéristiques morphologiques aussi bien des mâles que des femelles, l'effet étant particulièrement significatif pour les mesures morphométriques. Ainsi, il a été noté que les vaches et les taureaux du SET sont de grands animaux à longues pattes. Ceci reflète une adaptation à des transhumances sur de longues distances et au pâturage en terrain montagneux. Il peut être conclu que les bovins Achai ont du potentiel pour s'adapter aux besoins de systèmes d'élevage spécifiques. La conservation de ses traits adaptatifs s'avère donc nécessaire dans les deux systèmes d'élevage.

Mots-clés: *bovins Achai, caractérisation morphologique, système d'élevage sédentaire, système d'élevage transhumant*

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Introduction

It is increasingly recognized that the use, development and conservation of livestock biodiversity are of great importance to food security, rural development and the environment (Pilling *et al.*, 2008). Phenotypic characterization of the indigenous livestock breeds is critical in breed improvement and conservation (Jing *et al.*, 2010; Kugonza *et al.*, 2011). The Achai is an as yet undocumented but well-adapted indigenous cattle breed of the Hindu Kush Mountains in northern Pakistan (Saleem *et al.*, 2012). It is a dairy and light draught breed that can thrive under scarce fodder availability, and it can produce adequately under a hilly and sub-hilly subsistence production setup (Khan *et al.*, 2008). The Achai grazes freely, is resistant to diseases and is better adapted to high altitude areas, and has a better efficiency index than all other cattle breeds of Pakistan, except Jersey crosses and Sahiwal (Kenyanjui and Sheikh-Ali, 2009). Achai cows also have a better reproductive performance than other cattle breeds in Pakistan (Saleem *et al.*, 2012).

Though the official livestock census (Anonymous, 2006) has reported the total population to be 0.59 million with 55 percent concentration in Hindu Kush Mountains, however, these figures include all the non-descript crosses having some resemblance to Achai breed. We estimate the population of phenotypically true Achai breed to be no more than 0.15 millions. This population is limited to the less accessible Hindu Kush Mountain valleys, where the agro-pastoralists still depends on Achai bulls to plough the narrow mountain terraces and hence can afford keeping Achai bull for plough as well as breeding. In these areas the average herd size of Achai cattle is four and seven animals in sedentary farming system (SFS) and transhumant farming system (TFS), respectively (Saleem *et al.*, 2012).

Owing to its important role in the future, the public sector in Khyber Pakhtunkhwa has recently initiated an Achai cattle conservation programme (Khan *et al.*, 2008). However, such conservation programmes remain ineffective because of the lack of scientific information on phenotypically pure Achai cows and bulls (Yakubu *et al.*, 2010). The current investigation shall thus fill this gap while providing the crucial information needed to establish efficient conservation efforts. The generated information will also help breeders to select better animals to keep the breed in its best condition for subsisting in remote mountains. This will insure food security for the poorest segments of Pakistani society living in the Hindu Kush Mountain region.

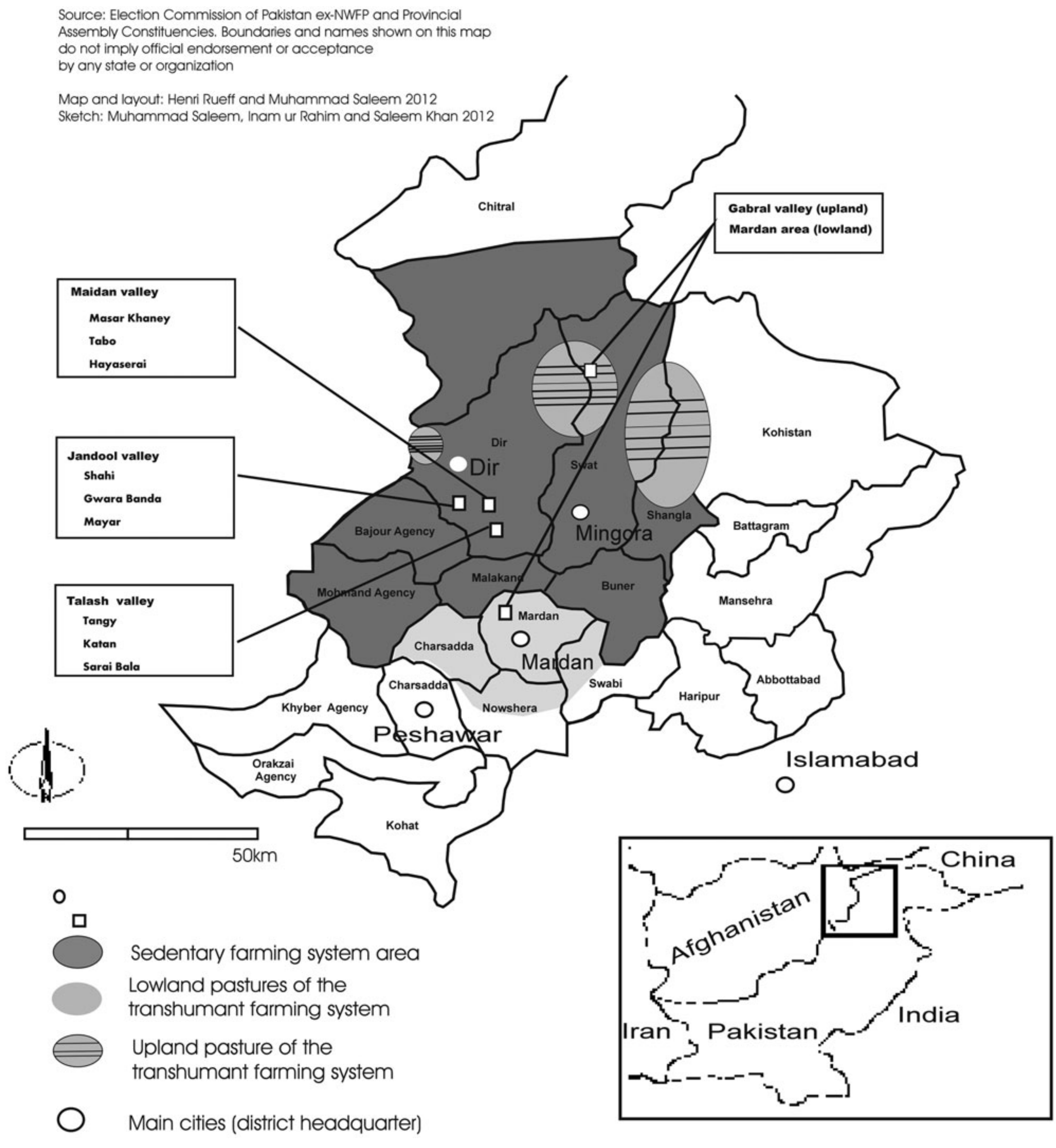
Material and methods

Study area

The broader home tract of the Achai cattle is spread over the northwestern Hindu Kush Mountains of the Khyber Pukhtunkhwa province in Pakistan. SFS are distributed over the mountain and rain-fed areas of the province. For the current study, the district of Lower Dir was taken as the study area for SFS (34°37′ to 35°07′N and 71°31′ to 72°14′E), with a mild, temperate climate, 700–1000 mm annual rainfall and 42 to 70 percent relative humidity (Anonymous, 1999). The SFS study area includes the mountainous Talash, Jandool and Maidan valleys (Figure 1). Under TFS, Achai herders spend summers in the uplands of Swat, Dir and Indus Kohistan, and winters in the major sugarcane growing lowlands of the Peshawar valley. The TFS involving transhumance between the Gabral uplands of Swat and the Mardan lowlands was taken as a representative area for the study (Figure 1). The Gabral valley lies between 35°20′ and 35°48′N and 72°12′ and 72°32′E, with a typical dry temperate zone climate (Hamayun, Afzal and Khan, 2006). The Mardan lowlands lay between 34°12′0N and 72°1′60E, and has a temperature range from 2.1 to 41.5°C, an average rainfall of 524.40 mm and humidity of 73 percent.

Attributes of the farming systems

The seasonal feeding in SFS is known as a cut-and-carry system, which provides wheat straw, weed thinning and hay in spring; wheat straw, tree leaves and hay in summer; wheat straw, maize stalks and weed thinning in fall; and wheat straw, maize stalks and hay in winter. Farmers also graze their cows on stubble fields (Saleem *et al.*, 2012). For TFS at Gabral (upland), the herders take dry cows, heifers and bulls to the high pastures for grazing, and keep milking cows at the settlements in the valley bottoms for homestead use. Milking cows are taken for grazing daily


Source: Election Commission of Pakistan ex-NWFP and Provincial Assembly Constituencies. Boundaries and names shown on this map do not imply official endorsement or acceptance by any state or organization

Map and layout: Henri Rueff and Muhammad Saleem 2012
Sketch: Muhammad Saleem, Inam ur Rahim and Saleem Khan 2012

Figure 1. Map of the study area and locations of the villages where adult Achai cows and bulls were sampled.

to the hillsides near the settlements. In the lowlands, sugarcane tops and maize stover are given during winter, and are complemented with grazing along the canal sides and on stubble fields. The breeding season spreads over the entire year. However, the majority of cows come into heat during summer. In uplands and lowlands, cows are served with the available Achai bulls (Saleem *et al.*, 2012).

Sampling pattern

The sampling pattern for the study in SFS and TFS is presented in Table 1.

Sedentary farming system

Three villages each from the Talash, Jandool and Maidan valleys in the Lower Dir district were randomly selected. From each village, 12 adult Achai cows and 12 adult Achai bulls were then randomly sampled.

Transhumant farming system

Three settlements were randomly selected in the Gabral valley where 36 adult Achai cows and 12 adult Achai bulls were observed at each settlement for physical and morphometric characteristics.

Table 1. Sampling pattern of adult Achai cows and bulls in SFS and TFS.

Management	Valley	Village/ settlement	Number of cows	Number of bulls
SFS	Talash	Tangey	12	12
		Katan	12	12
		Sarai Bala	12	12
	Jandool	Shahi	12	12
		Gwarabanda	12	12
		Mayar	12	12
	Maidan	Masar Khaney	12	12
		Tabo	12	12
		Haya serai	12	12
	Total		108	108
TFS	Gabral	Ghwai Bela	36	12
		Gul Abad	36	12
		Karin	36	12
	Total		108	36

Physical characteristics like colour of the coat, horns, eyelashes, muzzle, hooves and switch were recorded for each animal, and morphometric measurements including heart girth, body length, height at withers, height at hipbone, face length, horn length (along the greater and smaller curvature), horn circumference (at base, mid and tip), ear (length and width), neck (length and circumference), dewlap (length and circumference), chine length, loin length, rump (length and width), length below knee, hoof circumference, tail length and switch length were carried out with the help of measuring tape according to the Food and Agriculture Organization's (FAO) standard procedure (FAO, 1986). Body weight was estimated according to Shaffer's method as described by Al-Amin *et al.* (2007).

Statistical analysis

Chi-square test and Student's *t*-test was used to study the effect of a farming system (SFS, TFS) on physical and morphometric characteristics respectively performed in GraphPad Prism-5 software (GraphPad Software, San Diego, CA, USA).

Results

Physical characteristics

Physical characteristics of Achai cows and bulls in SFS and TFS are presented in Table 2.

The dominant coat colour of the cows and bulls in both farming systems is spotted reddish-brown (Figures 2 and 3). However, the farming system significantly ($P < 0.05$) affects the coat colour of Achai cows, with a higher percentage of spotted reddish-brown colour Achai cows in TFS as compared with SFS. Significant variations in the distribution of the colour of eyelashes ($P < 0.05$), muzzle ($P < 0.01$) and switch ($P < 0.01$) of the Achai cow were also observed between SFS and TFS. In the case of bulls, significant variations were observed only in the prevalence of the colour of the horn ($P < 0.01$) and the switch ($P < 0.05$) of the tail between the two systems.

Morphometric measurements and adult body weight

Morphometric measurements and body weight of Achai cows and bulls in SFS and TFS are shown in Table 3.

Table 2. Physical characteristics of Achai cows and bulls in SFS and TFS.

Colour	Description (%)	Cow		Significance	Bull		Significance
		SFS *n*=108	TFS *n* = 108		SFS *n* = 108	TFS *n* = 36	
Coat	Spotted reddish brown	59.26	72.22	*	66.67	68.57	NS
	Solid reddish brown	40.74	27.78		33.33	31.43	
Horn	Light brown with greyish black tip	44.44	25.93	NS	31.48	8.57	**
	Light brown with blackish tinge in the upper part	28.70	36.11		49.07	14.29	
	Light brown	26.85	20.37		14.81	62.86	
	Black	–	17.59		4.63	14.29	
Eyelashes	Red	76.85	62.04	*	77.78	80	NS
	Black	21.30	27.78		17.59	8.57	
	White	1.85	10.19		4.63	11.43	
Muzzle	Light brown	36.11	17.59	**	18.52	25.71	NS
	Light brown with black pigments	50.93	53.70		50.92	45.71	
	Black	12.96	28.70		30.56	28.57	
Hoof	Light brown	56.48	40.74	NS	31.48	48.57	NS
	Black	31.48	39.81		50.92	31.43	
	Light brown with black striations	12.04	19.44		17.59	20.00	
Switch	Reddish brown	55.56	22.22	**	32.41	45.71	*
	White	35.18	66.67		45.37	51.43	
	Black	9.26	11.11		22.22	2.86	

NS = not significant.
*$P < 0.05$; **$P < 0.01$.

Figure 2. Spotted reddish brown Achai (left) with Friesian cow (right) in SFS.

Achai cows in TFS have significantly higher values for most of the morphometric measurements and adult body weight than do Achai cows in SFS, except chine and loin length, which were significantly longer in SFS cows. There was no significant difference in horn length, ear length and width and height below the knee joint between Achai cows in SFS and TFS.

Achai bulls in SFS have significantly larger heart girth size, longer bodies, longer and thicker horns, long neck,

Figure 3. Spotted reddish brown Achai cows in a transhumant cattle herd in TFS.

Table 3. Mean values (±SEM) of morphometric measurements (cm) and adult body weight (kg) of Achai cows and bulls in SFS and TFS.

Variables	**Cows**		**Bulls**	
	SFS	**TFS**	**SFS**	**TFS**
Heart girth	134.33 ± 0.6	$138.60 \pm 0.64^{a**}$	140.50 ± 1.1	$134.12 \pm 1.9^{b**}$
Body length	112.20 ± 0.7	$116.11 \pm 0.71^{a**}$	116.26 ± 1.0	$112.12 \pm 1.85^{b*}$
Height at withers	101.80 ± 0.4	$103.69 \pm 0.53^{a**}$	107.62 ± 0.6	106.88 ± 1.1^{NS}
Height at hipbone	100.79 ± 0.3	$102.48 \pm 0.52^{a**}$	106.38 ± 0.4	106.09 ± 0.7^{NS}
Face length	41.27 ± 0.27	$42.57 \pm 0.20^{a**}$	41.93 ± 0.26	42.48 ± 0.46^{NS}
Horn greater curvature length	17.37 ± 0.42	17.72 ± 0.46^{NS}	19.73 ± 0.57	$16.45 \pm 0.99^{b**}$
Horn small curvature length	12.92 ± 0.34	13.81 ± 0.36^{NS}	16.09 ± 0.44	$13.04 \pm 0.77^{b**}$
Horn base circumference	11.86 ± 0.15	$12.82 \pm 0.22^{a**}$	16.75 ± 0.20	$15.94 \pm 0.54^{b*}$
Horn mid circumference	9.66 ± 0.19	$10.56 \pm 0.16^{a**}$	14.66 ± 0.24	$12.6 \pm 0.41^{b**}$
Horn tip circumference	5.22 ± 0.14	5.22 ± 0.08^{NS}	6.25 ± 0.15	5.88 ± 0.26^{NS}
Ear length	17.99 ± 0.21	16.56 ± 0.15^{NS}	16.14 ± 0.15	16.59 ± 0.26^{NS}
Ear width	11.59 ± 0.15	12.09 ± 0.11^{NS}	10.79 ± 0.11	11.34 ± 0.19^{NS}
Neck length	34.92 ± 0.52	$30.95 \pm 0.37\ ^{a**}$	33.22 ± 0.55	$30.26 \pm 0.97^{b**}$
Dewlap length	67.11 ± 1.02	$72.21 \pm 0.95^{a**}$	76.38 ± 0.97	$71.15 \pm 1.7^{b**}$
Chine length	36.81 ± 0.37	$33.08 \pm 0.26^{a**}$	39.66 ± 0.46	$34.96 \pm 0.8^{b**}$
Loin length	33.28 ± 0.45	$31.37 \pm 0.26\ ^{a**}$	29.44 ± 0.26	28.74 ± 0.45^{NS}
Rump length	30.92 ± 0.38	$36.04 \pm 0.19^{a**}$	33.45 ± 0.29	33.2 ± 0.52^{NS}
Rump width	30.55 ± 0.27	$32.00 \pm 0.18^{a**}$	27.72 ± 0.28	28.72 ± 0.49^{NS}
Length below knee	26.93 ± 0.31	26.95 ± 0.14^{NS}	27.94 ± 0.15	$28.67 \pm 0.26^{b*}$
Hoof circumference	27.94 ± 0.36	$33.49 \pm 0.22^{a**}$	33.49 ± 0.19	32.91 ± 0.33^{NS}
Tail length	78.81 ± 1.03	$91.04 \pm 0.79^{a**}$	95.06 ± 0.66	$89.39 \pm 1.16^{b**}$
Switch length	21.65 ± 0.89	$30.99 \pm 0.61^{a**}$	32.44 ± 0.5	$30.30 \pm 0.88^{b*}$
Body weight	188.23 ± 2.6	$207.13 \pm 2.59^{a*}$	215.83 ± 4.9	$190.32 \pm 8.20^{b*}$

^{a,b}Means with different superscript letters in the same row for the same sex differ significantly between SFS and TFS.
NS = not significant.
**P* < 0.05; ***P* < 0.01.

dewlap, chine, tail and switch and adult body weight than TFS Achai bulls. Achai bulls in TFS only have a significantly higher value for height below knee joint. There were no significant differences for the rest of the body measurements.

Discussion

Variation in coat colour in cattle depends upon geographical and climatic features and is reinforced by herder's preferences (Seo *et al.*, 2007; Desta, Ayalew and Hedge, 2011). The spotted reddish-brown coat colour of Achai cows and bulls in SFS and TFS may be due to the similar environmental condition in both farming system. However, the significantly ($P < 0.05$) higher percentage of spotted reddish-brown coat coloured cows in TFS could be due to the preference of the transhumant herders for this type of cows owing to better productivity. Such preference for spotting colour pattern has not been observed in SFS. Kugonza *et al.* (2012) also reported coat colour as the most important selection criteria among physical characteristics by the pastoralists rearing Ankole cattle in Uganda. In the case of bulls, the significant ($P < 0.01$) variations in the prevalence of horn colour between SFS and TFS may also be due to the herders' preference for light brown colour in TFS. In SFS, the herders give more attention to body frame followed by horn colour and orientation. Wurzinger *et al.* (2006) and Kugonza *et al.* (2012) also considered horn colour and shape as the most important phenotypic features among the physical characteristics, followed by coat colour, all of which are used as selection criteria in bulls as compared with cows.

Various morphometric measurements have been identified as the most appropriate variables to discriminate between and within cattle breeds (Mwacharo *et al.*, 2006; Yakubu *et al.*, 2010). Within the breed variation in morphometric measurements reflect adaptation to the specific production system (Hall, 1998; Kugonza *et al.*, 2011).

The significantly higher values (Table 2) for most of the morphometric measurements of Achai cows in TFS than Achai cows in SFS seem to be an adaptation to TFS, where tall (height at withers) and large body size (heart girt and body length) are suitable for trekking long distances to water and grazing points (Hall, 1998; Mwacharo *et al.*, 2006). Kugonza *et al.* (2011) also recorded significantly larger body dimensions for Ankole cattle in a pastoral system as compared with a crop-livestock production system.

Achai bulls in TFS have significantly lower values for most of the body measurements than Achai bulls in SFS, except for length below the knee joint, which was significantly higher for TFS bulls (Table 2). This could be an adaptation to mountain terrain grazing as the taller and

Table 4. Comparison of morphometric measurements (cm) of Achai cattle in SFS and TFS with other cattle breeds of Pakistan.

Breed		Sex	Heart girth	Body length	Height at wither	Source
Achai	SFS	Cow	134.33 ± 0.60	112.20 ± 0.77	101.80 ± 0.42	Present study
Achai	TFS	Bull	140.50 ± 1.12	116.26 ± 1.02	107.62 ± 0.68	
		Cow	138.60 ± 0.64	116.11 ± 0.71	103.69 ± 0.53	
		Bull	134.12 ± 1.97	112.12 ± 1.85	106.88 ± 1.16	
Lohani		Cow	139.78 ± 1.58	114.96 ± 0.79	111.84 ± 1.07	Joshi and Phillips (1953)
		Bull	160.02 ± 2.06	129.11 ± 3.05	121.92 ± 1.65	
Rojhan		Cow	152.40	124.46	106	Shah (1953)
		Bull	163.83	134.62	120.65	
Dhanni		Cow	142	137	119	Khan, Younas & Hanjra (1982)
		Bull	182	162	132	
Sahiwal		Cow	167	135	120	Khan, Younas & Hanjra (1982)
		Bull	200	160	136	
Red Sindhi		Cow	155	127	115	Khan, Younas & Hanjra (1982)
		Bull	185	145	132	
Tharparker		Cow	165.66 ± 1.35	133.25 ± 0.84	126.24 ± 1.04	Joshi and Phillips (1953)
		Bull	184.66 ± 1.60	139.95 ± 1.24	130.81 ± 0.99	
Bhagnari		Cow	169.15 ± 2.34	134.11 ± 1.02	129.54 ± 064	Wahid (1975)
		Bull	189.74 ± 1.80	156.03 ± 0.94	145.64 ± 0.68	
Dajal		Cow	205	145	136	Khan, Younas & Hanjra (1982)
		Bull	167	137	126	

leggier animals are more suitable for grazing in steep and rugged terrains than short-legged animals (Mwacharo *et al.*, 2006). The Achai bulls in TFS also have significantly ($t_{(141)} = 2.55$; $P < 0.01$) shorter body length to height at withers ratio than bulls in SFS (1.05 ± 0.01 and 1.08 ± 0.01, respectively), which indicates that TFS bulls are taller with respect to body length than SFS bulls. This sort of morphological feature is best suited to draught power in rocky mountains (Berthouly *et al.*, 2010).

The smaller body size of Achai cattle among all the cattle breeds of Pakistan, as indicated by the smaller heart girth, body length and height at wither (Table 4), seems to be an adaptive trait for survival during seasonal fodder fluctuation. This is because smaller animals are reported to be less susceptible to fodder shortages (Hall, 1998), and they can move more easily and quickly (Ouma *et al.*, 2004) on mountain slopes for grazing.

Conclusion

Because of the diversity of the Achai cattle production system, it has developed diverse morphological characteristics that suit mobility and draughtability in rugged mountain terrain, as well as better reproductive and productive performance under scarce fodder availability. These characteristics make it an ideal breed that can insure food security, particularly in relation to the changing climate that is predicted in the Hindu Kush and Himalayan regions (Hussain *et al.*, 2005). Our findings contribute to the basic information that characterizes this breed, and is relevant as a source of essential information to support the selection and conservation programmes of the Achai cattle breed under both SFS and TFS. However, comprehensive research is needed to find out the breeding goals of the relevant farming systems through which an *in situ* conservation can be made.

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Mammary immunity of White Park and Highland cattle compared with Brown Swiss and Red Holstein

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Summary

Mastitis is a frequent disease in modern dairy cows, but ancient cattle breeds seem to be naturally more resistant to it. Primary bovine mammary epithelial cells from the ancient Highland and White Park ($n = 5$) cattle and the modern dairy breeds Brown Swiss and Red Holstein ($n = 6$) were non-invasively isolated from milk, cultured, and stimulated with the heat-inactivated mastitis pathogens *Escherichia coli* and *Staphylococcus aureus* to compare the innate immune response *in vitro*. With reverse transcription quantitative polymerase chain reaction (RT-qPCR), the breeds differed in the basal expression of 16 genes. Notably CASP8, CXCL8, Toll-like receptors 2 and 4 (TLR2 and TLR4) expression were higher in the ancient breeds ($P < 0.05$). In the modern breeds, more genes were regulated after stimulation. Breed differences ($P < 0.05$) were detected in C3, CASP8, CCL2, CD14, LY96 and transforming growth factor β1 (TGFβ1) regulation. Principal component analysis separated the ancient from the modern breeds in their basal expression, but not after stimulation. ELISA of lactoferrin and serum amyloid A protein revealed breed differences in control and *S. aureus* treated levels. The immune reaction of ancient breeds seemed less intensive because of a higher basal expression, which has been shown before to be beneficial for the animal. For the first time, the innate immune response of these ancient breeds was studied. Previous evidence of breed and animal variation in innate immunity was confirmed.

Keywords: *breed comparison, primary bovine mammary epithelial cells, innate immune response, ancient and modern cattle breeds, mastitis*

Résumé

La mastite est une maladie fréquente chez les vaches laitières modernes. Or, les races bovines anciennes semblent être naturellement plus résistantes. Dans le présent travail, des cellules primaires bovines épithéliales mammaires des races anciennes *Highland* et *White Park* ($n = 5$), ainsi que des races laitières modernes *Brown Swiss* et *Red Holstein* ($n = 6$) ont été isolées du lait de façon non-invasive. Ensuite, elles ont été cultivées, puis stimulées avec les pathogènes de la mastite *Escherichia coli* et *Staphylocoque doré* – tous les deux préalablement inactivés par la chaleur – pour ainsi comparer la réponse immunitaire innée *in vitro*, utilisant la technique reverse transcription quantitative polymerase chain reaction (RT-qPCR). Il s'avère que les races diffèrent dans l'expression basale de 16 gènes. Notamment, les expressions de CASP8, CXCL8, TLR2 et TLR4 étaient élevées dans les races anciennes ($P < 0.05$). Dans les races modernes, c'est le nombre global des gènes régulés après stimulation qui était plus élevé. Des différences entre les races ($P < 0.05$) ont été détectées quant à la régulation de C3, CASP8, CCL2, CD14, LY96 et TGFβ1. L'analyse des composantes principales a permis de cloisonner les races anciennes des races modernes dans l'expression basale, mais pas après stimulation. Les mesures ELISA de lactoferrin et de sérum amyloïde A protéine ont dévoilé des différences interraciales entre le groupe du contrôle et du groupe *Staphylocoque doré.* Dans son ensemble, la réaction immunitaire de races anciennes apparaissait moins intensive en fonction d'une expression basale plus grande. Une telle atténuation avait préalablement été décrite comme étant bénéfique pour l'animal. Pour la première fois la réponse immunitaire innée de ces races anciennes a été étudiée ici. De précédentes preuves de la variation interraciale, ainsi qu'inter-animale, ont pu être confirmées par le présent travail.

Mots-clés: *comparaison de races, cellules primaires épithéliales mammaires bovines, réponse immunitaire innée, races bovines anciennes et modernes, mastite*

Resumen

La mastitis es una enfermedad de gran incidencia en ganado bovino moderno destinado a producción lechera. Sin embargo, razas más ancestrales y hoy en día casi en desuso parecen poseer una mayor resistencia natural a esta enfermedad. En el presente estudio se establecieron cultivos celulares de celulas mamarias provenientes de las razas ancestrales Highland y White Park ($n = 5$) y de las razas modernas Brown Swiss y Red Holstein ($n = 6$), para después ser infectados con los patógenos *Escherichia coli* y *Staphylococcus aureus*. Mediante reverse transcription quantitative polymerase chain reaction (RT-qPCR) se pudo determinar que la expresión basal de 16

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genes era diferente en las distintas razas. Los genes CASP8, CXCL8, TLR2 y TLR4 demonstran una mayor expresión en las razas ancestrales ($P < 0.05$). Un mayor número de genes sufría una estimulación de su expresión tras la infección con los patógenos en las razas modernas. Asi mismo fueron encontradas diferencias significativas ($P < 0.05$) entre razas en la regulación de C3, CASP8, CCL2, CD14, LY96 y TGFβ1. La concentración de las proteínas lactoferrina y serum amyloid A también es diferente en las distintas razas en células control y tratadas con *Staphylococcus aureus*. La reacción inmune tras infección fue generalmente menos intensa en células provenientes de razas ancestrales, posiblemente debido a una mayor expresión basal en estas razas, un hecho que ha sido demostrado beneficioso para el animal en trabajos previos. En resumen, los datos de este trabajo confirman la hipótesis previa de una mayor inmunidad innata en razas bovinas ancestrales en comparación con las razas modernas empleadas hoy en día.

Palabras clave: *comparación de razas, células primarias epiteliales mamarias bovinas, respuesta inmune innata, razas bovinas antiguas y modernas, mastitis*

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Introduction

Inflammation of the udder, or mastitis, causes major financial losses for farmers and diminishes the welfare of the animals. Gram-negative bacteria such as the environment-associated *Escherichia coli* mostly induce acute mastitis that can be mild or severe with grave systemic clinical symptoms (Burvenich *et al.*, 2003). In contrast with that the animal-associated Gram-positive *Staphylococcus aureus* often leads to subclinical and chronic infections with no or only mild symptoms (Riollet, Rainard and Poutrel, 2001). To better understand the disease process, primary bovine mammary epithelial cells (pbMEC) can be studied *in vitro*. Besides producing milk, these cells possess immune functions. Upon pathogen recognition via Toll-like receptors (TLRs) they secrete chemokines and inflammatory cytokines to attract immune cells and trigger the adaptive immune response. At the same time they also produce antimicrobial peptides and acute phase proteins to combat the pathogen directly (Rainard and Riollet, 2006). Modern dairy breeds are potentially more affected by mastitis than ancient breeds owing to intensive selection of milk production traits that have a negative genetic correlation with mastitis resistance (Strandberg and Shook, 1989). Observations from cattle farmers report that ancient cattle breeds that have never been selected for high milk yield seem to be naturally more resistant or tolerant to mastitis. This could be caused by different environmental and management conditions, but it could also be partly based on different genetics. However, prediction of traits by genetic values is only accurate if there are few large loci responsible for the trait rather than many small loci (Hayes *et al.*, 2010). Regarding the large number of so far identified candidate genes for mastitis traits (Ogorevc *et al.*, 2009) the latter can be assumed in the case of mastitis resistance. In addition, conventional estimation of breeding values showed that heritability of mastitis resistance is generally low (Heringstad, Klemetsdal and Steine, 2003). It is difficult to find genetic markers for phenotypic resistance when only the genomic architecture but not the resulting functional outcome is studied. That is why we looked at the functional phenotype of the innate immune system in pbMEC of two ancient and two modern cattle breeds. The Brown Swiss (BS) is one of the modern dairy breeds that are commonly used in Germany with 180 000 milk-controlled cows listed in Germany and an average milk yield of 6 800 kg/year (European Brown Swiss Federation, 2012). The Red Holstein (RH) cow is the red-allele carrying variant of the Holstein breed. It has been bred for high production traits for decades. Holstein is superior to most other dairy cattle breeds worldwide in terms of production and it is the most important dairy breed in Germany with 240 000 recorded RH and 2 million recorded Holstein cows that have an average milk yield of 8 245 and 9 008 kg/year (German Holstein Association, 2010). The British White Park (WP) cattle (Figure 1a) has been extensively described (Alderson, 1997) and is thought to be the oldest European cattle breed. Its descriptions as a sacred animal dates back to the pre-Christian Irish epics in the first century AD. It is hardy, robust and kept in extensive low-input grazing systems or parks for beef production (Alderson, 1997). Data from 11 male and 33 female WP cattle were available in Germany in 2009 (Biedermann *et al.*, 2009) and the breed has been considered as endangered-maintained in the UK, their country of origin (FAO, 2000). In Germany, the largest herd is kept in the Arche Warder, a zoological park for ancient domestic animal breeds (Biedermann *et al.*, 2009). The robust and hardy highland cattle (HLD) (Figure 1b) were originally bred in Scotland hundreds of years ago (Dohner, 2001). It was primarily used in extensive hill or mountain grazing systems for beef production, but was also used to some extent for dairy production (Dohner, 2001). With the herd book established in 1885, it is one of the oldest registered cattle breeds (Mason, 2002). Recent livestock numbers in Germany were 2 785 female and 385 male animals in 2010 (BLE, 2012). Our goal was to investigate possible phenotypic breed differences in the innate immune response against mastitis. Therefore, we cultivated pbMEC out of milk from these four breeds and stimulated them with the two major mastitis pathogens *E. coli* and

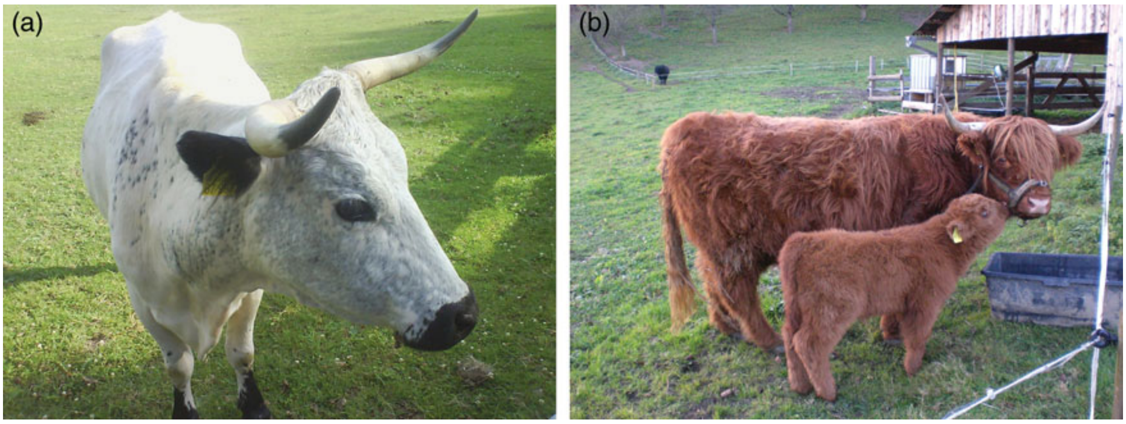

Figure 1. (a) White Park cow (Arche Warder, Zentrum für alte Haus- und Nutztierrassen e.V., Warder, Germany; photo: Diana Sorg). (b) Highland cow and calf (Rattenweiler, Germany; photo: Diana Sorg).

S. aureus. The breeds were compared in their mRNA expression of 39 target genes of the innate immune system via reverse transcription quantitative polymerase chain reaction (RT-qPCR) and in the synthesis of three antimicrobial proteins via enzyme-linked immunosorbent assay (ELISA).

Material and methods

Cell extraction from milk

Usually, pbMEC are cultivated from udder tissue after biopsy or slaughter. We chose to culture them from milk because it is a non-invasive method and therefore especially suited for rare and valuable animals. It yields less contamination by fibroblasts (Buehring, 1990) and has been shown to be an applicable alternative to tissue sampling (Sorg *et al.*, 2012). For the modern breeds, six healthy BS and six healthy RH cows (from research stations of Technische Universität München, Freising, Germany) in mid-to-late lactation were sampled in the milking parlour by machine milking into an autoclaved milk pail. For the ancient breeds, five healthy HLD (from Arche Warder and a private farm in Rattenweiler, Germany) and five healthy WP cattle (from Arche Warder) in mid-to-late lactation were automatically milked with a portable milking machine into an autoclaved milk pail or by hand milking into autoclaved glass bottles. The cells were extracted and cultivated with the method described in Danowski *et al.* (2012a) until third passage and stored in liquid nitrogen. Briefly, the milk was centrifuged at 1 850 ***g*** for 10 min to obtain the cell pellet. The pellet was washed twice with Hank's balanced salt solution (HBSS) containing 200 units/ml penicillin, 0.2 mg/ml streptomycin, 0.1 mg/ml gentamicin and 8.3 µg/ml amphotericin B (Sigma-Aldrich, Munich, Germany) and centrifuged at 600 ***g*** for 5 min. It was then resuspended in Dulbecco's modified Eagle's medium with nutrient mixture F12 Ham (DMEM/F12 Ham, Sigma-Aldrich) containing 10 percent fetal bovine serum (FBS, Gibco Life Technologies, Darmstadt, Germany), 1 × ITS supplement (Sigma-Aldrich), antibiotics as described above and 1.76 µg/ml amphotericin B (Sigma-Aldrich). The cells were cultivated in 25 cm^2 tissue culture flasks (Greiner, Frickenhausen, Germany) at 37 °C and 5 percent CO_2. For two subsequent passages, they were expanded into 75 cm^2 flasks (Greiner) by gently detaching them with accutase (PAA, Pasching, Austria). Growth and morphology was checked daily by light microscopy. After the third passage, they were resuspended in freezing medium (70 percent DMEM/F12 Ham, 10 percent FBS, 20 percent dimethyl sulfoxide (DMSO)) and stored in liquid nitrogen. Before freezing, a 16-well chamber slide (Nunc, Langenselbold, Germany) was cultivated for immunocytochemistry by seeding with 10 000 cells per well.

Bacteria

E. coli 1303 (Petzl *et al.*, 2008) and *S. aureus* 1027 (Petzl *et al.*, 2008) had been isolated from cows with clinical mastitis and shown to trigger the immune response *in vivo* (Petzl *et al.*, 2008) and *in vitro* (Gunther *et al.*, 2011). They were cultivated and harvested with the method used in Danowski *et al.* (2012a, b) and stored at −80 °C. Briefly, one colony of *E. coli* and of *S. aureus* was each cultured at 37 °C in Luria–Bertani (LB) medium containing 10 g/l yeast extract (Sigma-Aldrich), 10 g/l NaCl and 5 g/l trypton (Sigma-Aldrich) or in CASO-broth (Sigma-Aldrich), respectively, to the log-phase of growth. Bacterial density was determined photometrically at 600 nm. At several densities, a dilution series of *E. coli* and *S. aureus* was cultivated on LB agar (Roth, Karlsruhe, Germany) or on blood agar (Oxoid, Wesel, Germany, with sheep blood from Fiebig, Idstein-Niederauroff, Germany), respectively. The colonies were counted to determine the desired bacterial count and the corresponding optical density (OD). The cultivation was repeated up to the desired OD and stopped by placing the solutions on ice. The bacteria were harvested by centrifugation for 10 min at 1 850 ***g*** and washed in PBS twice. They were inactivated for 30 min at 63 °C in a water bath. A diluted sample of both harvested cell pellets was cultivated on a plate at 37 °C overnight to verify inactivation.

Cell stimulation

The 22 cultures were reseeded at 30 000 cells per well in one 12-well plate (Greiner) each and cultivated until confluent. Cells from three wells from each plate were then detached with accutase (PAA, Pasching, Austria) and counted manually for an estimate of the mean cell count per well in the other wells of the plate. Medium was removed and fresh medium without FBS, antibiotics and antimycotic was added. Heat-inactivated bacteria were added in a multiplicity of infection (MOI) of 30 colony forming units (cfu) per cell. This MOI was chosen as a typical bacterial load from other experiments with pbMEC (Danowski *et al.*, 2012a; Gunther *et al.*, 2009) to ensure that every culture received the same stimulation per cell. Control wells were left untreated. After 6 h of incubation, two wells each of control and *E. coli* treated cells were sampled from every plate. After 30 h, two wells each of control, *E. coli* and *S. aureus* treated cells, were sampled. After 78 h, two wells each of control and *S. aureus* treated cells were sampled. The incubation times were chosen to cover the often described earlier onset of the immune reaction to *E. coli* and the later reaction to *S. aureus* (Bannerman *et al.*, 2004; Gunther *et al.*, 2011; Petzl *et al.*, 2008). Cells were harvested with the lysis buffer of the Qiagen AllPrep RNA/Protein kit (Qiagen, Hilden, Germany).

Immunocytochemistry

Immunocytochemical staining of the epithelial marker cytokeratin was performed as described in Danowski *et al.* (2012a, b). Briefly, the cells were fixed on the slides and permeabilized in ice cold methanol/acetone (1:1) for 10 min. They were washed three times for 5 min in PBS-Tween (PBST). Endogenous peroxidases were blocked in 1 percent H_2O_2 for 30 min. After washing, background staining was reduced with goat serum (1:10 in PBST, DAKO, Glostrup, Denmark) for 10 min at room temperature. Monoclonal mouse anti-cytokeratin pan antibody clone C-11 (1:400 in PBST, Sigma-Aldrich) was incubated overnight at 4 °C in moist atmosphere protected from light. The negative control wells received goat serum (1:10 in PBST) instead. After washing, horseradish peroxidase (HRP) labelled goat anti-mouse-immunoglobulin (1:400 in PBST, DAKO) was incubated for 1 h. HRP was visualized with 0.01 percent diaminobenzidine and 0.01 percent H_2O_2 in PBST for 15 min at room temperature and protected from light. Nuclei were stained with Haemalaun after Mayer (Roth, Karlsruhe, Germany) for 15 s and developed with tap water. The slides were dehydrated in 50 percent ethanol, 100 percent ethanol and Rotihistol (Roth) for 2 min each and covered with Eukitt (Roth) and a cover slip.

RNA and reverse transcription

The AllPrep RNA/Protein Kit together with the RNAse-free DNAse set (both Qiagen, Hilden, Germany) was used to extract total RNA and protein from the lysed cells and remove DNA contamination following manufacturer's instructions. Concentration and purity of the obtained RNA samples were measured with the Nanodrop 1000 spectrophotometer (Peqlab, Erlangen, Germany) at 260 nm. The integrity of the RNA was analysed with the RNA 6000 Nano Assay kit on Agilent 2100 Bioanalyzer (Agilent Technologies, Waldbronn, Germany). For the reverse transcription to cDNA, a total amount of 100 ng RNA was used in a reaction volume of 30 µl containing 100 units of Moloney murine leukemia virus (M-MLV) H(−) reverse transcriptase and 5 × buffer (Promega, Mannheim, Germany), 0.5 mM dNTPs and 0.5 µM Oligo-d(T) primer (Fermentas, St. Leon-Rot, Germany), and 2.5 µM random hexamer primers (Invitrogen by Life Technologies, Darmstadt, Germany). Reverse transcription reaction was run with annealing (21 °C for 10 min), transcription (48 °C for 50 min) and degrading phase (90 °C for 2 min). To check for genomic DNA contamination, an RNA pool from each extraction run was incubated with the same protocol without reverse transcriptase.

PCR primer pairs

Primer pairs (Metabion, Martinsried, Germany) were designed with HUSAR (DKFZ, German Cancer Research Center, Heidelberg) or PrimerBLAST from NCBI (National Center for Biotechnology Information, National Library of Medicine, Bethesda, MD, USA) using mRNA sequences from the NCBI. Specificity of primer pairs was checked via melting curve analysis and gel electrophoresis of the amplified product. PCR efficiencies of the assays were measured with a five-point dilution series of three cDNA samples in qPCR triplicates and calculated as described in Bustin *et al.* (2009). Name and symbol, selected relevant functions taken from the Gene Ontology Annotation (UniProt-GOA) database (Dimmer *et al.*, 2012), NCBI reference sequence number, primer pair sequences and amplicon lengths of the genes measured in RT-qPCR are shown in Supplementary Table S1.

RT-qPCR

A primer-specific preamplification step was carried out to adjust cycle of quantification (Cq) values to the measuring range with the following temperature profile: 95 °C for 3 min followed by 18 cycles of 95 °C for 20 s, 55 °C for 3 min and 72 °C for 20 s. 4 µl cDNA were amplified in a volume of 20 µl with the iQ Supermix (Bio-Rad, Munich, Germany) and a primer concentration of 25 nM (Metabion, Martinsried, Germany) of each primer pair over 18 cycles. RT-qPCR was done on the microfluidic high-throughput BioMark™ HD system (Fluidigm, San Francisco, CA, USA) (Spurgeon, Jones and Ramakrishnan, 2008). One 48.48 Gene Expression (GE) Dynamic Array chip was used to measure PCR efficiencies of the assays and four 96.96 GE Dynamic Arrays were used to measure gene expression in the samples. One representative and stably expressed sample was chosen as between-chip calibrator and measured repeatedly on all chips. 5 ìl sample premix containing 2.5 µl SsoFast EvaGreen Supermix (Bio-Rad), 0.25 µl of sample loading reagent (Fluidigm), 0.1 µl ROX (diluted 1:3, Invitrogen), 1.25 µl preamplified and 1:9 diluted cDNA and water, as well as 5 µl assay premix containing 2 µl 10 µM primer pairs in the final concentration of 4 ìM, 2.5 µl Assay loading reagent (Fluidigm) and water were prepared and transferred to the primed GE Dynamic Array 96.96. The samples and assays were mixed inside the chip with the Nanoflex IFC controller (Fluidigm). The final concentration of primers in the individual reaction was 400 µM. The temperature profile was 98 °C for 40 s then followed by 40 cycles consisting of 95 °C for 10 s and 60 °C for 40 s. A melting curve of all PCR products was performed after the run to check for specificity. The Cq, where the fluorescence signal crossed the threshold, was detected by the BioMark Data Collection Software 2.1.1. built 20090519.0926 (Fluidigm, San Francisco, CA, USA). RT-qPCR was conducted following the minimum information for the publication of quantitative real-time PCR experiments (MIQE)-Guidelines (Bustin *et al.*, 2009).

Data analysis of RT-qPCR

Melting Curve Analysis Software 1.1.0. built 20100514.1234 (Fluidigm) and Real-time PCR Analysis Software 2.1.1. built 20090521.1135 (Fluidigm) were used to determine the valid PCR reactions. Invalid reactions were not used for later analysis and treated as missing data. Owing to loss of measurement precision, Cq values higher than 30 were treated as missing data and values between 25 and 30 were replaced by 25. Raw Cq values were processed with Genex 5.3.2 (MultID Analyses AB, Gothenburg, Sweden), using interplate calibration and reference gene normalization. Actin gamma 1 (ACTG1), keratin 8 (KRT8) and H3 histone, family 3A (H3F3A) were identified as suitable reference genes with the Normfinder tool within Genex 5.3.2. (MultID). The subtraction of reference gene Cq value index from target gene Cq value yielded the dCq value. Genex 5.3.2 (MultID) was also used for principal component analysis (PCA). All other statistical calculations were conducted with SigmaPlot 11 (Systat, Chicago, IL, USA) or SPSS Statistics Standard 21.0 (IBM, Armonk, NY, USA). Fold change in expression was calculated with the $2^{-\mathrm{ddCq}}$ method (Livak and Schmittgen, 2001). Independent *t*-tests were used to compare basal expressions and fold changes in expression between breeds ($P < 0.05$). Paired *t*-tests or signed rank tests on dCq values were used to find differentially expressed genes between treatment and control. Graphs were drawn with SPSS (IBM) or SigmaPlot 11 (Systat). It must be noted that no correction for multiple testing was imposed on the *P*-values. This study is of descriptive and explorative character only, not of a diagnostic one. Such a correction would have been too stringent and masked many of the differences.

Protein quantification with ELISA

Total protein content in the extracted cell protein was determined with the bicinchoninic acid (BCA) assay (Smith *et al.*, 1985) and measured with a photometer (Tecan, Männedorf, Switzerland). Lactoferrin (LF) was measured with the ELISA protocol and reagents used by Danowski *et al.* (2012b). Cell protein was diluted 1:1 in PBST and measured in duplicates. Interleukin-10 (IL-10) was determined using the ELISA protocol from Groebner *et al.* (2011) with minor modifications: the capture antibody mouse anti-bovine IL-10 antibody clone CC318 (AbD Serotec, Düsseldorf, Germany) was used at 5 µg/ml and the detection antibody biotinylated monoclonal mouse anti-bovine IL-10 antibody clone CC320 (AbD Serotec) was used at 1 µg/ml and incubated for 2 h. Samples were diluted 1:50 in PBST. Serum amyloid A (SAA) was measured in 30 h *E. coli* treated and control samples with the PHASE Serum amyloid A Multispecies ELISA kit (TriDelta, Maynooth, Ireland) according to manufacturer's instructions. Samples were diluted 1:67 in PBST.

Data analysis of ELISA

LF contents were calculated from the standard curve (Magellan data analysis software, Tecan, Männedorf, Switzerland). They were normalized to the total protein content of the sample and presented as ng LF/µg cell protein. A paired *t*-test in SigmaPlot 11 (Systat, Chicago, IL, USA) was used to test for differential expression of LF between treated and control samples at each time point ($P < 0.05$). Independent *t*-tests were used to compare treated and control levels between breeds. Owing to a lack of a commercial standard, relative IL-10 concentration was determined by normalizing the OD to the total protein content of the sample. To avoid interplate bias we gave the ratio of normalized ODs of treated and control samples that were each measured together on the same plate, multiplied by 100, this yielded IL-10 in % of control. SAA contents were determined with the standard curve as indicated in the manual. A paired *t*-test or signed rank test in SigmaPlot (Systat, Chicago, IL, USA) was used to compare SAA content in 30 h *E. coli* treated and control samples ($P < 0.05$). An independent *t*-test was used to compare breeds ($P < 0.05$).

Results

Cell culture and immunocytochemistry

An average of 5.98 million cells per animal with a range of 1–19 million cells was harvested for storage in liquid nitrogen. All the cultures showed a clear and continuous staining for cytokeratin, whereas the negative controls remained unstained. No cell types other than epithelial-like cells could be detected. All cultures showed the typical cobblestone-like shape with varying cell sizes. An example is shown in Supplementary Figure S2.

Gene expression

Table 1 shows the normalized basal expression of 16 innate immune genes in the untreated control samples after 6, 30 and 78 h incubation. These 16 genes were differentially expressed between breeds at one time point at least. CXCL8, LPO, CD68, CASP8, TLR2, TLR4 and MX2 were differentially expressed at all three time points. Six genes of the TLR pathway were differentially expressed at 6 h. Notably in CASP8, CXCL8, TLR2 and TLR4, the ancient breeds had lower Cq values and therefore higher expression levels than the modern breeds. WP had higher expression levels of CCL5, IL10, MX1 and MX2 than the other breeds. It also had a higher CCL20, CD68 and LPO expression than RH.

Tables 2 and 3 show the relative fold changes in gene expression of innate immune genes between control and treated cells. Only genes that were differentially expressed in one breed ($P < 0.05$) or were at least 1.5-fold up-regulated are presented. Table 2 shows the fold changes in gene expression after 6 and 30 h exposure to *E. coli*. After 6 h, HLD had lower fold changes than BS in complement component 3 (C3) and caspase 8 (CASP8), lower fold changes than RH in chemokine (C-C motif) ligand 2 (CCL2) and lymphocyte antigen 96 (LY96) and lower fold changes than WP in lactoperoxidase (LPO). C3, chemokines and cytokines were strongly up-regulated. Antimicrobial peptides were only up-regulated in the modern breeds. S100 and MX genes were more differentially expressed in the modern breeds. The most regulated gene after 6 h exposure to *E. coli* was SAA3 with nearly 290-fold in RH. After 30 h exposure to *E. coli*, BS had higher fold changes than RH in CD14. C3, chemokines, cytokines and antimicrobial peptides were strongly up-regulated. With the two *E. coli* treatments, more of the antimicrobial peptides were up-regulated in BS than in the other breeds. After 6 h exposure to *E. coli* there was no up-regulation of these in the ancient breeds. The S100 and MX genes were only up-regulated in the modern breeds. The most regulated gene after 30 h exposure to *E. coli* was SAA3 with 1900-fold in RH. Table 3 shows the fold changes in gene expression after 30 and 78 h exposure to *S. aureus*. There were no breed differences after 30 h exposure to *S. aureus*. The only differentially expressed genes were the antimicrobial peptides LPO and LYZ1 in WP and TLR4 in BS. After 30 h exposure to *S. aureus* LYZ1 had the highest significant fold change with 1.6 in WP. After 78 h exposure to *S. aureus*, HLD differed from BS in transforming growth factor β1 (TGFβ1). They were both down-regulated and differed from RH which was up-regulated. LY96 was slightly elevated in HLD compared with WP and RH. After 78 h exposure to *S. aureus,* the highest significant fold change was found in LF in RH with 1.6. SEM was generally very high. In general, the modern breeds had a higher number of regulated genes than the ancient breeds (Tables 2 and 3). Figure 2 shows the PCA on the dCq values of the control samples (Figure 2a) and the ddCq values, the differences between control and treated dCqs (Figure 2b). Each symbol represents all data of all respective samples from one animal. A visual clustering can be observed in the basal expression (Figure 2a): RH and BS form two subgroups in the lower half of the picture. WP and HLD are mixed together, but separated from the modern breeds in the upper half of the graph. No such separation is visible in the PCA on the ddCqs of gene expression.

Protein production

LF content in total cell protein is shown together with the inversed expression of its gene (20-dCq), so that higher bars represent higher gene expression (Figure 3). While an up-regulation in the gene expression could be observed in most *E. coli* treatments and after 78 h with *S. aureus*, only RH and WP had a significant protein increase with 30 h exposure to *E. coli*. BS even showed a down-regulation in LF protein with 30 h exposure to *S. aureus*. BS had higher gene expression levels than RH and HLD in 78 h control cells. HLD had higher control and *S. aureus* treated LF protein levels after 30 h compared with WP.

IL-10 was determined relatively as IL-10 in % of control and is shown together with the fold change of its gene expression (Figure 4). There were no significant breed differences. While there was an often significant up-regulation in IL10 gene expression (see Tables 2 and 3) the rise in protein production was not consistent throughout the breeds and the treatments. In BS, there was a qualitative increase of approximately 50 and 25 percent of IL-10 protein after 30 and 78 h exposure to *S. aureus*, respectively. RH had a qualitative increase of about 60 percent with 30 h exposure to *E. coli*. WP showed no visible changes compared with controls. In HLD, there was about 50 percent more IL-10 with 6 h *E. coli* and 78 h *S. aureus* treatments, as well as about 100 percent more with 30 h *S. aureus* treatment. SEM of the protein data was considerably high.

SAA content was measured in control and *E. coli* treated cells after 30 h stimulation and is shown together with the inversed expression of its gene (20-dCq), so that higher bars represent higher gene expression (Figure 5). Gene expression was significantly increased by the treatment, but only in BS this was also true for the protein production. BS and RH differed significantly from HLD in basal SAA levels (control). However, only BS differed significantly from HLD in *E. coli* treated SAA levels.

Table 1. Basal mRNA expression (mean dCq and SEM) of innate immune genes in pbMEC from four cattle breeds, unstimulated control after 6, 30 and 78 h.

Gene		Time											
		6 h				30 h				78 h			
		Breed				Breed				Breed			
		BS	RH	WP	HLD	BS	RH	WP	HLD	BS	RH	WP	HLD
Chemokines													
CCL20	Mean	12.21_{a}	15.40_{a}	11.94_{a}	13.96_{a}	13.01_{a}	15.05_{a}	12.79_{a}	13.83_{a}	13.71_{ab}	15.83_{a}	12.47_{b}	14.64_{ab}
	SEM	0.63	1.24	1.63	1.14	0.60	0.95	0.93	0.73	0.78_{a}	0.90	1.43	0.90
CCL5	Mean	15.12_{a}	15.19_{a}	12.44_{b}	15.60_{a}	15.01_{a}	14.79_{a}	13.48_{a}	15.29_{a}	14.49_{ab}	14.74_{ab}	13.15_{a}	15.37_{b}
	SEM	0.67	0.73	0.63	0.80	0.72	0.66	0.72	0.83	0.47	0.46	0.46	0.83
CXCL8	Mean	10.36_{ab}	11.51_{a}	9.22_{b}	9.25_{b}	10.96_{a}	11.37_{a}	9.45_{b}	10.07_{ab}	11.07_{ab}	12.36_{a}	9.76_{b}	10.60_{b}
	SEM	0.50	0.29	0.74	0.48	0.57	0.29	0.44	0.38	0.42	0.22	0.75	0.55
Cytokines													
IL6	Mean	7.22_{a}	6.88_{a}	8.92_{a}	8.03_{a}	7.66_{a}	7.52_{a}	9.56_{b}	7.92_{ab}	8.39_{a}	8.59_{a}	11.06_{b}	9.20_{ab}
	SEM	0.35	0.45	0.94	0.88	0.26_{a}	0.52	0.89	0.62	0.18	0.66	0.87	0.88
IL10	Mean	15.12_{a}	15.22_{a}	12.05_{b}	15.09_{a}	14.86_{a}	14.77_{a}	13.05_{a}	14.86_{a}	14.37_{a}	14.77_{a}	12.46_{b}	14.87_{a}
	SEM	0.68	0.68	0.76	0.77	0.67	0.66	0.67	0.87	0.44	0.44	0.38	0.98
Antimicrobial peptides													
LF	Mean	9.44_{a}	10.45_{a}	9.70_{a}	9.12_{a}	8.06_{a}	9.38_{a}	8.92_{a}	8.66_{a}	5.56_{a}	7.93_{b}	6.21_{ab}	7.11_{b}
	SEM	0.66	0.24	0.55	0.38	0.67	0.56	0.59	0.49	0.51	0.84	0.85	0.33
LPO	Mean	15.15_{ab}	15.97_{a}	14.20_{b}	15.37_{ab}	15.09_{ab}	15.87_{a}	14.34_{b}	15.26_{ab}	15.30_{ab}	15.62_{a}	13.96_{b}	15.06_{ab}
	SEM	0.63	0.28	0.50	0.18	0.53	0.36	0.63	0.16	0.42	0.50	0.67	0.27
Scavenger receptor													
CD68	Mean	13.28_{ab}	13.66_{a}	12.49_{b}	12.42_{b}	13.56_{a}	13.73_{a}	12.66_{b}	13.07_{ab}	14.16_{ab}	14.46_{a}	13.24_{b}	13.58_{ab}
	SEM	0.25	0.01	0.25	0.50	0.19	0.19	0.33	0.43	0.23	0.27	0.39	0.40
TLR pathway													
CASP8	Mean	7.61_{a}	7.82_{a}	6.62_{b}	6.64_{b}	7.90_{a}	7.90_{a}	6.85_{b}	7.01_{b}	7.76_{ab}	8.24_{a}	7.04_{c}	7.12_{bc}
	SEM	0.17	0.16	0.15	0.21	0.31	0.25	0.09	0.20	0.13	0.28	0.21	0.22
LBP	Mean	16.99_{a}	16.45_{ab}	16.60_{ab}	15.56_{b}	15.91_{a}	15.93_{a}	15.38_{a}	15.62_{a}	14.72_{a}	15.16_{a}	14.69_{a}	14.74_{a}
	SEM	0.44	0.35	0.21	0.56	0.55	0.26	0.34	0.51	0.40	0.58	0.91	0.43
LY96	Mean	4.92_{a}	5.53_{b}	4.43_{ac}	4.10_{c}	4.91_{a}	5.29_{a}	4.48_{a}	4.30_{a}	5.45_{a}	5.51_{a}	4.56_{a}	4.44_{a}
	SEM	0.08	0.29	0.18	0.21	0.13	0.63	0.20	0.28	0.34	0.52	0.27	0.27
MYD88	Mean	7.40_{a}	7.38_{ab}	7.18_{ab}	6.88_{b}	6.89_{a}	7.24_{a}	6.96_{a}	6.82_{a}	6.38_{a}	7.05_{a}	6.73_{a}	6.73_{a}
	SEM	0.18	0.15	0.19	0.17	0.20	0.39	0.19	0.21	0.18	0.38	0.08	0.29
TLR2	Mean	14.54_{a}	15.21_{a}	14.44_{ab}	13.47_{b}	14.04_{ab}	14.73_{a}	13.75_{b}	13.25_{b}	13.68_{ab}	14.57_{a}	13.34_{b}	13.02_{b}
	SEM	0.17	0.36	0.48	0.33	0.37	0.32	0.23	0.27	0.36	0.33	0.19	0.38
TLR4	Mean	8.87_{ab}	9.37_{a}	8.10_{c}	8.20_{bc}	8.76_{ab}	9.25_{a}	7.87_{c}	8.09_{bc}	7.91_{a}	9.14_{b}	7.58_{a}	7.97_{a}
	SEM	0.20	0.16	0.30	0.29	0.30	0.17	0.25	0.21	0.32	0.28	0.31	0.18
Others													
MX1	Mean	6.14_{ab}	6.54_{ab}	4.37_{a}	7.03_{b}	6.52_{a}	7.47_{a}	4.69_{a}	7.49_{a}	7.15_{a}	7.42_{a}	5.20_{a}	7.16_{a}
	SEM	0.34	0.88	0.54	1.27	0.41	0.89	0.87	1.48	0.71	0.68	0.27	1.56
MX2	Mean	11.59_{a}	11.42_{a}	8.22_{b}	11.61_{a}	11.29_{ab}	12.21_{a}	8.84_{b}	12.38_{a}	11.86_{ab}	12.59_{a}	9.20_{b}	12.05_{ab}
	SEM	0.72	0.97	0.63	1.24	0.57	1.06	1.08	1.28	0.84	0.96	0.45	1.33

Note: BS = Brown Swiss, RH = Red Holstein, WP = White Park, HLD = Highland. Means with different subscript letters are significantly different between the breeds ($P < 0.05$).

Table 2. Fold changes of the normalized relative gene expression of innate immune genes in pbMEC from four cattle breeds after 6 h and 30 h stimulation with *E. coli*.

Gene		**Treatment**							
		***E. coli* 6 h**				***E. coli* 30 h**			
		Breed				**Breed**			
		BS	**RH**	**WP**	**HLD**	**BS**	**RH**	**WP**	**HLD**
Complement system									
C3	Fold change	4.4_{a}**	4.2_{ab}**	6.1_{ab}*	1.9_{b}	8.6***	11.1**	6.8*	11.9*
	SEM	0.9	1.1	2.1	0.5	1.8	3.7	2.3	4.0
Chemokines									
CCL2	Fold change	28.8_{ab}**	10.8_{a}***	27.5_{ab}*	4.4_{b}	43.9***	27.3**	26.8*	18.2**
	SEM	12.3	1.9	11.8	1.0	13.1	9.0	12.1	9.2
CCL5	Fold change	24.1	4.0*	4.8*	2.0*	51.6**	26.6*	55.4*	3.9*
	SEM	18.3	1.7	1.5	0.5	33.3	14.1	37.7	1.3
CCL20	Fold change	39.4**	36.8**	110.8*	17.7*	50.2***	119.6*	74.5*	37.9*
	SEM	17.1	13.8	65.5	7.6	11.1	75.8	42.2	20.5
CXCL5	Fold change	8.1**	8.0***	11.7*	3.9*	7.8***	9.0**	7.2*	6.4*
	SEM	2.1	1.6	4.0	1.0	1.3	2.6	2.3	2.0
CXCL8	Fold change	20.1*	21.2***	33.8*	7.0*	21.9***	26.7**	16.0*	11.2*
	SEM	7.7	8.3	13.4	3.1	7.5	9.5	6.1	4.2
Inflammatory cytokines									
IL6	Fold change	3.6*	3.4**	7.7*	2.1*	5.3***	5.1*	11.2*	3.2*
	SEM	1.1	0.6	3.00	0.4	1.2	1.7	5.7	0.8
IL10	Fold change	18.8*	3.3*	4.1	1.7	53.1**	25.2*	57.5	3.5
	SEM change	11.0	1.1	1.8	0.4	35.1	13.3	33.8	1.2
TGFβ1	Fold change[1]					1.7	0.9	0.9	1.4
	SEM					0.7	0.0	0.1	0.4
TNF	Fold change	21.9**	21.6	54.0*	6.0*	21.5***	40.6**	65.1	13.1**
	SEM	7.0	9.0	32.7	2.0	4.1	17.2	35.7	6.5
Antimicrobial peptides									
LAP	Fold change	2.8**	1.5	6.8	2.1	19.5**	4.6	84	25.2
	SEM	0.6	0.5	2.7	0.8	8.0	1.0	53.5	14.3
LF	Fold change	3.2**	3.1*	2.8	1.7	8.6**	12.0**	9.3*	7.3*
	SEM	0.6	1.0	0.9	0.4	2.3	4.2	4.0	2.7
LPO	Fold change	1.9_{ab}	0.9_{ab}	2.9_{a}	0.9_{b}	4.2*	1.7	9.2*	2.2
	SEM	0.4	0.1	0.8	0.2	1.2	0.2	4.1	0.7
LYZ1	Fold change	2.1	2	3.7	1.9	40.2**	12.7*	32.1*	13.4*
	SEM	0.5	0.6	1.0	0.5	27.6	6.5	14.2	4.6
TAP	Fold change	54.8*	1.3	33.5	8.5	105.7**	11.8*	234.8	47.8
	SEM	32.8	0.1	12.9	6.1	57.9	1.7	117.8	41.0
Acute phase proteins									
SAA3	Fold change	98.7	289.4*	418.2	10.8	618.2**	1912.3**	1769.1*	69.9*
	SEM	90.1	263.4	172.5	3.7	272.4	1445.1	1076.6	39.1
TLR signalling									
CASP8	Fold change	1.3_{a}*	1.1_{ab}	1.2_{ab}	1.0_{b}	1.4*	1.3*	1.2	1.4
	SEM	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.2
CD14	Fold change	1.3	1.1	1.2	1.8	1.8_{a}*	1.0_{b}	1.1_{ab}	1.8_{ab}
	SEM	0.1	0.1	0.1	0.4	0.3	0.1	0.2	0.4
LBP	Fold change	2.5	2.2	1.4	1.2	1.2	1.4	1.2	2.7
	SEM	0.7	0.7	0.4	0.3	0.1	0.4	0.5	0.2
LY96	Fold change	1.0_{ab}	1.1_{a}*	0.9_{ab}	1.0_{b}				
	SEM	0.0	0.0	0.1	0.0				
TLR2	Fold change	5.7	1.7***	6.9*	1.5	5.0*	2.0*	2.8	2.2*
	SEM	2.1	0.1	3.3	0.2	2.1	0.3	0.9	0.4
Others									
MX1	Fold change	2.8	1.6*	1.2	1.5	4.4*	3.5**	3.1	2.9
	SEM	1.4	0.2	0.3	0.4	1.4	0.8	1.1	1.3
MX2	Fold change	11.6*	2.0*	1.5	1.8	8.6***	8.3*	6.5	3.9
	SEM	7.6	0.5	0.4	0.6	2.3	2.8	3.3	1.6
S100A9	Fold change	3.9**	2.4	8.6*	2.1	12.0***	12.6*	14.2	20.4
	SEM	0.8	0.9	4.0	0.6	4.1	4.1	6.0	15.9
S100A12	Fold change	2	MD[2]	6.5	2.6	4.2**	2.1	5.1	1.7
	SEM	0.5	MD	3.1	1.0	0.9	1.2	1.4	0.5
Regulated genes[3]		14	14	10	6	22	18	11	12

Note: BS = Brown Swiss ($n = 6$), RH = Red Holstein ($n = 6$), WP = White Park ($n = 5$), HLD = Highland ($n = 5$); Stars indicate significant differences between treated and control dCq: *$P < 0.05$, **$P < 0.01$, ***$P < 0.001$. Fold change means with different subscript letters differ between breeds ($P < 0.05$).

[1] Empty genes: no significant breed differences in expression fold changes and no fold changes >1.5 at this time point.

[2] Missing data.

[3] $P < 0.05$ for dCq difference between treatment and control.

Table 3. Fold changes of the normalized relative gene expression of innate immune genes in pbMEC from four cattle breeds after 30 h and 78 h stimulation with *S. aureus*.

Gene		**Treatment**							
		***S. aureus* 30 h**				***S. aureus* 78 h**			
		Breed				**Breed**			
		BS	**RH**	**WP**	**HLD**	**BS**	**RH**	**WP**	**HLD**
Complement system									
C3	Fold change[1]					1.1	1.6	1.1	1.2
	SEM					0.1	0.4	0.1	0.1
Chemokines									
CCL2	Fold change					1.0	1.3	1.3	1.6
	SEM					0.1	0.1	0.2	0.3
CCL5	Fold change					1.5*	1.6	1.3	1.2
	SEM					0.2	0.4	0.6	0.3
CCL20	Fold change					1.7	0.9	3.3	1.5
	SEM					0.6	0.2	1.3	0.4
CXCL8	Fold change					1.3	1.2	1.9	1.1
	SEM					0.2	0.1	0.6	0.2
Inflammatory cytokines									
IL10	Fold change					1.5*	1.5	1.0	1.1
	SEM					0.2	0.5	0.4	0.3
TGFβ1	Fold change					0.9^{*}_{b}	1.2^{*}_{c}	0.9_{abc}	0.8_{a}
	SEM					0.0	0.1	0.1	0.0
TNF	Fold change					1.2	1.2	4.5	1.8
	SEM					0.3	0.1	2.9	1.1
Antimicrobial peptides									
LAP	Fold change					1.2	MD[2]	5.1	1.9
	SEM					0.2	MD	3.4	0.8
LF	Fold change					1.0	1.6*	1.3	1.1
	SEM					0.1	0.2	0.4	0.1
LPO	Fold change	1.0	1.2	1.2*	1	1.2	0.9	1.7	1.5
	SEM	0.3	0.2	0.2	0.1	0.2	0.1	0.7	0.4
LYZ1	Fold change	1.1	0.9	1.6*	1.9	1.6	1.2	2.9	1.2
	SEM	0.1	0.2	0.3	0.5	0.5	0.2	1.2	0.1
TAP	Fold change	0.9	1.1	1.5	0.9	5.2	0.7*	6.9	1.5
	SEM	0.3	0.4	0.3	0.2	4.3	0.2	3.7	0.8
Acute phase proteins									
SAA3	Fold change	1.7	2.5	3	1.2	5.1	3.1	5.4	1.2
	SEM	0.5	1	1.7	0.3	3.8	1.5	4.3	0.2
TLR signalling									
LBP	Fold change					1.0	1.4	0.9	1.8
	SEM					0.2	0.4	0.2	1.0
LY96	Fold change					1.1_{ab}	1.0_{b}	1.0_{b}	1.1^{*}_{a}
	SEM					0.0	0.1	0.0	0.0
TLR2	Fold change					1.0	1.0	1.3	1.9
	SEM					0.1	0.1	0.2	1.1
TLR4	Fold change	1.3*	1.0	1.0	1.1	1.0	1.2*	1.0	1.0
	SEM	0.2	0.1	0.1	0.0	0.1	0.1	0.1	0.0
Scavenger receptor									
CD68	Fold change					1.1	1.3	1.2	1.7
	SEM					0.2	0.2	0.3	0.5
Others									
MX1	Fold change	2.1	1.2	1.0	1.7	1.7	1.2	1.1	0.8
	SEM	0.7	0.4	0.3	0.3	0.4	0.2	0.3	0.2
MX2	Fold change	1.9	1.9	1.1	1.9	2.9	1.3	1.4	1.0
	SEM	0.7	1.3	0.4	0.4	1.3	0.2	0.5	0.2
S100A9	Fold change					1.3	1.3	2.2	1.3
	SEM					0.2	0.2	0.6	0.2
S100A12	Fold change					1.3^{*}_{a}	0.8_{b}	1.2_{ab}	1.6_{ab}
	SEM					0.1	0.2	0.2	0.5
Regulated genes[3]		1	0	2	0	4	4	0	1

Note: BS = Brown Swiss ($n = 6$), RH = Red Holstein ($n = 6$), WP = White Park ($n = 5$), HLD = Highland ($n = 5$); Stars indicate significant differences between treated and control dCq: $*P < 0.05$, $**P < 0.01$, $***P < 0.001$. Fold change means with different subscript letters differ between breeds ($P < 0.05$).

[1] Empty genes: no significant breed differences in expression fold changes and no fold changes >1.5 at this time point.

[2] Missing data.

[3] $P < 0.05$ for dCq difference between treatment and control.

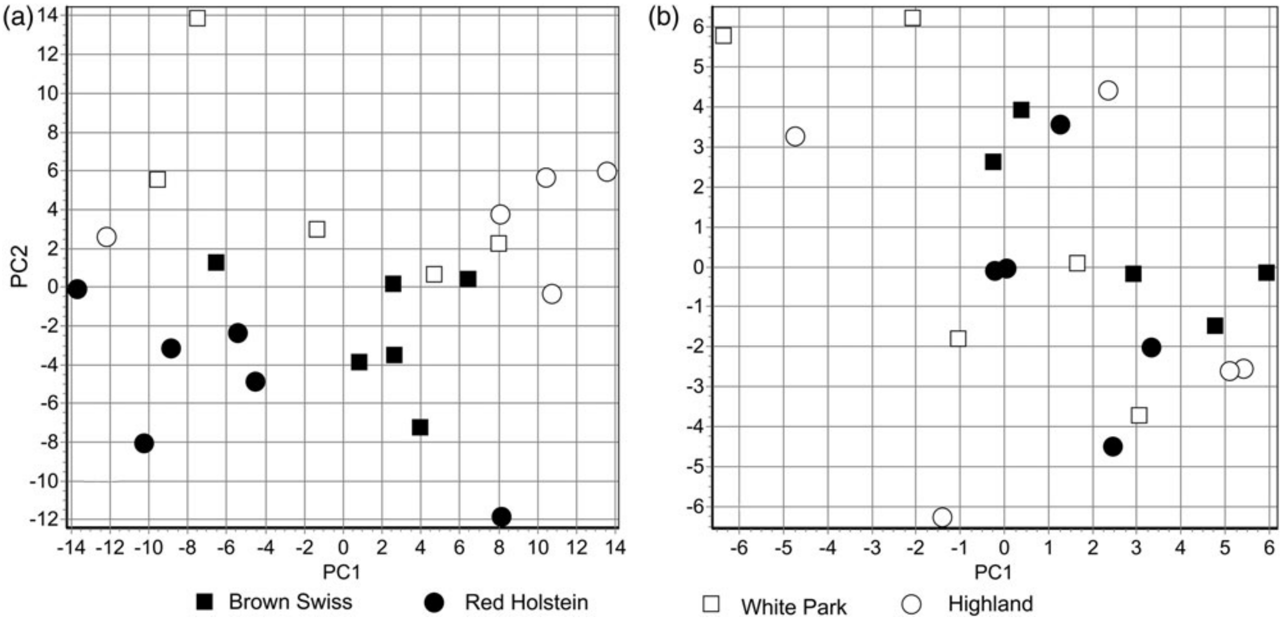

Figure 2. PCA of (a) dCq values (basal expression of unstimulated control) and (b) ddCq values (difference between treated and control dCq) of 28 target genes in pbMEC from four cattle breeds after stimulation with *E. coli* and *S. aureus*. Each symbol represents all respective samples of one animal.

Discussion

Breed comparison

On the level of basal expression in the PCA, there was a visible separation of ancient from modern breeds and within the two modern breeds. The higher basal expression of the components of the TLR pathway in the ancient breeds could be responsible for an earlier recognition of invading pathogens and therefore lead to an earlier and more effective immune response. The same could be true for the higher basal levels of SAA protein in the ancient breeds which could have a protective effect against

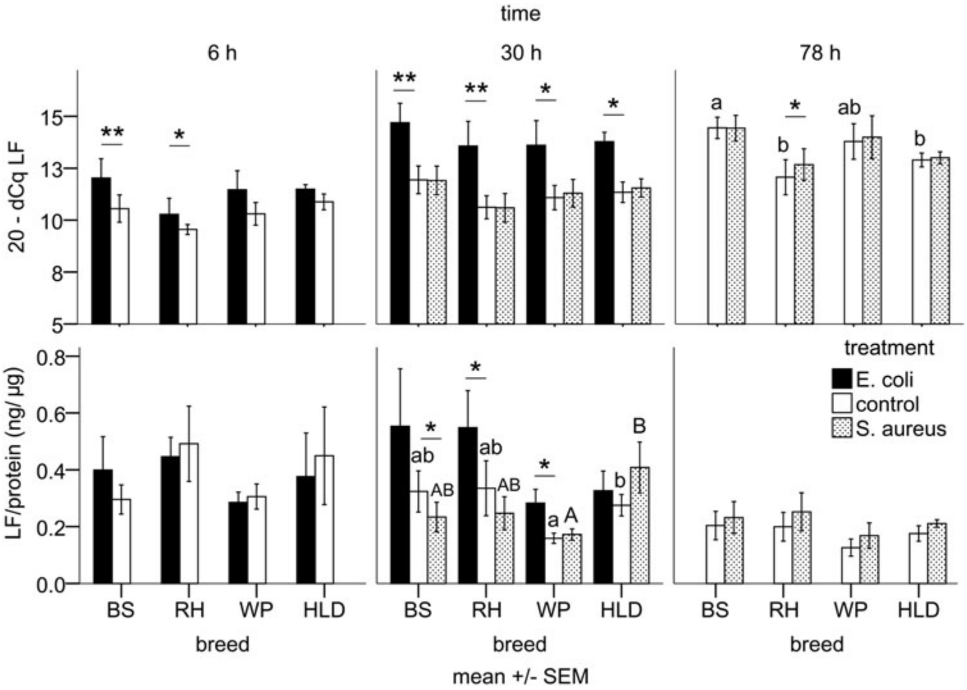

Figure 3. Relative gene expression and LF content in ng/μg cell protein in pbMEC from ancient (WP, HLD; $n = 5$) and modern (BS, RH; $n = 6$) cattle breeds stimulated with *E. coli* (6 and 30 h) and *S. aureus* (30 and 78 h). Stars indicate significant differences between the treatments, letters indicate significant differences of *S. aureus* treated (upper case letters) and control levels (lower case letters) between the breeds ($P < 0.05$). BS = Brown Swiss, RH = Red Holstein, WP = White Park, HLD = Highland cattle.

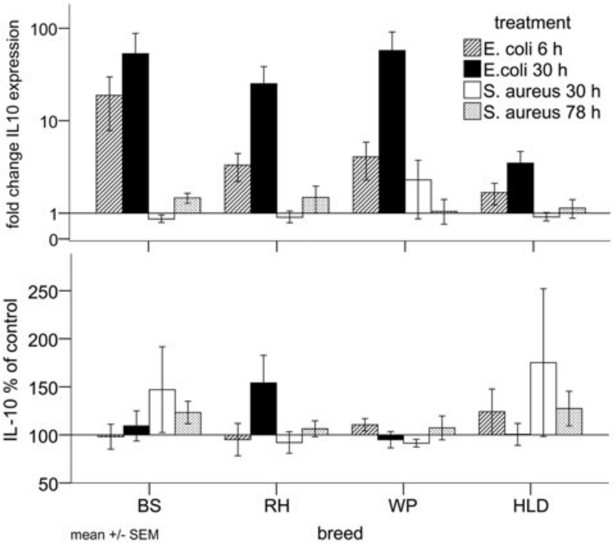

Figure 4. Fold change of IL10 expression and relative IL-10 content in % of untreated control in total cell protein of pbMEC from ancient (WP, HLD; $n = 5$) and modern (BS, RH; $n = 6$) cattle breeds stimulated with *E. coli* (6 and 30 h) and *S. aureus* (30 and 78 h). BS = Brown Swiss, RH = Red Holstein, WP = White Park, HLD = Highland cattle.

pathogens, as SAA is an opsonising agent (Shah, Hari-Dass and Raynes, 2006). Interestingly, basal LF protein levels were lower in the ancient breeds, but differed significantly only between WP and HLD. WP and HLD also differed in basal expression of MX1 and CCL5. So the breeds seem to be all different from each other and cannot just be grouped together in "modern" and "ancient". It is difficult to interpret the fold changes of gene expression, as the SEM were considerably high and led to weak significances for visibly high fold changes. In addition, the PCA on ddCq did not reveal any clustering of the animals. However, this set aside, there was a higher number of significantly up-regulated genes in the modern breeds, especially for the antimicrobial peptides, the TLR pathway and the MX genes. HLD had the lowest fold changes in SAA3 expression, but the highest basal levels of SAA protein after 30 h. Although the whole picture is diffuse and complex, it seems as if in those parts of the immune system where we found a difference between the breeds, a higher basal expression led to a lower response. Kandasamy *et al.* (2012) tested the extent of the immune response of cows that had before been classified as "high-" and "low-responder" animals to an intramammary *E. coli* challenge. They found that the weaker immune response of low-responder animals was more effective and led to a shorter resolution phase of the inflammation. Hence, a strong immune response is not necessarily a benefit for the animal. Another prominent example for this phenomenon is the well-studied tolerance of the *Bos indicus* Sahiwal cattle to the indigenous protozoan parasite *Theileria annulata.* Compared with Holstein calves *in vivo* (Glass *et al.*, 2005) they showed fewer clinical symptoms, recovered from a higher dose of pathogen and had lower acute phase protein levels. In another comparison with Sahiwal cattle, macrophages from Holstein cattle showed higher up-regulation of inflammatory and immune response genes (Glass *et al.*, 2012).

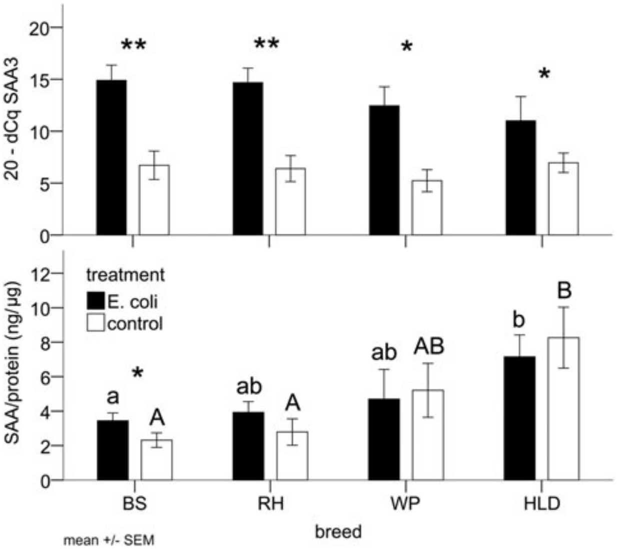

Figure 5. Relative expression of the SAA3 gene and SAA content in ng/µg cell protein in pbMEC from ancient (WP, HLD; $n = 5$) and modern (BS, RH; $n = 6$) cattle breeds stimulated with *E. coli* for 30 h. Stars indicate significant differences between treatments, different letters indicate significant differences of treated (lower case letters) and control cells (upper case letters) between breeds ($P < 0.05$). BS = Brown Swiss, RH = Red Holstein, WP = White Park, HLD = Highland cattle.

To our knowledge, there are no studies on the intramammary immune system of ancient cattle breeds such as WP and HLD. There has been evidence that the immune system of modern breeds shows differences in details, but overall is highly conserved (Bannerman *et al.*, 2008a, 2008b), which is in accordance with our results. The *in vivo* response of Holstein and Jersey cows to *E. coli* differed only in the time point of milk cytokine and somatic cell count (SCC) increase, not in overall levels (Bannerman *et al.*, 2008a). To an *S. aureus* challenge Holstein and Jersey animals also responded with similar overall levels of milk SCC and cytokines except for neutrophils and N-acetyl-beta-D-glucosaminidase (NAGase) activity (Bannerman *et al.*, 2008b). Different LF contents in milk have already been observed between Holstein, Jersey and Simmental cows (Krol *et al.*, 2010) as well as between dairy and beef cattle (Tsuji *et al.*, 1990), which adds to our findings of different LF contents in pbMEC. There are several polymorphisms located in the LF gene in different cattle breeds that could be the reason for differential LF expression and production (O'Halloran *et al.*, 2009). The different SAA contents in our pbMEC can be compared with a study where after an LPS challenge SAA in blood serum increased more rapidly in Angus than in Romosinuano steers (an indigenous Colombian breed) and remained at higher levels for 8 h (Carroll *et al.*, 2011). Although in the cells from our ancient breeds the absolute levels of SAA protein were higher than in the modern breeds, there was no significant rise after pathogen stimulation. Cattle breed differences in gene expression and protein production of the immune system have not been systematically studied so far, but our findings and the above-mentioned studies show that there is evidence for such diversity.

The considerable animal differences within each breed, reflected by the high SEMs and by the wide spread of the symbols representing animals in the PCAs, could be explained by the existence of a substantial between-cow variation in the immune response which has already been shown for Holstein cattle *in vitro* and *in vivo* (Kandasamy *et al.*, 2012). It could be caused by genetic polymorphisms that are linked to a certain breed, but could also be spread all over the cattle population. Furthermore, it has been suggested that a proportion of unexplained phenotypic variation in the dairy cow is because of epigenetic regulation (Singh *et al.*, 2010).

General remarks about the immune response

C3, chemokines, inflammatory cytokines and the inflammation marker SAA3 experienced a strong up-regulation by *E. coli* in all the breeds. The antimicrobial peptides were also strongly up-regulated after 30 h in *E. coli* treated cells. This confirms that our pbMEC continued to exert sentinel functions to trigger the innate immune response upon pathogen recognition as well as an active defence by attacking and opsonising bacterial cells. Interestingly, in our study the TLR pathway was not as markedly regulated, although it is one of the starting points of the immune signalling cascade and has been shown to be a source for potential mastitis resistance (Griesbeck-Zilch *et al.*, 2009). However, in another study the regulation of TLRs in pbMECs was similarly weak, but the authors still concluded that there was a functioning and locally effective immune system (Strandberg *et al.*, 2005). We also found a regulation of the genes we had termed as “others”. The calcium-binding, pro-inflammatory, regulatory and anti-oxidant S100 calcium-binding proteins A9 (S100-A9) and A12 (S100-A12) seem to be a class of protective and defence proteins (Hsu *et al.*, 2009) that act in addition to LF, lysozyme 1 (LYZ1), LPO and the β-defensins lingual antimicrobial peptide (LAP) and tracheal antimicrobial peptide (TAP). The antiviral myxovirus (influenza virus) resistance 2 (mouse) gene (MX2) has a yet unknown role in mastitis and remains a subject of further research.

Pathogen comparison

It has previously been shown that *S. aureus* elicits a different and often weaker immune response than *E. coli in vitro* (Griesbeck-Zilch *et al.*, 2008) and *in vivo* (Petzl *et al.*, 2008). The dose of inoculum could have been too low so that the cells did not receive enough signals to trigger the response. Our results can be compared with a similar study with pbMEC from milk and the same strains of pathogens (Danowski *et al.*, 2012a): in that study, too, the immune response to *S. aureus* was much weaker than to *E. coli*. Our data support the hypothesis that the often subclinical and chronic outcome of *S. aureus* mastitis is caused by this reduced reaction of the mammary immune system.

Gene expression and protein comparison

LF gene expression was generally better reflected by the ELISA measurements than the other two proteins. Although IL10 gene expression was significantly up-regulated in the two modern breeds there was no consistent rise of the protein in cell content. SAA3 expression was up-regulated by *E. coli* after 30 h, but the protein levels reflected that only in BS and RH. For all these three genes (in SAA for the SAA encoding-gene SAA2) microRNAs have been identified that could lead to a differential expression, translation and massive variation in protein levels (Longley, Steel and Whitehead, 1999; Sharma *et al.*, 2009; Liao, Du and Lonnerdal, 2010). These microRNAs could also be differentially expressed between the breeds and determine the breed differences in mRNA expression. LF was also secreted into the media, but the concentrations were mostly below the measuring range (data not shown). This and a delay between mRNA expression and protein synthesis of the three genes could also account for the differences.

Conclusions

To our knowledge this is the first time that the mammary immune system of the ancient WP and HLD cattle was studied *in vitro*. The four breeds BS, RH, WP and HLD were found to differ in parts of the gene expression and protein production. A higher basal expression of some genes and proteins in the cells from the ancient breeds seemed to lead to a lower immune response after pathogen recognition. However, the main immune system pathways that were activated were the same, indicating that the complex network of immune response is to some extent conserved between the *Bos taurus* breeds. With this experimental setup it is possible to study other breeds and other pathogens in the same way, especially with the non-invasive pbMEC extraction from milk which is suitable for the sampling of valuable animals of rare breeds. We confirmed the existence of previously described substantial cow-to-cow variation in immune response. The classification of high- and low-responder animals and the underlying genetic and epigenetic mechanisms remain subject to further analysis.

Acknowledgments

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Conflict of Interest statement

The authors declare that there is no conflict of interest.

Supplementary material

Supplementary materials of this paper is available at http://journals.cambridge.org/agr

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Vechur cattle – from extinction to sustainability

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Summary

The Vechur Cattle of South Kerala (India), once popular and known for its comparatively high milk yield compared with the other local varieties, had become almost extinct by the 1980s. This was due to the massive cross-breeding with exotic bulls implemented by the Government in order to enhance milk production. But the launching of a search for the last available specimens of the variety and the initiation of a conservation effort in 1989 in the Kerala Agricultural University by the author and a team of her students resulted in saving this valuable breed. With 10 years time the distribution of the progeny of the foundation stock to the farmers could be started. The conservation work was taken forward with strong determination in spite of unexpected events. The Vechur cattle was subsequently recognized as a cattle breed of India. The cow yields 2.5 litres of milk daily during the lactation period of about 8 months. It has emerged as a sustainable cow to farmers. The adaptability of the animal to the hot humid tropical countries has special significance as an insurance for the future. It also has the potential to be a small good beef breed. The value of the milk including the small fat globule size, presence of A2 beta-lactalbumin protein and higher arginine content has been proven scientifically. The total population size in Kerala is estimated to be 2000 animals.

Keywords: *conservation, indigenous cattle, meat, milk, Vechur breed, India*

Résumé

Les bovins Vechur du sud du Kérala (Inde), autrefois populaires et renommés pour leur relativement élevée production laitière par rapport à d'autres variétés locales, faillirent s'éteindre dans les années 80. Le croisement massif avec des taureaux exotiques mis en place par le Gouvernement afin d'améliorer la production laitière en fut la cause. Néanmoins, la recherche des derniers spécimens disponibles de la variété et l'engagement dans un effort de conservation en 1989 de la part de l'auteure et d'une équipe intégrée par certains de ses élèves de l'Université Agricole du Kérala aboutirent à la sauvegarde de cette race de grande valeur. Une période de 10 ans s'étant écoulée, la distribution de la progéniture du troupeau fondateur parmi les éleveurs put être commencée. Le travail de conservation se poursuivit avec une forte détermination malgré les imprévus. Les bovins Vechur furent par la suite reconnus comme une race bovine de l'Inde. La vache produit 2,5 litres de lait journaliers sur une lactation d'environ 8 mois. C'est ainsi que la race s'est positionnée comme une race bovine durable aux yeux des éleveurs. L'adaptabilité de cet animal aux pays à climat tropical chaud et humide a une signification spéciale comme garantie de futur. Ce bétail a aussi du potentiel comme race bouchère de petit gabarit. La valeur du lait a été démontrée scientifiquement de par la petite taille des globules de graisse, la présence de la protéine A2 béta-lactalbumine et sa teneur élevée en arginine. La taille totale de la population en Kérala a été estimée à 2000 animaux.

Mots-clés: *conservation, bovins indigènes, viande, lait, race Vechur, Inde*

Resumen

El ganado bovino Vechur del sur de Kerala (India), en su día muy popular y conocido por su proporcionalmente alta producción de leche en comparación con otras variedades locales, estuvo a punto de extinguirse en los años ochenta. Esto se debió al cruce masivo con toros exóticos que puso en práctica el Gobierno con el fin de mejorar la producción lechera. Sin embargo, la búsqueda de los últimos especímenes existentes de la variedad y el inicio de un esfuerzo de conservación en 1989 por parte de la autora y un equipo formado por estudiantes suyos de la Universidad Agrícola de Kerala permitieron salvar esta valiosa raza. Tras un plazo de diez años, fue ya posible distribuir la progenie del rebaño fundacional entre los ganaderos. El trabajo de conservación se llevó adelante con fuerte determinación a pesar de los imprevistos. El ganado bovino Vechur fue posteriormente reconocido como una raza bovina de la India. La vaca produce diariamente 2,5 litros de leche a lo largo de una lactación de aproximadamente 8 meses. Así, la raza se ha posicionado como una raza bovina sostenible a los ojos de los ganaderos. La adaptabilidad de este animal a los países de clima tropical cálido y húmedo tiene un significado especial como garantía de futuro. Este ganado tiene también potencial como raza cárnica de pequeño formato. El valor de su leche ha sido demostrado científicamente por el pequeño tamaño de los glóbulos de grasa, por la presencia de la proteína A2 beta-lactoalbúmina y por el alto contenido en arginina. Se estima que el tamaño poblacional total en Kerala es de 2000 ejemplares.

Palabras clave: *conservación, ganado bovino autóctono, carne, leche, raza Vechur, India*

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Introduction

Kerala is in the south western part of the Indian Peninsula, bordered by the Western Ghats in the east and by the Arabian Sea in the west, located between 76°23′ and 77° 23′E longitudes and 9°44′ to 10°18′N latitudes on the northern hemisphere. The area has a size of only 38 863 km^2, is from 11 to 121 km wide and has a coastal length of 590 km. The state has abundant rainfall through south-western (June to August, with an average rainfall of 2 250–2 500 mm) and north-eastern (September to November, rainfall of 450–500 mm) monsoon. The climate is hot and quite humid because of the proximity of the back-waters, which are a network of waterways, inlets, estuaries, brackish lagoons, lakes and canals lying almost parallel to the Arabian Sea coast. The network includes five large lakes including large ones like Vembabad and Ashtamudi and linked by canals and fed by 38 rivers. At the backwaters freshwater from the rivers and the brackish water from the Arabian Sea get mixed and have a unique ecosystem. The biodiversity of this coastal area is also unique as in the Western Ghats.

There is one long spell of dry weather between the two monsoons from November to June. There are 44 rivers originating from the Western Ghats with 41 flowing west and draining out to the backwaters in the coastal area or directly into the Arabian Sea. As the Western Ghats are less than 120 km from the sea, all these rivers are relatively short. Principal crops are rice, coconut, tea, coffee and spices. Before the recognition of Vechur breed by the Government of India by 2001 Kerala did not have a cattle breed of its own. The local cattle were referred to as nondescript (ND) (Velu Pillai, 1940) as they were not scientifically described. Among them had been a variety known as Vechur. The adaptability to hot humid environments and low feed requirements are just some of the valued attributes of the cows; however, the farmer's preference for the cow had mostly been due to their relatively higher milk yield (KAU, 1999).

The small Vechur cows were the pride of Kerala. This status was lost subsequently with their near 100 percent replacement with cross-bred cows. But with the revival of the breed they have a more elevated status now. The Vechur cows have relatively high milk production compared with those of the other native varieties of Kerala (Velu Pillai, 1940).

The name Vechur is believed to have originated from the place of origin – Vechur. This place is situated in a unique low-lying agricultural tract called Kuttanad, where farming is done below the sea level on a sizeable portion. Vechur cattle were an integrated part of the traditional agriculture, especially paddy cultivation in this lowland. The author used to observe, in her childhood in the 1950s, the bulls being used for ploughing in the marshy paddy fields and were excellent for this use because of their light weight.

Vechur cattle near extinction

In the 1960s, the Kerala Government launched a series of massive cross-breeding programmes with exotic bulls such as Brown Swiss, Jersey and Holstein Friesian in order to increase milk production. The implementation of the aggressive cross-breeding throughout the state with exotic bulls transformed the local animals. Local bulls were not permitted to be retained as per Kerala Livestock Improvement Act (1961) (Government of Kerala, 1961); however, temple bulls were exempted. The allure of the cross-bred cows was their higher (double the amount) yield of milk production in the first generation compared with that of the local animals. The Government wanted a complete transformation of the local cattle in favour of the exotic cross-breeds. This government policy, coupled with a cultivated preference on the part of the farmers for cross-bred cows, led to the near extinction of Vechur cows. It was actually believed that the Vechur had become extinct.

Conservation efforts

It was in 1988 that the author, a professor at the Kerala Agricultural University, started a serious conservation effort for Vechur cattle. This was not in accordance with the Government policy of that time. A student team led by Anil Zachariah volunteered to make a search for Vechur cattle and join the conservation attempt. After searching for many months, eight cattle were located. The spotting of a Vechur cow along with Manoharan, a toddy tapper of Ullala (formerly a part of Vechur village), was the first exciting step in the conservation effort in Kerala (Figure 1).

The students (most of them in their teens) literally jumped and danced in their excitement. A few other animals were also spotted in other places. This was reported by Iype (1996). This paper reports on the progress of this conservation project.

Figure 1. First spotted Vechur cow with the author (1989).

Materials and methods

In addition to reviewing available documented information about Vechur cattle in Kerala, this report used data generated by the Vechur cattle conservation project in Kerala Agriculture University and the cows with the farmers. The challenges faced in this project are also reported here as observations of the author. The size of the population was eight when it started and then two dozens of animals were purchased and added to this population. This basic stock and progenies in the conservation unit and those with farmers numbered totalled to about 2000.

Results and discussions

Starting of the nucleus herd

The owners of the cattle were convinced to sell these animals that were spotted by the team. With a stock of just eight animals, the project to conserve the germplasm of Vechur cattle was commenced on the 26 July 1989 at the Kerala Agricultural University. The searching for animals was continued by the team, and in 1 year 24 more animals were added to the initial lot of eight (Iype, 1996).

The first step in the conservation effort was selecting bulls and multiplication of the animals to the maximum possible, as the numbers were very low. Good bulls were selected. Next-generation bull is seen in Figure 2. Distributing a few animals to committed farmers was the next priority. By 1999, the first set of animals could be given back to farmers. This allowed them to be in different places.

Difficulties encountered

In the 1980s, it was difficult to convince people that conservation of native cattle is necessary. The team was mocked even by many scientists. But they tried hard to educate others. In the first leaflet for "Save Vechur" the author highlighted four points: (1) to conserve domestic animal biodiversity; (2) to retain the heat and disease-tolerant cow as an insurance in case of crisis; (3) to cater for farmers' needs who cannot give sophisticated management to the cow, but need milk just for domestic consumption; and (4) to save them as a raw material for scientific studies in future and unravel their potential for improvement. Since 1999, next-generation cows were being given to the farmers. But pure breeding of Vechur remained a problem as the bull semen was not available near the farmers.

Figure 2. Vechur bull with Anil Zacharia (1992).

A very disturbing experience was the death of a few animals in the conservation unit in the Kerala Agricultural University. Autopsy and forensic examination revealed that poisoning was the cause. This was an extremely difficult and confusing time. No one, even the author herself, knew on any given day what was in store for the animals. Next was the allegation that some western countries were trying to steal some of the germplasm for the patenting of genes. Vandana Siva came out with the allegation that the Roslin Institute in Scotland had patented the alpha lactalbumin gene of the cow. Siva cited a particular patent number EP 765390 (Jayaraman, 1998). Nobody could find such patent details. The Indian Council of Agricultural Research, Swaminathan Foundation, India, Rafi Canada and others after making searches intimated the Kerala Agricultural University that there is no such patent/application related to Vechur. Kumar interviewed Vandana Siva, Harry Griffin of the Roslin Institute, the author and the Kerala Agricultural University authorities (Kumar, 1999). It was reported that the EP number 765390 quoted by Siva was not submitted by the Roslin Institute, but by PPL Therapeutics and it was about a human gene and Holstein cow. It was not at all connected to the Vechur or the genes of any Indian cattle and the story by Siva was entirely groundless. The Vice Chancellor, Dr Syama Sundaran Nair, published a white paper on the whole issue to clarify the real situation. All the allegations and the poisoning of animals resulted in the loss of some of the valuable germplasm as well as all of the time and energy.

In spite of these disturbing circumstances, the conservationists were determined to push ahead with the effort. P. K. Uthaman and many environmentalists came forward in support of the conservation (Uthaman, 2000). Thirupathy Venketachalapathy, K. C. Jayan Joseph and his mother Rosakutty, N. Jayadevan, Joby George, K. C. Raghavan, the members of the student team, people of Vechur were all out to battle the war. Slowly things took a more positive turn, as more people became convinced that conservation was a necessity. All these made the conservationists feel that a nongovernmental agency with farmers and conservationists had to be formed for the continuation of conservation.

The Vechur Conservation Trust

The informal association since 1988 to conserve the Vechur cow was registered as The Vechur Conservation Trust with the objective of saving other native domestic animals and birds in 1998. It was felt necessary that a non-governmental organization with conservationists, farmers and breeders was initiated in the interest of sustainable conservation.

The Trust established a germplasm centre in the native tract of Vechur cattle in order to assure purity in the breeding of the Vechur; otherwise, the cows distributed to farmers would get crossbred due to lack of availability of Vechur bull semen. The bulls in the unit are with known pedigree for 4–5 generations. The cow in Figure 3 is of the seventh generation and the calf eighth generation from the foundation stock. The Trust has undertaken research and development work in spite of major financial constraints. Animal identification of native animals has been started with farmers but this effort has a long way to go. This being the first step towards the breed improvement and for the first time introduced for native cattle is a great achievement of the Vechur Conservation Trust. This identification is imperative to avoid fraud in the purchase and sale of animals.

Continued conservation and research work

The Council of Agricultural Research sponsored the conservation work in the Kerala Agricultural University from the next year of its start and made it possible to begin the research necessary to characterize the Vechur breed and undertake other works like embryo transfer. As a result, this small cow today has a place in the breed map of cattle published by the National Bureau of Animal Genetic Resources, ICAR, India (NBAGR, 2001). The FAO has also officially listed the Vechur cattle among the Indian breeds in their Domestic Animal Diversity Information System in the critical category and description given in the breed data sheet (DAD-IS, 2012). One cow made entry into The Guinness book, as the smallest cow of the world (Guinness, 2011). The Vechur Conservation Trust is active with its work with farmers. The Trust is also supported by the Government in a small way.

Figure 3. Cow and calf (generations 7 and 8).

Features of Vechur cattle

These cattle are small sized with an average weight of about 133.6 ± 3.7 and 173.5 ± 6.8 kg and a height of 89.0 ± 0.7 and 99.8 ± 1.4 cm for cows and bulls, respectively (Iype and Venketachalapathy, 2001). The animals have a solid colour. Red, black, white and their shades are commonly seen (Figure 4). Chocolate and grey colours are also seen; red, black or fawn and white colours. Hump is prominent for bulls.

Milk production and quality

The average daily yield is 2.5 kg per day (Iype, 2009). The lactation length was reported to be 242 days (Iype and Thirupathy, 2001). The milk of Vechur cows was considered to have high medicinal value and was extensively used in the Ayurvedic system of medicine (Vijayan Vaidyan Thennattu, personal communication). The traditional belief was that Vechur milk is good for infants and convalescing people, as it is more easily digested. The low-fat globule size (3.21 μm) found in the studies (Venkatachalapathy and Iype, 1996) gives an indication that this could be true.

Studies have shown that Vechur cattle are free from Bovine leukocyte adhesion deficiency (Aravindakshan and James, 2006). Growth studies showed that the rate of growth for Vechur is good under Kerala conditions. By 6 months the bull calves weigh 44 kg and by 9 months 64 kg and 173 for bulls over 2 years. It is around 4 times and 6 and 16 times of the birth weight of 11 kg for males (Iype and Venkatachalapathy, 2001).

This and the recent research finding on the β-casein A2 allele in the Vechur cow (Muhamed and Mathew, 2010), the finding that arginine content in Vechur cow milk is more than that in the milk of other cows (Anisha Bhasker and Mohankumar, 2011) and the experiences of

Figure 4. Different colours of Vechur.

people are increasing the popularity of the cow. Added to this is the use of dung and urine for natural farming, organic and zero budget farming systems. Compared with bigger cows Vechur cow is a pet and companion to farmers if reared affectionately (Figure 5).

Experience of farmers and economic feasibility

A survey undertaken with the farmers showed the below results (Iype, 2009). This was a part of a project undertaken by the Vechur Conservation Trust. The milk yield of Vechur cattle was recorded by asking the farmers. Same was the procedure with cross-bred cows. The cows were in one of the first three lactations. The average was 2.3 for crossbreds and 1.6 for Vechur. The Vechur cows were newer to the area and with advancing time the average parity number would increase. The observations were of 1 year (Table 1).

Table 1. A comparison of Vechur and cross-bred cows of the farmers (Iype, 2009).

	Vechur	Crossbred
Daily average milk production (litres)	2.5	7.9
Feed grass (kg)/day	10	25
Straw (kg)/day	1	3
Compounded feed/bran (kg)/day	0.5	4.5
Wages for milker per day (Rs)	Milking by owner	15
Income from milk (Rs)/day	75	160
Labour by owner (hours)	2	3
Frequency of washing and cleaning of animal	Once a week	Daily

Source: Unpublished progress report 2007 Vechur Conservation Trust (Iype, 2009).

Because the cost for feed, labour, fodder cultivation and grazing is increasing, cattle raising has become not viable for many. Farmers are also dejected with disease problems of the crossbreds as well as their heat intolerance. The management-intensive, exotic/cross-bred cows become a liability to many farmers forcing them out of the dairy business. Many farmers do not want to take the trouble of going out to sell the milk in the collection centres. In this context, a breed of cow that needs no sophisticated management is an answer for a good percentage of people.

The ideal cow is the one sustainable to the farmer and need not be a high producing one. Vechur cow rearing is a low-input, "eco-friendly" system, as the grass in the compound and by-products of agriculture are used as feed. The use of the urine and cow manure rather than chemical fertilizers is beneficial economically as well as environmentally. Now there is a big boost to native cow keeping as many farmers switch to organic farming or "zero budget natural farming".

The farmers having Vechur cows are of different economic status. Wealthy people who want really good milk and are concerned about food security is one group. Resorts are especially interested in maintaining Vechur cows as it is an attraction to the guests. They are used as lawn mowers in some eco-friendly resorts. Apart from energy saving for lawn the smallest cows in action in the lawn moving is a real attraction. Also the feeding becomes inexpensive.

Figure 5. The companion of the farmer (2001).

Middle-class people use them for food security and as an income through the sale of milk or ghee.

Organic/Natural/zero budget farmers are much interested in Vechur. The demand for Vechur cows is great. The problem is those who can afford buy the cows at a fancy price. So the poor are tempted to sell away the cows though the cow is sustainable.

Now the Kerala Government has started realizing the importance of this conservation. After 23 years of dedication and persistence, it is a great accomplishment to the pioneers that this effort is now recognized and acknowledged by the Kerala Government and also the people. But more has to be done for the farmers.

Further developmental work

A change in the government policy promoting indigenous breeds is absolutely essential. People are at the centre of any conservation effort. Only the livestock keepers can effectively do something to ensure survival of the native animals. But they need support. The experience of the past is that unilateral governmental policies have been detrimental to breeds and breeding. What is required now is the strengthening and supporting of livestock keepers. Native breed associations should be encouraged to be formed and they should fulfil their responsibilities and governments should recognize the farmers' rights. A change is required to the effect that the policies are with the concurrence of the farmers. Governments need to give only general guidelines. With global warming looming no one can afford to lose heat-tolerant animals like Vechur. Crossbreds have been a failure in India. Large-scale/factory farming is getting promoted in India and in other developing nations. The small farmers in Kerala are leaving cattle rearing, which is resulting in a drastic reduction in livestock. Kerala Livestock Census figures reveal a cattle population drop of 49 percent between 1996 and 2007 (Kerala Government, 2012). Now there is a great realization that the Vechur cow is invaluable to farmers; especially those with small land holdings. The Vechur cows are highly sought after by many farmers. They find it very economical to maintain this cow. It provides sufficient milk for home consumption and one cow can provide enough milk for two households. For those who wish to own a cost-effective cow for home use that frees one from having to consume processed milk, a Vechur is the perfect cow especially in hot and humid tropical climates! The Vechur cow is contributing to future food security. Considering the unique qualities of the Vechur, value addition programmes should be taken up. At least in the initial stage funding from national and international agencies would help and this cow would be used globally in future.

The Vechur Conservation Trust is making available the germplasm to more farmers near and far since 8 years. The demand is high. If supported, the work can be done more extensively.

Conclusion

Vechur cattle have been saved from extinction owing to a collective effort, despite many ordeals and obstacles. Instead of just being yet another variety listed among the thousands that have been going into oblivion, the Vechur is now a living reality, providing farmers with a viable, economical and sustainable resource. More financial support is needed to ensure that the number of these animals can be increased effectively, making them available for those who want.

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Cross-breeding cattle for milk production in the tropics: achievements, challenges and opportunities

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Summary

This paper reviews experiences with cross-breeding for milk production in the tropics. Data were compiled from 23 different studies evaluating the performance of different grades of cross-bred animals as well as local breeds. Relative performance of indigenous breeds compared with different grades of cross-breeds was calculated for three climatic zones. Traits considered were milk yield per lactation, age at first calving, services per conception, lifetime milk yield and total number of lactations completed. At 50 percent *Bos taurus* blood, lactation milk yields were 2.6, 2.4 and 2.2 times higher than those of local cattle in the highland, tropical wet and dry, and semi-arid climatic zones, respectively; lactation lengths increased by 1.2, 1.2 and 1.9 months in the above-mentioned climatic zones, respectively; there was a reduction in calving interval by 0.8 times and in age at first calving by 0.9 times. Similarly, cross-breds with 50 percent *B. taurus* genes had 1.8 times higher lifetime milk yields and a 1.2 times higher number of total lactations. Although cross-breeding faces a number of challenges such as better infrastructure, higher demand for health care, there are many advantages of using it. These are higher production per animal, higher income for the families and provision of high-value food. It is therefore likely to continue to be an important livestock improvement tool in the tropics in the future, where farmers can provide sufficient management for maintaining animals with higher input requirements and access to the milk market can be secured.

Keywords: *Cattle, cross-breeding, milk production, tropics*

Resumen

Este artículo hace un repaso por las experiencias obtenidas con el cruzamiento de razas para la producción de leche en los trópicos. Se recopilaron datos de 23 estudios diferentes que evaluaron los rendimientos de animales con distinto grado de cruce así como de animales de razas autóctonas. Se compararon los rendimientos de las razas autóctonas con los de animales con distinto grado de cruce para tres zonas climáticas. Las características consideradas fueron el rendimiento lechero por lactación, la edad al primer parto, el número de servicios por concepción, la producción lechera total a lo largo de la vida del animal y el número total de lactaciones completadas. Con un 50 por ciento de sangre Bos taurus, los rendimientos lecheros por lactación fueron 2,6, 2,4 y 2,2 veces mayores que los del ganado bovino autóctono en las zonas climáticas de las Tierras Altas, Tropical Húmeda y Seca y Semiárida, respectivamente; la duración de la lactación se incrementó en 1,2, 1,2 y 1,9 meses en las zonas climáticas anteriormente mencionadas, respectivamente; el intervalo entre partos y la edad al primer parto se redujeron, respectivamente, 0,8 y 0,9 veces. Asimismo, los animales cruzados con una genética 50 por ciento Bos taurus tuvieron rendimientos lecheros, para la totalidad de su vida productiva, 1,8 veces mayores y un número total de lactaciones 1,2 veces mayor. Si bien el cruzamiento implica afrontar una serie de retos como una mejor infraestructura o una mayor demanda de atención sanitaria, su uso presenta múltiples ventajas como son una mayor productividad por animal, mayores ingresos para las familias y el aprovisionamiento en alimentos de alto valor. Por ello, el cruzamiento seguirá seguramente siendo una importante herramienta de mejora del ganado en los Trópicos, donde los ganaderos pueden aportar las condiciones adecuadas de manejo para mantener animales con elevadas necesidades, garantizándose así el acceso al mercado de la leche.

Palabras clave: *Ganado bovino, cruzamiento, producción lechera, trópicos*

Résumé

Ce travail de synthèse fait le point des expériences obtenues avec le croisement de races pour la production laitière sous les tropiques. Les données de 23 études différentes ayant évalué les performances d'animaux avec différent degré de croisement ainsi que ceux d'animaux de races indigènes ont été compilées. Les performances des races indigènes ont été comparées à celles d'animaux avec différent degré de croisement pour trois zones climatiques. Les caractères considérés ont été la production laitière par lactation, l'âge au premier vêlage, le nombre de services par conception, la production laitière sur la durée de la vie de l'animal et le nombre total de lactations complétées. Avec un 50 pour cent de sang Bos taurus, les productions laitières par lactation ont été 2,6, 2,4 et 2,2 fois plus élevées que celles des bovins indigènes dans les zones climatiques des Hauts-Plateaux, Tropicale Humide et Sèche et Semi-aride, respectivement; la durée de la lactation a augmenté de 1,2, 1,2 et 1,9 mois dans les susdites zones climatiques, respectivement; l'intervalle entre mises bas et l'âge au premier vêlage ont été, respectivement, 0,8 et 0,9 fois plus bas. De même, les animaux croisés à 50 pour cent de sang Bos

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taurus ont eu des productions laitières, sur la durée de leur vie, et un nombre total de lactations 1,8 et 1,2 fois plus élevés, respectivement. Bien que le croisement suppose affronter des défis tels qu'une meilleure infrastructure ou une plus grande demande en soins sanitaires, son usage comporte de nombreux avantages, parmi lesquels une majeure productivité par animal, un revenu plus élevé pour les familles et l'approvisionnement en aliments de grande valeur. Ainsi, le croisement continuera certainement à être un outil important d'amélioration du bétail sous les Tropiques, où les éleveurs peuvent fournir les conditions adéquates d'élevage pour maintenir des animaux à forts besoins et s'assurer ainsi l'accès au marché du lait.

Mots-clés: *Bovins, croisement, production laitière, tropiques*

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Introduction

Cross-breeding native cattle, often of *Bos indicus* type, with exotic *Bos taurus* cattle is now a widely used method of improving reproduction and production of cattle in the tropics (VanRaden and Sanders, 2003). Although indigenous cattle are well adapted to local production conditions, they usually mature late and have poor growth rates and low milk yields (Syrstad, 1988).

Reports on cross-breeding in the tropics date back to 1875 (Gaur, Garg and Singh, 2005), when shorthorn bulls were crossed to native cows in India. Other reports (Buvanendran and Mahadevan, 1975) indicate that livestock improvement in the tropics using this method began more than 300 years ago when exotic cattle were introduced into what is today Sri Lanka. Results on the performance of such crosses in well-designed experiments have, however, only been available since 1930 and a great number of reports have been published since then. It has now become clear from studies carried out by Amble and Jain (1967); Mason (1974); Katpatal (1977); Kimenye (1978); Rege (1998); Demeke, Neser and Schoeman (2004a) and Gaur, Garg and Singh (2005) that where cattle management is good, the performance of cross-breds increases with the number of *B. taurus* genes, and that the breeds that have 50 or 75 percent of these genes perform better than all other levels of exotic inheritance. Animals with these levels of *B. taurus* blood calve earlier than the indigenous stock, produce more milk, and have longer lactations and shorter calving intervals (CIs). Cross-breeding is therefore a very attractive short-term livestock improvement tool as improvements can be made in a population within a single generation. However, despite the impressive results and high demand for milk in the tropics, well-organized and successful cross-breeding programmes remain few (McDowell, Wilk and Talbott, 1996). For example, in India only 12 percent of its 187 million head of cattle are cross-breeds (Ahlawat and Singh, 2005); similarly, in Bangladesh cross-bred cattle account for only 2 percent of all milking cows (Miazi, Hossain and Hassan, 2007). Reasons for this include (1) lack of strategies and policies to take advantages of crosses in most parts of the tropics (Rege, 1998); (2) gaps in knowledge as to what the appropriate levels of exotic inheritance should be for a particular production system (Kahi, 2002); (3) lack of in-depth analysis of the socio-economic and cultural values of livestock in the different production systems or production environments, which leads to wrong breeding objectives (Chagunda, 2002) and (4) small herd sizes that do not allow maintaining sufficiently large breeding stock for cross-breeding and often unknown exotic blood level.

This paper reviews the achievements that have been made in cross-breeding for milk production in the different climatic zones (climatic zones) in the tropics, and discusses the challenges and opportunities for its use in the future.

Cross-breeding: the genetic background and types of cross-breeding

Genetic background

The genetic basis of cross-breeding can be broadly divided into two components: additive and non-additive. The additive component is because of the average effect of the strains involved (breeds or parental lines), weighted according to the level of each parental breed in the cross-bred genotype. The non-additive component of cross-breeding is heterosis (Swan and Kinghorn, 1992). Heterosis is defined as the difference between the increase in cross-breeds' performance from the additive component based on the mean performance of the pure-bred parental lines. The levels of heterosis are presented as percentage values and can be used to calculate the expected performance of cross-bred individuals (Bourdon, 2000). Heterosis is caused by dominance (interactions within loci) and epistasis (interactions between loci) effects of genes. The positive effects of dominance are the result of increased levels of heterozygosity, which allow an individual to react to environmental challenges in different ways (Swan and Kinghorn, 1992). Epistasis interactions can have a negative effect because of a breakdown of favourable interactions between loci in pure-bred animals, which prior to cross-breeding developed by both natural and artificial selection within breeds (Roso *et al.*, 2005). These effects have been observed in cross-breeding studies for milk production in the tropics. Syrstad (1989) reviews results obtained from

F1 and F2 *B. indicus* and *B. taurus* crosses for milk production. In his article, a deterioration in performance because of the breakdown of epistatic gene effects was found to occur between the F1 and F2 for all traits studied (age at first calving (AFC), calving interval (CI), milk yields and lactation lengths (LLs)).

Types of cross-breeding

Cross-breeding can be grouped into three types. They are grading up, rotational crossing or criss-crossing and formation of synthetic or composite populations (Cunningham and Syrstad, 1987).

Grading up

This is a common cross-breeding strategy employed in most parts of the tropics. Usually an indigenous female animal is mated with an exotic male. The first cross generation (F1) performs very well in productive and reproductive traits: it has higher milk yields, shorter CIs and the animals calve at a younger age than the indigenous stock. Further upgrading, however, usually leads to mixed results (McDowell, 1985; Rege, 1998). These results are because of a reduction in heterozygosity as the generations proceed (Cunningham and Syrstad, 1987). Although the average performance of the F1 usually exceeds that of the indigenous breeds in milk yields, performance of the cross-breds can be variable. This could be because of the large variation in the environmental conditions that exist in the tropics, and a result of the two genotypes involved (Cunningham, 1981; McDowell, 1985; Dhara, Ray and Sinha, 2006).

Rotational crossing

Rotational crossing is used or widely advocated in different parts of the tropics as a strategy to maintain high levels of heterozygosity and at the same time achieve specific proportions of the domestic and exotic strains (Cunningham, 1981; Gregory and Trail, 1981). Madalena (1981) describes four forms of this method. In the first, two bulls (one exotic and one indigenous) are used in alternate generations; the exotic bull is bred to the indigenous cow, then the indigenous bull is bred to the resulting cross-bred cows, and so on. Within a few generations, the system stabilizes at two types of grades (2/3 and 1/3), which coexist on one farm at the same time. The second form also involves two breeds: one exotic and one indigenous bull. In this system, the indigenous bulls are only mated to cows with more than 75 percent exotic blood. This leads to a herd that is composed of three coexisting grades (3/7, 5/7 and 6/7). In other words, the exotic bull is used on two generations and followed by an indigenous bull for one generation. The third form is similar to the first one, but instead of an indigenous bull, a cross-bred bull is used. In the fourth form, three breeds are used: two exotic bulls and one indigenous bull. In the first stage, the exotic breed is mated with the indigenous breed to produce the F1 population. This new breed is mated to the second exotic breed to produce offspring with 75 percent exotic genes. To complete the cycle, these are mated to the local breed to produce offspring with 37.5 percent exotic genes.

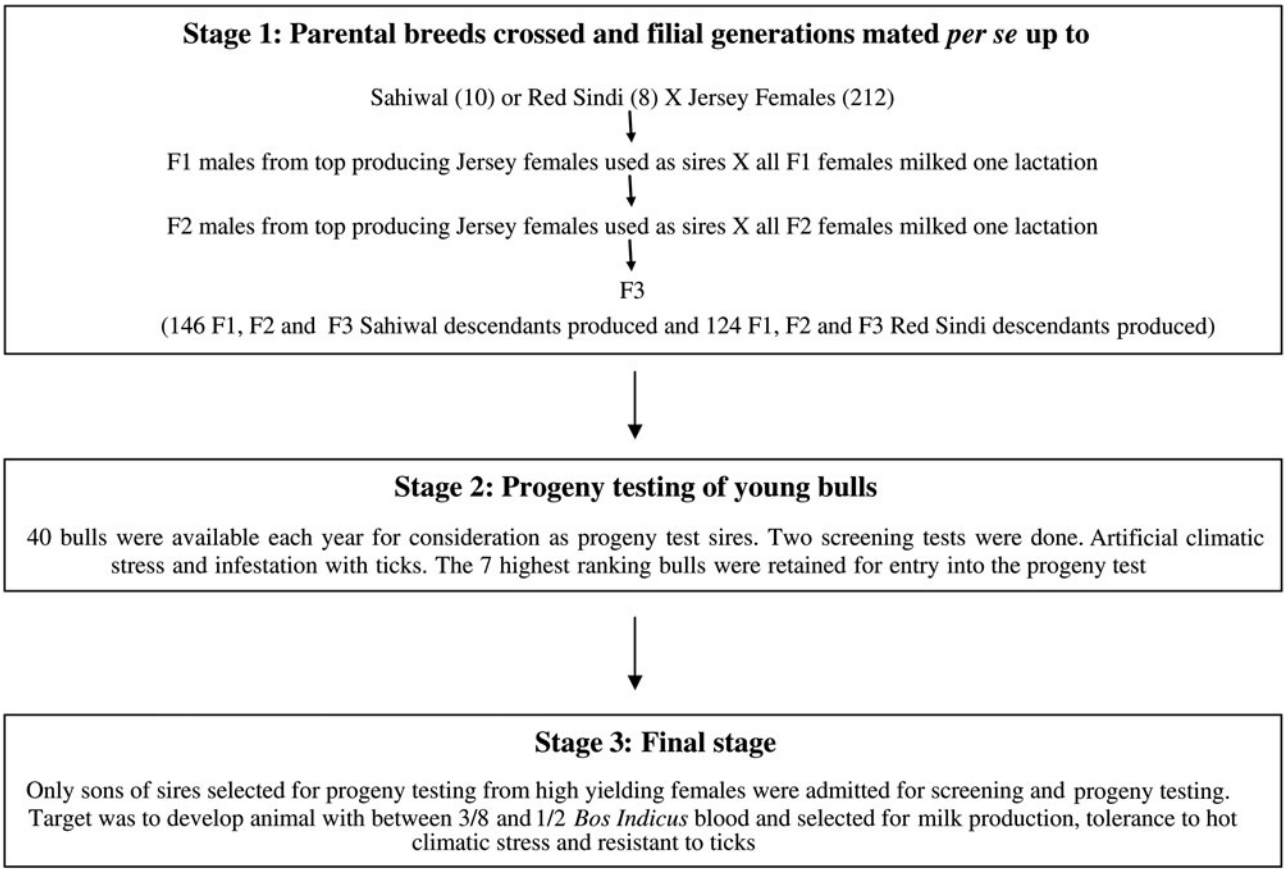
Rotational cross-breeding also has some limitations. First, in the two-breed rotational system the genes contributed by the two breeds fluctuate between 1/3 and 2/3 between generations. This makes it difficult to harmonize adaptability and performance characteristics to appropriately match the management level or the prevailing natural environment. Second, regular cross-breeding as described in the previous section is expensive to maintain.

Synthetic breeds

Synthetic breeds are made up of two or more component breeds, and are designed to benefit from hybrid vigour without crossing with other breeds (Bourdon, 2000). Synthetic breeds can be formed in many ways. Cunningham and Syrstad (1987) describe two methods: the simplest form involves two parental breeds which are crossed to produce the F1 generation. Selected F1 individuals are then *inter se* mated to produce the F2 generation. This process is repeated in subsequent generations. Figure 1 shows a summary of the cross-breeding programme that is followed in the development of the Australian milking Zebu (AMZ), a Sahiwal:Jersey synthetic. There are also other methods of forming synthetic breeds. A programme using three breeds, for instance, could produce a synthetic with 25 percent local genes (*B. indicus*), 25 percent from one of the *B. taurus* breeds and 50 percent *B. taurus* genes from a second exotic animal.

Materials and methods

The relative performance of different grades of crosses with the indigenous genotypes from different climatic zones in the tropics was compared. The data used in the study were obtained from published records for different parts of the tropics, and grouped into climatic zones according to the classification used by World Book (2009). Data were compiled from several studies on cross-breeding for dairy production in the tropics (the complete data set is provided in Supplementary Tables S1–S3). From these, a subset of studies was extracted that evaluated the performance of different grades of cross-breeds in comparison with local breeds (*B. indicus*). Reports that did not have local breeds in their design were excluded. At the end of the process, 23 studies were obtained, as can be seen in Table 1. Data were further clustered into three production environment groups according to whether the study was conducted on stations or on farms, and according to the climatic zone in which the study was undertaken. Studies undertaken on large commercial farms are marked on-farm 1, and studies conducted on small-scale farms on-farm 2. The final data set comprised data obtained from three climatic zones:



Stage 1: Parental breeds crossed and filial generations mated *per se* up to

Sahiwal (10) or Red Sindi (8) X Jersey Females (212)

F1 males from top producing Jersey females used as sires X all F1 females milked one lactation

F2 males from top producing Jersey females used as sires X all F2 females milked one lactation

F3

(146 F1, F2 and F3 Sahiwal descendants produced and 124 F1, F2 and F3 Red Sindi descendants produced)

Stage 2: Progeny testing of young bulls

40 bulls were available each year for consideration as progeny test sires. Two screening tests were done. Artificial climatic stress and infestation with ticks. The 7 highest ranking bulls were retained for entry into the progeny test

Stage 3: Final stage

Only sons of sires selected for progeny testing from high yielding females were admitted for screening and progeny testing. Target was to develop animal with between 3/8 and 1/2 *Bos Indicus* blood and selected for milk production, tolerance to hot climatic stress and resistant to ticks

Figure 1. Summary of the breeding programme used to develop the Australian Milking Zebu. Source: Developed from Hayman (1974).

highlands, tropical wet and dry and semi-arid. Owing to the small differences between the tropical wet and dry climatic zones, and because of the small amount of data obtained from the tropical wet zone, the data from these two zones were merged into one tropical wet and dry zone. Traits compared in the study were milk yield per lactation (MYL), lactation length (LL), CI, AFC, services per conception (SPC), lifetime milk yield (LMY) and total number of lactations completed (TLC). Some of the studies used did not evaluate all these traits; in that case only the traits reported were considered. Relative performance of the different grade crosses was compared with that of local breeds by dividing the least squares mean (LSM) of a given trait in the different cattle grades by the LSM of the same trait in the local breeds. Finally, means and standard deviations of the relative performance ratios for the different grade crosses for a given climatic zone were computed. The ratios obtained for every study under analysis are given in Supplementary Tables S4 and S5.

Most available cross-breeding studies are based on single lactation records, and therefore do not account for lifetime productivity of cows, which is an important measure of overall profitability of dairy cattle (Matharu and Gill, 1981). For the purpose of this paper, reports on LMY and lactations completed (LC) were compiled (Supplementary Table S4) for indigenous cattle and the different grades of crosses. Unlike for the other traits, results from the different climatic zones were analysed together because of the low number of available studies.

Results

Grading up

In all climatic zones, cross-breds had higher milk yields, increased LL, shorter CIs and lower AFC compared with the local breeds (Tables 2 and 3). In the highland climatic zone, it was observed that the mean MYL for cows with 50 percent *B. taurus* genes was 2.6 times higher than that of the indigenous cows. Cows at the next level of exotic inheritance with 75 percent *B. taurus* genes showed a similar performance, with an MYL 2.7 times higher than that of local cows. In the tropical wet and dry climatic zone, increasing the percentage of *B. taurus* genes beyond 75 percent resulted in lower milk yields than that observed in the 50 percent crosses. The F2 in this climatic zone performed significantly lower than the F1. In the semi-arid region, MYL increased by 2.2 times at the 50 percent *B. taurus* level. In all climatic zones, all cross-breds with the exception of the 25 percent cross in the tropical wet and dry climatic zone had longer LLs. The overall range of change for MYL was between 1.1 and 4.5. In the tropical wet and dry climatic zone, and in the

Table 1. Summary of data from 23 different studies used in the analysis.

No.	*Bos indicus*	*Bos taurus*	climatic zone	Country	Location	Production environment	Source
1	Boran	HF	Highlands	Ethiopia	Holeta station	On station	Demeke, Neser and Schoeman (2004a)
	Boran	Jersey	Highlands	Ethiopia	Holeta station	On station	Demeke, Neser and Schoeman (2004a)
	Boran	HF	Highlands	Ethiopia	Holeta station	On station	Demeke Neser and Schoeman (2004b)
	Boran	Jersey	Highlands	Ethiopia	Holeta station	On station	Demeke Neser and Schoeman (2004b)
2	Arsi	HF	Highlands	Ethiopia	Aresela region	On station	Kiwuwa *et al.* (1983)
	Arsi	Jersey	Highlands	Ethiopia	Aresela region	On station	Kiwuwa *et al.* (1983)
	Zebu	HF	Highlands	Ethiopia	Aresela region	On station	Kiwuwa *et al.* (1983)
3	Barca	HF	Highlands	Ethiopia	Aresela region	On station	Tadesse and Dessie (2003)
4	Sahiwal	Ayrshire	Highlands	Kenya	Nanyuki	On farm1	Gregory and Trail (1981)
	Sahiwal_S	Ayrshire	Highlands	Kenya	Nanyuki	On farm1	Gregory and Trail (1981)
5	Sahiwal	Ayrshire	Highlands	Kenya	Ngong	On station	Kimenye (1978)
	Sahiwal_S	Ayrshire	Highlands	Kenya	Ngong	On station	Kimenye (1978)
6	White Fulani	HF	Tropical WD	Nigeria	Vom	On station	Knudsen and Sohael (1970)
7	White Fulani	HF	Tropical WD	Nigeria	Vom	On station	Sohael (1984)
8	White Fulani	HF	Tropical WD	Nigeria	Vom	On farm1	Olutogun, Yode-Owolade and Abdullah (2006)
9	Sahiwal	HF	Tropical WD	India	Ambala	On station	Amble & Jain (1967)
	Sahiwal	HF	Tropical WD	India	Meerut	On station	Amble & Jain (1967)
10	Sahiwal	Brown Swiss	Semi-arid	India	Karnal OS	On station	Bala and Nagarcenkar (1981)
	Deshi	HF	Tropical WD	India	Haringhata	On station	Bala and Nagarcenkar (1981)
	Hariana	HF	Tropical WD	India	Haringhata	On station	Bala and Nagarcenkar (1981)
	Hariana	Brown Swiss	Tropical WD	India	Haringhata	On station	Bala and Nagarcenkar (1981)
11	Deshi	Jersey	Tropical WD	Srilanka	Karagoda -Uyan.	On station	Buvanendran (1974)
12	Sinhala	HF	Tropical WD	Srilanka	Karagoda -Uyan.	On station	Wijerante (1970)
13	Sindi	Jersey	Tropical WD	Srilanka	Undugoda	On station	Buvanendran and Mahadevan (1975)
	Sihala	HF	Tropical WD	Srilanka	Karagoda-Uyangoda	On station	Buvanendran and Mahadevan (1975)
14	Criollo	Jersey	Tropical WD	Costa Rica	Turrialba	On station	Alba and Kennedy (1985)
15	Local	Jersey	Tropical WD	India	Chalakudy	On station	Katpatal (1977)
	Local	Jersey	Tropical WD	India	Vikas Nagar	On station	Katpatal (1977)
	Local	Jersey	Tropical WD	India	Visakhapatnam	On station	Katpatal (1977)
16	Local	HF	Tropical WD	Bangladesh	Comilla	On farm2	Miazi, Hossain and Hassan, 2007
	Local	Jersey	Tropical WD	Bangladesh	Comilla	On farm2	Miazi, Hossain and Hassan, 2007
	Local	HF	Tropical WD	Bangladesh	Khulna	On farm2	Ashraf *et al.* (2000)
17	Local	HF	Tropical WD	Bangladesh	Dhaka	On station	Majid, Talukder and Zahiruddin (1996)
18	Local	Jersey	Tropical WD	Bangladesh	Dhaka	On station	Majid, Talukder and Zahiruddin (1996)
	Sahiwal	HF	Tropical WD	Bangladesh	Dhaka	On station	Majid, Talukder and Zahiruddin (1996)
	Local	Jersey	Tropical WD	Bangladesh	Dhaka	On station	Rahman, Islam and Rahman (2007)
19	Local	HF	Tropical WD	Bangladesh	Dhaka	On station	Rahman, Islam and Rahman (2007)
	Local	HF	Tropical WD	Bangladesh	Barisal/Patuakahli	On station	Al-Amin and Nahar (2007)
20	Sahiwal	HF	Semi-arid	Pakistan	Bahadurnagar	On station	McDowell, Wilk and Talbott (1996)
21	Sahiwal	HF	Semi-arid	India		On farm1	Matharu and Gill (1981)
22	Ratini	Red Dane		India	Bikaner	On farm1	Singh (2005)
23	Ongole	Jersey		India	Visakhapatnam	On farm1	Singh (2005)

Note: Tropical WD = tropical wet and dry.

Table 2. Relative performance of breed groups (F1 1/4 exotic; F1 1/2 exotic; F1 1/3 exotic; F2) in two selected production traits in different climatic zones.

climatic zone	Milk yield per lactation				Laction length			
	Breed group				Breed group			
	1/4	1/2	3/4	F2	1/4	1/2	3/4	F2
Highlands ($n = 10$)								
Mean	n.a.	2.6	2.7	3.4	1.2	1.2	1.3	n.a.
SD	n.a.	1	1	0.4	0.2	0.2	0.2	n.a.
Range	n.a.	1.4–4.5	1.8–4.5	3–3.6	1–1.3	1–1.5	1.2–1.5	n.a.
Tropical wet and dry ($n = 27$)								
Mean	1.7	2.4	1.8	1.9	1	1.2	1.1	1.1
SD	0.4	0.8	0.6	0.6	0.01	0.2	0.1	0.1
Range	1.1–2	1.2–3.9	1.4–2.8	1.2–2.9	1.05–1.07	1–1.7	0.9–1.3	1–1.3
Semi-arid ($n = 4$)								
Mean	1.4	2.2	1.5	1.4	n.a.	1.9	n.a.	n.a.
SD	0.5	0.4	0.5	0.5	n.a.	0.6	n.a.	n.a.
Range	1.1–1.7	1.8–2.6	n.a.	1.2–1.5	n.a.	1.2–2	n.a.	n.a.

Note: n.a = not available.

semi-arid climatic zone, the F2 had lower MYL as compared with the 50 percent. With the exception of the semi-arid climatic zone, where LL increased by 1.87, mean LL ranged between 1 and 1.3 times in all the other climatic zones.

There were also some unexpected results: for example, MYL of the F2 in the highlands zone was higher than that of the F1. This observation is in contrast with findings from other studies (Syrstad, 1989; Rege, 1998), and could be because of the small amount of data used, and the fact that no correction was made for the different breed combinations used in the different studies. The widest mean range (1.4–4.5) for relative performance was observed in MYL for the F1 and 75 percent crosses in the highlands. This could be the result of the large differences in management between farms, or because of the different *B. taurus* and *B. indicus* breeds used in the various cross-breeding programmes providing the data. For example, in the highlands of Ethiopia a MYL of 529 litres was observed for Boran cattle, as compared with the 809 litres obtained from the Arsi breed in the same area (Kiwuwa *et al.*, 1983; Demeke Neser and Schoeman, 2004b). Holstein–Friesian (HF) crosses had the highest relative performance for MYL, followed by Jersey and Ayrshire crosses. Similar effects of *B. taurus* blood on performance (MYL and AFC) have been reported in other earlier studies. Cunningham and Syrstad (1987) compared production traits in different projects in which two or more *B. taurus* breeds were used simultaneously. The study included HF, Brown Swiss and Jersey cows. Jersey crosses were the youngest and Brown Swiss crosses the oldest at first calving, both differing significantly from Friesian crosses. Friesian crosses had the highest and Jersey crosses

Table 3. Relative performance of breed groups (F1 1/4 exotic; F1 1/2 exotic; F1 3/4 exotic; F2) in three selected reproduction traits in different climatic zones.

climatic zone	Calving interval				Age at first calving			Service/conception	
	Breed group				Breed group			Breed group	
	1/4	1/2	3/4	F2	1/2	3/4	F2	1/2	F2
Highlands ($n = 7$)									
Mean	n.a.	0.9	1	0.9	0.8	0.8	0.9	0.8	0.89
SD	n.a.	0.1	0.1	0.01	0.01	0.01	0.01	0.1	0.1
Range	n.a.	0.8–1	0.9–1	0.91–0.92	0.8–1	0.8–0.9	0.92–0.93	0.7–0.8	0.8–0.9
Tropical wet and dry ($n = 16$)									
Mean	n.a.	0.92	1	1	0.8	0.9	0.9	1	n.a.
SD	n.a.	0.1	0.2	0.1	0.1	0.1	0.01	0.17	n.a.
Range	n.a.	0.8–1	0.8–1.3	0.9–1.1	0.6–1	0.8–1	0.84–0.85	0.8–1.2	n.a.
Semi-arid ($n = 4$)									
Mean	n.a.	0.9	1.01	1	0.83	0.7	0.8	n.a.	n.a.
SD	n.a.	0.01	0.06	n.a.	0.1	0.03	0.02	n.a.	n.a.
Range	n.a.	n.a.	0.9–1.0	n.a.	0.7–0.9	0.7–0.8	0.8–0.84	n.a.	n.a.

Note: n.a. = not available.

the lowest milk yields, and the differences between them were significant.

Cross-bred animals with 50 percent *B. taurus* genes had between 1.4–2.6 times higher LMY and 1.2 times more LC than the indigenous cattle. An increase in LMY and LC among cross-breds is also reported by Singh (2005), who reviewed lifetime parameters on two and three-breed crosses from different studies conducted on government and research farms in various parts of India involving several local and exotic breeds. HF crosses of 50 to 62.5 percent *B. taurus* genes had higher LMY and more LC than those above these levels of crossing (75 or 87.5 percent). These results were confirmed by a later study carried out by Goshu (2005), who compared lifetime performance of different grades of crosses of HFs with Ethiopian Boran cattle under an intensive grazing system with supplementation at Chefa farm in Ethiopia. The level of crossing significantly affected herd life and LMY. The 50 and 75 percent *B. taurus* cross-breeds had significantly higher LMY and longer herd life than animals with higher levels of exotic inheritance (87.5 or 93.7 percent).

To enable proper overall comparison of the different genotypes, some studies on upgrading have focused on economic performance in different production environments. Madalena *et al.* (1990) undertook a study involving 65 commercial cooperative farms in the states of Minas Gerais, São Paulo, Rio de Janeiro and Espírito Santo, and two research centres (Santa Monica and USEPA São Carlos) in Brazil. Six red and white HF × Guzera crosses (25, 50, 62.5, 75 and 87.5 percent crosses and pure HF) kept under two types of management systems were compared, one with high and the other with low-level management and inputs. The F1 had a longer herd life, and better productive and reproductive performance than the other groups, and therefore yielded higher profits. The superiority of the F1 over all HF backcrosses was more pronounced at low levels of management.

In a more recent study, Haile *et al.* (2007) conducted an economic comparison of Ethiopian Boran animals and their crosses of 50, 75 and 87.5 percent HF inheritance, which were all reared in an intensive, stall-feeding system in the central highlands of Ethiopia. The study covers one calendar year (2003) and collected its data from cattle kept on the Debre Zeit Research Station in Ethiopia. Returns per day and per cow were calculated from dung and milk production. Results showed that the cost of producing 1 litre of milk was significantly higher for the Ethiopian Borans than for the crosses. The 87.5 percent crosses returned a significantly higher profit per day per cow and profit per year per cow than the 50 percent crosses. The crosses of 75 percent, however, did not yield a significantly higher profit per day per cow and profit per year per cow than the 50 or 87.5 percent crosses. It was concluded that intensive dairy production with indigenous tropical breeds is not economically viable.

Variations in economic performance between crosses of different breeds have also been observed. Hemalatha, Prashanth and Reddy (2003) compiled reports in which Friesian crosses, Jersey crosses and local cattle kept in different parts of India were compared. These reports showed that the cross-breds produced higher profits per kilogram of milk produced than the indigenous Zebu animals. It was also observed, however, that maintenance costs were highest for Friesian crosses, followed by Jersey crosses and lowest for local cattle. The economic impact of cross-bred cows in smallholder farming systems has been demonstrated in a number of studies. Some of these studies (Patil and Udo, 1997; Bhowmik, Sirohi and Dhaka, 2006; Policy Note, 2007) reported that in areas where cross-bred animals can be maintained, farmers incorporating them into their production systems had higher household incomes than those with pure indigenous breeds.

Rotational cross-breeding

One well-documented rotational cross-breeding programme is the one conducted at Kilifi Plantations in the humid lowlands of Kenya. The rotational cross-breeding programme on this farm dates back as far as 1939. Gregory and Trail (1981) analysed data from two groups of cattle produced on this farm in a two-breed continuous rotational cross-breeding system. Group 1 consisted of 67 percent Sahiwal and 33 percent Ayrshire genes, whereas group 2 consisted of 67 percent Ayrshire and 33 percent Sahiwal genes. The records analysed were collected between 1972 and 1978. With regard to milk production, group 2 (463 observations) performed significantly better than group 1 in the following traits: AFC (1019 versus 1042 days), MYL (2843 versus 2662 kg) and annual lactation yield (2616 versus 2503 kg), but had significantly longer CIs (398 versus 390 days) than group 1. In a follow-up study, Thorpe, Morris and Kang'ethe (1994) analysed lifetime performance of the two groups and of the cross between them (interbreeds). LMY was 48 percent higher for group 2 (67 percent Ayrshire and 33 percent Sahiwal genes group) than for group 1. The interbreeds yielded 34 percent less than the average rotational cross (groups 1 and 2). This decline is thought to be because of recombination loss, which results from the breakdown of favourable epistatic interactions between genes in different loci (Table 4).

Later, two more breeds (Brown Swiss and HFs) were introduced into the breeding programme. Mackinnon, Thorpe and Barker (1996) analysed data from a three-breed rotation programme consisting of Brown Swiss, Ayrshire and Sahiwal cattle in various combinations. The data contained 8447 observations. MYL for the herd was 3268 kg, and the LL and CI were 322 and 398 days, respectively. The improvement in performance of the three-breed crosses as compared with the two-breed crosses was attributed to the large amount of heterosis from crossing Sahiwal and the two *B. taurus* genomes. In a more recent study (Kahi

Table 4. Relative performance of F1 with 50 percent exotic blood level in life time production traits summarized across all studies ($n = 6$) in which these traits have been assessed.

	Life time milk yield ($n = 6$)	Total lactations completed ($n = 6$)
Value	**F1 (50%)**	**F1 (50%)**
Mean	1.8	1.2
SD	0.5	0.03
Range	1.4–2.6	1.21–1.26

et al., 2000), performance of the herd was analysed after the introduction of HFs. The data set contained 25 cross-breed combinations of HF, Ayrshire, Brown Swiss and Sahiwal cattle. Overall herd MYL, CI and LL were 3446 kg, 402 and 326 days, respectively. Crosses with 50 percent HF genes had significantly higher MYL, longer LL and shorter CI than those with 50 percent Brown Swiss genes. It was concluded that, as farm management had not changed, the improvement in MYL for the herd relative to the earlier study (Mackinnon, Thorpe and Barker, 1996) was because of the introduction of the HFs.

Formation of synthetic populations

Several attempts have been made to form synthetic groups: Hayman (1974), Katyega (1987), Gaur, Garg and Singh (2005), Singh (2005) and Cerutti, Alvarez and Rizzi (2006) give accounts of 13 synthetic breeds at varying levels of development from different parts of the tropics. McDowell (1985) compared data of five of these groups and found that performance of each group was superior to that of the native breeds. Table 5 shows a summary of some of the traits that were compared. For comparison, the performance of the native breeds used is indicated in the same table. It should be noted that the figures given for the native breeds were selected from a few studies only to enable quick comparison. Performances of the same native breeds observed in different studies are summarized in Supplementary Table S1.

The Australian Friesian Sahiwal (AFS) is one of the successful synthetic breeds: the 50:50 Sahiwal:Friesian is a well-documented synthetic developed by the government of Queensland, Australia, from 1960 until 1994, when the programme was sold to a private company. The programme is now under the management of the AFS Association of Australia, which continues breed development, genetic management and progeny testing for AFS Bulls (Meat and Livestock Australia, 2006). The AFS was bred for milk letdown, tick resistance and milk yield. Under extensive grazing on tropical pastures, the AFS averaged 2556 litres of milk and 105 kg of fat, which compares favourably with the HF performance of 2291 litres of milk and 82 kg of fat (Alexander, 1986). Another equally successful synthetic is the Girolando, a 62.5:37.5 HF:Gir synthetic developed in Brazil. The Girolando produces 80 percent of the milk in Brazil and is characterized by an average of 3600 kg of milk with 4 percent fat content, and has a CI of 410 days (Girolando Associação Brasileira Dos Criadores de Girolando, 2005). In some parts of the tropics, where synthetic breeds have been successfully developed and reared by farmers, major increments in overall milk yields have been recorded. For instance, the Sunandini cattle have contributed greatly to the dairy economy of Kerala State in India. It

Table 5. Description of origin and composition of selected synthetic breeds and overview of performance parameters of selected synthetic and indigenous breeds.

	Description of synthetic breed				
	Jamaica Hope	**Pitanguei-Ras**	**Australian milking Zebu**	**Karan-Swiss**	**Sibovey**
Origin	Jamica	Brazil	Australia	India	Cuba
Composition	Jersey × Sahiwal	Red Poll × Zebu	Jersey × Sahiwal/Red Sindi	Brown Swiss × Sahiwal/Red Sindi	Holstein × Zebu
Performance of sythetic breeds					
AFC (months)	34.5	34.7	31	36.3	31.3
MYL (kg)	2930	2780	1987	2519	2897
LL (days)	282	281	244	324	298
CI (days)	439	414	422	415	405
Performance of the indigenous breeds used in establishment of synthetic breeds above					
	Sahiwal[2]	**Red Sindi**	**Zebu**[5]		
AFC (months)	37.4	40.5[3]			
MYL (kg)	1891	1270[4]	929		
CI (days)	439	414	422	415	405
Performance of the indigenous breeds used in establishment of synthetic breeds above					
	Sahiwal[2]	**Red Sindi**	**Zebu**[5]		
AFC (months)	37.4	40.5[3]			
MYL (kg)	1891	1270[4]	929		
LL (days)	305		303		
CI (days)	392	535[3]	451		

Source: [1]McDowell (1985), [2]Amble and Jain (1967), [3]Stonaker (1953), [4]Acharya (1970), [5]Kiwuwa *et al.* (1983).
Note: AFC = age at first calving; MYL = milk yield per lactation; CL = calving interval; LL = lactation length

is a synthetic breed developed by crossing nondescript local cows of Kerala State with Jersey, Brown Swiss and HF cows. It is estimated that through the active involvement of farmers in the breeding programme, milk production increased from 0.164 million tonnes in 1966 to 19.3 million tonnes in 1993 (Chacko, 2005).

Breeding strategies of smallholder farmers

A study of Ethiopian smallholder farmers keeping cross-breds has shown that farmers make informed decisions about the blood level they keep on their farm. Above 85 percent of all respondents ($n = 62$) prefer cross-bred cows with an exotic blood level between 50 and 75 percent. Main reasons for their preference are good level of income, adaptation of animals to environment and acceptable management level. A similar number of farmers (80 percent) also prefer their bulls/artificial insemination (AI) semen between 50 and 75 percent of exotic blood. However, 47 percent of farmers prefer their bulls/AI semen to have even more than 75 percent exotic blood. The percentages do not sum up to 100 percent, because farmers were allowed to give more than one exotic blood-level group. They like having a choice of more than one blood levels to be able to use higher grade bulls/AI for mating with local and low-grade cross-bred cows and lower-grade bulls/AI for mating with high-grade cross-bred cows (Roschinsky *et al.*, 2012). Madalena, Peixoto and Gibson (2012) also report that farmers with smaller herd sizes use bulls from different breeds in an often disorganized way in order to sustain their cross-bred herds.

Most farmers (88.7 percent) would advice other farmers to start with cross-breeding given proper management and accessible markets.

Challenges

In spite of the great potential of cross-breeding as a livestock improvement method, it has not led to a wide-spread increase in milk production in the tropics (Bayemi *et al.*, 2005). Owing to several challenges, cross-breeding has yet to be successfully and sustainably adopted and practised in the region (Rege, 1998; Kumar, Birthal and Joshi, 2003; Miazi, Hossain and Hassan, 2007). These include (1) limitations of cross-breeding methods; (2) mismatches between genotypes and production system, (3) intermittent funding of programmes and lack of appropriate policies and (4) lack of or limited involvement of farmers in the design of the interventions.

Limitations of cross-breeding methods

The many impressive results of grading up on record were mostly achieved at research stations and commercial farms, where the level of management and nutrition of stock is good (e.g. Katpatal, 1977; Thorpe, Morris and Kang'ethe, 1994; Tadesse and Dessie, 2003; Demeke, Neser and Schoeman, 2004a; Tadesse *et al.*, 2006). The smallholder sector in the tropics, which constitutes the majority of farmers, is at times unable to raise the levels of management and nutrition in line with the requirements of the new genotypes (Kahi, 2002). This often leads to low productivity and high mortality among the animals (Chagunda, 2002; Philipsson, Rege and Okeyo, 2006).

Although results from rotational cross-breeding have shown a marked improvement in animal productivity, this improvement method can only be used on large-scale operations, where management is good. The programmes associated with it are not practical for small-scale farmers, whose herd sizes may not justify keeping more than one bull. In the two-breed rotation system, there is great variability in genotypic composition from generation to generation, depending on the sire breed used. This is not practical for small-scale operations (Trail and Gregory, 1981; Syrstad, 1989; Madalena, Peixoto and Gibson, 2012). The most widely reported success, the Kilifi Plantation rotation programme (Mackinnon, Thorpe and Barker, 1996; Kahi *et al.*, 2000), has never been expanded beyond the single ranch programme or replicated elsewhere. Thus, this programme has had only limited impact as a source of improved genetics to the wider dairy farming community in the hot and humid coastal region of Kenya.

The development of synthetic populations has its drawbacks, too. First, it takes many years to develop a synthetic population, during which the production environment could change. Second, the development can be expensive. For example, the development of the AFS started in the 1960s and the costs amounted to $30 million Australian dollars. The breeding programme was later sold off to a private company, which has continued commercial development since 1994 (Chambers, 2006; Meat and Livestock Australia, 2006). During the development period of the AFS, there were drastic changes in Australia's infrastructure. As a result, milk production systems changed and the synthetic could not compete with breeds such as HF or Jersey under the new intensive production systems. It is now estimated that only 250 pure-bred AFS cattle remain in Australia, but exports of AFS cattle continues to many tropical countries including Mexico, Brunei, Thailand, India and Malaysia (Chambers, 2006). However, as will be later discussed in the section ‘Opportunities’, the innovative combination of emerging assisted reproductive technologies (ART), genomics and dense single nucleotide polymorphism (SNP) marker technologies can significantly speed up the development of synthetics.

Production environment and production system

Poor infrastructure and market access are major obstacles to the successful implementation of cross-breeding programmes, especially in rural areas with lower agricultural potential. In addition, pricing policies for milk in some countries are often poor. Prices paid to the farmers are low and cannot support the purchase of feeds or investment in the necessary infrastructure, all of which are necessary to make the production system economically viable (McDowell, 1985). The failure to recognize the different needs of different production systems has also affected the success rate of cross-breeding programmes. In many tropical countries, past, and, in some cases, ongoing cross-breeding programmes have often been based on a one-genotype-combination-fits-all premise, with HFs being the preferred improver breed even in the hot and humid tropics and under production systems such as stall feeding (zero grazing), where other breeds might be better suited (King *et al.*, 2006). Such genotype × production system mismatches that ignore the important genotype-by-environment interaction effects are partly responsible for the largely disappointing and poor performance of cross-bred cattle in the tropics and their often insignificant impact (McDowell, 1985; King *et al.*, 2006; Philipsson, Rege and Okeyo, 2006). The assumption that production systems can easily be changed and adapted to fit the needs of cross-bred animals seems in many circumstances wrong. In these cases the genetic improvement of local breeds should be considered a more realistic approach.

The choice of *B. taurus* breeds and the level of crossing for different production systems should not only be based on the genetic potential for milk yield, but also on farmers' ability to follow adequate husbandry practices as well as on the available healthcare services and markets. In addition, the availability of adequate, good-quality feeds and water needs to be taken into account, too. Increasing the genetic potential of the animals alone is not enough, the above factors must be considered as well for the full beneficial heterotic effects to be realized (Ansell, 1985; Chantalakhana, 1998).

Intermittent funding of programmes and lack of appropriate policies

A well-planned cross-breeding programme requires adequate funding (Kumar, Birthal and Joshi, 2003). However, funds in the required amount are not always available, which has caused the interruption of many programmes (Shem and Mdoe, 2003; Cardoso and Vercesi Filho, 2006; Shem, 2007). In addition, a lack of supportive national breeding policies and appropriate strategies has contributed greatly to the failure of many programmes. Rege (1998) and Chantalakhana (1998) observed that there is hardly a country in the tropics that has developed appropriate policies to take advantage of cross-breeding. This issue is of major concern to both farmers and technical personnel who are constantly seeking answers on how to maintain the appropriate level of crossing or determine which level of crossing is appropriate for a given production environment (Ansell, 1985; Chantalakhana, 1998). The lack of proper guidelines has led to undesirable consequences, especially at smallholder units where indigenous breeds are upgraded to higher exotic grades without following a defined cross-breeding programme (Kahi, 2002).

Participation of farmers

Ownership of farmers of any breeding programme, either for improving local breeds or cross-breeding with exotic breeds, is a crucial point for the success for any livestock improvement intervention. Farmers must have the right to express their opinion and should be involved in decision-making processes. This can ensure that new procedures such as data recording can be easily implemented, and that animals that better fit to the management of the individual farmers are bred.

Opportunities

Certain advantages exist to assist in addressing the challenges discussed in the previous section. These include: (1) availability of a large base population of indigenous tropical cattle; (2) advancements in ART; (3) availability of alternative recording methods; and (4) advances in genomic technology. Well-planned programmes using all or a combination of the existing advantages may lead to a large number of productive cross-bred animals in the tropics. In this section, the potential and impact of the advantages given above are discussed.

Availability of large base populations

A considerable number of cattle are found in the tropics. It is estimated that of the 1.4 billion cattle in the world, more than two-third are found in the tropics (Wint and Robinson, 2007). Most of these are indigenous cattle and belong to the Zebu type. The Zebu can be classified into a number of subgroups according to external traits, such as size, origin or utility. It has been proposed that improvement in tropical cattle should be made by selective breeding within the *B. indicus* race. This has however been shown to be a slow way to meet the fast-growing need for production (Ansell, 1985). The large number of existing animals with unique qualities provides an opportunity to make rapid improvements over a short period, if breeding programmes that cross-breed large numbers of animals with *B. taurus* milk breeds can be successfully implemented.

Assisted reproductive technologies

Recent developments in ART provide an opportunity for rapid multiplication of cross-bred populations. ART are defined as techniques that manipulate reproductive-related events and/or structures to achieve pregnancy with the final goal of producing healthy offspring in bovine females (Velazquez, 2008). ART began with the development of AI about 50 years ago. Widespread use of AI has been greatly enhanced by the possibility to freeze semen. In well-structured cross-breeding programmes in the tropics, AI has the potential of increasing the rate at which genetic change happens in the local population by increasing the reproductive rates of the bulls (Cunningham, 1999). Through AI it has been possible to transfer exotic genes to the tropics through imported semen. In some parts of the tropics, the persistent use of AI has yielded impressive results. In India, a well-planned cross-breeding programme resulted in the formation of the Sunandini synthetic breed. By 1993, Sunandini cattle had contributed greatly to the increase in milk production in Kerala State, India (Chacko, 2005).

A successful example for the use of AI for cross-breeding in the tropics is the dairy husbandry programme of the non-governmental organization (NGO) BAIF Development Research Foundation in India. Established in the 1970s in Maharashtra, India, with support from various international development agencies and the government of India, BAIF has built up a successful AI programme. BAIF's programme has served over 4.4 million families by establishing over 3500 cattle development centres across most states of India. The centres provide doorstep AI services to farmers accompanied by training and support concerning all aspects of dairy cattle farming (BAIF, 2011b). Farmers buy high-quality semen collected at BAIFs own bull station which houses 300 bulls of various exotic and indigenous breeds (BAIF, 2011a). The joint efforts of an NGO, the government of India, private sponsors and farmers benefitting from and recognizing the value of this ART have led to a successful, sustainable cross-breeding programme.

Following the success of AI, other methods of recovering, storing and implanting embryos, for instance multiple ovulation and embryo transfer (MOET), were developed. This opened up new possibilities for genetic improvement. It has been shown in some studies (e.g. Mapletoft and Hasler, 2005) that well-organized MOET programmes can result in increased selection intensity and reduced generation intervals, which eventually lead to higher genetic gains. It is for example estimated that if nucleus herds are established and heifers subjected to juvenile MOET (before first breeding), genetic gains twice than those obtained through traditional progeny testing programmes can be achieved. Since the middle of the 1990s, another important technique has been developed: ovum pick-up followed by *in vitro* embryo production (OPU-IVP). In this method, oocytes are harvested from females and fertilized *in vitro* (Cunningham, 1999; Van der Werf and Marshall, 2003). Through OPU-IVP, reproductive rates in females can be increased. For example, if two OPU-IVP sessions are carried out per week, up to 150 embryos and 70 calves per donor can be produced every year. There are two benefits for cross-breeding programmes: The number of females required in the programme is significantly reduced, and it is possible to multiply the number of animals with the required qualities rapidly (Cunningham, 1999). If sexed semen is used for *in vitro* fertilization, the sex of the offspring can be predetermined. This opens up additional opportunities for repeatedly and rapidly producing cross-breds of specific breed combinations and preferred sex (Wheeler *et al.*, 2006). It has also been proposed (Rutledge, 2001) that OPU-IVP be used widely as a method for continuous production of F1s by using oocysts from spent dairy cows and semen from adapted breeds. In this method, lactation in F1 cows can be initiated by transfer of F1 *in vitro* produced embryos. This strategy eliminates the loss of the heterosis effect and increases the phenotypic variation that results when F1 cattle are bred to either a pure-bred or cross-bred sire (Hansen, 2006). Wide-scale use of the technologies mentioned above (MOET, OPU-IVP and AI) is, however, not possible in the tropics at the moment because of the high costs involved, the poor infrastructure in many countries and the shortage of technical personnel (Kahi *et al.*, 2000). Madalena, Peixoto and Gibson (2012) report that there is one large cooperative in Brazil that offers to members F1 heifers pregnant with F1 or other female embryos.

Alternative recording methods

It has been pointed out (Cunningham, 1981) that any cross-breeding programme adopted for a population requires at some point in the programme an indigenous selection operation. A serious constraint on this is that performance records are not readily available in the tropics. The sort of extensive milk recording programmes which support dairy breeding in the temperate regions are virtually non-existent in the tropics (Syrstad and Ruane, 1998; Kahi *et al.*, 2000; Kosgey, Kahi and Van Arendonk, 2005). The reasons for this have been outlined by different authors (Ansell, 1985; Islam, Rahman and Faruque, 2002; Singh, 2005) and include: small herd sizes, scattered herds, poor communication, low level of farmer education, lack of incentives for farmers to record data, poor facilities for collecting and processing data and great diversity in feeding and management regimes. Mason and Buvanendran (1982) argue that recording systems in the tropics do not have to be as elaborate as in the temperate regions. They propose the following approaches, which are simpler, cheaper and easier to adopt for the farmers, but would still allow progeny testing to be done: (1) bi-monthly recording: in this system, the recorder visits the farm every alternate month and records the milk yield obtained during a 24-hour period; (2) AM–PM sampling: in this method, the morning milk is weighed one month, and the evening milk the next month. It maintains monthly visits but is cheaper; and (3) sampling at particular stages of lactation: sampling during early, mid or late lactation. This system is difficult to adopt for herds calving all year as the cows will always be at different stages of lactation.

Another approach that could be employed to reduce sampling costs is to contract selected herds in a given region to produce the desired cross-breeds. In this approach, detailed recording would only take place for the contracted herds. Farmers could be familiarized with these recording systems through community-based organizations for general improvement of livestock (CBOGIL), which have been established by several groups of farmers. Kahi *et al.* (2000) define CBOGIL as organizations owned by farmers in a community with the objective of improving livestock production through use of animal genetic resources. Other authors (Sölkner, Nakimbugwe and Valle-Zarate, 1998; Wurzinger *et al.*, 2008) refer to this livestock improvement approach as village breeding programmes. CBOGIL ensure effective participation of the local communities and other stakeholders, which can lead to the establishment of successful recording systems and breeding programmes, either for pure or cross-breeding programmes (Kahi *et al.*, 2000).

Genomic technology: current and future opportunities

Recent development in molecular genetics and the powerful new tool genomic selection are profoundly changing dairy cattle breeding in developed countries. Genomic selection refers to selection decisions based on genomic estimated breeding values (GEBV) or genomic breeding values (Hayes *et al.*, 2009). GEBV are the sum of the effects of dense genetic markers or the haplotypes of these markers across the genome (Hayes *et al.*, 2009). Genomic selection is now becoming feasible because of the availability of large numbers of SNP markers. In the case of cross-breeding, pure-breds can be selected for performance of cross-breds by estimating the effects of SNPs on cross-bred performance using phenotypes and SNP genotypes evaluated on cross-breds, and applying the results estimates to SNP genotypes obtained on pure-breeds (Dekkers, 2007). This is a major achievement because *B. taurus* breeds used in most cross-breeding programmes in the tropics are selected in the temperate regions under different management conditions. Owing to genetic differences between pure-breds and cross-breds, and the environmental differences between the two production systems, the performance of pure-bred parents is not a good predictor for that of their cross-bred descendants. This development now makes it possible to identify pure-breed parents whose descendants will perform best as cross-breds. Other benefits of genomic selection for cross-breeding include: (1) it does not require pedigree information on cross-breds; (2) once estimates of the SNP effects have been made, the genotype and phenotypic data can be used for several generations, and (3) it reduces the rate of inbreeding (Ibáñez-Escriche *et al.*, 2009).

The availability of large numbers of SNP makers has other benefits as well. It is, for example, possible to use certain techniques to accurately determine the breed composition of cross-bred animals without prior pedigree information. This is important because recording systems in the tropics are rare, and as a result many cross-bred populations exist whose breed compositions are unknown. Determining the breed composition of an animal enables inclusion of animals of unknown genotypes into breeding programmes and allows farmers to find out the accurate breed composition of the animals they wish to buy or sell.

The use of genomic technology in combination with ART opens up new possibilities of speeding up the formation of synthetic breed populations by taking advantage of reduced generation intervals and thereby multiplying the animals of the required breed combination (e.g. synthetic breeds) faster than is currently possible. The costs of these new technologies must, however, come down before they can be used on a wide scale.

General discussion

Results from over 60 years of research confirm that cross-breeding is the fastest way to improve milk production, but not necessarily to long-lasting genetic improvement of livestock, with the exception of the formation of synthetic breeds. However, results obtained at the various research centres have not been widely transferred to the farming community. This review has provided some reasons for this failure and proposed solutions for overcoming the still widespread problems. Results from a study point to the fact that the milk production performance of the F1 could be close to being the optimum, but other factors such as reproductive performance also need to be considered to give recommendations on the right combination of exotic inheritance for a particular production system. Maintaining the suitable breed inheritance through grading up and rotational breeding still remains a challenge. Implementing the proposal of continuous production of F1s (Rutledge, 2001) as described in subsection ‘Assisted reproductive technologies’ can only be guaranteed if technical and financial issues limiting the use of ART are addressed. Another way to acquire animals of the required breed combination could be through special contracts with rotational breeders who supply smallholder farmers at an agreed price. The impact of such a move, however, would be limited, as there are only a few large-scale rotational breeders in the tropics. What is more, this approach cannot guard against genetic variation when offspring are mated to animals of different breed composition. It appears, therefore, that maintaining the suitable breed combination from generation to generation will be best achieved through developing synthetic breeds for the different production environments. This approach ensures the creation of a self-replacing population. It also ensures that the farmers deal with one kind of animal, which makes management easier, especially in harsh production environments. The combination of ART with advanced molecular genetics plus the availability of simple recording schemes provide great opportunities for developing and multiplying synthetic breeds at a much faster rate than in previously conducted breeding programmes. Success of this kind of programme requires farmer involvement already at the development stage and long-term financial commitment of governments and funding bodies in the tropics. Innovative ways should be found to help deal with the high costs associated with ART and the use of genomic technology. The newly developed methods could, for example, initially be targeted at farmers that have established a community-based breeding programme in which recording and breeding information is shared. This approach also enables efficient use of technical personnel and equipment as it is available in a single place.

More and more exhaustive studies on the various merits of indigenous tropical genotypes still need to be undertaken. The findings of these studies will help determine which combinations of exotic and indigenous breeds to use, and the level of exotic blood to maintain in the new genotypes. The conservation of indigenous breeds should not only not be ignored but become part of national breeding programmes as this group of animals possesses qualities that make them a valuable resource for present and future generations.

Conclusion

Cross-breeding remains an attractive option for livestock improvement in the tropics because of the quick results that can be obtained by its use and the potential benefits it has for farmers. Nevertheless, careful assessment should be made on whether or not appropriate intervention strategies need to be put in place for each individual case. The required infrastructure for improved management and market access has to be secured. In most cases, the F1 crosses perform better than other genotypes, but the continuous production of F1s and animals of required genetic combinations for the different production environment still remains a big challenge. Production and multiplication of synthetic breeds is perhaps a solution to this problem. The success of any strategy followed to improve results obtained from cross-breeding depends greatly on long-term financial commitment of governments, active involvement of the beneficiary farming communities in the design as well as operationalization of the breeding programmes, and on the successful combination of advances in ART and molecular genetics in breeding programmes.

Supplementary material

Supplementary online material is available at http://cambridge.journals.org/agr.

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Breeding structure and genetic variability of the Holstein Friesian dairy cattle population in Kenya

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Summary

Pedigree data from 11 267 animals born between 1960 and 2004 were used to analyse population structure and genetic variability of the Holstein–Friesian population in Kenya. Parameters estimated were the pedigree completeness index, average inbreeding coefficient, number of founders, effective number of founders and ancestors, and genetically important herds. The hierarchy of registered herds and concentration of origin of individuals was also assessed. Pedigree completeness of the reference population was 67.1 percent. Average inbreeding level for the entire population was 0.09 and 1.7 percent among individuals with three complete generations, and 9.2 percent among inbred individuals. Inbreeding level increased with generation from 0.8 to 2.5 percent in the most recent generation among individuals with three complete generations. Effective number of founders and ancestors were 156 and 108, respectively. The ten ancestors with the largest marginal genetic contribution accounted for 19.52 percent of the total variation. The effective number of genetically important herds that contributed breeding males to the population was 5.2. Higher levels of inbreeding were detected among individuals with at least three complete generations. Few herds contributed breeding males, causing structural weakness to the breeding programme. Recruitment of herds into the breeding tier is needed to strengthen the breeding structure and pedigree recording enhanced to enable long-term management of genetic variability.

Keywords: *ancestors, dairy cattle, founders, genetic importance of herds, Kenya, pedigree*

Résumé

Les données généalogiques de 11267 animaux nés entre 1960 et 2004 ont été utilisées pour analyser la structure et la variabilité génétique de la population Holstein-Frisonne au Kenya. Les paramètres estimés ont été l'indice de complétude de la généalogie, le coefficient moyen de consanguinité, le nombre de fondateurs et le nombre effectif de fondateurs, d'ancêtres et de troupeaux génétiquement importants. La hiérarchie des troupeaux inscrits et la concentration de l'origine des individus ont aussi été évaluées. Le degré de complétude de la généalogie pour la population de référence a été du 67,1%. Le niveau moyen de consanguinité a été de 0,09% pour la population entière, de 1,7% pour les individus ayant trois générations complètes et de 9,2% pour les individus consanguins. Le niveau de consanguinité a augmenté d'une génération à l'autre, passant de 0,8 à 2,5% pour la génération la plus récente des individus ayant trois générations complètes. Le nombre effectif de fondateurs et d'ancêtres a été de 156 et 108, respectivement. Les dix ancêtres avec la plus grande contribution génétique marginale ont expliqué le 19,52% de la variation totale. Le nombre effectif de troupeaux génétiquement importants ayant apporté des mâles reproducteurs à la population a été de 5,2. Les niveaux les plus élevés de consanguinité ont été décelés parmi les individus ayant au moins trois générations complètes. Peu de troupeaux ont apporté des mâles reproducteurs, ce qui affaiblit la structure du programme de sélection. Le recrutement de troupeaux aux différents étages du programme de sélection s'avère nécessaire pour renforcer la structure du programme et pour améliorer l'enregistrement des généalogies afin de permettre la gestion à long terme de la variabilité génétique.

Mots-clés: *ancêtres, fondateurs, importance génétique des troupeaux, généalogie, bovins laitiers, Kenya*

Resumen

Los datos genealógicos de 11267 animales nacidos entre 1960 y 2004 fueron usados para analizar la estructura y la variabilidad genética de la población de ganado Holstein-Frisón en Kenia. Los parámetros estimados fueron el índice de compleción del pedigrí, el coeficiente medio de endogamia, el número de fundadores y el número efectivo de fundadores, de ancestros y de rebaños genéticamente importantes. También se evaluaron la jerarquía de los rebaños registrados y la concentración del origen de los individuos. El grado de compleción del pedigrí para la población de referencia fue del 67,1%. El nivel medio de endogamia fue del 0,09% para la población entera, de 1,7% para individuos con tres generaciones completas y de 9,2% para individuos endogámicos. El nivel de endogamia aumentó de una generación a otra pasando de 0,8% a 2,5% en la generación más reciente de individuos con tres generaciones completas. El número efectivo de fundadores y de ancestros fue de 156 y 108, respectivamente. Los diez ancestros con la mayor contribución genética marginal explicaron el 19,52% de la variación total. El número efectivo de rebaños genéticamente importantes que aportaron machos reproductores a la población fue de 5,2. Los mayores niveles de endogamia

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se detectaron entre los individuos con al menos tres generaciones completas. Fueron pocos los rebaños que aportaron machos reproductores, lo cual debilita la estructura del programa de mejora genética. La incorporación de rebaños a los distintos niveles del programa de cría se hace necesaria para fortalecer la estructura del programa y para mejorar el registro genealógico con el fin de posibilitar la gestión a largo plazo de la variabilidad genética.

Palabras clave: *ancestros, fundadores, importancia genética de los rebaños, pedigrí, ganado bovino lechero, Kenia*

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Introduction

Dairy cattle breeding programmes in developing countries rely on both local and imported genetic materials (semen and embryos) for genetic improvement (Murage & Ilatsia, 2008; Hammami *et al.*, 2009). Importation of semen is stimulated mainly by the need for increased milk production and failure of local breeding programmes to provide semen from locally proven bulls (Ojango, Ducrocq & Pollot, 2005). Most of the imported genetic materials are from dairy cattle populations that have low genetic variability owing to high levels of inbreeding (Kearney *et al.*, 2004; Sørensen, Sørensen & Berg, 2005) owing to increased use of a few genetically superior and often related individuals (Verrier, Colleau & Foulley, 1993). Increase in inbreeding leads to reduced genetic variability (Falconer and Mackay, 1996) and increased risk of breeding programmes owing to variance of genetic gains (Meuwissen, 1991), which seriously limits sustainability of breeding strategies.

Genetic variability of a population depends on the number of founder individuals, breeding strategy, selection intensity and genetic drift (Boichard, Maignel & Verrier, 1997). The variability of a population can be studied through estimation of probability of gene origin statistics (Boichard, Maignel & Verrier, 1997). Gene origin statistics provide a measure of the extent to which individuals influence genetic variability of a population, providing an historical overview of changes occurring in a population. Effective population size and inbreeding are useful for long-term management of genetic variability. Inbreeding and effective population size can therefore be used to monitor trends in genetic variability. However, inbreeding level of a population can be underestimated where pedigree information is incomplete. Effective population size would, on the other hand, be overestimated after a number of generations with missing pedigree information (Boichard, Maignel & Verrier, 1997; Faria *et al.*, 2009). Exchange of germplasm between populations can also change the population structure, making it difficult to interpret estimates of inbreeding (Boichard, Maignel & Verrier, 1997). Other factors that can change the population structure include periodic reductions in population size, decline in the number of contributing males and unequal contribution of ancestors.

Nucleus breeding programmes (NBS) have been recommended for genetic improvement in dairy cattle in developing countries (Kahi *et al.*, 2004) owing to a number of reasons. Firstly, NBS are easier and cheaper to implement since recording is carried out in nucleus. Since inception, the Kenya dairy cattle breeding programme has relied on both locally produced and imported bull semen for genetic improvement (Ojango & Pollot, 2002). In 1992, the Kenyan Artificial insemination sector was liberalized, allowing for increased use of imported semen. Since then, use of imported semen has been on the increase (Murage & Ilatsia, 2008), and it is not known to what extend this has affected the local breeding programme. Assessing hierarchy of herds using the method of Wiener (1953) as elaborated by Barker (1957) reveals the structure of populations by identifying the flow of genes in a breeding programme and herds that influence genetic change by contributing breeding individuals (Barker, 1957; Valera *et al.*, 2005), thereby assessing the robustness of a breeding programme by assessing the extent of the concentration of origin individuals in a population.

In dairy cattle, quantification of genetic variability has mainly been based on large country-specific populations with low or no importation of germplasm (Sölkner, Filipcic & Hampshire, 1998; Roughsedge, Brotherstone & Visscher, 1999; Hagger, 2005). These studies revealed high inbreeding levels and decreased genetic variability, raising concern over the long-term sustainability of their breeding strategies (Koenig and Simianer, 2006). Such studies in developing countries, where data recording is limited, are scarce. In Tunisia, Hammami *et al.* (2007) showed how extensive genetic connections can exist between populations in developed and developing countries using artificial insemination (AI). Dairy cattle breeding programmes in developing countries are more vulnerable to the effects of inbreeding as they are often characterized by inconsistent pedigree and performance recording (FAO, 1998). Incomplete pedigree recording leads to erroneous estimation of measures of population diversity, such as inbreeding levels and effective population size and probability of gene origin statistics (Te Braake, Groen & Van Der Lught, 1994; Boichard, Maignel & Verrier, 1997). The objective of this study was therefore to determine the breeding structure and assess the genetic variability of the Holstein–Friesian population in Kenya.

Materials and methods

Materials

Data source

Original data consisting of 7663 pedigree records of milk recorded cows born between 1979 and 2004, sired by 806 bulls. The registered ancestors of the cows were obtained from the Kenya Stud Book (KSB), a farmer organization responsible for performance recording in Kenya. Individual identity consisted of a cow number that consisted of a herd prefix followed by a cow number as assigned by the KSB. The pedigree of each cow was build up by tracing its ancestors as far back as possible from the KSB archive. The pedigree information of sires was obtained from the Central Artificial Insemination Station (CAIS), a government body that is legally mandated to process and store all semen used in the country. Pedigrees of imported sires were cross-checked and enriched from the following online sources: www.ABSglobal.com and www.ukcows.com. A database of all animals (male and female) was then created, which included identity of the animal, its sire and dam, the herd where it was born and year of birth. For imported sires, country of birth was also included. After data cleaning and cross-checking of pedigrees of imported sires, a database of 11 267 individuals born between 1960 and 2004 was available.

A separate database was created for individuals with at least three complete generations, to facilitate comparison of inbreeding level in the entire population. Females were retained in this database if information on both ancestors was available known up to the three generation.

When computing the probability of gene origin statistics, the definition of reference population was necessary to allow for comparisons. This population was made up of cows with at least a first parity lactation record and born between 1990 and 2004. The reference period, as defined above, represented individuals in the last two generations of cows available for this study.

Methods

Pedigree completeness

The quality of the pedigree was assessed by pedigree completeness index. Pedigree completeness index as proposed by MacCluer *et al.* (1983) was calculated for all individuals for four generations. The completeness of pedigrees per generation was determined by estimating the proportion of individuals with parental information (MacCluer *et al.*, 1983). For pedigree of depth d an index was calculated separately for paternal ($I_{d_{\text{pat}}}$) and maternal ($I_{d_{\text{mat}}}$) lines as:

$$I_{d_{\text{pat}}} = \frac{1}{d}\sum_{i=1}^{d} a_i,$$

where a_{i} is the proportion of known ancestors in generation i and d is the number of generations considered. In the current study, four generations were considered, thus $d = 4$. The average pedigree completeness for each animal, I_{d}, was computed as the harmonic mean of the paternal and maternal indices as follows:

$$I_d = \frac{4 I_{d_{\text{pat}}} I_{d_{\text{mat}}}}{I_{d_{\text{pat}}} + I_{d_{\text{mat}}}},$$

where $I_{\text{d}_{\text{pat}}}$ and $I_{\text{d}_{\text{mat}}}$ are the contributions from the paternal and maternal lines, respectively.

Complete generation equivalent

The second measure of quality of pedigree is the complete generation equivalent. For each individual j, the number of complete generation equivalents, CGEs, was computed as:

$$\text{CGE} = \sum_{i=1}^{n_j} \frac{1}{2^{g_{ij}}},$$

where n_j is the number of ancestors of individual j, and g_{ij} is the number of generations between individual j and its ancestor i (Sölkner, Filipcic & Hampshire, 1998). Computed this way, a parent accounts for 0.5, and a grandparent for 0.25 and so on.

Inbreeding coefficient (F)

Inbreeding, F, was computed as the probability that an individual had two alleles identical by descent according to the method of VanRaden (1992). This method makes it possible to compute inbreeding coefficients per generation, and also assumes founders are inbred or related founders, an assumption that is important when pedigrees are heterogeneous. Animals were classified according to sex and birth year. In the method described by VanRaden (1992), the estimated inbreeding coefficient of an animal with unknown origin is equal to half the average relationship between genetic groups of its phantom parents.

Effective population size

The effective population size, N_{e}, was calculated from the rate of inbreeding per generation as:

$$N_{\text{e}} = \frac{1}{2\Delta F_y L},$$

where ΔF_y is the annual rate of inbreeding and L is the generation interval. The effective population size was calculated for three sub-sets of data; cows born between 1985 and 1994 and those born between 1995 and 2004, and cows with complete pedigree information for at least three generations. As average co-ancestry of animals within a population predicts the average inbreeding coefficient in the next generation (Falconer and Mackay, 1996), the rate of increase in co-ancestry, Δf_y, can be interpreted as the future rate of inbreeding per year. The expected future effective population size can then be calculated by replacing ΔF_y with Δf_y.

Concentration of origin of genes

Gene origin statistics reveal the historical development of a population since the founder generation, by estimating probability of gene origin statistics. Changes in the population structure owing to migration, bottlenecks and changes in breeding strategy, are accounted for by comparing the genetic variability in the reference population to that of the founding population (Boichard, Maignel & Verrier, 1997). Parameters estimated were pedigree completeness, average inbreeding coefficient, number of founders, effective number of founders and effective number of ancestors. Ratios of effective number of founders to number of founders and effective number of ancestors to effective number of founders were computed to determine the historical development of the population (Boichard, Maignel & Verrier, 1997).

Number of founders (f)

In the computation of this parameter, all animals with both parents unknown were regarded as founders. Also, if an animal had an unknown parent, the unknown parent was regarded as a founder.

Effective number of founders

Computation of number of founders assumes that founders are assumed unrelated since their parents are unknown, which may not be the case. When computed this way, numbers present little information on the genetic basis of a population. Another shortcoming of this parameter (number of founders) is that all founders are assumed to contribute equally to the reference population. In real sense, founders do not contribute equally to the current population, since depending on the breeding objective of the population some founders are used more intensively than others. The differential contribution of founders to a population is corrected by estimating the effective number of founders. The effective number of founders, f_e, is the number of equally contributing founders that would be expected to generate similar amount of genetic diversity as in the studied population (Lacy, 1989) and was calculated according to Boichard, Maignel & Verrier (1997) as

$$f_e = 1 \Big/ \sum_{k=1}^{f} q_k^2,$$

where f is the number of founders and q_k the genetic contribution of the kth founder to the reference population. Animals with both parents unknown were regarded as founders, as was any unknown parent. When each founder contributes equally to the reference population, the effective number of founders is similar to the total number of founders; therefore, a ratio f_e/f of close to 1 indicates an equal contribution of founders to the reference population, otherwise the effective number of founders remains smaller than total number of founders (Boichard, Maignel & Verrier, 1997).

Effective number of ancestors

The genetic contribution of founders is expected to converge after five to seven generations, and populations with deep pedigrees (more than seven generations) can have a high effective number of founders even after a severe bottleneck (Bijma & Woolliams, 1999). In genetic improvement programmes, founders more often than not contribute differentially, and therefore, the effective number of founders would be overestimated. To overcome this problem, Boichard, Maignel & Verrier (1997) proposed a method to find the minimum number of ancestors (founders or not) required to explain the genetic diversity observed in the reference population. Ancestors are chosen based on their expected marginal genetic contribution (p_k). The sum of the marginal contributions adds to 1 if the ancestors are assumed unrelated. However, since the non-founders are included in this definition, some of the ancestors may be related, and the marginal contributions may add up to more than 1. Therefore, only the marginal genetic contribution of each ancestor not explained by others should be considered (Boichard, Maignel & Verrier, 1997). The ancestor chosen first is the one with the largest expected marginal contribution, and the other ancestors are selected through an iterative process. This way, in round n of the process, the nth major ancestor is chosen on the basis of its marginal contribution, p_k, which is defined as the contribution of the kth ancestor not yet explained by the $k-1$ ancestors already chosen. The genetic contribution of the first major ancestor is $p_k = q_k$; that of the nth ancestor, p_k is defined as the genetic contribution of ancestor k, not yet explained by the $n-1$ already selected ancestors, and is calculated as follows:

$$p_k = q_k \left(1 - \sum_{i=1}^{n-1} a_i \right),$$

where a_i is the variation already explained by the $n-1$ already selected ancestors. Individual k may be an ancestor to some of the $n-1$ already selected ancestors, whose contributions are already accounted for, and therefore cannot be attributed to individual k. Therefore, after every iteration during which a major ancestor is found, its sire and dam identifications are deleted, making it a pseudo-founder. After every iteration, the pedigree is therefore updated to eliminate the redundancies and ensure that the marginal genetic contributions sum up to 1.

The effective number of ancestors, f_a, is calculated using genetic contributions of ancestors with the largest marginal genetic contributions to the reference population. This measure, therefore, is able to account for loss of allelic diversity since the founding population (Boichard, Maignel & Verrier, 1997) and was computed as:

$$f_{\mathrm{a}} = 1 \Big/ \sum_{k=1}^{f} p_k^2,$$

where p_k is ancestor i's marginal genetic contribution. The genetic contribution was determined for 1000 ancestors in the current study. If the ratio of $f_{\mathrm{a}}/f_{\mathrm{e}}$ is close to unity, the population has been stable in terms of numbers of effectively contributing animals. If the ratio is lower than 1, bottlenecks have played an important role in the population's formation (Boichard, Maignel & Verrier, 1997).

Population structure

The concentration of origin of animals was estimated to assess the extent to which dairy herds or semen exporting countries influenced the genetic variability of the Kenyan Holstein–Friesian population by following the criteria proposed by Wiener, (1953) and further expanded by Barker (1957) and later integrated into the ENGOG software (Gutierrez and Goyache, 2005). A herd belonged either to the nucleus (N), multiplier (M), commercial (C) or isolated (I) class of herds, thus determining the breeding structure of a population. A herd was classified as N if all the calves within the herd were sired by a sire born within the herd and that sire also had progeny in other herds. Herds in the category M were those which in addition to using semen from own bulls and selling bulls, also used semen of bulls born in other herds. Herds that used semen of bulls born in other herds and did not sell bulls were categorized as commercial herds. A herd was considered isolated if it is used for breeding purposes, only semen of sires born within the herd and did not contribute breeding males to other herds.

Genetically important herds

This parameter aimed at identifying herds that supplied sires, grandsires and great-grand sires, and was analysed using the three methods proposed by Barker (1957) and Wiener (1953):

(1) total number of appearances of each herd in any of the 15 male positions of the pedigree;
(2) total score of these male appearances; and
(3) number of appearances of each herd in the sire of sire line only.

An appearance in one generation was given twice the weight of an appearance in the preceding generation The parameter was computed based on whether a herd produced a bull that was a sire of a sire, grandsire, great-grand sire or great-great grand sire. A score of 8 was assigned to any herd with a bull that was a sire, 4 for a grand sire, 2 for a great-grand sire and 1 as a great-great-grand sire (Barker, 1957). To calculate the genetic contribution of herds to the Holstein–Friesian population in Kenya, the method of Wiener (1953) was used. At each of the 30 positions of the four-generation pedigree, the number of appearances of a herd independent of an earlier appearance from the same herd was recorded. The genetic contribution of sires and dams within each generation was calculated, and the results summed to give the total genetic contribution of the herd.

Effective number of genetically important herds

Effective number of genetically important herds was computed as the inverse of probability when two animals taken at random in the population have their parent in the same herd (Robertson, 1953). This was repeated for each path to know the effective number of herds supplying sires (HS), grandsires (HSS), great-grandsires (HSSS) and great-great grandsires (HSSSS).

Genetic similarity (GS) between tiers

GS between the levels of the breeding structure identified above (see section on population structure) was computed according to Rekaya, Weigel & Gianola (2003) as the ratio of the number of daughters of common bulls to that of all bulls in any two levels, i and j as follows:

$$\mathrm{GS}(i,j) = \frac{\sum_{r=1}^{n} \sum_{k=1}^{C(i,j)} \mathrm{ND}_{k,r}}{\sum_{r=1}^{n} \sum_{k=1}^{T(i,j)} \mathrm{ND}_{k,r}},$$

where $C(i,j)$ is the number of bulls in common between any two levels i and j, $T(i,j)$ is the total number of bulls used in the two levels and $\mathrm{ND}_{\mathrm{k},r}$ is the total number of daughters of bull k in level r.

The software package Pedig by Boichard (2002) was used to calculate generation intervals, number of founders, effective number of founders, effective number of ancestors and marginal contribution of ancestors and inbreeding. The computer software ENDOG (Gutierrez and Goyache, 2005) was used to assess herd hierarchy and to compute number of herds contributing breeding males, number of genetically important herds and effective number of genetically important herds.

Results

Pedigree completeness for the Holstein–Friesian population in Kenya was 67.1 percent. From Figure 1, it is clear that 79.0. percent of the individuals in the population had parents known, while 70.2, 52.0 and 48.6 percent had information on their grandparents, great grandparents and great–great grandparents, respectively.

Table 1 shows population parameters for the pedigreed Holstein–Friesian cattle population of Kenya. The average inbreeding coefficient for the entire pedigreed population was 0.09 percent. Individuals with both parents known up to the third generation had an average inbreeding level of 1.7 percent.

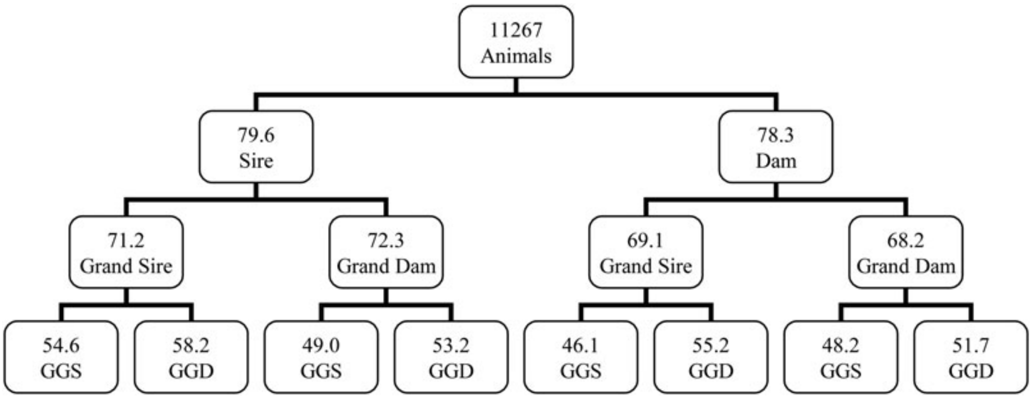

Figure 1. Pedigree completeness level (%) for Holstein–Friesian cattle population of Kenya.

The level of inbreeding increased with generation and was 0.8, 1.7 and 2.5 percent from the first to the most recent generation. Among animals in the entire pedigree, 1144 were inbred and had an average value of 9.2 percent. Inbreeding level was higher among individuals with at least three complete generations compared with the whole population. As average inbreeding level for the entire population was low, its trend was not estimated.

Table 2 shows the distribution of animals within different inbreeding levels. There were a total of 1144 inbred animals with inbreeding level ranging from 0.04 percent to 12 percent. The maximum inbreeding level for a single animal was 12 percent recorded in 2006. Among the inbred animals, majority (72.9 percent) had inbreeding levels below 1 percent.

Effective population size for the Holstein–Friesian population in Kenya was lower in the more recent years (Table 3) because of an increase in average inbreeding level. The change in co-ancestry also showed a similar trend. Based on the upward trend in co-ancestry, future effective population size also decreased for the Kenyan Holstein–Friesian population.

The generation interval dropped slightly from earlier to later period. This could have been because of the change in the breeding strategy, which saw an increase in the use of imported semen (Murage and Ilatsia, 2008), after the Artificial Insemination sector was liberalized in 1992. Also, the earlier cohorts included the age of animals that actually reproduced, whereas the later group was composed of all animals, including those that had not reproduced.

Table 1. Number of animals, average inbreeding coefficient (*F*%), and average complete generation equivalents for the Holstein–Friesian population of Kenya.

Parameter	Whole pedigree	Inbred	Individuals[1]
Number of animals	11 267	1 144	3 985
Average *F* (%)	0.09	9.2	1.7
Average complete generations	1.5	1.8	3.1

[1] Cows in the reference population with complete pedigree information for at least three generations.

Estimates of probabilities of gene origin statistics are shown in Table 4. The number of animals in the reference population was 4684, with 1942 founders contributing to this population. The effective numbers of founders and ancestors for the reference population were 156 and 108, respectively.

The number of ancestors (founder or not) explaining 50 percent of the variation in the registered Holstein–Friesian population of Kenya was 89. The ten most popular ancestors that had the largest marginal genetic contribution to the Holstein–Friesian population in Kenya and their country of origin are given in Table 5. These ancestors accounted for 19.52 percent of the total variation in the reference population. The ancestor contributing most (Kapsoen Kebenei 34th) explained 2.24 percent of the total genetic variation (Table 5). Most of the important ancestors (8) were foreign, and the majority came from the USA (3) and Israel (3). Two of the ancestors were born in Kenya, but were both sons of UK born sires.

The breeding structure of registered Holstein–Friesian herds in Kenya, based on origin and use of sires, is presented in Table 6. Up to 10.2 percent of the herds contributed breeding bulls to the Kenyan population during the period of study. This group of herds used semen of own sires and from each other, and were therefore classified as the nucleus. The rest of the herds formed the commercial tier, as they did not contribute any reproductive males. None of the herds was genetically isolated (Table 6).

Table 2. Percentage of inbred Holstein–Friesian cows within different inbreeding levels.

Inbreeding class, %	*N*	%
0	10 123	89.8
$0 < F \geq 1.0$	834	7.4
$1.0 < F \geq 5.0$	251	2.2
$5.0F \geq 12.0$	59	0.5

Table 3. Average generation interval, rate of inbreeding and rate of increase in co-ancestry per generation in Holstein—Friesian of Kenya.

Period	Generation interval	Rate of inbreeding per generation, %	Rate of co-ancestry per generation, %	N_e	Future N_e
1985–1994	4.1	0.11	0.14	454	357
1995–2004	3.7	0.29	0.31	263	238
Cows with three complete generations	3.5	0.85	0.92	59	54

N_e was calculated based on rate of inbreeding; Future N_e was calculated based on the rate of co-ancestry.

The number of calvings within each of the tiers is given in Table 7. Within the nucleus, a total of 4765 calvings were recorded within the study period. Majority of the calvings (83.9 percent) were by sires born in other herds, while only 16.1 percent were by sires bred within the herds.

In general, Kenyan born bulls sired fewer progeny within their herd of birth (13.5 percent) compared with other herds. Bulls born within the nucleus herds in Kenya sired 16.3 percent of the registered animals within the commercial tier, with the rest (83.7 percent) being daughters of sires of foreign origin. As expected, all registered animals within the commercial tier were progeny of sires born in other herds.

Table 8 shows the number of herds supplying ancestors of sires up to the fourth generation. Effective number of herds contributing breeding sires was 5.2 (Table 8). This parameter decreased to 3.9, 2.6 and 1.9 for those producing sire of sires, grand sires and great-grand sires, showing a limited concentration of herd of origin of the animals.

Estimates of genetic similarities between Holstein–Friesian populations in the nucleus and commercial tiers are given in Table 9. The number of sires with daughters in both nucleus and commercial tiers were 131. The percentage of registered daughters sired by common bulls in the nucleus and commercial level were 72.8 and 64.9 percent, respectively, of the total females registered in each population.

Discussion

Despite the existence of a local dairy cattle progeny testing scheme for over 40 years, the results of this study show a low level of pedigree completeness and continued reliance on imported semen. The proportion of known pedigree in this study is similar to that of Tunisian Holstein and Luxembourg Holstein populations (Hammami *et al.*, 2007). Inbreeding level was low, though in Kenya, only a few number of sires per dairy breed are selected annually (Ombura, *et al.*, 2007), and a small number of herds contributed breeding males (Table 8). In recent years, inbreeding increased at a rate of 0.11 percent per generation, and is expected to increase at the rate of change in co-ancestry (0.14 percent). Among individuals with at least three complete generations, the average inbreeding level was 1.7 percent with a mean change of 0.85 percent per generation, just below the recommended 1 percent (Franklin and Frankham, 1998), beyond which a population begins to lose its fitness. Higher values of inbreeding have been reported among various Holstein populations which have deeper pedigree and more complete ancestral information (Sørensen, Sørensen & Berg, 2005; Hammami *et al.*, 2007). Effective population size for individuals in the reference population in the more recent group of years reported in this study of 263 was higher than values of 75 for Holstein–Friesian cattle populations in Ireland (McParland *et al.*, 2007) and the range of 47–53 for Danish dairy breeds (Sørensen, Sørensen & Berg, 2005). In the United States, values of 39 and 40 were reported for USA Holstein and Jersey populations (Weigel, 2001).

Table 4. Parameters characterizing gene origin statistics for the registered Holstein–Friesian population of Kenya.

Parameter	Number
Total number of animals	11 267
Animals in the reference population	4684
Number of founders	1942
Effective number of founders	156
Number of ancestors explaining 50% variation	89
Effective number of ancestors	108

Table 5. Marginal genetic contributions of the most popular ancestors in the Kenyan Holstein–Friesian population.

Ancestor	Rank	Contribution, %	Country of birth
Kapsoen Kebenei 34th (312)	1	2.24	Kenya
To-Mar Blackstar-ET 1929410 EX-93	2	2.10	USA
Tintawn Rex Winston (307)	3	1.98	Kenya
Bernd (IMP)(294)	4	1.97	Germany
Walkway Chief Mark	5	1.94	USA
Round Oak Rag Apple Elevation	6	1.89	USA
Navon [Imported Semen] 856	7	1.86	Israel
Ensdon Herald (IMP) (263)	8	1.86	United Kingdom
Perek (IMP) 834	9	1.85	Israel
Pidion [IMP.Semen] 730	10	1.83	Israel
Total contribution		19.52	

Table 6. Classification of registered Holstein–Friesian herds in Kenya according to origin and use of sires.

Type of herd	Herd characteristics			Number of herds
	Used semen of sire born in another herd	Used semen of sire born within the herd	Sold breeding bulls	
Nucleus	No	Yes	Yes	8
Multiplier	Yes	Yes	Yes	0
Commercial	Yes	No	No	70
Isolated	No	Yes	No	0

However, when the estimate was based on individuals with at least three complete generations, the estimate (59) was within the range reported for various dairy cattle populations (Weigel, 2001; Sørensen, Sørensen & Berg, 2005; McParland *et al.*, 2007).

Inbreeding level and effective population size are dependent on quality and depth of pedigree (Gutierrez *et al.*, 2003). In the current study, pedigree completeness was fairly low and could have led to underestimation of inbreeding (Boichard, Maignel & Verrier, 1997). As such, the two parameters are not very informative when pedigree is shallow; the number of inbred animals and average inbreeding coefficient are underestimated, while the inbreeding coefficient of inbred animals is exaggerated (Te Braake, Groen & Van Der Lught, 1994). However, the current study revealed a tendency of inbreeding level to increase with improved pedigree information (Table 1).

The concentration of the origin of genes was assessed by calculating number of founders, effective numbers of founders and ancestors. Probabilities of gene origin statistics estimated in this study show that the Holstein–Friesian population in Kenya is derived from a large number of founding individuals. Revealed also is the continued influence of imported germplasm to the Kenyan population, as most of the genetically important ancestors were foreign. Number of founders is usually proportional to the population being studied (Gutierrez *et al.*, 2003; McParland *et al.*, 2007). Although the large number of founder animals represented in the reference population in the current study imply that the population is not at risk for inbreeding, the value could be an overestimate because of the missing pedigree information, as any individual with either of parent unknown is regarded as a founder in the computation of this parameter (Gutierrez and Goyache, 2005).

Table 8. Genetically important herds and effective number of herds for the Kenyan Holstein–Friesian population.

Herds supplying	Number of herds	Effective number of herds
Sires	8	5.2
Sire of sires	7	3.9
Great grand sires	5	2.6
Great-great grand sires	3	1.9

Effective number of founders for the Kenya Holstein–Friesian population of 156 was higher than 112 for Holstein–Friesian crosses reported by McParland *et al.* (2007) in Ireland and 70 and 115.7, respectively, for Holstein and Jersey cattle populations in Denmark (Sørensen, Sørensen & Berg, 2005), but lower than 207.2 reported for Red dairy cattle population in Denmark (Sørensen, Sørensen & Berg, 2005). The effective number of ancestors of 108 found in this study is higher than 20.6, 23.8 and 34.6 reported for Danish Holstein, Jersey and Red breed populations, respectively (Sørensen, Sørensen & Berg, 2005), 44 for Tunisian Holstein (Hammami *et al.*, 2007), 93 for British Holstein–Friesian population (Roughsedge, Brotherstone & Visscher, 1999) and 40 for Holstein–Friesian crosses in Ireland (McParland *et al.*, 2007). This parameter is most affected by the quality of pedigree (Boichard, Maignel & Verrier, 1997), as it includes all animals with missing pedigree information. The large value in the current study could mainly be because of missing pedigree information, though lack of objective selection in the studied population (Ilatsia *et al.*, 2007) could lead to more ancestors passing on genes to subsequent generations.

Ratios of probability of gene origin statistics help to understand the historical development of a population, since the founder population (Boichard, Maignel & Verrier, 1997). The ratio f_e/f describes whether the founders were used in a balanced manner and/or the extent of pedigree completeness. A low ratio implies that the population has gone through bottlenecks and/or lack of pedigree information. This study found a ratio of 0.08, which was higher than those reported for Tunisian (0.02), Luxembourg Holstein (0.04) (Hammami *et al.*, 2007) and Irish Holstein (0.002) populations (McParland *et al.*, 2007). From these studies, it can be noted that the ratios seem to be dependent on population size and selection intensity, with lower values being reported for larger populations, which also have more complete pedigree information.

Table 7. Frequency of use of sires in Nucleus (N) and commercial (C) tiers of the Kenyan Holstein–Friesian population.

Tier	Number of herds	Registered calvings	Number of registered progeny		Number of times a sire has progeny	
			Own bred sire	Sire born in other herd	In herd of birth	In other herds
N	8	4765	766	3999	766	5669
C	70	5539	0	5539		

Table 9. Genetic links between nucleus and commercial Holstein–Friesian populations.

Total number of sires	Number of common sires	Daughters of common sires as percentage of all cows		Genetic similarity
		Nucleus	Commercial	
251	131	0.73	0.65	0.46

The ratio f_a/f_e is important when describing the history of a population (Boichard, Maignel & Verrier, 1997). A low ratio implies the population has gone through bottlenecks, which leads to reduction in genetic variability. In the current study, a ratio of 0.69 was reported indicating that the population has generally been genetically stable. The ratio reported in this study is higher than previous estimates of 0.15 for Tunisian (Hammami *et al.*, 2007) and 0.29 Danish Holsteins, (Sørensen, Sørensen & Berg, 2005). The observed value indicates a balanced contribution of ancestors to the reference population of the Kenyan Holstein–Friesian, which could be attributed to lack of effective selection in the studied population (Ilatsia *et al.*, 2007).

The large number of foreign ancestors with large marginal genetic contributions (eight of ten ancestors with the largest marginal genetic contribution were foreign) underscores the continued importance of imported germplasm in the development of the dairy sector in Kenya (Murage and Ilatsia, 2008). However, contribution per ancestor was low, ranging from 1.82 to 2.24 percent. High marginal genetic contributions per ancestor of up to 10.35 percent for Tunisian Holstein (Hammami *et al.*, 2007) and 13.8 percent for Danish Holstein (Sørensen, Sørensen & Berg, 2005), have been reported. Two of the important ancestors, Round Oak Rag Apple Elevation and To-Mar Blackstar-ET 1929410 EX-93, were reported to contribute heavily to the German (Koenig and Simianer, 2006), Danish (Sørensen, Sørensen & Berg, 2005) and American (Young and Seykora, 1996) Holstein populations. The low contribution per ancestor in the Kenyan Holstein–Friesian population, are reflected by the lack of genetic progress for milk yield (Ilatsia *et al.*, 2007) and could partly be explained by continued importation of germplasm from genetically diverse populations.

Identification of herds contributing sires and their relative influence on genetic diversity is important in determining the breeding structure of a population (Wiener, 1953). The environment under which progeny testing of young bulls is done, can then be identified and the robustness of a breeding programme assessed. This study shows that only a small number of effective number of genetically important herds (5.2) influenced variability of the Holstein–Friesian population in Kenya. This characterizes the Kenyan Holstein–Friesian as a weak population based on a small number of herds, presenting a high structural risk (Gama and Delgado 2000; Goyache *et al.*, 2003). Studies on breed structure in dairy cattle populations are scarce. A similar unbalanced population structure, where only a few herds supply reproductive males, was reported for the Xalda sheep in Spain (Goyache *et al.*, 2003). Increased concentration of origin of individuals predisposes a breeding programme to structural risks as the withdrawal of some herds seriously affects the sustainability of breeding strategies.

Herds that contribute breeding males and replacement stock influence the rate of genetic improvement in the commercial tier. Genetic gains achieved in these herds are usually passed onto the commercial tier through semen and replacement stock. Measure of GS revealed the presence of genetic links between the nucleus and commercial tiers. The proportions of daughters with common sires in the current study are higher than 2.8 and 2.3 percent in Swedish and Finnish Holstein populations, 10.0 and 1.3 percent in Danish and Finnish Holstein populations, and 10.2 and 20.7 percent in Swedish and Danish Holsteins, respectively (Pedersen *et al.*, 2001). In another study, Hammami *et al.* (2007) reported daughters of common sires to be 14.9 and 13.2 percent, respectively, in Tunisian and Luxembourg Holsteins. Based on the proportion of daughters of common sires to total number of daughters for all sires in both environments, GS index can be calculated (Rekaya, Weigel & Gianola, 2003). For Tunisian Holsteins, a genetic linkage of 0.19 was reported (Hammami *et al.*, 2007). Rekaya, Weigel & Gianola (2003), using a structural model, found five geographical regions in the USA to be highly genetically identical based on genetic connectedness and moderately similar when based on management information. In the current study, strong genetic links were found, though the small data size should be considered when referring to this value. Nevertheless, the existing genetic linkages imply that the herd hierarchy identified can be used to evaluate whether the resultant genetic improvement can be applied across herds within the country.

Among the different measures of diversity, rate of increase in co-ancestry is the most important measure of diversity as it uses all currently available information to predict future trend in inbreeding. Future breeding strategy of the population should make use of tools designed to balance rate of gain and the rate of inbreeding in future (Wray and Goddard, 1994; Koenig and Simianer, 2006). Based on the results of the current study estimated for a sub-population with more complete pedigree information, and the small number of herds contributing breeding males, future mating plans needs to be cautiously planned to avoid further increase in inbreeding. The other measures of diversity: probability of gene origin statistics, inbreeding and effective population size, are historical in nature and provide an insight on the formation of the population to date (Boichard, Maignel & Verrier, 1997). Effective population in the last decade declined slightly, indicating some loss of genetic diversity. However, the results of the current study have to be used cautiously in view of the moderate pedigree completeness.

Conclusions

The Kenyan Holstein–Friesian population is derived from a diverse population, but has low pedigree completeness, leading to overestimation of effective population size and other measures of genetic variability and underestimation of inbreeding levels. However, there was a tendency for inbreeding level to increase with increasing pedigree completeness beyond acceptable levels. The breeding structure of the population is weak as only a small number of herds contributed for breeding males. The breeding programme can be strengthened by recruiting more herds into the breeding tier and enhancing pedigree recording to enable long-term management of genetic variability and genetic improvement.

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Breeding management and assessment of Curraleiro cattle in Northeastern Brazil

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Summary

The Curraleiro, also called Pé-Duro, is the only naturalized bovine breed of Northeastern Brazil. The breed originated via admixture of different Iberian breeds that were introduced during the sixteenth century and the subsequent natural adaptations to the semi-arid environment. The introduction of zebu bovine breeds during the twentieth century led to the replacement of the Curraleiro, which is now on the brink of extinction. With the aim of supporting the establishment of a conservation programme, the present study focused on assessing the management of the existing Curraleiro populations. Data on 2 366 head of cattle were obtained by interviewing 22 owners of Curraleiro herds. The number of animals in the herds varied from 4 to 384. The average herd size was 131.4 (standard deviation = 120.3). All animals were bred under extensive conditions, without any supplementary feed, and in 50 percent of all cases without any specialized technical assistance. Data indicated that breeders maintain the cattle not for economic reasons, but because of tradition. The Curraleiro was characterized by the breeders as being resistant to water stress and parasites. The animals can be bred without feed supplements on all kinds of native-grass pastures. These characteristics, in addition to its low production costs, could make the Curraleiro attractive, especially for low-income families.

Keywords: *Bos taurus, Curraleiro cattle, locally-adapted breed, Northeastern Brazil*

Résumé

Le bétail Curraleiro, aussi appelé Pé-Duro, représente la seule race bovine naturalisée du Nord-est du Brésil. La race s'est formée suite au croisement de différentes races ibériques introduites au cours du seizième siècle et par l'adaptation naturelle à l'environnement semi-aride. Les races zébuines introduites pendant le vingtième siècle ont remplacé la race Curraleiro qui se trouve actuellement au bord de l'extinction. Afin de soutenir l'établissement d'un programme de conservation, cette étude s'est concentrée sur la caractérisation de la conduite des élevages de race Curraleiro encore existants. Les données de 2 366 animaux ont été obtenues en enquêtant 22 propriétaires de troupeaux Curraleiro. Le nombre d'animaux par exploitation a varié de 4 à 384. La taille moyenne des troupeaux était de 131,4 avec un écart type de 120,3. Tous les animaux ont été élevés dans des conditions extensives, sans aucun complément alimentaire, et dans le 50 pour cent des cas sans aucune assistance technique spécialisée. Les données indiquent que les éleveurs maintiennent la race non pas pour des raisons économiques mais par tradition. Les éleveurs ont souligné que la race Curraleiro est résistante au manque d'eau et aux parasites. Les animaux peuvent être élevés, sans aucune supplémentation alimentaire, sur la base de n'importe quel pâturage natif. Ces caractéristiques, liées aux faibles coûts de production, pourraient rendre la race Curraleiro attirante, en particulier pour les familles à faibles revenus.

Mots-clés: *Bos taurus, bétail Curraleiro, race naturalisée, Nord-est du Brésil*

Resumen

El ganado Curraleiro, también llamado Pé-Duro, constituye la única raza bovina naturalizada del Noreste de Brasil. La raza se originó por la mezcla de diferentes razas ibéricas, introducidas a lo largo del siglo XVI, y por las sucesivas adaptaciones naturales al ambiente semiárido. La introducción de razas bovinas cebuinas durante el siglo XX fue desplazando la raza Curraleiro, que a día de hoy se halla al borde de la extinción. Con el fin de apoyar el establecimiento de un programa de conservación, este estudio se centró en caracterizar el manejo de las poblaciones existentes de ganado Curraleiro. Se recabaron datos de 2 366 animales encuestando a 22 propietarios de rebaños Curraleiro. El número de animales por explotación varió de 4 a 384. El tamaño medio de los rebaños fue de 131,4 con una desviación estándar de 120,3. Todos los animales eran criados bajo condiciones extensivas, sin ningún tipo de complemento alimenticio, y en el 50 por ciento de todos los casos sin ningún tipo de asistencia técnica especializada. Los datos indicaron que los ganaderos mantienen la raza no por razones económicas, sino por tradición. Los ganaderos destacaron de la raza Curraleiro su resistencia al estrés hídrico y a los parásitos. Los animales pueden ser criados, sin suplementación alimenticia, en base a todo tipo de pastos nativos. Estas características, junto con sus bajos costes de producción, podrían hacer de la raza Curraleiro un ganado atractivo, en especial para las familias con escasa renta.

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Palabras clave: *Bos taurus, ganado bovino Curraleiro, raza naturalizada, Noreste de Brasil*

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Introduction

The Food and Agriculture Organization of the United Nations (FAO) aims to support the conservation of rare livestock breeds, as they represent important genetic resources for breeding and conservation programmes (FAO, 2007). The most prominent breeds in Brazil today are Indian zebu breeds such as Nelore, Gyr and their hybrids, which have been introduced as exotic breeds over the last 100 years (Egito *et al.*, 2007). These exotic breeds are characterized by strong artificial selection and low effective population sizes. The other group of breeds, termed Creole, are referred to "naturalized", because after their introduction several centuries ago they developed new morphological and physiological traits (Rangel, Zucci and Ferreira, 2004; Mariante and Cavalcante, 2006).

Brazil is the only country in South America where naturalized breeds are descended not only from Spanish but also from Portuguese breeds (Mariante and Egito, 2002). The five extant naturalized bovine breeds – Pantaneiro, Crioulo, Lageano, Mocho Nacional and Curraleiro – originated via the hybridization of distinct Portuguese and Spanish breeds that adapted over the centuries to a wide range of local environmental conditions (Egito, Mariante and Albuquerque, 2002; Fioravanti *et al.*, 2011).

In 2012, the Brazilian Ministry for Agriculture officially recognized the Curraleiro, which is also known as Pé-Duro (Figure 1), as a distinct bovine breed (Process No. 21038.001530/2011-89). Curraleiro originated from an admixture of the three *Bos taurus ibericus* breeds, Alentajana, Galega and Mirandesa, whose introduction to Brazil, from Spain, Portugal and the Cape Verde Islands started in the first half of the sixteenth century (Primo, 1992; Britto and Mello, 1999; Rangel, Zucci and Ferreira, 2004; Mariante and Cavalcante, 2006). It developed initially in the states of Pernambuco, Sergipe, Alagoas, Paraíba, Ceára, Maranhão and Piauí, and also spread to the north into the state of Pará and to the southwest into the states of Tocantins and Goias (Britto and Mello, 1999; Carvalho *et al.*, 2010; Fioravanti *et al.*, 2011). Today, the Curraleiro is the only naturalized bovine breed in Northeastern Brazil (Figure 2), a large territory of about 980 000 km^2 mainly dominated by the Caatinga, a semiarid bush–savannah characterized by a mean precipitation of 900 mm/year, high levels of evaporation and relative humidity that is sometimes lower than 30 percent during the dry season (Bianchini *et al.*, 2006).

Previous studies have indicated that the Curraleiro shows several adaptations to the harsh local conditions of this semiarid region. Animals are considered to have some level of tolerance to the worm parasites and toxic plants (e.g. *Stryphnoden droncoriaceum* and *Palicourea marcgravii*) found in their production environment (Carvalho and Girão, 1999;Mariante and Cavalcante, 2006). They perform well on pastures consisting of native grass species of a low nutritional value, and graze even in the natural bush-land of the Caatinga (Carvalho *et al.*, 2010; Fioravanti *et al.*, 2011).

Compared with zebu breeds, individuals are small and light. The average shoulder height and mean weight of adult males is 122.29 cm and 342.94 kg, respectively; the equivalent figures for females are 106.98 cm and 220.92 kg (Carvalho *et al.*, 2010). This may be advantageous in the bush-land, with its lack of feed resources and its dry and hot tropical climate. The breed's adaptive characteristics have developed over 400 years as a result of the selective pressures of the local environment and the extensive breeding conditions, with little or no artificial selection by humans (Carvalho and Amorim, 1989; Fioravanti *et al.*, 2011).

Despite the low costs of breeding the Curraleiro, and its good adaption to local environmental conditions, the absence of artificial selection has been accompanied by low economic efficiency (Fioravanti *et al.*, 2011). In order to intensify agricultural production, more productive European and (mainly African) zebu breeds were introduced to Brazil and started to displace the Curraleiro at the end of the nineteenth century (Mariante and Egito, 2002; Egito *et al.*, 2007; Oliveira, 2008). Little is known about the Curraleiro's total population size. Fioravanti *et al.* (2011) estimated that there may be between 1 000 and 5 000 reproductive cows. A breed with a population size of less than 5 000 reproductive females is considered to be at risk of extinction (Hodges, 1992). The Domestic Animal Diversity Information System (DAD-IS; http://www.fao.org/dad-is) classifies the Curraleiro as an endangered-maintained breed.

In 2011, the Associação Brasileira de Criadores de Bovinos Curraleiro Pé-Duro (ABCBCP) (Brazilian Association of Breeders of Curraleiro Pé-Duro) was founded by fusing existing breeders' associations (http://abcpd.com.br/). Salles *et al.* from the Instituto Nacional do Semiarido (INSA; National Institute of the Semiarid Region) developed a conservation and breeding programme for the breed (Salles *et al.*, 2011). No molecular data on the population genetics of the Curraleiro have been published, but because of the low effective population size, inbreeding within single herds may be high and gene flow between herds may be low. In addition, a

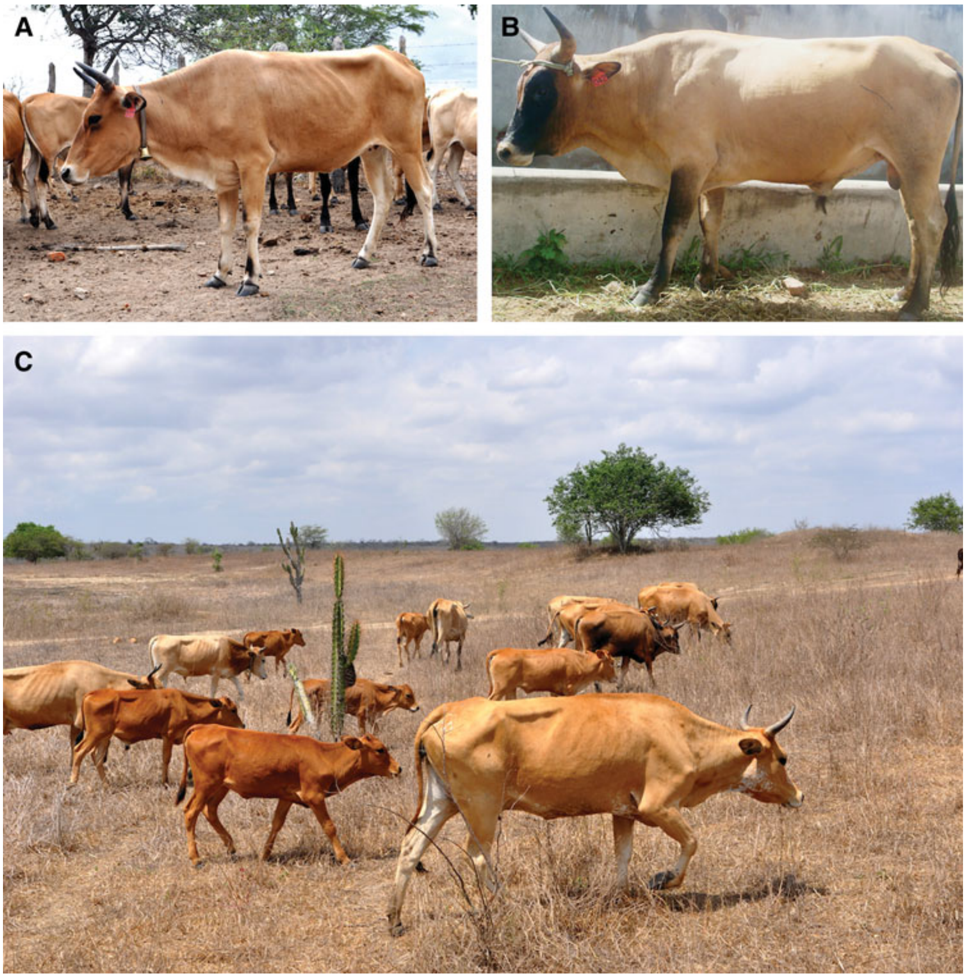

Figure 1. An adult cow (A), bull (B) and a herd (C) of Curraleiro cattle on an INSA pasture. Photos (A) and (C) were taken during the dry season in December, whereas (B) was taken during the raining season in July.

large proportion of existing Curraleiro herds may have interbred with other breeds.

This paper describes a study, undertaken in collaboration with ABCBCP, that aimed to obtain information about existing Curraleiro herds and their owners in Northeastern Brazil. The study focused on the identification of herds and on the breeding practices of registered breeders, with the objective of facilitating the future establishment of a conservation programme. It sought to obtain information on the degree of admixture between Curraleiro and other breeds and to identify breeders who would be interested in participating in a programme of conservation and improvement for the Curraleiro.

Methods

The data collection protocol and the consent procedure were reviewed and approved by the National Committee for Research Ethics (CONEP; http://conselho.saude.gov.br/web_comissoes/conep/index.html; Brazil).

Data were obtained by interviewing 22 Curraleiro breeders belonging to the ABCPD. Owing to the large distances involved, interviews were carried out with the help of questionnaires and by telephone. In addition, data were obtained from one herd owned by INSA in the state of Paraíba. The number of sampled herds, their sizes and their locations in the states of Ceará, Maranhão, Paraíba and Piaui are summarized in Table 1 and Figure 2. Data were analysed using the software program Microsoft Excel® (version 14.2.3).

Results

The average size of the 22 sampled cattle herds was 131.4 (standard deviation = 120.3), varying from 4 to 384 animals. Results obtained from the interviews are summarized in Table 2.

The findings indicate that breeding targeted not only the production of dairy products but also the production of beef for home consumption and animals for sale. When asked about the breed's main positive attributes, the breeders described the Curraleiroas having high levels of tolerance to diseases and parasites and excellent maternal

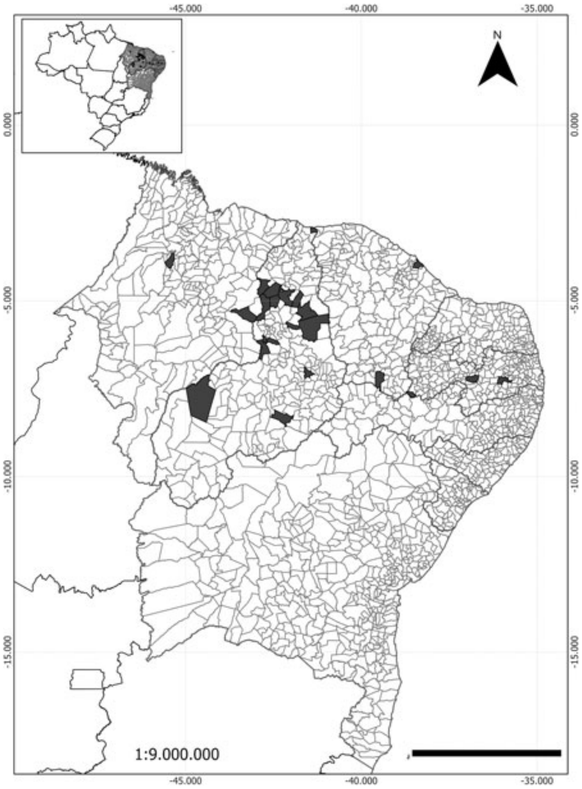

Figure 2. The Northeast Region of Brazil is marked in grey within the inlay. *Notes*: The magnification of Northeast Region shows the geographic distribution of the 22 municipal districts with Curraleiro herds. Numbers at the borders indicate the geographic latitudes and longitudes. Scale bar: 500 km.

abilities. It was also pointed out that animals are tame and that the breed is very tolerant of drought and water stress. All the herds in the study sample were bred under extensive conditions. All 20 breeders who provided a response cited the native grass species *Andropogon gayanus*,

Table 1. Number of studied herds, animals and their location

Locality		Number	
State	Municipal district	Herds	Animals
Piauí	JardimMulato	1	36
	Castelo do Piauí	1	384
	Sigefredo Pacheco	1	139
	Campo Maior	5	244
	Barras	1	105
	São João do Piauí	1	176
	Amarante	1	47
	Teresina	1	291
	Cajueiro da Praia	1	80
	Angical	1	14
	Altos	1	4
	São Miguel do Tapuio	1	280
	Ininga	1	9
Ceara	Crato	1	17
Paraíba	Campina Grande	1	69
	Taperoa	1	31
Maranhão	Santa Inês	1	300
	Matões	1	140
Total		22	2 366

Table 2. Frequency of reported husbandry practices of Curraleiro cattle

Variable	Number of responses	Percentage of responses
Main uses		
Milk	1	4.76
Beef	6	28.57
Breeding	5	23.81
Beef and breeding	3	14.29
Beef and milk	4	19.05
All	2	9.52
Land area per herd (hectares)		
23–300	13	59.09
300–600	2	9.09
600–1 000	2	9.09
1 000–3 000	3	13.64
>5 000	2	9.09
Main advantages of the breed		
Tolerance of parasites	2	9.09
Tolerance of drought and water stress	10	45.46
Good conformation, good quality of meat and other services	10	45.46
Pasture type		
Andropogon gayanus	14	70.00
Brachiaria decumbens	3	15.00
Cenchrus ciliares	3	15.00
Main feed that improves quality of beef		
Axonopus purpusii	12	100.00
Technical assistance		
Yes	11	50.00
No	11	50.00
Ectoparasites and endoparasites		
Controlled	21	95.46
Not controlled	1	4.54
Application of vaccines against rabies, foot and mouth disease and botulism	22	100
Disinfection of the navel of new born calves		
Not practised	8	36.36
Practised	14	63.64
Mating of Curraleiro cows with males of other breeds is avoided	22	100
Controlled mating		
Not controlled	19	86.36
Controlled	3	13.64
Cows and bulls remain together		
Not controlled	3	13.64
Controlled time period	19	86.36
Duration of the mating period		
5–48 h	4	66.67
More than 48 h	2	33.33
Factors that influence mating positively		
Rainy season	8	61.54
Feed	5	38.46
Main period of mating		
December/January	6	37.50
February/April	6	37.50
May/June	4	25.00
Age of cows at first calving		
Between 2 and 3 years	11	57.90
Between 3 and 4 years	8	42.10

Continued

Table 2. Continued

Variable	Number of responses	Percentage of responses
Age of oldest bull used for reproduction		
3–6 years	8	40.00
7–10 years	9	45.00
More than 10 years	3	15.00
Duration of lactation period		
Six months	3	33.33
Six to eight months	6	66.67
Production of milk and beef		
Notes of quantities taken	5	22.73
Quantity not controlled	17	77.27
Quantity of milk produced per day in kg		
Unknown	9	82.00
About 5 kg	2	18.00
Water source for the animals		
Tap water	7	31.82
Water reservoir	9	40.91
River	6	27.27
Slaughter age		
1–2 years	6	40.00
4–5 years	9	60.00
Weight at slaughtering (kg)		
100–150	7	58.33
150–200	3	25.00
200–250	2	16.67
Location of slaughtering		
Own farm	8	57.14
Butcher	6	42.86
Number of dead animals per year		
0–1	17	77.27
1–3	5	22.73
Main cause of death		
Unknown	10	45.45
Snake bites	9	40.91
Worm parasites	3	13.64
Carcass disposal		
Burning	10	45.46
Burial	8	36.36
Other forms of disposal	4	18.18

Brachiaria decumbens or *Cenchrus ciliares* as the most important feed resources. All the breeders reported that Curraleiro cattle can survive on all types of native grass.

Only half the breeders stated that they obtained specialized technical assistance for their livestock, but nearly all stated that their animals were treated for parasites and vaccinated. All breeders said that they avoided deliberately mating Curraleiro cows with males of other breeds. Most breeders stated that they did not control mating, but that they controlled the period of time during which cows and bulls stayed together.

About 58 percent of the breeders who provided a response stated that the first offspring were born when cows were between 2 and 3 years old. We did not obtain reliable data about the birth weight of new-born calves. Six breeders out of nine stated that the length of the lactation period was between 6 and 8 months. In about 77 percent of all cases, breeders stated that milk production, which is mainly used for home consumption, was not systematically recorded. Two breeders estimated that a cow is able to produce about 5 kg of milk per day during the lactation period; the other respondents were unable to provide an estimate. No breeders reported that their animals received any kind of supplementary feed, with the exception of minerals in the form of salt. Fifteen out of 22 breeders reported that their animals use natural water sources.

Nine breeders reported that animals were slaughtered between 4 and 5 years of age and six reported that animals are slaughtered between 1 and 2 years of age. Seven breeders reported that the weight of slaughtered animals was between 100 and 150 kg and five reported that the weight of slaughtered animals was between 150 and 250 kg. In most cases, only one animal per year was killed by natural causes. Nine breeders cited snake bites as a main cause of death.

Discussion

Previous studies have indicated that most Curraleiro herds and animals are found in the states of Tocantins and Goiás (Fioravanti *et al.*, 2011). In contrast, the ABCBCP indicated that the state of Piauí has the most herds and animals (Personal communication with Fernando Gayoso). The latter opinion could reflect the true distribution of Curraleiro herds within Northeastern Brazil. This idea is supported by the fact that the Curraleiro can be regarded as part of the heritage of the state of Piauí, where until beginning of the twentieth century beef production was mainly based on this breed (Carvalho, 1985, 1997). However, it could also represent a biased view, influenced by the fact that the ABCBCP is located in Teresina, the capital of Piauí, and therefore attracts mainly breeders from this region. It is also important to point out that all members of the ABCBCP pay a monthly membership fee, which may discourage breeders with a low income from registering as members. Therefore, the results presented in this paper may not necessarily be representative for the whole population of the breed in the state of Piauí. The breeders that participated in the present study did not practise other agricultural activities, and Curraleiro cattle were not their main source of income. Their income was based on non-agricultural activities; they included lawyers, health professionals, professors and civil servants.

When asked about the advantages of the Curraleiro, breeders mainly referred to its tolerance of drought and water stress, the tameness of the animals and the good quality of their meat. Fioravanti *et al.* (2011) found identical arguments among breeders living mainly on agriculture in the states of Tocantins and Goias. This previous study also showed that all herds were bred under extensive conditions. Breeders applied 4 (46.4 percent) or 8 (53.6 percent) out of 12 management techniques that had been defined to determine the technical level of breeding (Fioravanti *et al.*, 2011). The cattle in the present study were also bred exclusively under extensive conditions and only about half of them received specialized technical assistance. This is similar to the observations made by Fioravanti *et al.* (2011). Also similar to the previous results, the present study found that mating and production of milk and beef were in most cases not recorded and that in 8 out of 22 herds the navel of new-born calves was not disinfected. However, when asked about vaccination and parasite control, all breeders reported that animals were vaccinated against most serious diseases and in most cases also treated for ecto- and endoparasites. Interestingly, several breeders pointed out that ecto- and endoparasites did not represent a serious problem for the Curraleiro. This indicates that technical services did not focus on production but on the care and conservation of the animals. The idea of conservation was further supported by the fact that breeders claimed never to cross Curraleiro cows with bulls of other breeds.

The mean number of animals was 131.4 per herd, compared with 77.5 and 66.5 found by Fioravanti *et al.* (2011) in Goias and Tocantins, respectively. This could indicate more productive pastures in regions covered by the present study or may mean that herds of sampled cattle populations are generally larger. As Curraleiro animals do not need supplementary feed, and can live on native grass pastures, they can be bred at low costs and without destruction of the autochthonous flora and fauna. However, it will be important to determine maximal population densities that do not overburden pastures. Data indicate that the Curraleiro is ecologically attractive for the semi-arid region of Northeast Brazil, as it could help to decrease the burning of natural vegetation, a process that accelerates land degradation and desertification in the region (Bianchini *et al.*, 2006; Fioravanti *et al.*, 2011).

As in the study of Fioravanti *et al.* (2011), first calving was reported to occur between 2 and 3 years of age. However, some breeders reported that first calving occurs between 3 and 4 years of age.

The data indicate that Curraleiro animals are slaughtered at 48–60 months old and at a weight of between 200 and 250 kg. In comparison, animals of the zebu Nelore breed are slaughtered at mean weights of 353.8–424.8 kg at the age of 24–30 months (Lôbo *et al.*, 2002). The quantity of milk produced by the Curraleiro cows was reported to be about 5 kg per day, with a lactation period of about 6–8 months. According to the Associação Brasileira dos criadores de Gir leiteiro (Association of breeders of the Dairy Gir) the zebu breed Gir produces an average of 12 kg of milk per day over a 10-month lactation period (http://www.girleiteiro.org.br). This underlines the fact that it would be desirable to determine the potential for improving the milk production of the Curraleiro.

Conclusions

The Curraleiro's low breeding costs and its tolerance of drought and water stress indicate that it would be advantageous for low-income families living on small areas of farmland. A conservation and breeding programme should include this perspective and monitor Curraleiro cattle keeping. To date, estimates of the number of Curraleiro cattle in Northeastern Brazil remain speculative because many breeders may not be members of any association. The ABCBCP, in collaboration with cattle farmers involved in the present study, could serve as a basis for breed improvement and a conservation programme. A conservation and breeding programme would need to identify definitive morphological and molecular characteristics of the Curraleiro for crossing pure animals, but would also need to avoid inbreeding. Subsequently, productive traits of the breed should be improved.

Statement

None of the authors have any conflict of interest.

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The domestic livestock resources of Turkey: sheep breeds and cross-breeds and their conservation status

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Summary

Turkey's 21.8 million head of sheep comprise a rich array of fat-tailed and thin-tailed native breeds and crosses of these with animals of exotic origin. The structure of agriculture is such that most farms are predominantly subsistence oriented, of small size, keep few animals and provide only minimal inputs. Native breeds have evolved to meet these conditions and are generally well adapted to the natural environment, inadequate and unbalanced nutrition and disease stress. In the last 80 years, there have been attempts to modify the natural gene pool and many distinct breed types are in danger of or have already suffered extinction. This paper describes some of the major sheep genetic resources and their conservation status. The government is now aware of the danger of impoverishment or loss of this important aspect of biodiversity and has established programmes for conservation and preservation of several native breeds. Government, research institutions and producers should work together to ensure that the local gene pool is preserved and can thus continue to contribute to biodiversity and sustainable livestock production.

Keywords: *native breeds, biodiversity, production systems, cross-breeding, risk status, extinction, conservation*

Résumé

Les 21,8 millions d'ovins de la Turquie comprennent une vaste gamme de races indigènes à queue grasse et fine ainsi que des animaux de ces races croisés avec d'autres d'origine exotique. La structure de l'agriculture est telle que la plupart des fermes s'orientent principalement vers une agriculture de subsistance, sont de petite taille, élèvent peu d'animaux et ont une faible productivité. Les races indigènes ont évolué avec ces contraintes et sont en général bien adaptées à l'environnement naturel, à une alimentation pauvre et déséquilibrée et au stress causé par diverses maladies. Au cours des 80 dernières années, les modifications du pool génétique naturel ont été nombreuses, ce qui a fait que, de nos jours, plusieurs races différentes se trouvent menacées d'extinction ou se soient déjà éteintes. Cet article fournit des détails sur quelques-unes des principales ressources génétiques ovines, y compris leur état de conservation. Le gouvernement a actuellement pris conscience du danger qui découle de l'appauvrissement ou la perte de cette importante composante de la biodiversité et a, en conséquence, établi des programmes pour la conservation et préservation de plusieurs races indigènes. Le gouvernement, les instituts de recherche et les producteurs devraient travailler ensemble pour assurer la préservation du pool génétique local, contribuant ainsi au maintien de la biodiversité et au développement de la production animale durable.

Mots-clés: *races indigènes, biodiversité, systèmes de production, croisement, état de risque, extinction, conservation*

Resumen

Los 21,8 millones de cabezas de ganado ovino de Turquía comprenden un amplio abanico de razas nativas de cola grasa y cola fina así como cruces de estas razas con animales de origen exótico. La estructura de la agricultura es tal que la mayoría de las explotaciones están orientadas a la subsistencia, son de pequeño tamaño, mantienen pocos animales y presentan una baja productividad. Las razas nativas han ido evolucionando con estos condicionantes y, por lo general, se han adaptado adecuadamente al medio natural, a una alimentación pobre y desequilibrada y al estrés causado por diversas enfermedades. A lo largo de los últimos 80 años, se han producido modificaciones del acervo genético natural que han llevado a que muchos de estos tipos raciales se encuentren actualmente en peligro de extinción o se hayan extinguido ya. Este artículo describe algunos de los principales recursos genéticos ovinos así como su estado de conservación. En la actualidad, el gobierno es consciente del peligro que entraña el empobrecimiento o pérdida de este importante componente de la biodiversidad y por ello, ha puesto en marcha programas de conservación y preservación de varias razas nativas. Gobierno, centros de investigación y productores deberían trabajar conjuntamente para garantizar el mantenimiento del acervo genético local, contribuyendo así al desarrollo de la biodiversidad y la producción ganadera sostenible.

Palabras clave: *razas nativas, biodiversidad, sistemas de producción, cruzamiento, estado de riesgo, extinción, conservación*

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Introduction

The sheep was one of the first animals to be domesticated by man (Yilmaz, 1995) and ancient Turkey played a major role in the domestication process (Zeder, 2008). Sheep have been an important element in Turkey's household and national economies for some 10 000 years from the Neolithic to the present time (Arbuckle *et al.*, 2009). In 2010, the country had a population of 21.8 million sheep and it is one of the world's most important producers of sheep in spite of the fact that this number is less than half of the sheep population of the early 1980s (Turkstat, 2011). Over the millennia many breeds have been differentiated, but morphologically Turkish breeds are clearly divided into two groups, one being fat tailed and the other thin tailed (Anon., 1987). Recent phylogenetic analyses based on genetic distance estimates have shown the close relationships among the Akkaraman, Morkaraman and Tuj breeds (which are all fat tailed) and a clear separation between the fat-tailed group and those belonging to the thin tailed one (Uzun *et al.*, 2006).

Sources differ in the numbers they consider to be the types or breeds of Turkish livestock and there is considerable confusion in the nomenclature not only outside but also within the country. Many native or indigenous and exotic types and various crosses between these (although some of the crosses have had limited utility and an ephemeral life) are listed by various sources. Thus, according to one authority domestic sheep comprise 13 varieties, but none are identified individually (MARA/FAO, 2001). An earlier publication on Turkish biological diversity identifies and names 14 types and several subtypes of sheep (Anon., 1987). A search of one authoritative source (Mason, 1996) brings to light several to many more breeds and types of sheep to provide a total of 27 breeds. The Domestic Animal Diversity Information System of the Food and Agriculture Organization lists 35 sheep types although 15 of these are given as extinct (DAD-IS, 2010).

In spite of the importance of sheep in Turkey there have been relatively few recent publications on the species in the international literature. Those that have been published include ones on short-term fattening experiments (Macit, 2002; Macit *et al.*, 2002; Oflaz *et al.*, 2010), health and disease (Yilmaz *et al.*, 2002), reproduction (Ekiz *et al.*, 2007; Oflaz *et al.*, 2010) and production economics (Atsan *et al.*, 2009; Keskin *et al.*, 2010). The current paper aims to provide information on some of the main native and cross-bred sheep populations of Turkey, some perceptions of their production and current conservation activities and is one of a series (Wilson *et al.*, 2011; Yilmaz *et al.*, 2011a, 2011b, 2012) that will eventually cover all the nation's domestic animal species.

Production systems

Turkish sheep are produced under four distinct husbandry systems and in two of them production is generally secondary to crop production. The first system is the "small household" one common in western and northwestern Turkey. A family has an average of 3–5 sheep with a maximum holding of 10–15 per head. The second type is a "settled village flock" system common all over Turkey. Family flock sizes range from 8–10 to as many as 100 sheep. In this system, sheep are released by their owners early in the morning and a village flock is constituted. This flock is managed by a shepherd who is assisted in protecting them with several dogs. In both, the first two systems, sheep are grazed on common land in the spring and recover much of the body condition they have lost during the winter when they have been fed on cereal straws and brans. By the end of June, the grass has matured but the cereal harvest takes place in July and stubbles become available. Animals now reach peak condition and lay down fat under the skin, around the intestines and kidneys and, classically in the fat-tailed breeds, in the tail. The third system is denominated as "highland" and is common in northeastern, eastern and southern Turkey. Sheep are kept in the villages during the winter season and in the early spring. As the grass matures and dries in late spring and early summer the flocks are taken to the highlands whence they return, after 3–5 months when the feed is exhausted and cold sets in, to their villages for the winter. The "nomadic" system is found in eastern and southeastern Turkey. Some traditional nomadic tribes have as many as 100 000 to 200 000 sheep. Sheep stay and graze during the cold season in the lower lands of the southeastern plains of Turkey. During the hot season, the tribes migrate to the higher lands of eastern Turkey. Members of nomadic tribes always live in goat hair tents when they are with their flocks (Sonmez, 1978; Ertugrul *et al.*, 1993).

Sheep breeds and types

Fat-tailed

Turkey has 12 recognized breeds of fat-tailed sheep with several subtypes or varieties. Fat-tailed sheep are found over much of Turkey. Only four of the breeds are not at risk, four are at some risk and four are at severe risk. Other than the fat tail, the breeds vary in morphology and colour and in production characteristics and as may be expected in animals that have adapted through millennia to survival performance and especially reproductive performance is low (Table 1).

The *White Karaman* (Turkish = *Akkaraman,* Figure 1) is a rather small breed of central Anatolia and is a dual purpose meat and milk type that also produces a small amount of coarse wool (Table 1). Kangal, Karakas (which is classed as at severe risk (Sonmez, 1978)) and Southern are varieties of this type (Mason, 1996). Similar breeds are the Barazi in Syria and the Makui in Iran. The dominant breed of East Anatolia is the *Red Karaman* (*Morkaraman*, Figure 2) which is somewhat larger than the White variety and also a producer of meat and milk

Table 1. Conservation status, areas of distribution, morphological characteristics and some production traits of Turkish fat-tailed native sheep.

Trait	**Breed/type (Turkish name in brackets)**					
	White Karaman (Akkaraman)	**Red Karaman (Morkaraman)**	**Awassi (Ivesi)**	**Kangal Karaman (Kangal Karaman)**	**Norduz (Norduz)**	**South Karaman (Guneykaraman)**
Conservation status	Not endangered	Not endangered	Not endangered	Not endangered	Endangered	Endangered
Main area of distribution	Central Anatolia	East Anatolia	Southeast Anatolia	Sivas and adjacent provinces in Central Anatolia	Norduz area, Gurpinar County, Van Province	Antalya, Merin, Hatay and Gaziantep Provinces
Colour	White body, black spots on muzzle, ears and feet	Light to dark brown	White body, black or brown spots on head, neck and legs	White body, black spots around mouth and eyes	Commonly white, rarely grey or grey brown	White, grey, brown, red, black and pied
Horns	Male horns, female polled	Male horns, female polled	Male horns, female polled	Male 10% horns, female polled	Male horns, female 50% polled	Male horns, female rarely horns
Withers height (cm)	–	75♂, 68 ♀	66 ♂, 65 ♀	–	71 ♀	68 ♂, 63 ♀
Body length (cm)	–	72 ♂, 67 ♀	62 ♂, 59 ♀	–	68 ♀	63 ♂, 58 ♀
Birth weight (kg)	4.0–4.9	3.9 ♂, 3.5 ♀	4.6 ♂, 4.4 ♀	–	4.3 ♂, 4.0 ♀	4.2 ♂, 3.6 ♀
Adult weight (kg)	50–60 ♂, 35–40 ♀	50–90 ♂, 40–60 ♀	53 ♂, 46 ♀	–	60 ♀	52 ♂, 37 ♀
Products	Meat, milk	Meat	Milk, meat	Meat, milk	Meat, milk	Meat, milk
Average feedlot daily gain (g)	–	192 ♂	264 ♂	–	279 ♂	275 ♂
Milk lactation yield (kg)	38–60	60	172	–	137	25–30
Lactation length (days)	125	126	185	–	182	–
Greasy fleece weight (kg)	1.5–2.0	1.5–2.0	2.3	–	–	2.7
Age at puberty (months)	–	18	18	–	–	18
Litter size (lambs per birth)	1.05	1	1.1	–	1.1	1

Trait	**Breed/type (Turkish name in brackets)**					
	Hem in (Hem in)	**Herik (Herik)**	**Daglic (Daglic)**	**Cine Capari (Cine Capari)**	**Karagul (Karagul)**	**Tushin (Tuj)**
Conservation status	Endangered	Endangered	Nearly extinct	Nearly extinct	Nearly extinct	Nearly extinct
Main area of distribution	Artvin and Rize Provinces	Amasya Province	Central-Western Anatolia	Cine and Bozdogan Counties, Aydin Province	Tokat and neighbouring provinces	Ardahan and Igdir Provinces, Cildir County, Kars Province
Colour	Brown to black, occasionally light grey	White body, occasional black or dark brown spots on head and legs	White body, black or brown spots on muzzle, ears and feet	Beige or light grey body, dark spots on head, ears, legs and abdomen	Commonly black, rarely brown, grey or white	Shiny white body, dark spots on head and legs
Horns	Male spiral horns, female occasional horns	Male horns, female polled	Male spiral horns, female polled	Male large spiral horns, female usually polled	Male horns, female 87% polled	Male spiral horns, female mainly polled
Withers height (cm)	79 ♂, 73 ♀	65 ♂, 61 ♀	67 ♂, 61 ♀	70 ♂ 65 ♀	65 ♂, 58 ♀	61 ♀

Continued

Table 1. Continued

Trait	**Breed/type (Turkish name in brackets)**					
	Hem in (Hem in)	**Herik (Herik)**	**Daglic (Daglic)**	**Cine Capari (Cine Capari)**	**Karagul (Karagul)**	**Tushin (Tuj)**
Body length (cm)	72 ♂, 68 ♀	67 ♂, 62 ♀	65 ♂, 63 ♀	64 ♂ 62 ♀	66 ♂, 58 ♀	71 ♀
Birth weight (kg)	3.4 ♂, 3.1 ♀	3.5 ♂, 3.3 ♀	3.5 ♂, 3.5 ♀	4.0 ♂, 3.5 ♀	3.3 ♂, 3.1 ♀	3.8 ♂, 3.7 ♀
Adult weight (kg)	55–70 ♂, 55–60 ♀	60 ♂, 47 ♀	53 ♂, 46 ♀	55–60 ♂, 35–40 ♀	58 ♂, 38 ♀	50–55 ♂, 45–50 ♀
Products	Meat, wool	Meat, wool	Meat, milk	Meat, milk	Meat, milk, skin	Meat, wool, milk
Average feedlot daily gain (g)	215 ♂ 180 ♀	–	241 ♂	210 ♂	–	190 ♂
Milk lactation yield (kg)	110	–	57	50	–	45
Lactation length (days)	135–170	–	75–105	145–150	–	124
Greasy fleece weight (kg)	1.7	1.8–3.5	2.3	1.2	1.8–3.0	–
Age at puberty (months)	18	18	18	–	11–18	–
Litter size (lambs per birth)	1.1	1.1	1	1.1	1	1.2

Source: Sonmez (1975, 1978), Ertugrul *et al.* (1993), Anon. (2009).

Figure 1. White Karaman.

(in slightly large amounts than its white counterpart) with a subsidiary output of coarse wool (Table 1) (Anon., 2009). The *Karacadag* of Diyarbakir Province (the Appendix map at the end of this paper provides an outline of Turkey showing the locations of all the Provinces mentioned throughout this paper) is a local variety of the Red Karaman (Mason, 1996). In Turkey, the *Awassi* (*Ivesi*, Figure 3) is found mainly in the southeastern part of the country but this animal is part of the widespread and important breed that is found throughout the Arab Middle East and Israel as well as Turkey (Mason, 1996). The Turkish type (Table 1) is a medium-sized animal with a good milk yield over a long lactation, a rapid growth rate for meat production and a medium-heavy fleece of coarse wool (Ertugrul *et al.*, 2009). Usually considered as a local variety of the White Karaman, the

Figure 2. Red Karaman.

Figure 3. Awassi.

Kangal Karaman (Table 1) is localized in Sivas and Malatya provinces of central Anatolia (Mason, 1996), but a peculiarity is that only a small proportion of males are horned (Anon., 2009).

An endangered but extremely local breed is the *Norduz*, which is found in only a small area of Van Province in eastern Turkey. The medium-sized sheep has good growth rates, produces good quantity of milk and is unusual in that 50 percent of females are horned. A group of 11 farmers maintain 200 sheep for conservation purposes (Anon., 2009; Ertugrul *et al.*, 2009). An often-coloured variety of the White Karaman is the medium-sized *South Karaman* (*Guneykaraman*, Figure 4), which is found, as indicated by its name in the provinces of southern Anatolia (Mason, 1996). It is mainly a meat type with poor milk production but yields moderate coarse wool (Table 1). The government's International Bahri Dagdas Agricultural Research Institute maintains a small conservation flock which numbered 24 rams and 22 females in 2009 (Ertugrul *et al.*, 2009). Another endangered breed is the *Hem in* (Figure 5) which is a variety of Red Karaman found in northeastern Turkey (Mason, 1996). The tall but medium-weight breed has a moderate growth rate for meat, produces a fair mount of milk and provides a moderate clip of coarse wool (Table 1). One farmer in Ardanuc County of Artvin Province was maintaining a conservation flock of 200 sheep in 2009 (Ertugrul *et al.*, 2009). A fourth endangered fat-tailed breed is the *Herik* (Figure 6) of north Anatolia is similar to the Daglic but has a rather shorter tail than most others in the group (Mason, 1996). It is classed as a meat type but produces a fair to heavy clip of coarse wool (Table 1). Some 200 sheep were in conservation herds maintained by three farmers in its home tract in Amasya Province in 2009 (Ertugrul *et al.*, 2009).

Figure 4. South Karaman.

Figure 5. Hem in.

Severely at risk is the *Daglic* (Figure 7) of western Anatolia. This medium-sized coarse wool and meat type is limited in its distribution to central-western Anatolia

Figure 6. Herik.

Figure 7. Daglic.

(Table 1). In 2009, three farmers had about 200 sheep in conservation flocks in Bolvadin County in Afyon Province (Ertugrul *et al.*, 2009). Reputed to be resistant to disease the small-sized *Cine Capari* (Figure 8) from Aydin Province has only a moderate growth rate and produces small quantities of milk and coarse carpet wool (Table 1, Mason, 1996). Some 120 animals were being maintained by two farmers in Aydin Province in 2009 (Ertugrul *et al.*, 2009). Classed as at high risk in Turkey the local *Karakul* (*Karagul*, Figure 9) is part of the larger Central Asia type of fat-tailed sheep and in common with them a proportion of the females carry horns (Mason, 1996; Anon., 2009). Similar in size to other Turkish fat-tailed sheep, the local variety is commonly black but there are also some brown, grey or white animals (Table 1). In addition to meat and milk the Karakul produces skins (pelts) of various colour and type. Some 200 sheep were in conservation flocks managed by two farmers in Tokat Province in 2009 (Ertugrul *et al.*, 2009). The *Tushin* breed of Georgia is known as *Tuj* (Figure 10) in Turkey and is mainly confined to Cildir County in Kars Province with other populations in other parts of the extreme northeast of the country (Table 1). This rather small sheep with a small fat tail or even a fat rump (Mason, 1996; Anon., 2009) produces moderate amounts of wool and milk and is at very high risk (Ertugrul *et al.*, 2009).

Figure 9. Karakul.

Thin-tailed

There are six recognized breeds of thin-tailed sheep in Turkey. These are largely confined to the western part of the country including the southern shore of the Black Sea. It is considered that three of the breeds are not endangered, two are at some risk and one, which is confined to three counties in Izmir Province, is at severe risk. Among them the breeds have a thin tail in common but otherwise vary in morphology and in production characteristics (Table 2).

The rather large *Kivircik* (Figure 11) is common in northwest Turkey. This triple purpose meat, milk and medium/coarse wool type is similar to the Karnmobat of Bulgaria and the Tsigai of southeast Europe in general and may have originated from them (Koban, 2004). The breed is a constituent member of the Ruda (Balkans) breed group but has more uniform and slightly less coarse wool than the Zackel type (Mason, 1996). One of the bigger and

Figure 8. Cine Capari.

Figure 10. Tushin.

Figure 11. Kivircik.

heavier of Turkey's thin-tailed breeds the Kivircik shows good feedlot performance, produces a moderate amount of milk in a long lactation, matures sexually somewhat late and has a small litter size (Table 2). The Kivircik is the origin of the Karacabey Merino and has also been crossed with the Daglic to produce the Kamakuyruk (=wedge tail) (Mason, 1996). Some 286 sheep (15 rams and 271 females) are in a conservation flock at the government's Marmara Agricultural Research Institute (MARI) and 200 sheep are under protection by a farmer in Kirklareli (Ertugrul *et al.*, 2009). Largely confined to northern Anatolia, the *Karayaka* (Figure 12) is a triple purpose breed producing meat, wool and milk (Mason, 1996; Arat, 2011). This animal falls in the medium-size and weight in the thin-tailed group. Late maturing and with a small litter size, the breed's milk yield is low but is compensated for to some extent by the heaviest fleece weight of all thin-tailed sheep (Table 2). Similar to the Greek Zackel breed, the *Imroz* (*Gokceada*, Figure 13) is a milk, meat and coarse wool type (Table 2). A synonym for this breed is Gokceada (Mason, 1996). In 2009, a total of 94 sheep (18 rams and 76 females) were under protection by the government at MARI with 200 sheep in farmer flocks in Gokceada and Canakkale being conserved (Ertugrul *et al.*, 2009).

The *Pirlak* (*Pirlack*) of Afyon, Burdur, Isparta, Kutahya, Manisa and Usak Provinces is considered to be at some risk (Ertugrul *et al.*, 2009). This mid-sized coarse wool sheep also produces meat and milk (Table 2) and has a long tail with some fat at the base (Anon., 2009). Also endangered (Ertugrul *et al.*, 2009) is the *Karya* of Aydin, Izmir, Manisa, Usak and Denizli. This small breed produces coarse wool, meat and milk (Table 2) and terminates in a long thin tail (Anon., 2009). The most critically at risk of the thin-tailed types is the *Sakiz* (Figure 14), which is confined to a small area around Izmir and was originally bred from the Chios (Mason, 1996). A producer of coarse wool, milk and meat (Table 2) the breed has a long thin tail with fat at the base. A total of 130 sheep (35 rams and 95 females) were under protection by the government at MARI and 113 sheep were in conservation flocks managed by four farmers in Cesme in Izmir Province in 2009 (Ertugrul *et al.*, 2009).

Cross-breeds

Attempts to increase the output of the sheep subsector by cross-breeding started in 1928 (Ertugrul *et al.*, 2009, 2010). Cross-breeding programmes – which have often been somewhat unstructured and over the years have produced an enormous variety of animals (Table 3) – had three objectives: increased wool production for the textile industry; increased meat production to feed people and support the food industry; and increased milk production for the food industry. Four principal cross-breeding strategies have been followed: use of exotic sires on native females and then breeding *inter se* from the F1 generation; backcrossing the new cross-bred to the same or another exotic breed; using the new cross-bred for further crosses on native breeds; and simple crossing of two native breeds. Various exotic breeds with the supposedly required traits to achieve these objectives have been used in Turkey for more than 80 years. Principal in the early days were German Mutton Merino and Ile de France to improve growth rates and fleshing and the East Friesian for milk, which is still an important output of sheep. Under programmes aimed at increasing milk production, however, native sheep were also targeted either by selection within a single breed or by crossing two native breeds (Ertugrul *et al.*, 1993). In addition, all new breeds were also expected to improve both the quantity and quality of wool over the native breeds. All Turkish cross-bred sheep – there are, or have been, at least 17 named varieties – with the exception of Acipayam, Wedge tail or Kamakuyruk and Malya, which have long tails with fat at the base, have thin tails.

The first German Wool-Mutton Merino imports by the Ministry of Agriculture in 1928 were crossed on native Kivircik sheep at Karacabey State Farm in western Anatolia to produce the *Karacabey Merino* (*Karakabey Merinosu*, Figure 15). The large, heavy and early maturing, both physically and sexually, Karacabey Merino (Table 3) has 90–95 percent Merino blood and is mainly a meat-medium wool type with a rapid growth rate, a good yield of carpet wool and of good prolificacy (Mason, 1996; Kaymakci, 2008). In a manner analogous to the Karacabey Merino, the German Mutton Merino was used to produce the *Anatolian Merino* (Figure 16) by crossing with the White Karaman at Konya State Farm (Sonmez, 1978; Anon., 2009). This is a mid-sized, sheep that is heavier than its native progenitor and produces more milk and a good crop of finer wool (Table 3). Of similar provenance to the Anatolian Marino but with a greater proportion of German blood is the *Central Anatolian Merino* (*Orta Anadolu (Konya) Merinosu*, Figure 17). Development was started in 1952 at the Konya State Farm (Mason, 1996; Anon., 2009)

Table 2. Conservation status, areas of distribution, morphological characteristics and some production traits of Turkish thin-tailed native sheep.

Trait	**Breed/type (Turkish name in brackets)**					
	Kivircik (Kivircik)	**Karayaka (Karayaka)**	**Imroz (Golceada)**	**Pirlak (Pirlak)**	**Karya (Karya)**	**Sakiz (Sakiz)**
Conservation status	Not endangered	Not endangered	Not endangered	Endangered	Endangered	Nearly extinct
Main area of distribution	Thrace, Marmara and North Aegean	Sinop, Sansu, Ordu, Giresun and Trabzon Provinces	Gokceada Island, Canakkale Province	Kutahya, Afyon, Usak, Manisa, Isparta and Burdur Provinces	Aydin, Izmir, Manisa, Usak and Denizli Provinces	Cesme, Urla and Seferihisar in Izmir Province
Colour	White body, occasionally black or pied	White body, black spots on head and neck	White body, black spots around mouth, eyes, ears and legs	White body, black spots around mouth, eyes and ears	White body, black spots around mouth, eyes and ears	White body, black spots around mouth, eyes, ears and legs
Horns	Male spiral horns, female polled	Male horns, female polled	Male spiral horns, female polled	Male spiral horns, female polled	Male spiral horns, female polled	Male horns, female polled
Withers height (cm)	69 ♂, 64 ♀	66 ♂, 62 ♀	61 ♀	63 ♀	67 ♀	75 ♂, 73 ♀
Body length (cm)	80 ♂, 66 ♀	71 ♂, 63 ♀	63 ♀	60 ♀	64 ♀	75 ♂, 72 ♀
Birth weight (kg)	4.0 ♂, 3.7 ♀	3.5 ♂, 3.2 ♀	3.8 ♂, 3.7 ♀	4.0 ♂, 3.5 ♀	4.5 ♂, 3.5 ♀	3.2 ♂, 3.0 ♀
Adult weight (kg)	60–70 ♂, 45–55 ♀	55 ♂, 40 ♀	55 ♂, 48 ♀	45–50 ♀	55 ♂, 45 ♀	70 ♂, 50 ♀
Products	Meat	Meat, wool, milk	Milk, meat	Meat, milk	Milk, lamb	Milk, lamb
Average feedlot daily gain (g)	263 ♂	220 ♂	191 ♂	150 ♂	182 ♂	242 ♂
Milk lactation yield (kg)	83	40–50	121	75–80	100	180–200
Lactation length (days)	180	100–160	204	120	170	190
Greasy fleece weight (kg)	1.5	2.0–3.5	2.2	2.0–2.5	1	2
Age at puberty (months)	16–18	18	16	18	10–14	8–9
Litter size (lambs per birth)	1.2	1.1	1.2	1.2–1.5	1.6	2

Source: Sonmez (1975, 1978), Ertugrul *et al.* (1993), Anon. (2009).

Figure 12. Karakaya.

and has resulted in a sheep somewhat larger than the Anatolian Merino, with a more rapid growth rate, slightly heavier wool clip but a reduced milk yield (Table 3).

Originating in the 1970s at Malya State Farm in central Anatolia the homonymous *Malya* (Figure 18, Table 3) is a fine wool, meat and milk type derived from the German Mutton Merino (35 percent) and the Akkaraman (Yilmaz, 1984; Ertugrul *et al.*, 1993; Anon., 2009). The low proportion of exotic blood enables this animal to do well under less than optimum husbandry and has left it with a fat tail. The International Bahri Dagdas Agricultural Research Institute (IBDARI) in Konya Province south of Ankara bred the *Hasak* (Figure 19) via a three-way descent German Mutton Merino and Hampshire sire lines and an Akkaraman dam line. This is a strong, heavy mid-sized and coloured sheep with a rapid growth rate and a good carcass yield that is often used for early lamb production (Table 3). It has a long tail that is fat at the base (Kaymakci, 2008; Sonmez 2009; bdutae.gov.tr 2011). Also bred at IBDARI and unusual in Turkish cross-breeding programmes because there is no Native Turkish sheep blood is the *Hasmer* (Figure 20), which is a milk, meat and wool type with a strong mid-sized body, a rapid growth rate and good carcass yield (Table 3). Unlike the previous cross-bred this type has a thin tail (Kaymakci, 2008; Sonmez, 2009; bdutae.gov.tr 2011).

Figure 13. Imroz (Gockeada).

Figure 14. Sakiz.

Developed at Istanbul University from 1969 onwards with American Rambouillet (65–70 percent) sire and Daglic (30–35 percent) dam lines the *Ramlic* is a heavy meat breed with a rapid growth rate that also carries a rather fine fleece (Table 3, Anon., 2009). Two cross-breds are of mainly Ile de France parentage. The *Menemen* is a medium heavy type developed in the Izmir area and is a cross of Ile de France (75 percent) and Tahirova (25 percent). It has a rather slow growth rate, but produces quality lamb and a low yield of wool, but is reputed to have a good milk yield (Table 3). It is considered that there is further need for selection and breeding before this cross achieves its potential (Sonmez, 2009). The *Polatli* (Figure 21) has been developed since 1998 at Bafra State Farm in central Anatolia from the Ile de France and Akkaraman (www.tigem.gov.tr 2011; Anon., 2009). This medium-heavy sheep is bred as a triple purpose fine wool, meat and milk type (Table 3).

The East Friesian has been used in several cross-breeding programmes. In cooperation with Hohenheim University, the Faculty of Agriculture at Cukurova University has produced the *Asaf* from the East Friesian and the Awassi (Table 3). The Asaf has been developed through *inter se* crossing of the F1 to produce the F2 (Kaymakci, 2008; Sonmez, 2009). The *Acipayam* (Table 3) is a fat-tailed cross-bred of the southern provinces of Denizli, Afyon, Isparta and Antalya, and is a light weight milk, meat and wool type bred from East Friesian rams on Awassi ewes with some Daglic blood introduced to improve wool quality. Originating from East Friesian sire and Kivircik dam lines the *Tahirova* (Figure 22) was developed at the Tahirova State Farm (Mason, 1996) and was bred for the lowlands of Izmir Province on Turkey's Mediterranean coast. This medium-heavy breed is among the most prolific of Turkey's sheep, produces a considerable amount of milk and clips a heavy fleece (Table 3, Anon., 2009). The

Table 3. Genetic make up, morphological characteristics and some production traits of Turkish cross-bred sheep.

Trait	**Breed/type (Turkish name in brackets)**					
	Karacabey Merino (Karakabey Merinosu)	**Anatolian Merino (Anadolu Merinosu)**	**Central Anatolian Merino (Orta Anadolu (Konya) Merinosu)**	**Malya (Malya)**	**Hasak (Hasak)**	**Hasmer (Hasmer)**
Sire and dam lines	German Mutton Merino ♂ × Kivircik ♀	German Mutton Merino ♂ × Akkaraman ♀	German Mutton Merino ♂ × Akkaraman ♀	German Mutton Merino ♂ × Akkaraman ♀	German Mutton Merino × Hampshire × Akkaraman	German Mutton Merino × Hampshire × Merino
Foreign genotype (%)	90	65	80	35	100	100
Colour	White	White	White	White	Pied, black or brown	White, dark spots on head and legs
Characteristics	Thin tail, heavy with rapid growth	Thin tail, higher milk yield than Akkaraman	Thin tail, higher milk yield than Akkaraman	Long fat tail, does well under Akkaraman conditions	Thin tail, rapid growth, quality meat and lamb	Thin tail, strong and heavy body, fine wool
Withers height (cm)	77 ♂ 73 ♀	75 ♂, 66 ♀	76 ♂ 68 ♀	70 ♀	–	–
Body length (cm)	73 ♂ 72 ♀	86 ♂, 74 ♀	88 ♂ 75 ♀	68 ♀	–	–
Birth weight (kg)	4.5 ♂, 4.3 ♀	4.3 ♂, 4.1 ♀	4.4 ♂, 4.1 ♀	4.0 ♂, 3.6 ♀	4.2	4.6
Adult weight (kg)	80–100 ♂, 60–65 ♀	80–90 ♂, 50–55 ♀	85–90 ♂, 55–60 ♀	80 ♂, 58 ♀	75–90 ♂, 60–65 ♀	75–85 ♂, 60–65 ♀
Products	Meat, wool	Meat, wool	Meat, wool	Meat	Meat, lamb	Milk, meat, wool
Average feedlot daily gain (g)	322 ♂	240 ♂	290 ♂, 235 ♀	240 ♂	–	–
Milk lactation yield (kg)	78	70–90	60–70	35	–	–
Lactation length (days)	140	120	150	90	–	–
Greasy fleece weight (kg)	3.6	3.0–3.5	3.6–3.8	2.7	3.1	3.5
Age at puberty (months)	10–14	18	18	18	–	16–18
Litter size (lambs per birth)	1.4	1.4	1.4	1.2	1.2	1.2

Trait	**Breed/type (Turkish name in brackets)**					
	Ramlic (Ramlic)	**Menemen (Menemen)**	**Polatli (Polatli)**	**Asaf (Asaf)**	**Acipayam (Acipayam)**	**Tahirova (Tahirova)**
Sire and dam lines	Rambouillet ♂ × Daglic ♀	Ile de France ♂ × Tahirova ♀	Ile de France ♂ × Akkaraman ♀	East Friesian ♂ × Awassi ♀	East Friesian ♂ × Awassi ♀ × Daglic ♀	East Friesian ♂ × Kivircik ♀
Foreign genotype (%)	65–70	75	?	25	25	75
Colour	White	White	White	–	White, black spots on head and neck	White

Characteristics	Thin tail, fine wool and heavy weight	Thin tail, quality meat, high milk yield	Thin tail, fine wool and heavy weight	Thin tail	Long fat tail, crossed with Daglic for carpet wool	Thin tail, highly prolific
Withers height (cm)	74 ♂, 70 ♀	68 ♀	–	–	66 ♂, 62 ♀	–
Body length (cm)	75 ♂, 72 ♀	71 ♀	–	–	71 ♂, 63 ♀	–
Birth weight (kg)	4.5 ♂, 4.0 ♀	–	–	–	3.5 ♂, 3.2 ♀	–
Adult weight (kg)	80–90 ♂, 60–65 ♀	70 ♂, 60 ♀	–	–	55 ♂, 40 ♀	60–85
Products	Meat, wool	Meat, milk	Meat, milk	Milk, lamb	Milk, meat, lamb	Milk, meat,
Average feedlot daily gain (g)	265 ♂	122–183 ♂	–	–	220 ♂	–
Milk lactation yield (kg)	50–60	–	–	–	40–50	250–300
Lactation length (days)	130–150	–	–	–	100–160	–
Greasy fleece weight (kg)	2.5–3.0	1.8	–	–	2.0–3.5	3.0–4.0
Age at puberty (months)	40829	–	–	–	18	–
Litter size (lambs per birth)	1.3	1.3	–	–	1.1	1.6–1.8

Trait	**Breed/type (Turkish name in brackets)**				
	Sonmez (Sonmez)	**Turkgeldi (Turkgeldi)**	**Wedge tail (Kamakuyruk)**	**Cukurova (Cukurova)**	**Bafra (Bafra)**
Sire and dam lines	Tahirova ♂ × Sakiz ♀	Tahirova ♂ × Kivircik ♀	Kivircik ♂ × Daglic ♀	Sakiz ♂ × Awassi ♀	Sakiz ♂ × Karakaya ♀
Foreign genotype (%)	75	75	0	62.5	75
Colour	White	White	White	–	White, black spots on head
Characteristics	Thin tail, fine wool and heavy weight	Thin tail, moderately prolific	Long fat tail	Thin tail	Thin tail, fine wool and heavy weight
Withers height (cm)	–	–	–	–	68 ♀
Body length (cm)	–	–	–	–	71 ♀
Birth weight (kg)	–	–	–	–	4.0 ♂, 3.8 ♀
Adult weight (kg)	80–90 ♂, 60–65 ♀	70–80 ♂, 40–50 ♀	–	–	70 ♂, 60 ♀
Products	Meat, milk	Milk, meat, wool	Meat	Milk, lamb	Lamb, milk, meat
Average feedlot daily gain (g)	–	–	–	–	240 ♂
Milk lactation yield (kg)	350–400	150–180	–	–	120
Lactation length (days)	–	172–186	–	–	120
Greasy fleece weight (kg)	3.0–4.0	3.0–4.0	–	–	2.2
Age at puberty (months)	–	–	–	–	12
Litter size (lambs per birth)	–	1.4–1.5	–	–	1.8

Source: Sonmez (1975, 1978), Ertugrul *et al.* (1993), Anon. (2009).

Figure 15. Karacabey Merino.

Figure 16. Anatolian Merino.

Tahirova has been used within Turkey as a sire line in the production of further cross-breds.

Bred at Ege University in western Anatolia by a team led by a scientist whose name is synonymous with the type the

Figure 17. Central Anatolian Merino.

Figure 18. Malya.

Figure 19. Hasak.

Sonmez (Figure 23) is a backcross of the Sakiz to the Tahirova (Ertugrul *et al.*, 1993). This is an animal with a high milk yield, a heavy clip of fine wool and a medium-heavy producer of meat (Table 3). Originating at Turkgeldi

Figure 20. Hasmer.

Figure 21. Polatli.

Figure 22. Tahirova.

State Farm in Thrace in the European part of Turkey from Tahirova (75 percent) and Kivircik (25 percent) the *Turkgeldi*is a medium heavy and reasonably prolific meat, milk and wool type (Table 3, Kaymakci, 2008).

Three named cross-breds derive directly from other Turkish native breeds with no admixture of exotic blood. The *Wedge tail* – so-called because of the fat at the base of the otherwise thin tail – or *Kamakuyruk* originates from two local breeds, in this case the Kivircik and Daglic (Sonmez, 1978; Mason, 1996). This is a breed of Balikesir, Izmir, Bursa and Canakkale Provinces in the extreme west of Asian Turkey and is mainly a meat type (Table 3). Bred at the Faculty of Agriculture at Cukurova University is the *Cukurova*, which is a composite of Sakiz and Awassi sheep (Table 3). This is a milk and early lamb type (Kaymakci, 2008; Sonmez, 2009). The *Bafra* (Figure 24) originated in 1998 at Bafra State Farm in Samsun Province in the north of Anatolia and on the Black Sea from Sakiz (75 percent) and Karayaka (25 percent) (www.tigem.gov.tr 2011). This medium-heavy fast growing sheep is highly prolific and also produces a moderate amount of milk and a light fleece (Table 3).

The *Candir* is a cross of Daglic and White Karaman found in western Anatolia with the synonym *Kesber* sometimes also being used (Sonmez, 1978).

Attempts to achieve the three original objectives of cross-breeding continue to the present day. At least eight State Farms continue to pursue programmes to produce new types of sheep, often using exotic breeds that have not been used in earlier programmes (Table 4).

Extinct breeds

Three breeds of sheep considered to be indigenous Turkish types are known to have become extinct. The first is the Halkali about which very little is known (Ertugrul *et al.*, 2009). The Karakachan (Figure 25) is a widespread Balkans breed of the Zackel type (Mason, 1996) that has disappeared from Turkey (Kaymakci, 2008; Ertugrul *et al.*, 2009; Sonmez, 2009). The Odemis (Figure 26), a triple purpose meat-milk-wool fat-tailed breed (Figure 27) that was largely confined to the small Menderes Valley

Figure 23. Sonmez.

Figure 24. Bafra.

Table 4. Sheep cross-breeding programmes being carried out on Turkish state farms in the 21st century.

State farm and location	Cross-breeding programme
Turkgeldi State Farm, Kirklareli	Teasel × Kivircik
Inanli State Farm, Tekirdag	Teasel × Kivircik
Gokhoyuk State Farm, Amasya	Border Leicester × Karayaka
Alpaslan State Farm, Mus	Lincoln × Red Karaman
Bala State Farm, Ankara	Dorset Down × White Karaman
Ulas State Farm, Sivas	Hampshire Down × White Karaman
Acipayam State Farm, Denizli	German Mutton Merino × Ramlic; German Mutton Merino × Acipayam
Pasture, Grassland and Animal Breeding Research Institute, Ankara	Ile de France × White Karaman; Ile de France × Anatolian Merino

Source: Sonmez (2009).

Figure 25. Karakachan.

of west Turkey (Mason, 1996; Anon., 2009) is now also thought to be extinct (Ertugrul *et al.*, 2009).

Conservation measures

The number of sheep in Turkey has fallen steadily since the middle of the 20th century. Concomitant to the loss in numbers has been a reduction in the genetic resource with the result that at least three Turkish native breeds are known to have become extinct and several others are of such low numbers or of such limited geographic distribution that they are considered to be endangered and at possible risk of extinction in the future. Alarmed, perhaps belatedly, by this situation the Turkish government began to apply conservation policies in an attempt to prevent further decline and to preserve Turkish indigenous sheep breeds.

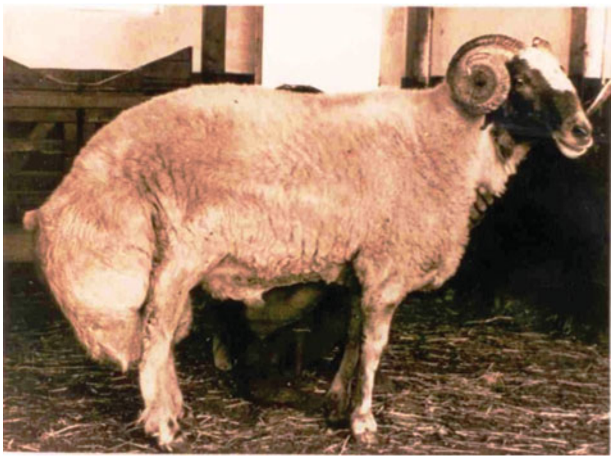

Figure 26. Odemis.

Figure 27. Odemis showing fat tail.

The Genetic Engineering and Biotechnical Institute (GEBI), Marmara Research Centre (MRC), the Scientific and Technological Research Council of Turkey (STRCT) Gebze, Kocaeli, prepared a project entitled the "*In Vitro*

Table 5. Locations and breeds of sheep under conservation activities at government centres.

Location	Breed/line
Lalahan Livestock Research Institute (LLRI), Ankara	Awassi, Herik, Daglic, Karagul, Cine Capari, Karayaka
Marmara Livestock Research Institute (MLRI), Balikesir	Kivircik, Imroz (Chios), Sakiz how does Chios get here?
IBDARI, Konya	White Karaman, Red Karaman, Norduz, Hem in

Source: Anon. (2009).

Conservation and Preliminary Molecular identification of some Turkish Domestic Animal Genetic Resources (TURKHAYGEN-I)" in 2005 (Arat, 2011). Consequent to several iterations the project was approved by the STRCT in March 2007 with a budget of 9.1 million Turkish Lira (about US$5.0 million). The implementation period was 4.5 years with the project expected to be completed by the end of 2011 (Arat, 2011).

As indicated in the project document its expected outcomes were:

- Establishment of DNA and viable cell banks (gametes, embryos, somatic cells and tissue samples) of animal genetic resources through cryopreservation at GEBI and at Lalahan Livestock Central Research Institute (LLCRI);
- Genetic characterization and registration of valuable species and breeds; and
- Enhancement of the competitiveness of national human resources in the area of animal husbandry and the building of a critical mass of researcher capacity.

Collection of genetic material for cattle had begun in 2006 and sheep were included in the programme in 2007. Some 14 conservation flocks of sheep have been established at various research stations (Table 5) and an extensive bank of genetic material has been established for 13 breeds as a result of the project (Table 6). It is expected that this resource will be expanded for preservation, conservation and use of Turkey's native genetic resources in the future.

Discussion

Sheep numbers decreased steadily from more than 48 million head in 1980 to a little over 21.6 million head in 2009 (Turkstat, 2010). Among the manifold reasons for the reduction are changes in the structure of agriculture, smallholder farmers turning to other products or other employment, low output from sheep, changing market conditions and a move away from red meat by consumers and lack of government support. Unlike the cattle

Table 6. Genetic material conservation status of Turkish sheep breeds in May 2011.

Breed	Institute and type of material							
	GEBI				Lalahan Livestock Central Research Institute			
	Embryo	Sperm	DNA	Cell	Embryo	Sperm	DNA	Cell
White Karaman (Akaraman)			50 animals	49 animals, 490 vials	65	23 animals, 704 straws	50 animals	44 animals, 440 vials
Red Karaman (Morkaraman)			50 animals	44 animals, 184 vials	173	13 animals, 556 straws	50 animals	
Awassi (Ivesi)			51 animals	51 animals, 183 vials	50	23 animals, 681 straws	51 animals	
Norduz (Norduz)	–	–	54 animals	49 animals, 490 vials	36	23 animals, 807 straws	54 animals	49 animals, 490 vials
Hem in (Hem in)	–	–	48 animals	48 animals, 284 vials	64	18 animals, 550 straws	48 animals	
Herik (Herik)	–	–	49 animals	48 animals, 480 vials	50	18 animals, 103 straws	49 animals	47 animals, 470 vials
Daglic (Daglic)			50 animals	50 animals, 192 vials	8	19 animals, 635 straws	50 animals	
Cine Capari (Cine Capari)			39 animals	39 animals, 390 vials	38	16 animals, 530 straws	39 animals	34 animals, 340 vials
Karagul (Karagul)	–	–	50 animals	48 animals, 283 vials	60	13 animals, 465 straws	50 animals	
Kivircik (Kivircik)			45 animals	43 animals, 195 vials	185	21 animals, 656 straws	45 animals	
Karayaka (Karakaya)	–	–	49 animals	64 animals, 292 vials	136	25 animals, 292 straws	49 animals	
Imroz (Gokceada)	–	–	50 animals	49 animals, 490 vials	102	23 animals, 730 straws	50 animals	49 animals, 490 vials
Sakiz			49 animals	47 animals, 470 vials	22	7 animals, 298 straws	49 animals	47 animals, 470 vials

Source: www.turkhaygen.gov.tr 2011.

subsector where reduced numbers have been compensated for by higher individual performance (Yilmaz *et al.*, 2012), there has been no increase in output per head of sheep production because of poor performance. Much of the market for meat has been taken over by the enormous increase in the numbers of poultry and structural changes in poultry production from low input extensive to high input very intensive systems.

In spite of many years of effort by the government and universities to produce new genetics that would give higher output for similar input there has been little success. The new cross-breds are in many cases only marginally better than the breeds they are meant to replace. After more than 80 years of effort there is little evidence of improvement in the sheep industry. In recent years, and in spite of the effort of both government and universities only 20 percent of targets to produce cross-bred progeny have been achieved. Programmes have been started and then terminated for a variety of reasons including unstructured programmes serving the interests of individual scientists rather than the industry as a whole, failure of the cross-breds to perform as expected, susceptibility to disease, inadequate funding and a distinct lack of enthusiasm by farmers to make use of the new genetic material. In 2010, only 4 percent of the national sheep population was cross-bred. A major reason for this is the inappropriateness and unadapted nature of the cross-breds to local conditions. Some 90 percent of native Turkish sheep, for example, are fat-tailed types. Native breed are capable of lifting the female tail to mate but foreign thin-tailed rams do not have this ability. On government or university farms handlers are present to assist the foreign thin tails to mate but under small farm conditions the owners are unwilling to do this. Hence, the cross-bred is not the right animal in the right place (Wilson, 2009).

Locally developed species are a pool of irreplaceable genetic material of unacknowledged merit and value that must not be lost but must be conserved for possible unknown and unseen future use (Wilson, 2009). Impoverishment of the nation's natural capital is not acceptable under any circumstances but the modest start of conservation measures by government augurs well for the future and for safeguarding of the country's heritage. Livestock production will not remain sustainable if the nation's gene pool is not fully characterized and preserved for use by future generations who will face as yet unforeseen circumstances.

Turkey is a country that is still on the road of development. Livestock production remains an important economic activity, but its product is inadequate to supply the nutritional requirements of its people. Native sheep are generally of low output but still constitute the vast majority of the national flock. Efforts should continue to characterize and improve their productive traits alongside the use of exotic breeds with possibly and potentially superior productivity but lower adaptability. Government, universities and the mass of livestock producers and ancillary industries should work together to conserve and improve the native sheep breeds of Turkey.

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Appendix: Outline map of Turkey showing locations of Provinces

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Recent Publication

China yellow cattle, culture and industry

Chen Youchun

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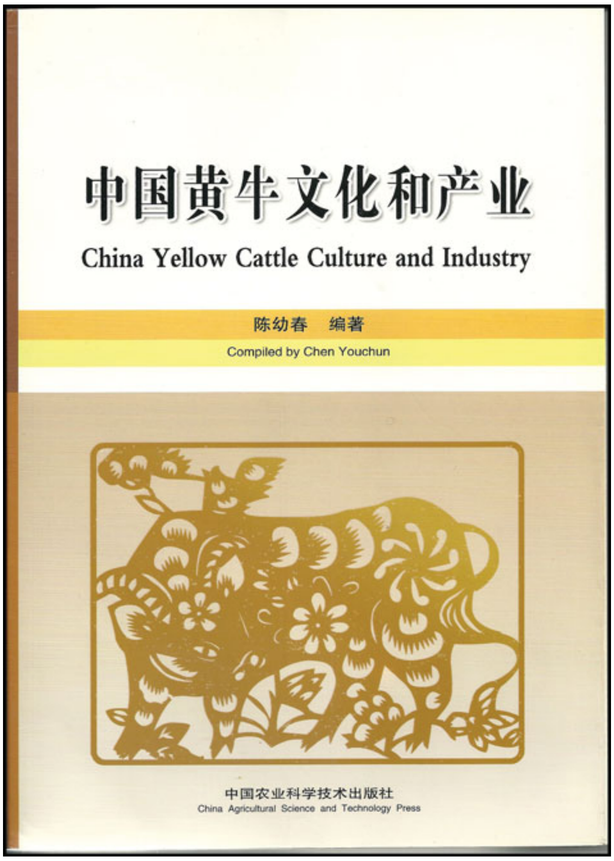

This book brings together a wealth of information on the China Yellow Cattle that is of interest to animal scientists, geneticists, developmental specialists, historians, livestock producers and others engaged in farming. The author provides a scientific narrative drawing particularly upon genetics that shows the Yellow Cattle in the context of history and culture over several millennia, assesses their socio-economic contribution in improving the quality of life and recognizes their essential role in the production of food today. The book is written in parallel with English on one page and Chinese on the opposite page.

The Yellow Cattle of China are not simply one breed, as one might think of the Sahiwal, N'Dama or Charolais. The Yellow Cattle are a broad category embracing numerous distinct breeds that exhibit many different qualities of phenotype, genetic structure, adaptation, meat and milk products and suitability for work. The various types or breeds of Yellow Cattle are scattered throughout the huge landmass of China from high elevation and extensive grassland to temperate crop farming in river plains and semi-tropical lush areas. In each place, they are known by local and regional names. The huge diversity of around 30 breeds within this single genetic group is displayed by the 96 high-quality colour photographs at the end of the book. This attractive feature enlightens the narrative, but should not lead one to conclude that this book follows the pattern of some earlier livestock publications that simply offer classifications of breed by their physical features such as coat colour, ear anatomy, weight and height. The recent discoveries of molecular genetics facilitate new ways of distinguishing different breeds. In this book, results from advanced genetic research are combined with the increasing knowledge of the origins of the Yellow Cattle from history, art, culture and archaeology. Thus, the author brings together information from ancient and new sources to provide a fresh understanding of the genetic structure of the breeds, both within the Yellow Cattle group and by comparison with other species including Bali cattle, yak, water buffalo and wild relatives such as the mithun and banteng. The book explores the different contributions made by *Bos taurus* and *Bos indicus* to the Yellow Cattle, resulting in variations in hump and adaptation. The *B. taurus* influence is greater in the northern high-elevation regions, while the *B. indicus* type is more evident in the south of China. The author uses phylogenetic trees to explain these relationships. Various parameters now being used in molecular genetic analyses are employed to measure genetic relationships between the breeds in the Yellow Cattle group, and these are portrayed using dendrograms.

In addition to the wealth of detail described above, the book gives the reader a valuable overall picture of what is happening in livestock production in China today. The author considers there have been three great periods in Chinese history during which the Yellow Cattle have passed through change and development. The first two were the Qin–Han Dynasty and the Tang–Song Dynasty. He considers that the present period of the Peoples Republic of China is the third such period. In the last 50 years, China has moved and continues to move from an agrarian to an industrial society. Yet the process is far from complete and millions of Chinese citizens live in rural areas where agriculture and livestock production are central to their economic welfare and quality of life. Although pigs and poultry are the most numerous domestic animal species in China, the Yellow Cattle are an extremely important structural resource for the countryside. They contribute substantially as work animals in fields and for transport. In cropping areas they are part of integrated mixed small-scale farming where they consume arable by-products and build soil fertility. They are vital for the livelihoods of pastoralists and for the management of extensive grasslands and mountain rangelands up to about 3000 m, above which yak are better adapted.

Apart from the cattle found in Tibet and associated mountainous areas, the author broadly classifies the Yellow Cattle breeds into three types found in three distinct regions. These are the Northern Pastures, Central Regions with more cultivated land and the Southern Region. The Yellow Cattle have always been multipurpose – for work, meat and milk – although some breeds are valued more for one or other of these functions. The rapid development of cities with an increasing demand for milk is resulting in greater use of the Holstein–Friesian, especially in large and often intensively managed systems. Some specialized beef breeds from Europe are also found, usually under more intensive management. The author has no doubt that, despite the huge socio-economic revolution taking place in China today, the Yellow Cattle continue to have a vital and important place in the Chinese economy and way of life, evident from the fact that 78 percent of all cattle in China today are found in herds of five animals or fewer, indicating the value of the Yellow Cattle for the family farm. The current great global debates about migration from rural to urban civilization and feeding the world leave no doubt in the minds of thinking people that cattle, as herbivores able to use vegetation instead of grain, are guaranteed as vital a role in the future of mankind as they have had in the past. The China Yellow Cattle are an essential resource for millions of small-scale Chinese farmers and they deserve the recognition that is given in this book.

Animal Genetic Resources, 2013, 52, 167. © Food and Agriculture Organization of the United Nations, 2013
doi:10.1017/S2078633613000167

Recent Publication

Zelena knjiga izvornih pasmina Hrvatske / Green book of indigenous breeds of Croatia

Z. Barać, L. Bedrica, M. Čačić, M. Dražić, M. Dadić, M. Ernoić, M. Fury, Š. Horvath, A. Ivanković, Z. Janječić, J. Jeremić, N. Kezić, D. Marković, B. Mioč, R. Ozimec, D. Petanjek, F. Poljak, Z. Prpić and M. Sindičić
Ministry of Environmental and Nature Protection, State Institute for Nature Protection, Croatian Agricultural Agency, Krka National Park, COAST, Republic of Croatia
Published in 2011, pp. 388
ISBN 978-953-7169-88-6

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zelena knjiga
IZVORNIH
PASMINA
Hrvatske/
GREEN BOOK OF INDIGENOUS
BREEDS OF CROATIA

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Državni zavod za zaštitu prirode/
State Institute for Nature Protection

Ministarstvo zaštite okoliša i prirode/
Ministry of Environmental
and Nature Protection

HPA Hrvatska poljoprivredna agencija/
Croatian Agricultural Agency

REPUBLIKA HRVATSKA/ REPUBLIC OF CROATIA 2011.

This book begins with a substantial bilingual (Croatian and English) introductory section covering the history of livestock domestication; the development of agriculture in Croatia; livestock breeding and the use of Croatia's traditional breeds; the influence of traditional breeds on the country's environment, landscape, habitats and biodiversity; a list of indigenous breeds; methods used in estimating risk status; the legislative and institutional framework for the management of Croatia's animal genetic resources; the conservation of indigenous breeds as part of nature conservation in Croatia; and threats facing the country's livestock breeds. The latter part of the book, written in Croatian, consists of a catalogue of Croatia's indigenous breeds, and features chapters on horses, donkeys, cattle, sheep, goats, pigs, dogs, poultry and bees. A further chapter is devoted to extinct and "data deficient" breeds. Each breed description features the breed's risk-status category according to various classifications, along with descriptions of its origin, cultural-historical importance, ecology, characteristics, population and current significance. Also included are descriptions of the threats facing the breed, legal measures in place to protect it and proposed conservation measures. The book is illustrated throughout with colour photographs of Croatian livestock, mostly in their home production environments, along with a number of historical photographs and other images.

Animal Genetic Resources, 2013, 52, 168. © Food and Agriculture Organization of the United Nations, 2013
doi:10.1017/S2078633613000179

Recent Publication

Sustainable management of globally significant endemic ruminant livestock in West Africa: estimates of livestock demographic parameters in Mali

M. Ejlertsen, J. Poole and K. Marshall
International Livestock Research Institute (ILRI)
Published in 2012, pp. 35
ISBN 92-9146-282-9
Available at http://mahider.ilri.org/bitstream/handle/10568/25060/ilriResearchReport_31.pdf?sequence=2

doi:10.1017/S2078633613000179

This report describes the results of a 12-month retrospective survey for estimating livestock demographic parameters (including parturition, prolificacy and mortality rates, as well as replacement rates) of endemic ruminant livestock kept by smallholders at selected sites in Mali. The study covered cattle, goats and sheep, the majority of which belonged, respectively, to the N'Dama, West African Dwarf and Djallonke breeds. It was carried out as one of several baseline surveys under the PROGEBE-Mali project (PROGEBE = Regional Project on Sustainable Management of Endemic Ruminant Livestock in West Africa). The objectives of the study were to estimate demographic parameters for herds/flocks at the PROGEBE-Mali project sites, which combined with other information sources, could be used for prioritizing project interventions, to compare demographic productive parameters between endemic ruminant livestock and non-endemic animals, and to provide a baseline for evaluating the effects of project interventions. The second of these objectives could not be met because very few non-endemic animals were present at the study locations. The report describes the background of the study, the methods used and the results obtained. It offers recommendations for the future work of the PROGEBE project.

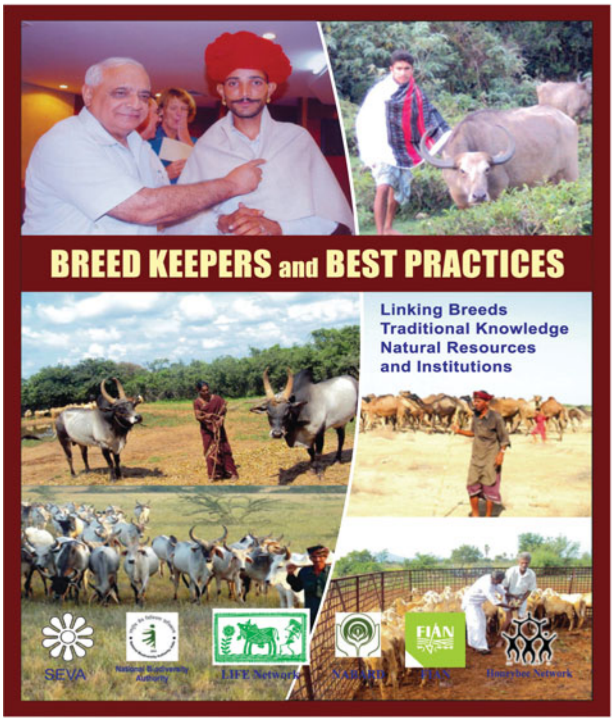
Animal Genetic Resources, 2013, 52, 169. © Food and Agriculture Organization of the United Nations, 2013
doi:10.1017/S2078633613000180

Recent Publication

Breed keepers and best practices. Linking breeds, natural resources, indigenous knowledge and institutions

Edited by P. Vivekanandan
Sustainable-Agriculture & Environmental Voluntary Action (SEVA)
Published in 2012, pp. 167

doi:10.1017/S2078633613000180



This publication describes the efforts of livestock keepers and grassroots NGOs in India to maintain and utilize locally adapted livestock breeds and the knowledge and practices associated with them. A short introduction describes a context in which India’s locally adapted breeds are threatened by a number of factors including loss of access to grazing lands and loss of traditional knowledge about livestock keeping and government policies that promote the use of exotic breeds and cross-breeds. The next section presents the “breed keepers” – 50 case studies focusing on the work of individual livestock keepers who have contributed to the conservation and development of breeds in their local areas. Each case study includes a description of the livestock keeper’s family background, followed by a description of his or her livestock conservation and/or breeding activities. A number of case studies include descriptions of traditional practices such as those used to treat animals when they are sick. More information on traditional practices is provided in the next section of the publication, which is entitled “Best practices”. Five case studies present information on, *inter alia*, treatments for bluetongue in sheep, herbal dewormers and treatments for infertility in cows. The next set of case studies focuses on the use of grazing lands, access rights to such resources and strategies for managing them sustainably. This is followed by a final set of case studies focusing on local initiatives undertaken by gaushalas (cow shelters), NGOs and breeders’ associations to conserve locally adapted breeds.

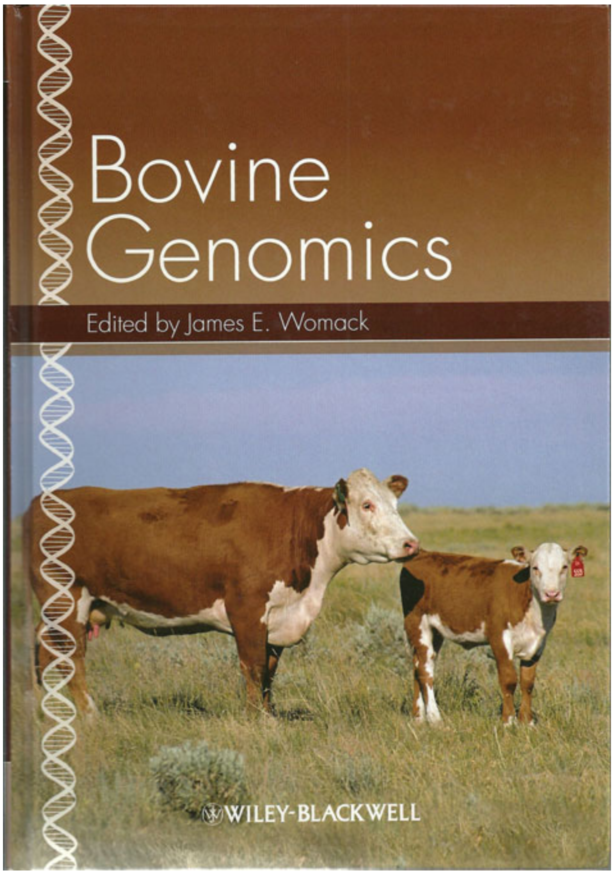
Animal Genetic Resources, 2013, 52, 170–171. © Food and Agriculture Organization of the United Nations, 2013
doi:10.1017/S2078633613000192

Recent Publication

Bovine genomics

Edited by J. E. Womack
Wiley-Blackwell, UK
Published in 2012, pp. 271
ISBN 978-0-8138-2122-1 (hardcover)

doi:10.1017/S2078633613000192



This is an excellent book. Why? First, because it comprehensively covers the whole topic of bovine genomics, which is a new scientific discipline that has grown rapidly in a few years. The book documents the new information. Second, each chapter is well written by a specialist and covers a precise aspect of the topic; and the book has been shaped and edited by one from the group of pioneers who originally defined the field of bovine genomics and who has spent the years since then as an active researcher. The book is solid and trustworthy and avoids wandering into attractive by-paths such as the application of the new knowledge to cattle breeding which, although important and relevant for the future, is a specialist topic of its own. So, the book focuses directly and competently on the exciting new scientific discoveries of the last couple of decades about the structure, function and nature of the molecular genome of bovines. The book is ideal for the reader who wants a clear statement, perhaps even a revelation, of what is now known.

Genomics is the scientific study of all the hereditary material of an organism or a species at the molecular level. The concept of genomics, although not the name, was visualised by some early pioneers of genetics early in the twentieth century when Mendel's discovery of discrete hereditary particles was integrated into a mathematical understanding of genetics. However, progress to the point of actually being able to study the structure, mechanism and behaviour of the molecules of heredity is new and has become possible in recent years because of new microtechniques in the laboratory and an improved understanding of biochemistry. In the process, the study of heredity has added population genetics, quantitative genetics, BLUP and QTL mapping, and has now arrived at the study of the molecules of the genome. Genomics research operates in highly specialized territory with innovative analytical methods and instrumentation allied to computers, and is embellished by new terminology. Genomics research is in progress in many species. However, documenting the genomes of farm animal species is a special category, as these mammalian genomes are complex and the perceived applications of genomics in improving animal production are great. Consortia have therefore been set up to address the genomes of each of the principal livestock species. This book is concerned with the bovine genome, and some of the leaders of the global consortium studying the bovine genome have contributed chapters. Although the scientists engaged in this research are physically scattered in laboratories in many parts of the world, the internet enables them to remain in constant contact with each other. By self-identification they are a relatively small scientific group, and they are bound to each other by this instant communication system and are constantly briefed on each stage of progress. While this situation has many advantages for promoting research in a rapidly moving field, the outsider, scientist or not, often experiences difficulty in keeping up-to-date. This book provides the answer.

To understand this new field, two major components need to be considered. First, one needs to keep up, in general, with the new science of genomics, which is exploring the frontiers of knowledge about life in any species, with the result that new concepts, assumptions and hypotheses are frequently created and, using an expanded vocabulary, are built into the models depicting genomes. With each individual species, there is the second level of knowledge concerning specific genes, fine-scale mapping, gene expression, the proteins involved and the control mechanisms that trigger or inhibit expression. Of course, constant updates could be gained by regular and systematic tracking of the scientific journals dedicated to this topic. However, this approach provides one with a collection of disparate papers from which a coherent understanding has to be synthesized – a much easier task when one is actually engaged in some aspect of the research as a daily occupation. The authors and editor of this book provide this synthesis for the reader, along with extensive references.

The value of the book is that it covers the historic development of genomics, especially as applied to livestock, places it within the meta-narrative of heredity, explains the concept of bovine genetics, mentions the analytical methods, and gives chapters that deal with specialised topics within the bovine genome – even to the extent, in some chapters, of listing arrays of genes and their known functions. I know of no other book that so competently brings the reader into the fold of understanding the molecular inheritance of cattle. The inevitable proviso is that specialist chapters have a limited half-life. The book will need updating.

For an overview of the whole subject, the reader is indebted to two of the authors: Morris Soller and James Womack, the latter also being the book editor. Morris Soller has written what he calls: “From quantitative genetics to quantitative genomics: a personal odyssey”. This chapter provides a timeline of progress in animal genetics over the last 60 years, during which Morris Soller has given and continues to give a lifetime of service to research and teaching. Early in his career he was one of the few to see that livestock selection as then practised was valuable but limited and he looked forward to a time when tools and knowledge would be available to map the genome at the molecular level. His personal memories provide an honest and exciting narrative that at times reads like a thriller with many twists and turns, nevertheless offering a clear account of the journey to the present. James Womack writes on “The cartography of the bovine genome” and provides the reader with the descriptions and conceptual tools needed by the explorer wishing to navigate the newly discovered bovine genome.

The other more specialized chapters are all valuable and well written, although the depth of detail varies. These are the chapter titles: Origins of cattle as documented by molecular studies; Mendelian inheritance; Genetics of coat colour; History of linkage mapping; X & Y chromosomes; Comparative genomics and chromosomal evolution; Sequencing the bovine genome; Genome architecture; Epigenetics and epigenomics; Quantitative trait loci; Genome-wide association studies and linkage disequilibrium; Genomic selection; Identification of genes and variants.

This is an excellent book for the busy specialist and the livestock generalist wanting an authentic account of what is happening in the science of the heredity of cattle.

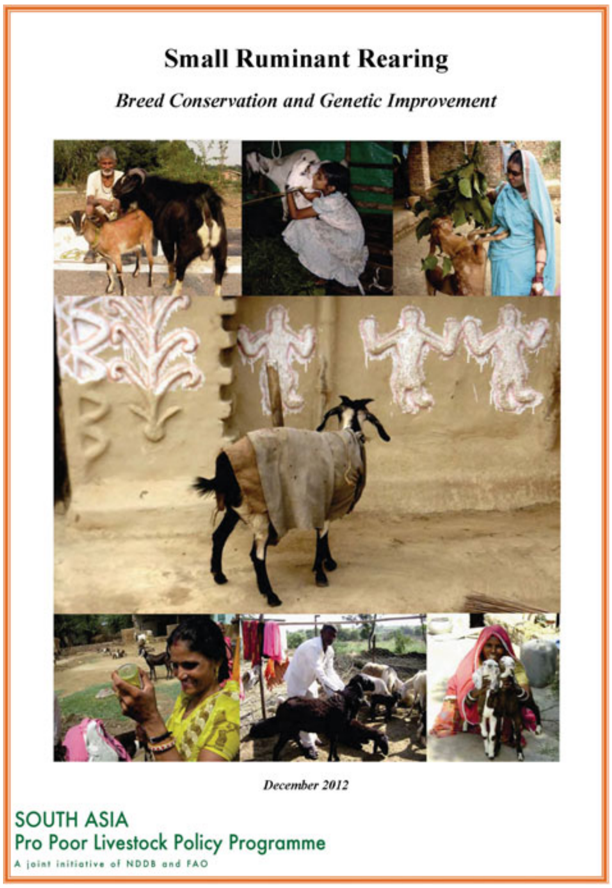
Animal Genetic Resources, 2013, 52, 172. © Food and Agriculture Organization of the United Nations, 2013
doi:10.1017/S2078633613000209

Recent Publication

Small ruminant rearing: breed conservation and genetic improvement

C. Nimbkar and P. Ghalsasi
South Asia Pro Poor Livestock Policy Programme
Published in 2012, pp. 69
Available at http://sapplpp.org/goodpractices/smallruminants/small-ruminant-rearing-breed-conservation-and-genetic-improvement

doi:10.1017/S2078633613000209



This report documents approaches, interventions and good practices related to small ruminant breed conservation and improvement in India and their impacts on the livelihoods of smallholder livestock keepers. It describes major small ruminant breeding and conservation interventions undertaken during the past 30 years and presents a comparative assessment of small ruminant breed populations in the country. It ends by summarizing the impact of breed conservation and improvement interventions in India and identifying policy actions that need to be taken to help secure sustainable livelihoods for small ruminant keepers and facilitating their participation in the expanding market for small ruminants.

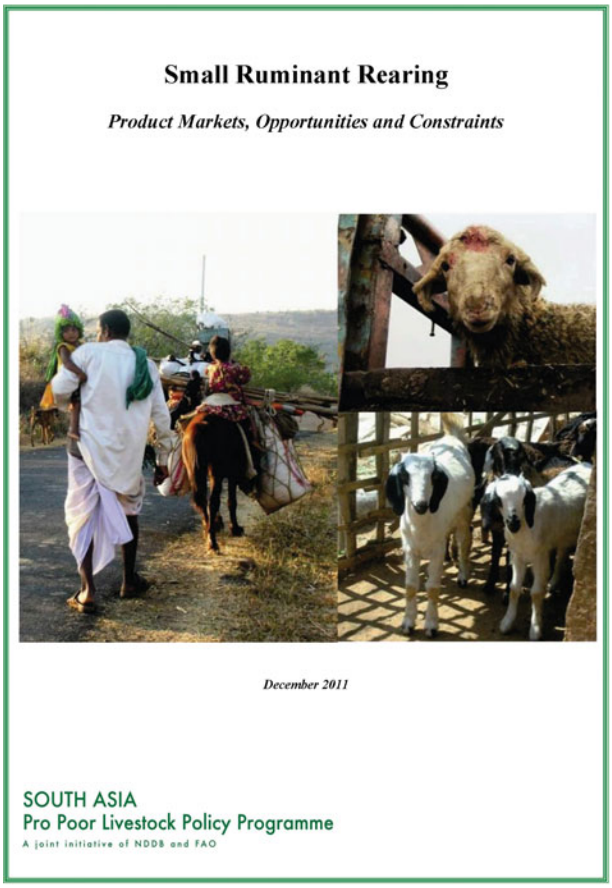
Animal Genetic Resources, 2013, 52, 173. © Food and Agriculture Organization of the United Nations, 2013
doi:10.1017/S2078633613000210

Recent Publication

Small ruminant rearing: product markets, opportunities and constraints

V. Mehta
South Asia Pro Poor Livestock Policy Programme
Published in 2011, pp. 66
Available at http://bit.ly/wAJL44

doi:10.1017/S2078633613000210



This report presents the outputs of a study that aimed to document and analyse small ruminant marketing in India and to identify opportunities for facilitating the access of smallholder livestock keepers to more remunerative markets. The report seeks to place the economic context of small ruminant rearing within broader policy and institutional frameworks. It documents some approaches and practices in small-ruminant production submitted in response to a call by the South Asia Pro Poor Livestock Policy Programme. Following a short overview of the small ruminant sector in India (distribution of animals by state and by size of landholding, etc.), the report discusses first the meat sector and then the leather and wool sectors, describing the main characteristics of the marketing chains in each sector. Issues highlighted among the conclusions and recommendations are, for the meat sector, a lack of organization in the marketing chain, a lack of value addition in the marketing chain, and a generally inefficient use of by-products; for the leather sector, problems with the availability and quality of raw materials reaching manufacturers; and for the wool sector, loss of grazing lands, declining flock sizes, rising costs and shrinking markets. Cross-breeding with exotic breeds in the wool sector is reported to have run into problems, *inter alia*, because the cross-bred animals have been unable to withstand the nutritional stress and difficult terrain associated with local production environments.

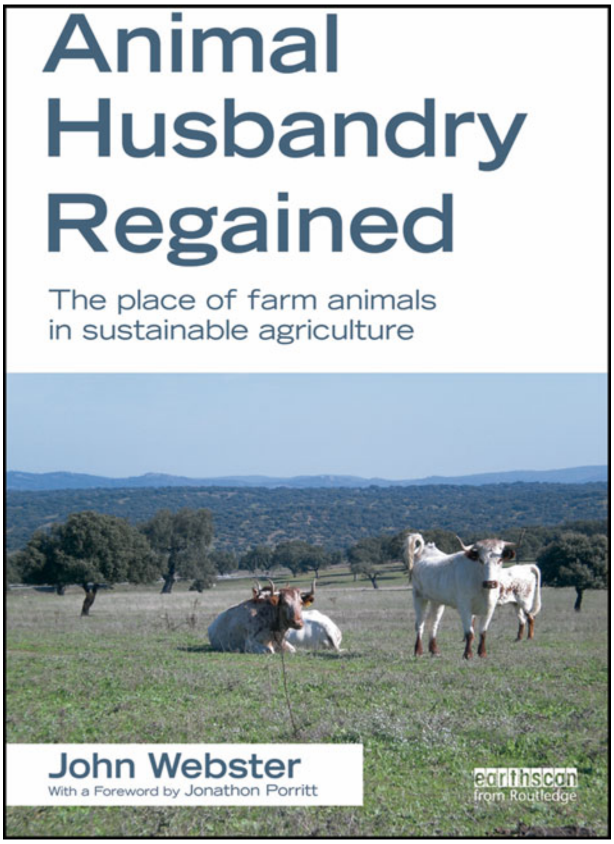
Animal Genetic Resources, 2013, 52, 174. © Food and Agriculture Organization of the United Nations, 2013
doi:10.1017/S2078633613000222

Recent Publication

Animal husbandry regained. The place of farm animals in sustainable agriculture

J. Webster
Earthscan from Routledge
Published in 2013, pp. 243
ISBN 978-1-84971-421-1

doi:10.1017/S2078633613000222



This book aims to describe ways in which the influence of livestock production on animal welfare and the environment can be improved. It is divided into two parts. The first, "Engaging with the problems", introduces the principles and arguments that the author regards as the basis for dealing with the challenges facing animal agriculture. The second, "Embarking on solutions", presents some practical proposals for the future. Part 1 features a chapter on the question of "audits of animals in agriculture", which starts with the question of animals' efficiency in converting metabolizable energy into food, and then adds additional layers of complexity by discussing, *inter alia*, the efficiency in the use of protein, lifecycle analysis (in terms of energy and water use and methane production), carbon sequestration in grasslands and the roles of grazing animals in grassland conservation. This is followed by a chapter on animal welfare and health, and another on the role of food from animals in the human diet. The final chapter of Part 1 considers animal husbandry from the perspectives of philosophy, economics and politics. Part 2 begins with a chapter on "Better, kinder food", which discusses potential means of improving the welfare of a range of livestock species in a range of production systems. Next comes a review of the prospects for improving animal husbandry through science and technology – nutrition, breeding and reproduction and animal health (including the genetics of disease resistance) and the science of animal welfare. A chapter on "planet husbandry" discusses potential means both of reducing the negative effects of livestock production on the environment and of increasing positive contributions such the roles of grazing animals in maintaining wildlife habitats and more general stewardship of the countryside. The final chapter explores the mechanisms through which the ideas discussed in the preceding chapters might be realized. This includes another dip into philosophy (featuring an unusual "pig's eye" assessment of human behaviour and human–animal relations), followed by discussions of the roles of awareness, understanding, education and propaganda in influencing the development of the livestock sector, the significance of quality assurance schemes and the potential of collective action – legislation (prescriptive laws and incentives) and so-called "politics by other means" (referring largely to pressure exerted by consumers via the market).

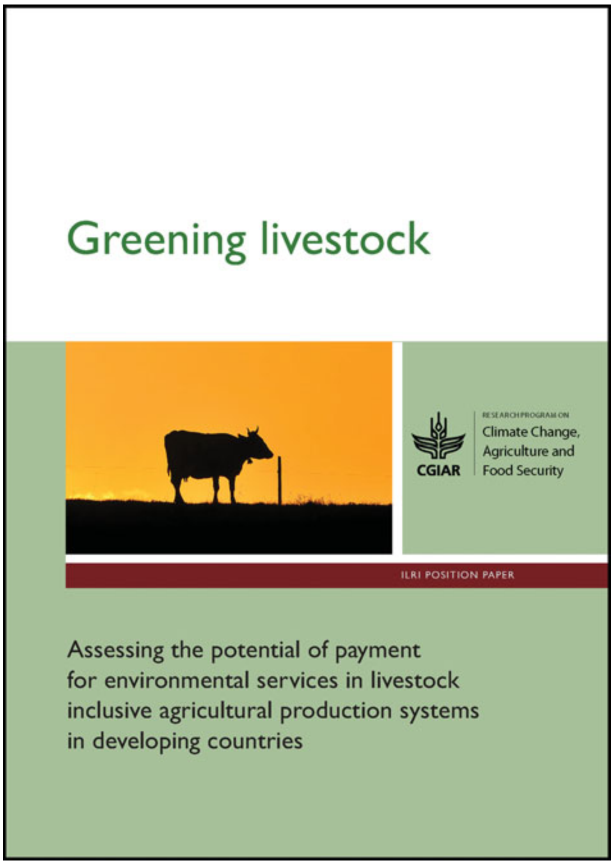
Animal Genetic Resources, 2013, 52, 175. © Food and Agriculture Organization of the United Nations, 2013
doi:10.1017/S2078633613000234

Recent Publication

Greening livestock: assessing the potential of payment for environmental services in livestock inclusive agricultural production systems in developing countries

S. Silvestri, Osano, J. de Leeuw, M. Herrero, P. Ericksen,
J. Kariuki, J. Njuki, C. Bedelian and A. Notenbaert
International Livestock Research Institute (ILRI)
Published in 2012, pp. 55
ISBN 92-9146-283-7
Available at http://cgspace.cgiar.org/bitstream/handle/10568/21188/GreeningLivestock.pdf?sequence=6

doi:10.1017/S2078633613000234



The subject matter of this ILRI Position Paper is clear from the title. It begins with a short introduction to the various environmental services and disservices (grouped according to whether they relate to soil, water, biodiversity or "landscape and air") that are associated with various livestock production systems. Next comes an overview of institutional arrangements in payment for environmental services (PES) schemes. The application of PES schemes in the livestock sector is then discussed, focusing on three types of service: climate regulation; watershed and hydrological services; and biodiversity conservation. Each is described via an introduction to the problem that needs to be addressed, an assessment of the extent of "demand" for the service, a description of how and by whom the service is or could be provided, and a discussion of existing or potential PES schemes related to the service. Enabling factors and constraints (legislation, property rights and land tenure regimes) affecting the implementation of PES schemes are then discussed. This is followed by a discussion of equity issues in PES schemes. Finally, a set of recommendations are presented along with a list of knowledge gaps that need to be addressed through further research. Among these knowledge gaps is the answer to the question "What are the opportunities of using PES to conserve animal genetic resources (AnGR) in the context of the agro-biodiversity conservation?" The significant potential of PES schemes as a means of promoting crop and livestock diversity – so-called payments for agro-biodiversity conservation services or PACS – is noted in the section on biodiversity conservation. Such schemes are reported to be currently limited to crops, but their application in the management of livestock genetic resources is noted as a potentially promising area for the future.

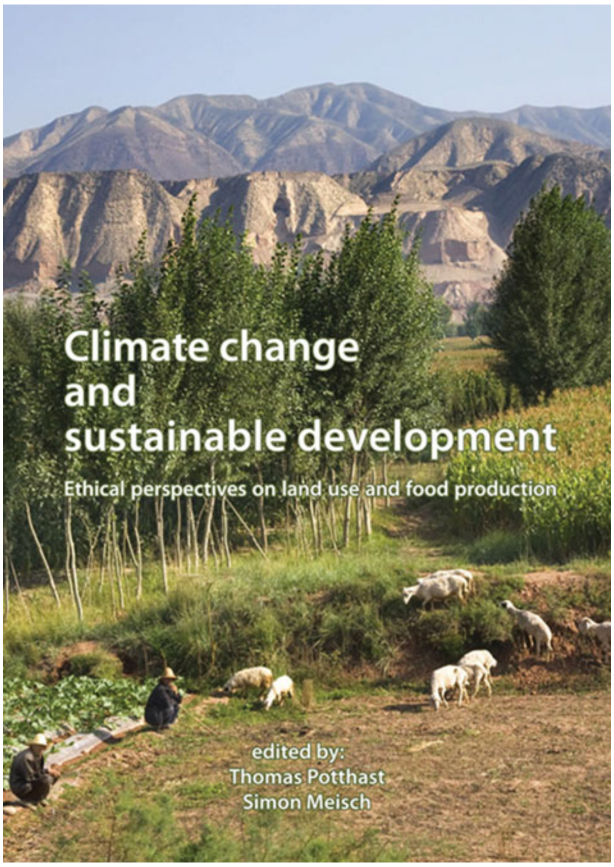
Animal Genetic Resources, 2013, 52, 176. © Food and Agriculture Organization of the United Nations, 2013
doi:10.1017/S2078633613000246

Recent Publication

Climate change and sustainable development: ethical perspectives on land use and food production

Edited by T. Potthast & S. Meisch
Wageningen Academic Publishers
Published in 2012, pp. 526
ISBN 978-90-8686-197-2
e-ISBN 987-90-8686-753-0

doi:10.1017/S2078633613000246



This book brings together about 80 papers from the EurSAFE (European Society for Agricultural and Food Ethics) 2012 Congress. The themes of climate change, sustainable development, ethics, land use and food production give plenty of scope for a wide range of papers. Animals – and livestock in particular – feature quite prominently, but there is little specific mention of animal genetic resources and their management, although a paper presenting an “ethically sound vision for the future” of agriculture and food production discusses the need to breed for animals that are suitable for use in such ethical (in animal welfare, environmental and social terms) agricultural systems. The section on biotechnology includes a short paper on the implementation of ethical standards in a cattle improvement company (the descriptions suggest that the standards relate more to questions of animal welfare, the use of biotechnologies and zoosanitary matters than to the question of ensuring the sustainable use or conservation of genetic resources). A section on “intensive versus extensive production” comprises eight papers all focusing on the livestock sector and its relationship to animal welfare, production efficiency and the environment. Another whole section is dedicated to the subject of “animal ethics”, focusing for the most part on the theoretical foundations for animal welfare debates, with some papers addressing changing attitudes to animals and animal welfare associated with socio-economic and cultural changes.

Livestock also feature heavily in the section on climate change adaptation and mitigation, which includes a paper on the question of a climate tax on meat and another that takes the question of adapting ruminant nutrition as a basis for a discussion of decision-making strategies in a context of uncertainty. Other sections of the book address, *inter alia*, property rights and the commons, non-agricultural land management, agro-energy, food policy, fisheries, science and governance, and ethics education.

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