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ANIMAL GENETIC RESOURCES

an international journal

RESSOURCES GÉNÉTIQUES ANIMALES

un journal international

RECURSOS GENÉTICOS ANIMALES

una revista internacional

2011-2020
United Nations Decade on Biodiversity

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ANIMAL GENETIC RESOURCES • RESSOURCES GÉNÉTIQUES ANIMALES • RECURSOS GENÉTICOS ANIMALES
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ANIMAL GENETIC RESOURCES

RESSOURCES GÉNÉTIQUES ANIMALES

RECURSOS GENÉTICOS ANIMALES

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Animal Genetic Resources is an international journal published under the auspices of the Animal Genetic Resources Branch of the Animal Production and Health Division, Food and Agriculture Organization of the United Nations (FAO).

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Recursos genéticos animales es una revista internacional publicada bajo los auspicios de la Subdivisión de los Recursos Genéticos Animales de la División de Producción y Sanidad Animal, la Organización de las Naciones Unidas para la Alimentación y la Agricultura (FAO).

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Online edition: Cambridge University Press online platform at www.journals.cambridge.org/agr. Please visit the homepage to access the fully searchable text with reference linking and also to submit your paper electronically. The electronic version is also available in the library of the Domestic Animal Information System – DAD-IS at www.fao.org/dad-is.

Édition en ligne: Plateforme virtuelle de «Cambridge University Press» accessible sur www.journals.cambridge.org/agr. Veuillez consulter la page d'accueil pour accéder aux textes qui contiennent des liens de référence et dont tout le contenu peut être recherché; ainsi que pour soumettre vos articles par voie électronique. La version électronique est aussi disponible dans la bibliothèque du Système d'information sur la diversité des animaux domestiques, DAD-IS accessible sur www.fao.org/dad-is.

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Editorial

Animal Genetic Resources celebrates its fiftieth volume

More than 400 papers were published in 50 volumes of *Animal Genetic Resources* over a period of nearly 30 years. The journal began in 1983 as *Animal Genetic Resources Information* and was renamed *Animal Genetic Resources* in 2010 – the International Year of Biodiversity. The journal was launched and initially published by the Food and Agriculture Organization of the United Nations (FAO) and the United Nations Environment Programme (UNEP) "with the aim of facilitating the spread of knowledge on animal genetic resources". Since 2009, FAO publishes the journal jointly with Cambridge University Press. Since mid 2011, papers have been published on the Cambridge University Press web site about eight weeks after they have been accepted (*FirstView*) independently of the completion of the next print volume. This allows readers to access newly published papers earlier.

The editors endeavor to publish the journal regularly twice a year in June and December, and increasingly encourage submission of high-quality papers with the aim of being indexed in Thomson Reuters Journal Citation Reports, which would include the journal's *Impact Factor*.

The original aim of the journal still remains valid but the objectives became more structured in 2007 following the adoption of the first internationally agreed framework for the management of animal genetic resources for food and agriculture – the *Global Plan of Action for Animal Genetic Resources*.[1] Papers are published related to the four strategic priority areas of the Global Plan: 1. Characterization, inventory and monitoring of trends and associated risks; 2. Sustainable use and development; 3. Conservation; and 4. Policies, institutions and capacity-building. *Animal Genetic Resources* has provided a forum for nearly 1 000 authors from 81 countries (see figure 1).

Animal Genetic Resources is a trilingual journal. Main papers are published in English, French or Spanish, with a summary in all three languages. Papers have mainly been published in English (77%) with the remaining papers divided equally between Spanish (12%) and French (11%). In the period from July 2009 to February 2012, 109 manuscripts were submitted of which 25 were rejected.

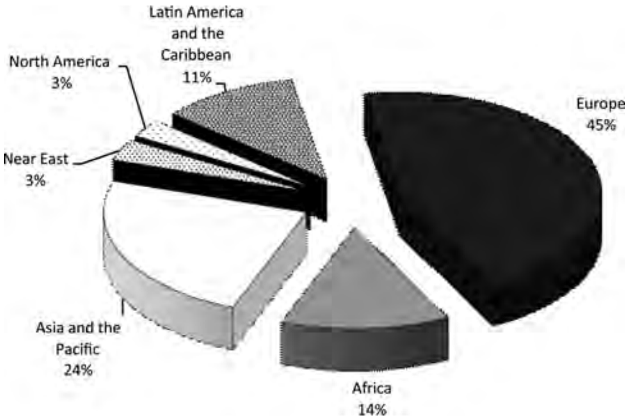

Figure 1. Regional distribution of authors

An analysis of more than 400 papers reveals that the majority focused on large ruminants (38% of the papers), followed by small ruminants (33%), poultry and mini livestock (13%), equines (8%), pigs (5%) and camelidae (3%). Classifying the papers according to the four strategic priority areas of the Global Plan shows that the majority of papers addressed characterization, inventory and monitoring of trends and associated risks (63%); sustainable use and development (11%); conservation (17%); and policies, institutions and capacity-building (9%). The high percentage of papers falling within the strategic priority area 1 can be explained by the fact that *Animal Genetic Resources* is the main forum for this topic. Competing and high-ranking specialized journals exist particularly for strategic priority areas 2 and 3. This is not the case for strategic priority area 4. However, the number of publications falling within this category is only slowly increasing.

Two special issues of the journal have been produced – *Animal Genetic Resources Information 45*[2] in 2009 dedicated to the International Year of Natural Fibres and *Animal Genetic Resources 47*[3] in 2010 dedicated to the International Year of Biodiversity.

The way in which the journal is accessed by its readers has also changed drastically over the years. The early volumes were printed and physically distributed; today all volumes are accessible online in the FAO document repository[4], in library of the Domestic Animal Diversity Information System[5] and paper by paper on the web site of Cambridge University Press.[6] In addition to individual downloads, 1 700 institutions subscribe to *Animal Genetic Resources* (see figure 2), and 3 200 copies of the journal are printed and distributed to readers in 187 countries (see figure 3). In 2007, a CD-Rom was produced containing

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

[2] http://www.fao.org/docrep/012/i1102t/i1102t00.htm

[3] http://www.fao.org/docrep/013/i1823t/i1823t00.htm

[4] http://www.fao.org/documents/en/search/advanced?%20forward=advanced&%20titleOfJournal=Animal+genetic+resources+information&%20connector=1

[5] http://www.fao.org/dad-is/

[6] http://journals.cambridge.org/action/displayJournal?jid=AGR

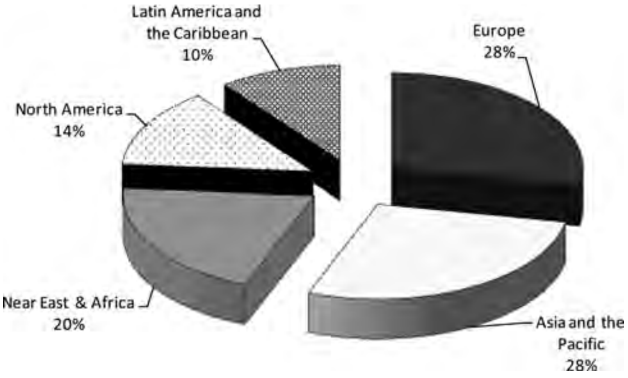

Figure 2. Regional distribution of the readership of *Animal Genetic Resources* (institutional electronic subscriptions)

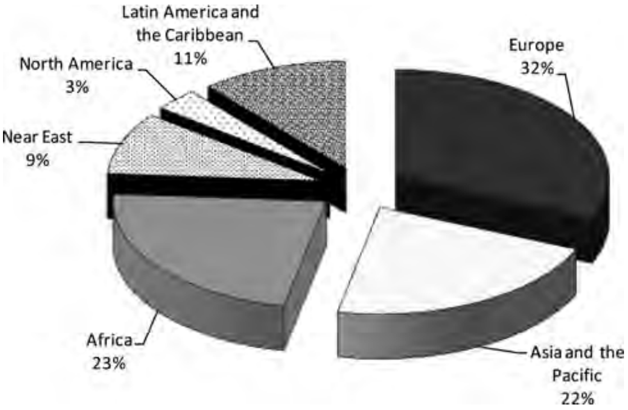

Figure 3. Regional distribution of the readership of *Animal Genetic Resources* (hard-copy subscriptions)

volumes 1 to 41, with a search engine providing easy access to individual papers.

The figures show that printed volumes are still in high demand, particularly in Africa and in Asia and the Pacific. In North America, relatively few individuals are interested in receiving *Animal Genetic Resources* in printed form, but this is compensated by the relatively high institutional electronic subscription rate.

Reporting on the implementation of the Global Plan of Action

Countries, regional networks and international organizations have been asked to report on their implementation of the Global Plan of Action. The questionnaire forms and reports have been published online.[7]

Forthcoming Seventh Session of the Intergovernmental Technical Working Group on Animal Genetic Resources for Food and Agriculture

The Seventh Session of the Intergovernmental Technical Working Group will be held at FAO headquarters in Rome from 24 to 26 October 2012. Issues to be addressed include:

- review of the progress made in the implementation of the Global Plan of Action for Animal Genetic Resources;
- implementation and review of the Funding Strategy for the Implementation of the Global Plan of Action;
- preparation of The Second Report on the State of the World's Animal Genetic Resources for Food and Agriculture; and
- indicators to measure progress made in the implementation of the Global Plan of Action, and the further development of the headline indicator of the Convention on Biological Diversity for trends in genetic diversity of domesticated animal species of major socio-economic importance.

Documentation for this meeting will be uploaded over the coming months to the web site.[8]

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

[8] http://www.fao.org/ag/againfo/programmes/en/genetics/angrvent.html

Animal Genetic Resources, 2012, 50, v–vi. © Food and Agriculture Organization of the United Nations, 2012
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Éditorial

Le journal *Ressources génétiques animales* célèbre son cinquantième volume

Sur une période de presque 30 ans, plus de 400 articles ont été publiés dans 50 volumes de *Ressources génétiques animales.* Le journal a démarré en 1983 sous le nom de *Bulletin d'information sur les ressources génétiques animales* et a été rebaptisé *Ressources génétiques animales* en 2010 – Année internationale de la biodiversité. Le journal a été lancé et initialement publié par l'Organisation des Nations Unies pour l'alimentation et l'agriculture (FAO) et par le Programme des Nations Unies pour l'environnement (PNUE) «dans le but de faciliter la diffusion des connaissances sur les ressources zoogénétiques». Depuis 2009, la FAO publie le journal en collaboration avec Cambridge University Press. Depuis la seconde moitié de 2011, les articles sont publiés sur le site Web de Cambridge Université Press environ huit semaines après leur première acceptation (*FirstView)*, indépendamment de l'achèvement du volume imprimé, ce qui permet aux lecteurs d'accéder plus rapidement aux articles nouvellement publiés.

Les éditeurs s'efforcent de publier le journal régulièrement deux fois par an, aux mois de juin et décembre, et encouragent de plus en plus la présentation d'articles de haute qualité dans le but de l'indexer dans le Thomson Reuters Journal Citation Reports, qui comprend le *facteur d'impact* du journal.

Le but original du journal demeure valable, mais les objectifs sont devenus plus structurés en 2007 suite à l'adoption du premier cadre convenu au niveau international pour la gestion des ressources zoogénétiques pour l'alimentation et l'agriculture – le *Plan d'action mondial pour les ressources zoogénétiques*[1]. Les articles sont publiés selon les quatre domaines prioritaires du Plan d'action: 1. Caractérisation, inventaire et surveillance des tendances et des risques associés; 2. Utilisation durable et mise en valeur; 3. Conservation; et 4. Politiques, institutions et renforcement des capacités. *Ressources génétiques animales* a assuré un forum pour presque 1 000 auteurs de 81 pays (voir figure 1).

Ressources génétiques animales est un journal trilingue. Les articles principaux sont publiés en anglais, en français ou en espagnol, et le résumé est présenté dans les trois langues. Les articles ont été principalement publiés en anglais (77 pour cent), et le restant a été partagé entre l'espagnol (12 pour cent) et le français (11 pour cent). Entre juillet 2009 et février 2012, 109 manuscrits ont été présentés, dont 25 ont été refusés.

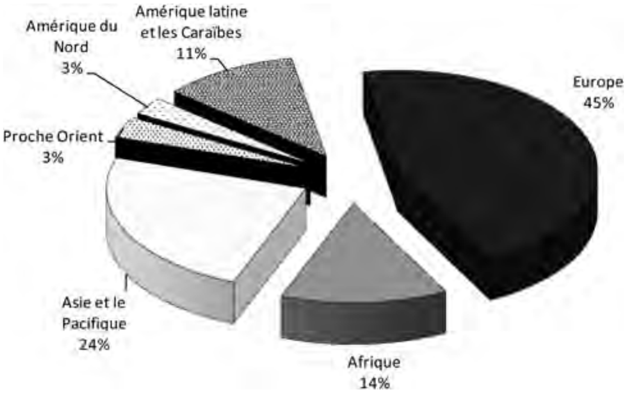

Figure 1. Répartition régionale des auteurs

L'analyse des 400 et plus articles indique que la majorité est concentrée sur les grands ruminants (38 pour cent des articles), suivie par les petits ruminants (33 pour cent), par les volailles et le mini-élevage (13 pour cent), par les équidés (8 pour cent), par les porcs (5 pour cent) et par les camélidés (3 pour cent). Le classement des articles selon les quatre domaines prioritaires du Plan d'action montre que la majorité a abordé la caractérisation, l'inventaire et la surveillance des tendances et des risques associés (63 pour cent); l'utilisation durable et le développement (11 pour cent); la conservation (17 pour cent); et les politiques, les institutions et le renforcement des capacités (9 pour cent). Le pourcentage élevé d'articles qui s'inscrivent dans le domaine prioritaire 1 peut s'expliquer par le fait que *Ressources génétiques animales* représente le forum principal pour cette thématique. D'autres revues spécialisées concurrentielles et haut placées existent surtout pour les domaines prioritaires 2 et 3, mais non pas pour le domaine prioritaire 4. Cependant, le nombre de publications relatives à cette catégorie n'augmente que lentement.

Deux numéros spéciaux du journal ont été produits – *Bulletin d'information sur les ressources génétiques animales 45*[2] en 2009, consacré à l'Année internationale des fibres naturelles, et *Ressources génétiques animales 47*[3] en 2010 consacré à l'Année internationale de la biodiversité.

La façon d'accéder au journal de la part de ses lecteurs a aussi évolué radicalement au fil des années. Les premiers volumes étaient imprimés et matériellement distribués; aujourd'hui, tous les volumes sont accessibles en ligne dans les archives de documents de la FAO[4], dans la bibliothèque du Système d'information sur

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[1] www.fao.org/docrep/010/a1404f/a1404f00.htm

[2] http://www.fao.org/docrep/012/i1102t/i1102t00.htm

[3] http://www.fao.org/docrep/013/i1823t/i1823t00.htm

[4] http://www.fao.org/documents/en/search/advanced?%20forward=advanced&%20titleOfJournal=Animal+genetic+resources+information&%20connector=1

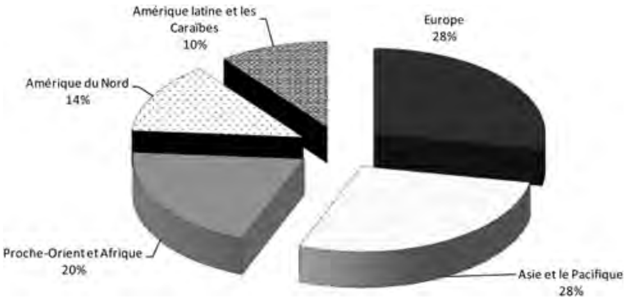

Figure 2. Répartition régionale des lecteurs de *Ressources génétiques animales* (abonnements électroniques des institutions)

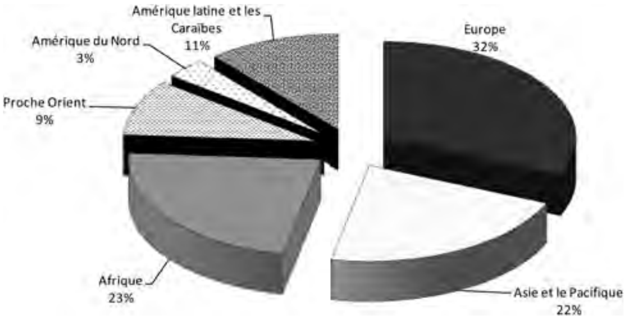

Figure 3. Répartition régionale des lecteurs de *Ressources génétiques animales* (abonnements à la version papier)

la diversité des animaux domestiques[5] et, par article, sur le site Web de Cambridge University Press.[6] Outre les téléchargements individuels, 1 700 institutions sont abonnées à *Ressources génétiques animales* (voir figure 2) et 3 200 copies du journal sont imprimées et distribuées aux lecteurs de 187 pays (voir figure 3). En 2007, on a produit un CD-Rom qui contenait les volumes 1 à 41 et un moteur de recherche fournissant un accès facile aux articles.

Les chiffres indiquent que les volumes imprimés sont encore très demandés, surtout en Afrique et dans la région Asie et le Pacifique. En Amérique du Nord, un nombre relativement faible de particuliers sont intéressés à recevoir la version papier de *Ressources génétiques animales*, ce qui est compensé par un taux relativement élevé d'abonnements électroniques des institutions.

Établissement de rapports sur la mise en œuvre du Plan d'action mondial

Il a été demandé aux pays, aux réseaux régionaux et aux organisations internationales d'établir des rapports sur leur mise en œuvre du Plan d'action mondial. Les formulaires des questionnaires et les rapports ont été publiés en ligne.[7]

Septième session du Groupe de travail technique intergouvernemental sur les ressources zoogénétiques pour l'alimentation et l'agriculture

La septième session du Groupe de travail technique intergouvernemental se tiendra à Rome au siège de la FAO du 24 au 26 octobre 2012. Les sujets qui seront abordés comprennent:

- l'examen des progrès accomplis dans la mise en œuvre du Plan d'action mondial pour les ressources zoogénétiques;
- la mise en œuvre et la révision de la Stratégie de financement pour la mise en application du Plan d'action mondial;
- la préparation du Deuxième Rapport sur l'état des ressources zoogénétiques pour l'alimentation et l'agriculture dans le monde; et
- les indicateurs pour mesurer les progrès accomplis dans la mise en œuvre du Plan d'action mondial, et la poursuite du développement de l'indicateur principal de la Convention sur la diversité biologique de l'évolution de la diversité génétique des espèces animales domestiquées d'importance socio-économique majeure.

La documentation pour cette réunion sera mise en ligne dans le site Web au cours du mois prochain.[8]

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[5] http://www.fao.org/dad-is/

[6] http://journals.cambridge.org/action/displayJournal?jid=AGR

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

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Editorial

Recursos Genéticos Animales celebra su quincuagésimo volumen

Se han publicado más de 400 artículos en 50 volúmenes de *Recursos Genéticos Animales* a lo largo de cerca de 30 años. La revista se comenzó a editar en 1983 como *Boletín de Información sobre Recursos Genéticos Animales*, pasando a llamarse, posteriormente, *Recursos Genéticos Animales*, en 2010, el Año Internacional de la Biodiversidad. Dicha revista se puso en marcha y fue publicada, inicialmente por la Organización de las Naciones Unidas para la Alimentación y la Agricultura (FAO, por sus siglas en inglés) y el Programa de las Naciones Unidas para el Medio Ambiente (PNUMA), "con el propósito de facilitar la difusión de conocimientos acerca de los recursos zoogenéticos". Desde 2009, la FAO publica la revista de forma conjunta con el servicio de publicaciones de la Universidad de Cambridge. Desde mediados de 2011, los trabajos son publicados en el sitio web del servicio de publicaciones de la Universidad de Cambridge unas ocho semanas después de haber sido aceptados *(FirstView)*, independientemente de la finalización del siguiente volumen impreso. Esto permite a los lectores tener acceso a los trabajos publicados con más antelación.

Los editores se esfuerzan por publicar la revista de forma regular dos veces al año, en junio y en diciembre, y animan a la presentación de trabajos de alta calidad con objeto de poder indexarla en *Thomson Reuters Citation Reports Journal*, que incluiría el Índice de Impacto de la revista.

El objetivo inicial de la revista sigue siendo el mismo, con la diferencia de que estos objetivos se estructuraron mejor en 2007, tras la aprobación del primer marco de trabajo internacional para la gestión de los recursos zoogenéticos para la alimentación y la agricultura – el Plan de Acción Mundial sobre los Recursos Zoogenéticos.[1] Los trabajos se publican en base a las cuatro áreas estratégicas prioritarias del Plan Mundial: 1. Caracterización, inventario y seguimiento de los riesgos asociados y las tendencias; 2. Utilización sostenible y desarrollo; 3. Conservación, y 4. Políticas, instituciones y creación de capacidad. *Recursos Genéticos Animales* ha proporcionado un foro para casi 1.000 autores de 81 países (véase la figura 1).

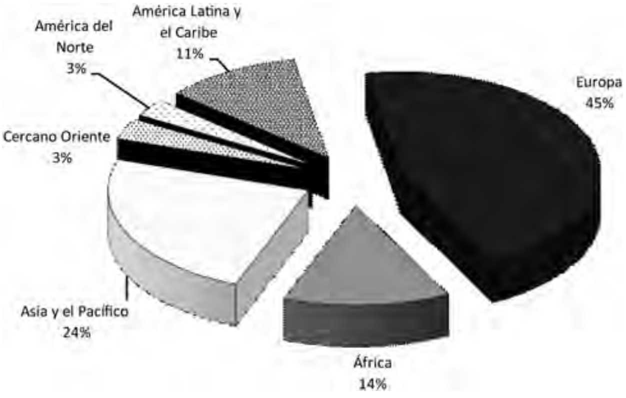

Figura 1. Distribución regional de los autores

Recursos Genéticos Animales se edita en tres idiomas. Los trabajos principales se publican en inglés, francés o español, con un resumen en los tres idiomas. Dichos trabajos se han publicado sobre todo en inglés (77%), y los restantes casi a partes iguales entre el español (12%) y francés (11%). En el período comprendido entre julio de 2009 y febrero de 2012 se han presentado 109 manuscritos, de los que 25 fueron rechazadas.

El análisis de más de 400 trabajos revela que la mayoría de ellos se centró en los grandes rumiantes (38% de los trabajos), seguidos de los pequeños rumiantes (33%), aves de corral y el ganado de talla pequeña (13%), équidos (8%), cerdos (5%) y camélidos (3%). La clasificación de los trabajos, de acuerdo con las cuatro áreas estratégicas prioritarias del Plan Mundial, muestra que la mayor parte de éstos tratan sobre la caracterización, inventario y seguimiento de los riesgos asociados y las tendencias (63%), utilización sostenible y desarrollo (11%), conservación (17%), y políticas, instituciones y creación de capacidad (9%). El alto porcentaje de trabajos centrados en el área estratégica prioritaria 1 puede ser explicado por el hecho de que *Recursos Genéticos Animales* es el principal foro para tratar este tema. Existen revistas especializadas de alto nivel, sobre todo, para las áreas estratégicas prioritarias 2 y 3, no siendo ése el caso del área estratégica prioritaria 4, dado que el número de publicaciones centradas en esa categoría aumenta, pero muy lentamente.

Se han publicado dos ediciones especiales de la revista – *Boletín de Información sobre Recursos Genéticos Animales* 45[2], en 2009, dedicado al Año Internacional de las Fibras Naturales, y *Recursos Genéticos Animales* 47[3], en 2010, dedicado al Año Internacional de la Biodiversidad.

La forma en que los lectores tienen acceso a la revista ha cambiado también de manera importante a lo largo de los años. Los primeros números se imprimían y distribuían físicamente. Hoy en día todos los volúmenes pueden ser consultados en el repositorio[4] de documentos

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[1] www.fao.org/docrep/010/a1404s/a1404s00.htm

[2] http://www.fao.org/docrep/012/i1102t/i1102t00.htm

[3] http://www.fao.org/docrep/013/i1823t/i1823t00.htm

[4] http://www.fao.org/documents/en/search/advanced?%20forward=advanced&%20titleOfJournal=Animal+genetic+resources+information&%20connector=1

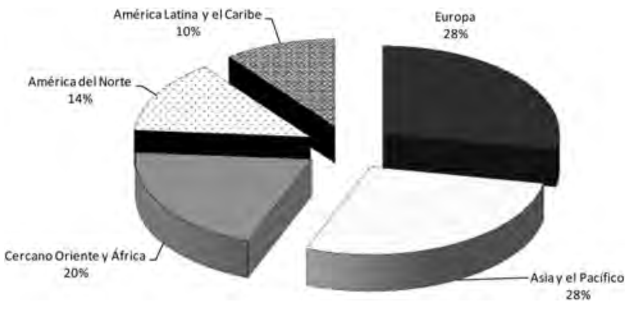

Figura 2. Distribución regional de los lectores de *Recursos Genéticos Animales* (suscripciones electrónicas institucionales)

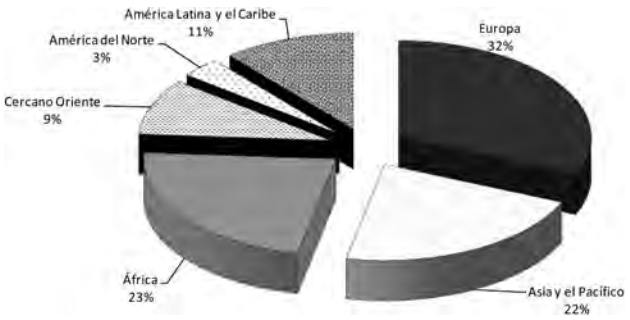

Figura 3. Distribución regional de los lectores de *Recursos Genéticos Animales* (suscripciones en papel)

de la FAO, en la biblioteca del Sistema de Información sobre la Diversidad de los Animales Domésticos[5] y, trabajo por trabajo, en el sitio web del servicio de publicaciones de la Universidad de Cambridge.[6] Además de las descargas individuales, 1.700 instituciones están suscritas a *Recursos Genéticos Animales*, (véase la figura 2) y 3.200 ejemplares de la revista se imprimen y distribuyen a lectores de 187 países (véase la figura 3). En 2007, se editó CD-ROM que contenía desde el volumen 1 al 41, con un motor de búsqueda que ofrecía un fácil acceso a los diferentes trabajos de forma individual.

Las cifras muestran que los números impresos siguen teniendo una gran demanda, especialmente en África y en Asia y el Pacífico. En América del Norte, pocas personas están interesadas en recibir *Recursos Genéticos Animales* de manera impresa; sin embargo, esto es compensado con un relativo elevado número de suscripciones electrónicas institucionales.

Informe sobre la implementación del Plan de Acción Mundial

Se ha solicitado a los países, las redes regionales y las organizaciones internacionales que informen acerca del grado de implementación del Plan de Acción Mundial. Los formularios de los cuestionarios y los informes han sido publicados en internet.[7]

Próxima sesión del Grupo de Trabajo Técnico Intergubernamental sobre los Recursos Zoogenéticos para la Alimentación y la Agricultura

La séptima Sesión del Grupo de Trabajo Técnico Intergubernamental tendrá lugar en la sede central de la FAO en Roma, del 24 al 26 de octubre de 2012. Los temas a abordar incluyen:

- Examen de los progresos realizados para la aplicación del Plan de Acción Mundial sobre los Recursos Genéticos Animales.
- Aplicación y revisión de la Estrategia de financiación para la aplicación del Plan de Acción Mundial.
- Preparación del segundo informe sobre La situación de los recursos zoogenéticos mundiales para la agricultura y la alimentación.
- Indicadores para medir los progresos realizados en la implementación del Plan de Acción Mundial, y el posterior desarrollo del indicador principal del Convenio sobre la Diversidad Biológica para el estudio de las tendencias de la diversidad genética en las especies animales con mayor importancia socio-económica.

La documentación de esta reunión será subida el próximo mes a la página web.[8]

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[5] http://www.fao.org/dad-is/

[6] http://journals.cambridge.org/action/displayJournal?jid=AGR

[7] http://www.fao.org/ag/againfo/programmes/es/genetics/Reporting_system.html

[8] http://www.fao.org/ag/againfo/programmes/es/genetics/angrvent.html

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Morphological diversities and ecozones of Ethiopian horse populations

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Summary

Using standard survey approaches, we carried out a nationwide survey to morphologically characterize and identify ecozones of Ethiopian horse populations. Accordingly, we explored one new feral horse population previously unreported and seven other distinct horse populations. A total of 17 selected morphological variables were recorded on 503 horses (293 stallions and 210 mares) that belong to five out of eight identified horse populations. Pair-wise multiple mean comparisons (PMMC) using one-way analysis of variance and multivariate analyses were performed separately for each sex and least-squares means was used in the case of aggregated sexes. Results of PMMC showed that there were significant differences ($P < 0.05$) between the means for most of the variables recorded. Principal component analysis showed that height at wither, height at back, height at rump, body length, back length and barrel length jointly account for about 80 percent of the variations. All squared Mahalanobis distance between populations were significant ($P < 0.01$). The greatest phenotypic divergence was observed between Bale and Selale horse populations and the least phenotypic divergence was between Horro and Kafa populations. Canonical discriminant function analysis showed that 77.05 percent of individuals were correctly categorized into their respective populations. Moreover, cluster analysis based on squared Mahalanobis distances grouped the five measured Ethiopian horse populations into three major breed groups and five distinct horse populations.

Keywords: ecozones*, horse population, feral horses, morphological diversity, morphological variables*

Résumé

Nous avons réalisé une enquête sur l'ensemble du territoire pour caractériser morphologiquement les populations de chevaux éthiopiens et pour en identifier les écozones en utilisant des méthodes d'enquêtes standardisées. Par conséquent, nous avons étudié une nouvelle population marronisée de chevaux qui n'avait pas été déclarée auparavant et sept autres populations distinctes. Au total, nous avons enregistré 17 variables morphologiques sélectionnées de 503 chevaux (293 étalons et 210 juments) qui appartiennent à cinq des huit populations identifiées. Des comparaisons multiples moyennes par paires en utilisant des analyses de variance simple et des analyses multivariables ont été réalisées séparément pour chaque sexe tandis que la moyenne des moindres carrés a été utilisée pour l'étude des deux sexes agrégés. Les résultats des comparaisons ont indiqué des différences significatives ($P < 0.05$) entre les moyennes pour la plupart des variables enregistrées. L'analyse en composantes principales a montré que la hauteur au garrot, au dos et à la croupe, et la longueur du tronc, du dos et du ventre expliquaient ensemble environ 80 pourcent des variations. Toutes les distances carrées de Mahalanobis entre les populations étaient considérables ($P < 0.01$). La divergence phénotypique la plus importante a été observée entre les populations de chevaux Bale et Selale et la plus faible entre les populations Horro et Kafa. L'analyse canonique discriminante a indiqué que 77.05 pourcent des animaux avaient été classés correctement dans les populations respectives. De plus, l'analyse typologique basée sur les distances de Mahalanobis a regroupé les cinq populations mesurées de chevaux éthiopiens dans trois groupes principaux de races et dans trois populations distinctes de chevaux.

Mots-clés: *écozones, population de chevaux, chevaux marronisés, diversité morphologique, variables morphologiques*

Resumen

Utilizando un enfoque de encuestas estándar, se llevó a cabo una encuesta a nivel nacional para caracterizar morfológicamente e identificar las ecozonas de las poblaciones equinas caballares de Etiopía. Como consecuencia, se ha estudiado una nueva población de caballos asilvestrados no investigada con anterioridad y otras siete poblaciones de caballos diferentes. Se estudió un total de diecisiete variables morfológicas en 503 caballos (293 sementales y 210 yeguas), pertenecientes a cinco de las ocho poblaciones equinas caballares identificadas. Las comparaciones múltiples entre medias por pares (PMMC por sus siglas en inglés), utilizando un modelo lineal y análisis multivariantes, se realizaron por separado para cada sexo y los mínimos cuadrados medios se utilizaron en el caso de los sexos agregados. Los resultados del PMMC mostraron que existían diferencias significativas ($P < 0.05$) entre las medias de la mayoría de las variables estudiadas. El análisis de los componentes principales mostró que la altura a la cruz, la altura al dorso, la altura a la grupa,

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longitud corporal, la longitud dorsal y la longitud ventral en conjunto representaban alrededor del 80 percent de las variaciones. Todas las distancias de Mahalanobis al cuadrado entre las poblaciones fueron significativas ($P < 0.01$). Las mayores diferencias fenotípicas fueron observadas entre las poblaciones equinas caballares de Bale y Selale y las menores entre las poblaciones Horro y Kafa. La función del análisis canónico discriminante mostró que el 77.05 percent de los individuos fueron clasificados correctamente dentro de sus respectivas poblaciones. Por otra parte, el análisis de agrupamiento, basado en las distancias de Mahalanobis al cuadrado, agrupó las cinco poblaciones equinas caballares estudiadas de Etiopía en tres grandes grupos y en cinco poblaciones de caballos diferentes.

Palabras clave: *ecozonas, población equina caballar, caballos asilvestrados, diversidad morfológica, variables morfológicas*

Submitted 20 July 2011; accepted 7 December 2011

Introduction

Domestication of the horse has profoundly affected the course of human civilization (Vila *et al.*, 2001), and world history could be quite different without this species (Goodall, 1973; Bowling and Ruvinsky, 2000). In human history, no other domestic animal has played such a direct role in accelerating social processes and political developments as the horse; it has been central to the rise and fall of empires and the conquest of the entire continents (Bowling and Ruvinsky, 2000). Horses had a paramount role to the spread of Indo-European languages and culture and the collapse of ancient societies (Diamond, 2002). No other domestic species has been used so widely in warfare and peace, communications, transportation, agricultural progresses and sports as the horse (Bowling and Ruvinsky, 2000).

Horses continue serving their destiny in the epoch of motorized vehicles, tractors and planes for different purposes than those for which they were originally domesticated.

For instances, horse sports became part of the popular Olympic Games since Stockholm Olympic in 1956 and elite horses of different breeds continue competing at World Championship level, competitive show ring events and other recreation sports, particularly in the Gulf States. This indeed led to the development of several horse breeds that revolutionized equestrian sports (Khadka, 2010). However, all this wealth is limited to a handful of horse breeds. The vast majority of local breeds still are poorly documented despite their active role in agrarian communities in the developing world and very little is known about their phenotypic diversity. It is our current standing that livestock species populations, across the time, have been subjected to differential selection pressures (e.g. farmers and environment) that resulted in a myriad of peculiar phenotypes. The correct characterization of each of these populations is the first step to better conserve this multitude of phenotypes for uncertain future (e.g. environmental changes and market demands).

Cursory reviews show that Ethiopia has no history of horse breeding. Epstein (1971) indicated that in the Horn of Africa, horses seem to have been absent and unknown before the great Arab invasion of the 11th century AD. He suggested that the southern influx of the Hillalian invasion of Egypt in 1048 seems to have carried out a fair number of Arab horses into Sudan from where they were introduced into the Horn of Africa. Despite this historical background, Ethiopia is among the top ten countries in the world in terms of number of horses (FAO, 2007). The Central Statistical Authority of Ethiopia (CSA, 2009) estimated that Ethiopia possesses about 1.9 million horses with many more unreported. They are not uncommon in most agro-ecologies and livestock production systems with more population density concentrated in the north central, central, eastern and southern highlands of the country.

Horses serve many purposes in the multicultural and multiethnic society of Ethiopia. They are the main sources of land transport systems in the rural areas. They are widely used during social festivals, cultural and other public events. Often, outstanding horses in such occasions are recognized as status symbols. Moreover, horses are the most highly valued and culturally respected domestic mammals, particularly in Borana pastoralists in Ethiopia. However, the horses of Ethiopia have not been systematically characterized and documented in terms of their observed phenotypic characteristics, geographical distributions and production environments. Generally, equines of Ethiopia have not been a focus of research in the past and were neglected regardless of their contributions in supporting the livelihoods of many resource-poor farmers.

Therefore, this study was carried out to phenotypically characterize and avail baseline information on the geographical distributions of Ethiopian horses that may serve as a basis to make informed management and conservation options for the needs of present and future generations.

Materials and methods

Sampling strategy

We followed the general phenotypic characterization guideline developed by FAO (2010) and procedures developed by Kefena *et al.* (2011) for donkey phenotypic characterizations. Sampling sites and the 17 measured morphological variables are shown in Figure 1 and

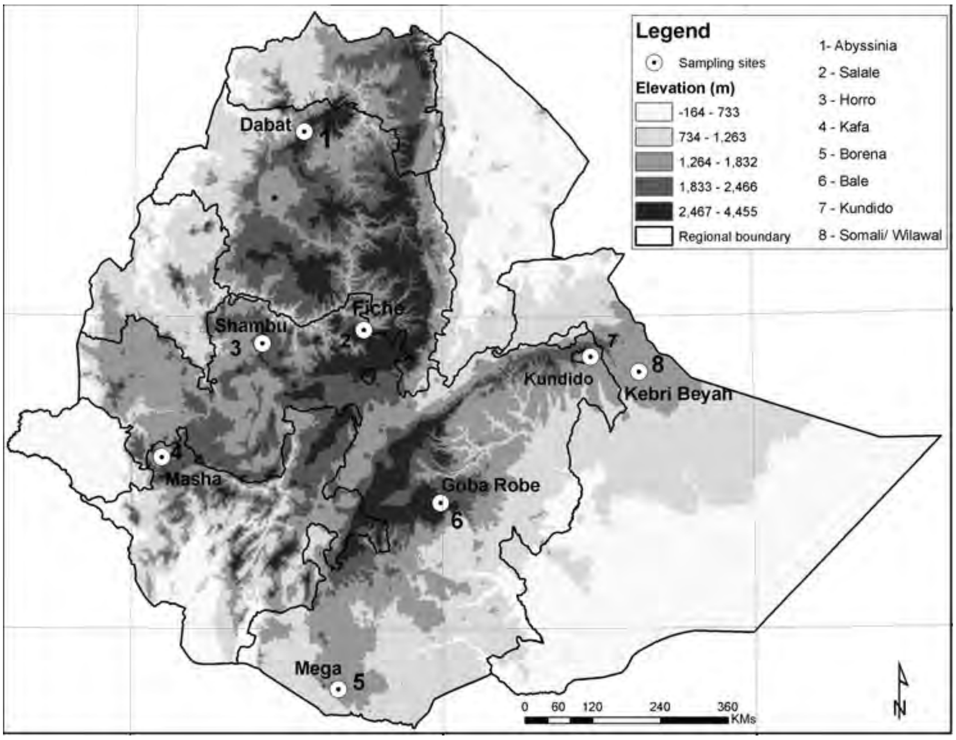

Figure 1. Sampling sites and ecozones of Ethiopian horse populations.

Table 1. Description of measuring devices and definitions of the 17 morphological variables recorded on Ethiopian horse populations.

No.	Definition of quantitative morphological variables	Measuring device
1	*Height at wither*: distance from the highest point of the processus spinalis of the vertebra thoracic to the ground	Measuring stick
2	*Height at back*: Distance from the deepest point of the back to the ground	Measuring stick
3	*Height at rump*: Distance from the highest point of rump to the ground	Measuring stick
4	*Body length*: Distance from the most cranial point of the shoulder joint to the most caudal point of the pin bone	Measuring tape
5	*Back length*: Distance from the caudal point of shoulder joint of perpendicular to the wither to the most cranial point of hip joint measured in a saddle place	Measuring tape
6	*Barrel length*: distance from the most caudal point of the scapula to the most cranial and dorsal point of the point of hip	Measuring tape
7	*Neck length*: Distance from the highest point at wither to nape by normal posture of the head	Measuring tape
8	*Head length*: Distance from the nape to the alveolar edge of the incisors I of the upper jaw	Slide caliper
9	*Length of cannon bone (forearm)*: Distance from the lateral toberculum of the os metacarpale IV to the fetlock joint	Slide caliper
10	*Cannon bone circumference (forearm)*: The smallest circumference of the cannon bone of the forelimb	Measuring tape
11	*Length of cannon bone (hind leg)*: Distance from the lateral tuberculum of the os metatarsale IV to the middle of fetlock joint	Slide caliper
12	*Cannon bone circumference (hind leg)*: The smallest circumference of the cannon bone of hind leg	Measuring tape
13	*Depth of chest*: Distance from wither to the sternum	Measuring tape
14	*Depth of shoulder*: Distance from the withers to the shoulder joint	Measuring tape
15	*Width of hip*: Distance from the left to the right point of hip	Measuring tape
16	*Chest circumference*: Measured in a place of the saddle girth	Measuring tape
17	*Length of rear quarter*: Distance from the most cranial and most dorsal point of the point of hip to the most caudal point of the pin bone	Measuring tape

Table 1, respectively. At the initial stage, we scanned through all previous reports that addressed Ethiopian horse populations. We also reviewed a country report of Ethiopian horse populations that have been officially reported in the Domestic Animal Diversity-Information System (DAD-IS) of the Food and Agricultural Organization of the United Nations at (http://www.dad.fao.org/). We, then, considered horses as a breed if they qualify the definition outlined in the FAO/UNEP (2000) and Oklahoma State University (http://www.ani.okstate.edu/populations/). We also set additional criteria that a given population is considered unique if a particular environment/s which they inhabit is a true breeding tract for that particular population/s. Using these main platforms as criteria, we carried out both confirmatory and exploratory nationwide surveys to confirm previous reports, explore new population/s previously unreported and locate their specific ecozones. All regional agricultural officers were consulted and participated in all the stages of breed identification processes. We also held group discussions with local elders and horse owners to know about the historical background of each identified horse population. Breed/population names were assigned on the basis of their ethnic belongings, eco-geographical nomenclatures and/or how communities name their horses. To avoid measurement errors, a single person recorded all the measurements from identified horse populations.

Data collection

Morphological variables

Generally, there are no universally standardized and consistent equid phenotypic characterization guidelines. Different authors developed different horse phenotypic characterization guidelines that they think are more complete and perhaps fits to their research objective/s. For instance, Zechner *et al.* (2001) used 37 different distances and angular variables, Pretorius *et al.* (2004) used 8, Rastija *et al.* (2004) used 15 and Brooks *et al.* (2010) used 35 different morphological variables. Brooks *et al.* (2010) excluded chest circumference, a commonly recorded morphological variable used in phenotypic characterization of almost all domestic mammals. These evidences indicate the absence of standardized and consistent phenotypic characterization guidelines in horses.

Thus, taking into account the temperamental status of Ethiopian horses, production environments and availability of specific measuring devices, we selected 17 quantitative morphological variables (Table 1) to phenotypically characterize and describe Ethiopian horse populations. These morphological variables are subsets of the variables developed by Oulehla (1996) for horse phenotypic characterization. Identified morphometeric variables were recorded on a randomly selected 503 adult horses (293 stallions and 210 mares) (Table 2) that belong to five horse populations. Horses were carefully handled by trained labourers or by horse owners themselves and were positioned to stand properly on flat and hard grounds with parallel legs apart. Data were not recorded on aggressive and improperly standing horses until they became calm and properly positioned.

Table 2. Summary of the number each horse populations sampled and their proportion to the total populations.

Breed/populations	Stallion	Mare	Total	Proportion
Abyssinian	54	52	106	0.21
Bale	55	45	100	0.20
Horro	57	38	95	0.19
Kafa	67	32	99	0.20
Selale	60	43	103	0.20
Total	293	210	503	1.0

Five major reference points were carefully marked before body measurements were taken. These points were: (1) the point of wither; (2) the point of back; (3) the point of rump; (4) the point of shoulder joint (5) and the point of pin bone. Measurements were regularly taken from the right side and exceptionally repeated on the left side when we become doubtful that horses were not properly standing on leveled grounds. If the measurements vary, the averages values were recorded.

Owing to bad temperamental status of animals and other factors, measurements were not recorded on Borana, Kundido feral and Somali/Wilwal horse populations. Borana horses were highly resistant to restraint. Besides, during survey period, there had been sustained drought in the area and they drastically lost their body condition. Thus, we did not record any data on this population. Moreover, due to small sample sizes, we further excluded morphological data from Kundido feral and Somali/Wilwal horses (Table 3).

Statistical analysis

Population means were estimated separately for stallions, mares and aggregated gender. Tests for significant differences between population means for stallions and mares were separated by *t*-test using the Bonferroni adjustment procedure in Holm (1979) with the step-down procedure using the SPSS package (SPSS, 2006). However, preliminary analysis showed that the interactions were significant only for five variables of the 17 measured morphological variables and, therefore, least-squares means were computed in the case of aggregated gender using SAS (2004).

The data were standardized following standard procedures of Manly (1986) before squared Mahalanobis distances and principal component analysis were computed. Squared Mahalanobis distances were computed between populations using the formula $D_{ij}^2 = (\bar{Y}_i – \bar{Y}_j)\ \mathrm{COV}^{-1}(\bar{Y}_i – \bar{Y}_j)$, where D_{ij}^2 is the distance between population i and j and COV^{-1} the inverse of the covariance matrix of measured variables x and $\bar{Y}_i$ and $\bar{Y}_j$ are the means of variable x in the ith and jth populations, respectively. Squared Mahalanobis distance matrix was used via agglomerative hierarchical cluster procedure to build a dendrogram using unweighted pair-group method using arithmetic mean (UPGMA) using tree procedure in SAS (2004).

Discriminant function analysis was used to determine percentage assignment of individuals into their own populations. Principal component analysis was performed to minimize overall variables into few meaningful variables that contributed most to variations in the populations. We also performed canonical discriminant function analysis to find out a linear combination of quantitative morphological variables that provide maximal separation between different horse populations. The scored canonical variable was used to plot pairs of canonical variable to aid visual interpretation of group differences. Multivariate analysis

Table 3. Summary of recognized Ethiopian horse populations with respect to their distinct phenotypic characteristics and ecozones.

Populations	Distinct phenotypic characteristics	Ecozones
Abyssinian	Unsound conformation, heavily working animals, mostly used for plowing and load carrying	North central Ethiopia, around Semien Mountains in Gonder
Bale	Unsound conformation, paunchy belly with dipped top line and course body. Primarily used for transport and load carrying	Mainly on Bale mountains on the eastern side of the Great Rift Valley
Borana[1]	Bay coat coloured and typical low-land horses raised by well-known Borana Oromo pastoralists in southern Ethiopia	Borana zone with typical representative populations around Megga
Horro	Unsound conformations. Primarily used for load carrying and transport, and occasionally for plowing	Western central highland, Horro district
Kafa	Heavy horse type with sound body conformation. Primarily used for transport and load carrying. Rarely housed. Mares are mainly live in the forests and used for foaling only	South-western Ethiopia in, in the tropical rainforest of Kafa-Sheka zone
Kundido feral horses[1]	Unsound conformation, short-backed, paunchy belly with dipped top line. Feral horses currently under domestication process	Kundido Mountain and nearby areas in Eastern Ethiopia
Ogaden/Wilwal[1]	Heavy horses with sound conformation. Mares are with dipped topline and paunchy belly	Somali Regional State around Jijjiga, Waju and Aware areas
Selale/Oromo	Symmetrical body conformation. Elegant and typical riding horses in Ethiopia. Top lines are straight with well developed crests in stallions	Central Ethiopia, North Shoa zone with typical population in Jidda district

[1] Horse populations for which body measurements were not taken.

for each sex and aggregated gender were carried out separately using SAS (2004).

Results

Breed means

Mean values of morphological variables and their standard errors (s.e) are depicted in Tables 4 and 5 for each sex and least-squares means for aggregated gender are shown in Table 6. Pairwise mean comparison showed significant differences for most of the morphological variables between stallion populations. Major morphological variables such as height at wither (HW), height at back (HB), height at rump (HR), body length (BOL), back length (BAL), barrel length (BRL) and length of rear quarter (LRQ) were significantly longer ($P < 0.05$) for Kafa and Selale stallions as compared with any other stallions considered in this study. Kafa stallions were also significantly superior ($P < 0.05$) in the measurements of their depth of chest (DC), depth of shoulder (DS) and chest circumference (CC) than any other stallions studied (Table 4).

Similar study for mares showed that Selale mares were significantly superior ($P < 0.05$) in their HW, HB, HR, BOL

Table 4. Means and pairwise comparison of morphological variables with their standard errors in each populations: stallions.

Traits[1]	Populations					
	Abyssinian	Bale	Horro	Kafa	Selale	Mean
HW	129.0 (0.5)^{b}	129.2 (0.5)^{b}	128.2 (0.4)^{b}	133.2 (0.5)^{a}	133.7 (0.6)^{a}	130.8 (0.3)
HB	123.1 (0.5)^{b}	123.4 (0.6)^{b}	121.6 (0.5)^{b}	126.8 (0.5)^{a}	127.8 (0.6)^{a}	124.7 (0.3)
HR	128.0 (0.5)^{b}	126.6 (0.6)^{b}	127.7 (0.5)^{b}	132.6 (0.5)^{a}	133.0 (0.6)^{a}	130.1 (0.3)
BOL	131.1 (0.6)^{b}	131.7 (0.8)^{b}	131.4 (0.5)^{b}	135.2 (0.4)^{a}	135.8 (0.4)^{a}	133.2 (0.3)
BAL	56.7 (0.5)^{b}	53.6 (0.4)^{c}	54.5 (0.2)^{c}	58.6 (0.5)^{a}	60.4 (0.5)^{a}	56.8 (0.2)
BRL	66.6 (0.4)^{b}	67.0 (0.5)^{b}	66.8 (0.4)^{b}	70.2 (0.4)^{a}	69.1 (0.3)^{a}	68.1 (0.2)
NL	64.3 (0.4)^{bc}	65.2 (0.4)^{ab}	63.5 (0.3)^{cd}	65.1 (0.3)^{ab}	64.2 (0.4)^{bd}	64.5 (0.2)
HL	48.8 (0.2)^{d}	50.2 (0.2)^{c}	49.3 (0.2)^{cd}	51.2 (0.2)^{b}	52.9 (0.3)^{a}	50.5 (0.1)
LCB_f	23.2 (0.2)^{c}	23.4 (0.1)^{c}	24.5 (0.1)^{b}	24.6 (0.1)^{b}	25.7 (0.2)^{a}	24.4 (0.1)
CBC_f	15.9 (0.1)^{b}	15.9 (0.1)^{b}	16.3 (0.1)^{ab}	17.6 (0.7)^{a}	16.7 (0.2)^{ab}	16.5 (0.2)
LCB_h	26.8 (0.2)^{b}	26.8 (0.2)^{b}	27.3 (0.2)^{b}	27.3 (0.2)^{b}	28.1 (0.2)^{a}	27.3 (0.1)
CBC_h	17.1 (0.1)^{c}	17.4 (0.1)^{bc}	17.5 (0.1)^{bc}	18.4 (0.1)^{a}	18.0 (0.1)^{ab}	17.7 (0.1)
DC	65.3 (0.4)^{d}	69.8 (0.5)^{b}	67.7 (0.4)^{c}	71.8 (0.4)^{a}	67.9 (0.4)^{c}	68.6 (0.2)
DS	50.8 (0.3)^{c}	53.5 (0.4)^{b}	51.6 (0.4)^{c}	55.2 (0.3)^{a}	53.8 (0.3)^{b}	53.1 (0.2)
WH	41.2 (0.3)^{e}	44.3 (0.4)^{ab}	42.7 (0.3)^{d}	44.6 (0.4)^{ab}	44.0 (0.4)^{bd}	43.4 (0.2)
CC	141.6 (0.7)^{c}	147.3 (0.9)^{b}	147.0 (0.8)^{b}	155.2 (0.9)^{a}	137.7 (0.9)^{d}	146.0 (0.5)
LRQ	41.0 (0.3)^{b}	44.7 (0.7)^{b}	43.9 (0.3)^{b}	49.9 (0.4)^{a}	45.1 (0.4)^{b}	45.1 (0.3)

[1] HW = height at wither; HB = height at back; HR = height at rump; BOL = body length; BAL = back length; BRL = barrel length; NL = neck length; HL = head length; LCB^f=length of cannon bone (forelimb); CBC_f = cannon bone circumference (forelimb); LCB_h = length of cannon bone (hindlimb); CBC_h = cannon bone circumference (hindlimb); DC = depth of chest; DS = depth of shoulder; WH = width of hip; CC = chest circumference; LRQ = length of rear quarter; f = forelimb.

Table 5. Means and pairwise comparison of morphological variables with their standard errors in each populations: mares.

Traits^{1}	Populations					
	Abyssinian	Bale	Horro	Kafa	Selale	Mean
HW	125.0 (0.6)^{b}	125.5 (0.5)^{b}	125.0 (0.5)^{b}	126.2 (0.6)^{b}	129.6 (0.8)^{a}	126.2 (0.3)
HB	120.8 (0.5)^{b}	118.2 (0.5)^{c}	119.4 (0.5)^{bc}	121.3 (0.7)^{ab}	123.8 (0.7)^{a}	120.7 (0.3)
HR	126.1 (0.6)^{b}	124.9 (0.5)^{b}	126.2 (0.4)^{b}	126.6 (0.6)^{b}	130.9 (0.8)^{a}	126.9 (0.3)
BOL	130.1 (0.7)^{b}	129.0 (0.6)^{b}	131.0 (0.7)^{ab}	131.0 (0.9)^{ab}	132.9 (1.0)^{a}	130.8 (0.4)
BAL	61.4 (0.4)^{b}	53.5 (0.5)^{e}	56.5 (0.6)^{d}	58.9 (0.6)^{c}	64.1 (0.5)^{a}	59.0 (0.4)
BRL	66.5 (0.3)^{b}	68.0 (0.5)^{b}	66.3 (0.4)^{b}	66.9 (0.5)^{b}	70.7 (0.8)^{a}	67.7 (0.3)
NL	64.2 (0.5)^{ab}	64.6 (0.4)^{ab}	63.1 (0.4)^{b}	63.7 (0.5)^{ab}	65.6 (0.7)^{a}	64.3 (0.2)
HL	48.2 (0.2)^{b}	49.1 (0.2)^{ab}	48.5 (0.2)^{ab}	49.3 (0.4)^{a}	49.1 (0.3)^{ab}	49.0 (0.1)
LCB$_{f}$	22.3 (0.2)^{c}	22.9 (0.3)^{ac}	22.3 (0.3)^{bc}	23.4 (0.3)^{ab}	23.6 (0.1)^{a}	22.9 (0.1)
CBC$_{f}$	15.2 (0.1)^{b}	15.6 (0.1)^{ab}	15.6 (0.1)^{ab}	16.1 (0.2)^{a}	15.5 (0.1)^{b}	15.7 (0.1)
LCB$_{h}$	25.5 (0.2)^{c}	26.4 (0.3)^{bc}	25.9 (0.2)^{c}	26.9 (0.2)^{b}	27.2 (0.2)^{ab}	26.3 (0.1)
CBC$_{h}$	16.3 (0.1)^{c}	16.7 (0.1)^{bc}	16.7 (0.1)^{bc}	17.4 (0.2)^{a}	17.1 (0.2)^{ab}	16.8 (0.1)
DC	62.8 (0.4)^{d}	67.8 (0.6)^{a}	65.3 (0.4)^{bc}	67.1 (0.5)^{ab}	65.0 (0.6)^{c}	65.4 (0.2)
DS	49.2 (0.3)^{c}	54.0 (0.6)^{a}	49.8 (0.4)^{bc}	51.8 (0.3)^{b}	51.5 (0.5)^{b}	51.2 (0.2)
WH	41.0 (0.2)^{d}	45.3 (0.4)^{a}	42.1 (0.3)^{cd}	44.0 (0.5)^{ab}	43.6 (0.5)^{bc}	43.1 (0.2)
CC	139.0 (0.6)^{c}	143.2 (0.9)^{b}	144.0 (0.9)^{b}	150.1 (1.0)^{a}	145.6 (1.0)^{b}	143.9 (0.5)
LRQ	40.3 (0.2)^{d}	43.7 (0.5)^{ab}	42.5 (0.3)^{bc}	44.3 (0.5)^{a}	41.5 (0.3)^{cd}	42.3 (0.2)

[1] HW = height at wither; HB = height at back; HR = height at rump; BOL = body length; BAL = back length; BRL = barrel length; NL = neck length; HL = head length; LCB^{f}=length of cannon bone (forelimb); CBC$_{f}$ = cannon bone circumference (forelimb); LCB$_{h}$ = length of cannon bone (hindlimb); CBC$_{h}$ = cannon bone circumference (hindlimb); DC = depth of chest; DS = depth of shoulder; WH = width of hip; CC = chest circumference; LRQ = length of rear quarter; f = forelimb.

and BRL but nearly similar in some morphological variables with Kafa mares (Table 5). On the other hand, DC, DS, WH and LRQ were significantly higher ($P < 0.05$) for Bale and Kafa mare populations.

The least-squares means for aggregated gender showed that Selale horse populations were consistently taller and longer bodied ($P < 0.05$) as compared with other Ethiopian horse populations but had similar BOL with Bale and Kafa horse populations (Table 6). Bale and Kafa horse populations were deep-chested and deep-shouldered ($P < 0.05$) as compared with any horse populations. Kafa and Selale horse populations had relatively longer lengths of both fore and hind leg cannon bones showing that they are the tallest horse population in Ethiopia (Table 6). Moreover, the circumferences of both

Table 6. Estimates of least-squares means (s.e.) of morphological variables for Ethiopian horse populations: aggregated gender.

Trait^{1}	Populations					
	Abyssinian	Bale	Horro	Kafa	Selale	Mean
HW	126.8 (0.4)^{bc}	127.9 (0.4)^{bc}	126.3 (0.4)^{c}	128.2 (0.4)^{b}	131.2 (0.4)^{a}	128.1 (0.4)
HB	122.1 (0.4)^{bc}	122.8 (0.4)^{b}	120.4 (0.4)^{c}	122.9 (0.4)^{b}	125.6 (0.4)^{a}	122.8 (0.4)
HR	127.3 (0.4)^{b}	128.2 (0.4)^{b}	127.0 (0.4)^{b}	128.1 (0.4)^{b}	131.7 (0.5)^{a}	128.5 (0.2)
BOL	130.7 (0.5)^{b}	132.7 (0.5)^{ab}	131.2 (0.6)^{b}	132.1 (0.6)^{ab}	133.6 (0.5)^{a}	132.1 (0.5)
BAL	59.0 (0.4)^{b}	53.6 (0.3)^{d}	55.4 (0.3)^{c}	58.7 (0.4)^{b}	61.9 (0.4)^{a}	57.7 (0.4)
BRL	66.6 (0.3)^{b}	67.5 (0.3)^{b}	66.6 (0.3)^{b}	68.6 (0.3)^{a}	69.9 (0.4)^{a}	67.8 (0.3)
NL	65.4 (0.4)^{bc}	67.8 (0.4)^{a}	64.3 (0.4)^{c}	67.0 (0.4)^{a}	66.4 (0.4)^{ab}	66.2 (0.4)
HL	48.5 (0.1)^{c}	49.7 (0.2)^{a}	49.0 (0.1)^{bc}	49.0 (0.2)^{a}	49.3 (0.3)^{ab}	49.8 (0.1)
LCB$_{f}$	22.8 (0.1)^{b}	23.2 (0.2)^{b}	23.5 (0.2)^{b}	24.3 (0.1)^{a}	24.7 (0.2)^{a}	23.7 (0.2)
CBC$_{f}$	15.6 (0.1)^{b}	15.8 (0.1)^{b}	16.0 (0.1)^{b}	16.9 (0.5)^{a}	16.1 (0.1)^{ab}	16.1 (0.1)
LCB$_{h}$	26.2 (0.1)^{b}	26.6 (0.2)^{b}	26.6 (0.2)^{b}	27.1 (0.1)^{a}	27.7 (0.2)^{a}	26.8 (0.6)
CBC$_{h}$	16.7 (0.1)^{b}	17.1 (0.1)^{b}	17.1 (0.1)^{b}	18.0 (0.1)^{a}	17.6 (0.1)^{a}	17.3 (0.1)
DC	64.1 (0.3)^{c}	68.8 (0.3)^{a}	66.5 (0.3)^{b}	69.2 (0.3)^{a}	66.2 (0.4)^{b}	67.0 (0.3)
DS	50.0 (0.2)^{c}	53.7 (0.3)^{ab}	50.9 (0.3)^{c}	53.5 (0.3)^{a}	52.7 (0.3)^{b}	52.2 (0.3)
WH	41.0 (0.3)^{c}	44.8 (0.3)^{a}	42.4 (0.3)^{b}	44.1 (0.3)^{a}	43.8 (0.3)^{a}	43.2 (0.3)
CC	140.4 (0.5)^{c}	145.3 (0.7)^{b}	145.5 (0.6)^{b}	152.6 (0.7)^{a}	146.6 (0.8)^{b}	146.1 (0.7)
LRQ	40.6 (0.2)^{d}	43.5 (0.2)^{b}	43.1 (0.2)^{b}	44.1 (0.2)^{a}	42.1 (0.2)^{c}	44.0 (0.2)

[1] HW = height at wither; HB = height at back; HR = height at rump; BOL = body length; BAL = back length; BRL = barrel length; NL = neck length; HL = head length; LCB^{f}=length of cannon bone (forelimb); CBC$_{f}$ = cannon bone circumference (forelimb); LCB$_{h}$ = length of cannon bone (hindlimb); CBC$_{h}$ = cannon bone circumference (hindlimb); DC = depth of chest; DS = depth of shoulder; WH = width of hip; CC = chest circumference; LRQ = length of rear quarter; f = forelimb.

Table 7. Principal component analysis: eigenvalues of the correlations coefficients, proportions accounted for by each variable and cumulative proportion.

Trait[1]	Eigenvalue	Difference	Proportion	Cumulative
HW	8.25	6.35	0.49	0.49
HB	1.9	0.93	0.11	0.60
HR	0.97	0.03	0.06	0.65
BOL	0.94	0.11	0.06	0.71
BAL	0.83	0.16	0.05	0.76
BRL	0.67	0.05	0.04	0.80
NL	0.62	0.12	0.04	0.83
HL	0.50	0.09	0.03	0.86
LCB_f	0.41	0.01	0.02	0.89
CBC_f	0.40	0.02	0.02	0.91
LCB_h	0.38	0.02	0.02	0.93
CBC_h	0.37	0.06	0.02	0.95
DC	0.31	0.11	0.02	0.97
DS	0.20	0.03	0.01	0.98
WH	0.17	0.11	0.01	0.99
CC	0.06	0.02	0.003	0.998
LRQ	0.03		0.002	1.00

[1] HW = height at wither; HB = height at back; HR = height at rump; BOL = body length; BAL = back length; BRL = barrel length; NL = neck length; HL = head length; LCB^f = length of cannon bone (forelimb); CBC_f = cannon bone circumference (forelimb); LCB_h = length of cannon bone (hindlimb); CBC_h = cannon bone circumference (hindlimb); DC = depth of chest; DS = depth of shoulder; WH = width of hip; CC = chest circumference; LRQ = length of rear quarter; f = forelimb.

hind and foreleg cannon bones were generally higher in Kafa and Selale horse populations than in any horse populations. Bale horses had the shortest BAL ($P < 0.05$), but were longer necked ($P < 0.05$) than any horse population. Chest circumference is significantly lower ($P < 0.05$) for Abyssinian but similar in other horse populations except in Kafa horses.

Multivariate analysis

Estimates of PCAs explained by six morphological variables (HW, HB, HR, BOL, BAL and BRL) jointly accounted for about 80 percent of the total variations (Table 7). HW is the most influential single variable representing for about 49 percent of the total variations.

Squared Mahalanobis distances using Mahalanobis procedure (Mahalanobis, 1936) are shown in Table 8 for stallions (above diagonal) and mares (below diagonal) and for aggregated gender in Table 9. All squared Mahalanobis distances were highly significant ($P < 0.01$). In stallions, the greatest morphological divergences were observed between Kafa and Selale followed by between Bale and Selale stallions. According to estimated squared Mahalanobis distances, the least morphological divergences were found between Bale and Horro followed by between Horro and Kafa. In mares, however, the greatest morphological divergences were observed between Abyssinian and Bale mares followed by between Bale and Selale mares. However, the least morphological divergences were observed between Horro and Kafa mares followed by between Abyssinian and Selale mare populations.

Table 8. Squared Mahalanobis distances between stallion (above diagonal) and mares (below diagonal) in Ethiopian horse populations.

Breed	Abyssinian	Bale	Horro	Kafa	Selale
Abyssinian	0	11.17	12.21	22.54	22.51
Bale	30.39	0	7.40	11.64	27.92
Horro	11.89	9.69	0	9.08	26.18
Kafa	12.84	11.75	3.96	0	34.61
Selale	8.04	29.89	16.00	12.51	0

Table 9. Squared Mahalanobis distances between Ethiopian horse populations.

Breed	Abyssinian	Bale	Horro	Kafa	Selale
Abyssinian	0				
Bale	27.70	0			
Horro	17.04	11.79	0		
Kafa	32.03	17.88	10.33	0	
Selale	12.23	35.64	27.96	35.23	0

For the aggregated gender, however, the greatest morphological divergences were observed between Bale and Selale followed by between Kafa and Selale horse populations. The least morphological divergences were found between Horro and Kafa horse populations followed by between Bale and Horro horse populations (Table 9).

Furthermore, we performed hierarchical cluster analysis using overall squared Mahalanobis distances computed for aggregated gender (Table 9) and found that the five identified Ethiopian horse populations were categorized into three major horse groups and five distinct populations: (1) The elegant, well built and racing type Selale and heavy and forest type Kafa horses that jointly represent bigger horse populations in Ethiopia; (2) pony type and short-backed Bale horses that predominantly inhabit the highlands of Bale on the eastern side of the Great Rift Valley; and (3) heavily working horses of Abyssinia and Horro that are characterized by poor body conformation (Figure 2).

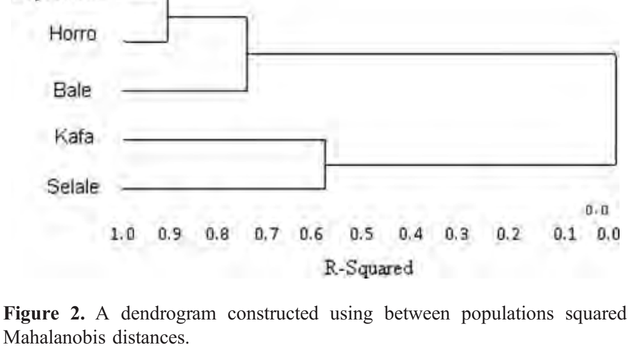

Figure 2. A dendrogram constructed using between populations squared Mahalanobis distances.

We also carried out discriminant function analysis to determine the percentage of individuals correctly classified into their respective populations. Accordingly, we found that, on average, 77.05 percent of the horses were classified into their own population from which they were actually sampled (Supplementary Table S1). Only 22.95 percent of individuals were misclassified into other populations.

Figure 3 shows the result of two canonical variates that separate the five Ethiopian horse populations. The first canonical variate, can 1, separates only between two horse populations: (1) Bale as one group and (2) Kafa as another group with other three populations found scattered between the two separated populations. The second canonical variate, can 2, separates between two groups: (1) Abyssinian and Selale as one group and (2) Bale, Horro and Kafa as another group.

Discussion

Breed comparisons

By fitting breed and sex as fixed effects in the preliminary analysis, we observed that the interaction effects were significant for only five morphological variables (data not shown). Generally, overall mean comparisons show that stallions were significantly taller and longer-bodied ($P < 0.05$) than mares. This indicates the existence of little sexual dimorphism in Ethiopian horses. Such sex-based differences in some morphological variables in horses have already been reported in literatures (e.g. Pinto *et al.*, 2008).

Significantly longer forearm cannon bone, body heights and relatively least CC in Selale stallions probably indicate that they are typical riding and saddle horses type in Ethiopia. Traditionally, Selale stallions have already been recognized as a status symbol and widely known as typical riding horses in Ethiopia.

In the case of aggregate gender, Selale and Kafa horse populations are taller and are longer bodied but higher DC, DS, CC and WH in Kafa horse population indicate that they are voluminous and heavy horse type that adapted to the tropical rainforest in Kafa-Shaka zone in southwestern Ethiopia. The shortest BAL but longer DC and DS in Bale population show that they are also voluminous and compact type of horses in Ethiopia. However, lower CC, WH and LRQ observed in Abyssinian horses probably shows they were low in body condition throughout the year as they regularly involved in intensive agricultural and related activities.

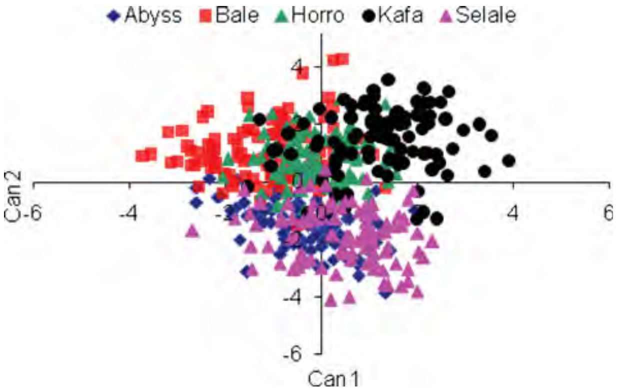

Figure 3. Plot of canonical discriminant analysis showing the first against the second canonical variant for five of the eight identified Ethiopian horse populations.

Relative comparison of Ethiopian horse populations with other studies indicates that they are generally smaller than large European horse breeds. For instance, overall mean HW (128.1 cm) obtained in the present study is by far lower than the mean values obtained for Friesian stallions (160.3 cm) and even the overall mean reported for mares (157.4 cm) in South Africa and Namibia by Pretorius *et al.* (2004). Likewise, mean BOL reported for Friesian horses (165.7 cm for stallions and 166.5 cm for mares) reported in Pretorius *et al.* (2004) is far longer than the mean BOL (132.1 cm) obtained in the present study. Zechner *et al.* (2001) also reported that HW ranges from 153.6 to 158.2 for stallions in Lippizan horses, which is by far higher than the mean HW obtained in the present study. This study supports the report of Epstein (1971) who suggested that in the Savanna belt south of the Sahara, extending from West Africa to Somalia, the majority of native horses, whatever racial types are distinguished, are characterized by small bodies. Epstein (1971) emphasized that the term pony usually applies to horses not over 140 cm in height. From this general assertion, though there exists high body size variations within and between populations, the majority of Ethiopian horse populations may be classified under pony horses.

Multivariate analysis

The six morphological variables (HW, HB, HR, BOL BAL and BRL) jointly account for about 80 percent of the total variations where HW alone accounts for about 49 percent of the total variations among populations. We also noticed that these variables had the highest correlations among themselves (data not shown). Manly (1986) demonstrated that morphological variables that have the highest correlation among themselves are good raw materials for multivariate analysis. This implies that selecting horses for one of these morphological variables, especially for HW simultaneously improves other variables that have high correlation with it.

Squared Mahalanobis distances differ between genders. The highest phenotypic distances between Kafa and Selale stallions probably reflect differences in body size rather than body height or lengths. For instance, Kafa stallions are characterized by having the highest CC, DC and DS as compared with Selale stallions. Bale stallions, which are characterized by higher DC and DS, are also morphologically distant from Selale horses. Relatively large differences in these traits than any other traits probably caused the highest differences between them. Generally, such phenotypic divergence between populations might be partly associated with the differences in management practices, biophysical resources and relative breeding objectives practised between these two distinct horse populations. Bale stallions are mostly blocky and shapeless with paunchy belly, deeper top line and the shortest BAL whereas Selale stallions are elegant and have symmetrical body conformation and are taller and long bodied.

Review of available literatures show that differences in squared Mahalanobis distances between stallions is apparent even within the same Lippizan stallions at different studs in Europe (Zechner *et al.,* 2001). Therefore, differences in squared Mahalanobis distances between different populations and sexes are highly likely to exist. The longest squared Mahalanobis distances observed between Bale and Selale followed by between Kafa and Selale might be attributed to the highest DC and DS differences observed between these pairs of populations. Generally, however, the squared Mahalanobis distances show only relative size differences among the Ethiopian horse populations. It may or may not represent actual genetic differences among them as most domestic animals become morphologically divergent depending on various factors (Zechner *et al.,* 2001).

Phenotypic descriptions and geographical distributions of Ethiopian horse populations

Evidences (e.g. Gubitz, Thorpe and Malhotra, 2000; Storz, 2002) clearly showed that morphological character systems such as coat colour patterns, body dimension or both are strongly influenced by ecological variables and population history. From this general tenet, large phenotypic divergence noticed in the present Ethiopian horse populations could also be associated with differences in production environments, specific population history and to some extent to community breeding practices. Therefore, we realized that it is fair to briefly highlight historical backgrounds, population history and geographical distribution of major indigenous Ethiopian horse populations.

Selale horses

Selale horses of central Ethiopia have a unique population history and are particularly known for their riding aptitudes. They are elegant, have straight top lines, fine legs, symmetrical and sound conformation with well-developed crest in stallions (Figures 4 and 5). They are also known as Oromo horses (a name of ethnic group that raise them) (Epstein, 1971). Their breeding tract is limited to the central highland plateau of Ethiopia, North Shoa zone, commonly known as Selale (Figure 1). In Selale areas, typical representative population of the breed is found at a particularly place known as Jida district; the horse of this place is commonly known as Jida horse. Historically, Jida is the place where the former Ethiopian King, Emperor Hailesilasie established two horse farms in the early 1930s and 1940s. According to local informants, Emperor Halesilasie imported few stallions from England (breed type unknown) for breeding whereby their genes possibly admixed with local horse populations. Phenotypic appearances of Selale horses may reflect this hypothesis. However, this hypothesis needs further genetic studies such as male-specific Y-chromosome and mitochondrial DNA to find out whether the blood of exotic horses was incorporated into the indigenous Selale horse population as hypothesized. Generally, Selale horses are often considered as status symbol in the community.

Figure 4. Horse show at Jida horse market in Ethiopia.

Most selected Selale riding horses receive better managements by the local Oromo community. Such horses are used only during yearly cultural events and horse show locally known as “*gugsii*” or during particular public holidays and other events such as during funeral ceremonies. Horses used in such particular events are locally known as “*farda teesumaa*”, means saddle horse while others are known as “*baataa*”, meaning simply load carriers. Jida market is a main open horse market in Selale area where a large number of horse traders congregate and attend horse show and then compete for outstanding stallions/colts. Selale farmers hardly sell non-castrated colts.

Figure 5. Typical Selale riding horse.

Kafa horses

Kafa horses are typical heavy forest type horses in Ethiopia. Coarse body, big body sizes and well-sprung ribs are among their distinct phenotypic characteristics (Figure 6 and Supplementary Figure S1). They have also long manes usually lying on the right side of their neck. Though they have nearly similar body heights and body length with Selale, they are deep-chested and deep-shouldered and their chest circumference surpasses all Ethiopian horse populations. Their breeding tract is restricted to the tropical rainforest and coffee-growing areas of Kafa-sheka zone in Southwestern Ethiopia.

Kafa horses serve as major sources of land transport system in the inaccessible areas in the tropical rainforests of Kafa and particularly they are used to transport forest coffee and spices from remote areas to the main highways or nearby coffee markets. Mares are hardly tamed and they are almost idle. They are exclusively used for foaling. All horses are rarely housed and mares in particular stay in the forest all year round.

Abyssinian horses

Abyssinian horses are found mainly in the north and north central parts of Ethiopia, particularly in northern Gonder following chains of mountains known as Semien Mountains. They have unsound conformation, paunchy belly and deep back. They are heavily working animals serving for various purposes. They are the chief sources of animal power for crop production and rural transport system in this part of the country (Figure 7).

Bale horses

Bale horses are found in the highlands of Bale zone on the eastern side of the Great Rift Valley that dissect Ethiopia into the eastern and western highlands. They have also unsound conformation, a punchy belly and a deep back with a coarse body. They are also deep-chested, deep-shouldered, long-necked and long-tailed. They are typical pony type of horses in Ethiopia (Supplementary Figures S2 and S3).

Figure 6. Kafa stallion.

Figure 7. Pair of Abyssinian horses engaged in crop land cultivation.

The Kundido feral horses of Ethiopia

Historically, it is only the Namibian feral horses that are known to exist in a feral state in Africa, south of the Sahara. However, the newly explored Kundido feral horses in eastern Ethiopia (Figure 8) show the extent of research gaps and how available information is poorly communicated in Ethiopian horse genetic resources. Recently, we explored Kundido feral horses on Kundido Mountain in the eastern part of Ethiopia (refer to Figure 1). They acquired their name from the name of the mountain where they live in a feral state.

As there is no written provenance on this horse population, their historical backgrounds are not clearly known. Local elders in a focused group discussion suggested that they had been roaming on Kundido Mountain plateau for an unknown period of time with few anecdotic theories. Local elders suggest that the Kundido feral horses might be the remnants of the historically known Ethiopian Muslim–Christian war that took place from 1528 to 1560 between Ahmed Gragn (leader of the Muslim army) and Atse Lebna Dengel (leader of Christian army). Kundido Mountain is situated in a strategic place and local elders speculated that one of the army leaders had been using this mountain as a military strategy to control the progress of their enemy into the area. For the time being, however,

Figure 8. Kundido feral horses.

no other hard evidences are available to substantiate these speculations.

Currently, Kundido feral horses are critically endangered. During a field survey in October 2010, we recorded 18 Kundido feral horses near Kundido Mountain. Recently, however, all these horses are successfully captured by local inhabitants, shared among a few households and are under the process of domestication. We noticed that horses are generally uncommon in the area and, therefore, poor knowledge of horse management practices, high rate of inbreeding and extreme market demands for new born foals are major threatening factors to Kundido feral horses. Therefore, urgent intervention and conservation options are needed by responsible bodies to rescue Kundido feral horses before they get extinct.

Borana horses

In his continent-wide study of the origin of the domestic animals of Africa, Epstein (1971) described Borana horses of Ethiopia as one of the ponies of Africa. In the present study, we re-explored that the major breeding tract of this horse population is around Megga town in Borana zone, in the southern rangelands of Ethiopia. They are kept by the well-known Borana Oromo pastoralists and are typical representative of lowland horses in Ethiopia (Supplementary Figure S4). All horses are characterized by uniform bay coat colour and are good looking.

Borana pastoralists have long-standing cultural system known as the "*Gadaa*" system that obligates every member of the community to give superior respect to horses. For instance, neither human nor any other species precede horses at any watering points in Borana pastoralists. Local Borana elders in a focused group discussion informed that they never allow horse to pull carts. Moreover, dead male horses receive similar burial ceremony as humans in Borana pastoralists. Borana horses are regularly affected by severe droughts occurring in the area. During the dry season of the year, we noticed that they are taken to the watering points every other day. Generally, they are the hardy breed type that adapted to moisture stress and stressful environments of southern Ethiopia.

Somali/Wilwal horses

Somali or Wilwal horses are found in the Somali lowland pastoral areas of eastern Ethiopia. Local pastoralists also call them "Dirdaa'u" or "Wilwal" horses. Local elders reported that the name Wilwal was given after the name of well known Somali warlord and local governor called Wilwal Farah Hersi who had been using these horses to fight the British colonialist during the early colonial period in Ethiopian Somali and Somalia. Moreover, Wilwal Farah Hersi had been using Wilwal horses to exchange information with the central Ethiopian government of the time and also to transport weapons supplied by the central government. This needs further demographic and historical study. They are common around Jijjiga town at specific places known as Dhik, Kebribeya and Waju. Other horse populations are exclusively living in a feral state at a place known as Aware, located at the border between Somalia and Ethiopia. There is also no written provenance for this horse population and, therefore, the origin of the Wilwal horses is not clearly known. Local informants suggested that they might have entered into Ethiopia from Nugal Valley, Somalila. Wilwal horses have sound conformation, a smooth body and are generally elegant and large (Supplementary Figure S5).

Conclusion

This preliminary nationwide study on morphological characters and ecozones of Ethiopian horse populations reveals a myriad of horse genetic resources that Ethiopia is endowed with. Among the studied native Ethiopian horse populations, Selale/Oromo horses are elegant, taller and long bodied with good stature that made it recognized as typical riding horses in Ethiopia. Therefore, targeted selection accompanied by well-designed breeding strategies could help to enhance their inherent genetic potential and develop them into locally adapted riding horses in Ethiopia. Kafa horse populations are also as tall as Selale horses, but are bigger and heavy forest type horses. This horse population could potentially develop for other purposes, such as for draft. The rest of the Ethiopian horse populations have unsound body conformations and are multipurpose types and, therefore, we cannot certainly recommend them to be improved for specific purposes. Therefore, information generated from the present study can help responsible body to make informed decision on priorities for the management and sustainable utilization of native Ethiopian horse populations.

At this point, it is important to also note that there are no well-developed and standardized phenotypic characterization guidelines for equids in general and for horses in particular. Available information is inconsistent and lack uniformity to make comparative analysis of one horse population with others. Therefore, a responsible organization must consider and address this issue in the future.

Supplementary material

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

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Genetic diversity analysis of the mitochondrial *D-loop* of Nigerian indigenous sheep

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Summary

Indigenous livestock resources are strategic in the socio-economics of rural agricultural systems to ensure food security in resource-poor countries. Therefore, better understanding of genetic variation holds the key to future utilization through conservation. We report the first analysis of genetic diversity of Nigerian sheep based on the *D-loop* region of the *Ovis aries* mitochondrial genome using 1 179 bases between sites 15 437 and 16 616 base pairs. A sample of 290 animals made up of Balami, West African Dwarf (WAD), Uda and Yankasa breeds were randomly collected from across Nigeria. Ninety-six haplotypes were observed with a high mean haplotype diversity of 0.899 ± 0.148. Gene diversity was highest in Uda (0.921 ± 0.021) and lowest in WAD (0.852 ± 0.061). Population specific F_{ST} indices varied from 0.00133 in Uda to 0.00335 in WAD. Yankasa had the highest number of polymorphic sites (201), while the least was in Uda (96). Analysis of molecular variance revealed that 0.23 percent of the variation is found among populations compared with 99.77 percent variation found within populations. The phylogenetic tree indicates that the mitochondrial lineages of these sheep breeds originated from a common source consistent with first divergence of Yankasa followed by WAD, while Balami and Uda remain more closely related. These results suggest that evolutionary divergence of Nigerian sheep breeds based on mitochondrial DNA *D-loop* sequence may be coincident with geographical distribution in Nigeria and suggest significant interbreeding. This could have implications for managing improvement and conservation strategies and long-term conservation of Nigerian indigenous sheep.

Keywords: *mitochondrial DNA, genetic distance, genetic diversity, Nigerian sheep*

Résumé

Les ressources des animaux d'élevage indigènes représentent une valeur stratégique dans la socio-économie des systèmes agricoles ruraux qui permettrait de garantir la sécurité alimentaire dans les pays pauvres en ressources. Par conséquent, l'utilisation future de ces ressources par le biais de la conservation dépend d'une meilleure compréhension de la variation génétique. Nous signalons la première analyse de la diversité génétique des moutons nigériens basée sur la région de la *boucle D* du génome mitochondrial d'*Ovis aries* en utilisant 1 179 bases entre les sites 15 437 et 16 616 paires de bases. Des échantillons de 290 animaux provenant des races Balami, West African Dwarf, Uda et Yankasa ont été collectés au hasard dans tout le Nigéria. On a observé 96 haplotypes avec une moyenne élevée de diversité d'haplotype de 0,899 ± 0,148. On a relevé la diversité génétique la plus élevée chez les moutons Uda (0,921 ± 0,021) et la plus faible chez les moutons West African Dwarf (0,852 ± 0,061). Les indices spécifiques de population F_{ST} variaient entre 0,00133 pour les Uda et 0,00335 pour les West African Dwarf. Les moutons Yankasa présentaient le nombre le plus élevé de sites polymorphiques (201) tandis que le plus bas a été repéré chez les Uda (96). L'analyse de la variance moléculaire a indiqué que 0,23 pour cent de la variation se trouve parmi les populations tandis que 99,7 pour cent se situe au sein des populations. L'arbre phylogénétique indique que les lignées mitochondriales de ces races de moutons proviennent d'une source commune cohérente avec la première divergence des Yankasa suivie par les West African Dwarf, tandis que les races Balami et Uda restent plus étroitement apparentées. Ces résultats semblent indiquer que la divergence évolutive des races de moutons indigènes basée sur la séquence de la boucle D d'ADN mitochondrial pourrait coïncider avec la distribution géographique au Nigéria et suggérer un croisement considérable. Cette conclusion pourrait avoir des retombées dans la gestion des stratégies d'amélioration et de conservation et dans la conservation à long terme des moutons indigènes du Nigéria.

Mots-clés: *DNA mitochondrial, distance génétique, diversité génétique, moutons nigériens*

Resumen

Los recursos ganaderos autóctonos son de carácter estratégico en los aspectos socioeconómicos de los sistemas agrícolas para garantizar la seguridad alimentaria en los países de escasos recursos. Por lo tanto, conocer mejor la importancia de la variabilidad genética es vital para su futura utilización, por medio de la conservación. Se presenta el primer análisis de la diversidad genética en ovejas de

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Nigeria basado en la región de control (D-loop) del *Ovis aries* del genoma mitocondrial, utilizando 1.179 bases entre las posiciones 15.437 y 16.616 de pares de bases. Una muestra de 290 animales, compuesta por las razas Balami, West African Dwarf (WAD), Uda y Yankasa, fue tomada al azar de toda Nigeria. Se observaron noventa y seis (96) haplotipos, con una alta diversidad media en cuanto a éstos de 0,899 ± 0,148. La diversidad genética fue mayor en la raza Uda (0,921 ± 0,021) y menor en la raza WAD (0,852 ± 0,061). Los índices de población específicos F_{ST} variaron de 0.00133 en la raza Uda a 0,00335 en la raza WAD. La raza Yankasa presentó el mayor número de posiciones polimórficas (201), mientras que el menor lo mostró la raza Uda (96). Análisis de la varianza molecular reveló que 0,23% de la variación se encuentra entre las poblaciones, en comparación con el 99,77% de variación que se encuentra dentro de las poblaciones. El árbol filogenético indica que los linajes mitocondriales de las razas ovinas partieron de un origen común en conformidad con la primera divergencia de la raza Yankasa, seguida por WAD, mientras que las razas Balami y Uda se encuentran más estrechamente relacionadas. Estos resultados demuestran que la divergencia evolutiva de las poblaciones ovinas de Nigeria, basados en el ADN mitocondrial de la región control, puede coincidir con la distribución geográfica en Nigeria e indican una tasa importante de cruzamiento entre ellas. Esto podría tener ventajas desde el punto de vista de la gestión de la mejora y las estrategias de conservación y preservación a largo plazo de las ovejas autóctonas de Nigeria.

Palabras clave: *ADN mitocondrial, distancia genética, diversidad genética, oveja nigeriana*

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Introduction

Animal genetic resources are defined as animal species that are used, or may be used for the production of food and fibre (FAO, 2007). Livestock currently contribute about 30 percent of agricultural gross domestic product in developing countries, with a projected increase to about 40 percent by 2030. The World Bank has estimated that it will be necessary to increase meat production by about 80 percent between 2000 and 2030 (FAO, 2011). Sheep are very important in the socio-economic lives of the people of Nigeria (Abdullahi, 2002). However, their potential value is not realized because of low productivity resulting from high mortality and poor performance among others. Geographical isolation, natural and artificial selection for physical or productive characters, genetic drift, mutations and interpopulation gene flows have altered gene frequencies over many generations (Pariset *et al.*, 2011), and this could affect fitness and adaptive potentials of animals (Luikart and Allendorf, 1996). The current loss of genetic resources concerns not only the extinction of traditional breeds, but also the loss of genetic diversity within breeds (Taberlet *et al.*, 2011). In terms of biodiversity, conservation and utilization, these genetic resources require further identification and evaluation to assess their potential contribution to food and agricultural production in the future.

The initial step in characterization is identification of distinct populations using information on their geographic and ecological isolation, traditional nomenclatures (traditionally recognized populations), phenotypic distinctness and the level of genetic differentiation among the populations (Gizaw *et al.*, 2011). Since the beginning of the 1990s, molecular data have become more relevant to the characterization of genetic diversity (Groeneveld *et al.*, 2010), and the identification of genetically distinct breeds is commonly based on these state-of-the-art techniques (Gizaw *et al.*, 2011). Mitochondrial DNA (mtDNA) diversity is a useful molecular tool in establishing phylogenetic relationships among breeds and at species level (Tanaka *et al.*, 2011; Zhao *et al.*, 2011). According to Ajmone-Marsan and The GLOBALDIV Consortium (2010), studies of mtDNA, microsatellite DNA profiling and Y-chromosomes have revealed many details about the process of domestication, diversity retained by breeds and the relationships between breeds.

Although a preliminary study of natural genetic variation among Nigerian sheep breeds using microsatellite markers was reported by Adebambo *et al.* (2004), the full extent of molecular variation and diversity remain largely unknown, and studies based on other molecular markers capable of unraveling phylogenetic history and development to better understand the genetic structure of the Nigerian sheep population are scarce. As part of efforts to better understand the genetics of Nigerian sheep for improvement and conservation goals, we report the first study undertaken to assess population structure and genetic diversity of Nigerian sheep using *D-loop* sequence of the ovine mitochondrial genome.

Materials and methods

Study area and study population

This study was carried out using samples collected across all over Nigeria. Nigeria is located in West Africa on the Gulf of Guinea between latitude 10° north of the equator and longitude 8° east of Greenwich Meridian with a total area of 923 768 km^2. Nigeria is bounded by Niger, Benin and Cameroon Republics on the North, West and East, respectively (Figure 1). The five agro-ecological zones include Sahel and Sudan Savannah, Guinea Savannah, derived Guinea Savannah and Rainforest/Mangrove swamp. For the purposes of sampling, Sahel and Sudan savannas were combined into Sahelo-Sudan; derived Guinea and Guinea

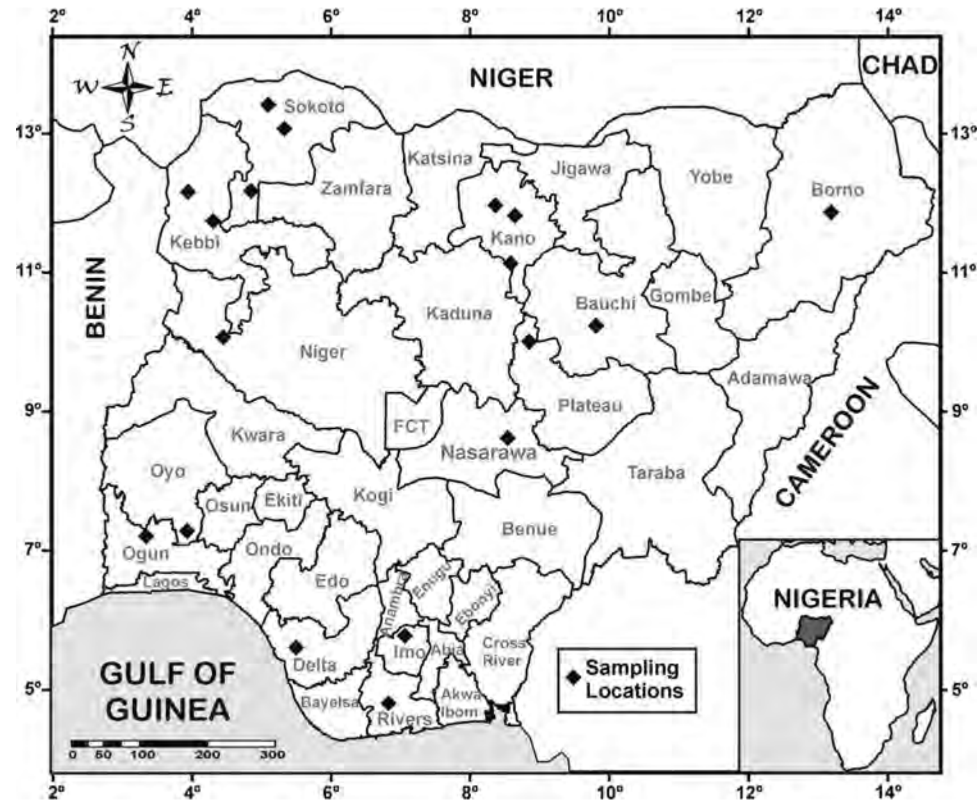


Figure 1. Map of Nigeria showing sampled locations.

savannas were combined into Guinea savanna and sampling was carried out from three main agro-ecological zones of Sahelo-Sudan Savannah, Guinea Savannah and Rainforest/Mangrove swamp.

Two hundred and ninety sheep were sampled from the three main agro-ecological zones of Nigeria comprising 98 Balami, 43 Uda, 110 Yankasa and 39 West African Dwarf (WAD) breeds. Approximately 5 ml of blood was collected into heparinized tubes from the jugular vein of the sheep, stored on ice before transfer to the laboratory for analysis.

DNA extraction, polymerase chain reaction amplification and sequencing

DNA was extracted from 50–100 µl of whole blood using the ZymoBead^{TM} Genomic DNA Kit (Zymo Research Corp. Irvine, CA, USA) according to the manufacturer's recommendations. Quantification of DNA yield and assessment of quality were done using the Nanodrop ND-100 Spectrophotometer (Thermo Scientific, Wilmington, DE, USA). The DNA was amplified via polymerase chain reaction (PCR) in a MyCycler^{TM} Thermal Cycler (Biorad, Hercules, CA, USA) using primers designed from published ovine sequences (Genbank Accession Number AF010406) (Hiendleder *et al.*, 1998): tRNA-proline (5-CAGTGCCTT GCTTTGGTTAAGC-3) and tRNA-phenylalanine (5-CA CCATCAACCC CAAAGCTGAAG-3). The total volume of 20 µl amplification reactions contained 20–50 ng template DNA, 2.0 µl each of forward and reverse primers, and 16 µl nuclease-free water in a BIONEER AccuPower$^{®}$ TLA PCR Premix (containing NTPs, $MgCl_2$ and DNA polymerase) (BIONEER Corporation, Alameda, CA, USA). PCR used the following protocol: initial denaturation at 94°C for 5 min, 35 cycles of amplification at 94°C for 30 s, annealing at 62°C for 30 s, extension at 72°C for 1 min, final extension at 72°C for 5 min and held at 4°C until analysis. Ten microlitres of the PCR product were separated in a 1.5 percent agarose gel prestained with 0.5 µg/ml ethidium bromide. Electrophoresis was carried out at room temperature for 40 min at 100 V using a Bio-Rad Power Pac^{TM} electrophoresis apparatus (Biorad). The resulting amplified bands were visualized with UV light and photographed using the AlphaImager^{TM} 2200 electrophoresis documentation and analysis system (Cell Biosciences, CA, USA), and were scored using GENEMate Quanti-Marker 100 bp DNA ladder (BioExpress, UT, USA). Amplified PCR products were sequenced with the Applied Biosystems Automated 3730 DNA Analyzer (Applied Biosytems, Foster City, CA, USA) using the Big Dye Terminator chemistry and AmpliTaq-FS DNA polymerase. Sequencing reactions used tRNA-proline primer (5-CAGTGCCTTGCTTTGGTTAAGC-3).

Statistical analysis

Sequence alignment of the 1 179 bp PCR-amplified fragment (after excluding the 75 nt tandem-repeat elements) was done using DNA alignment software (Fluxus Technology, http://www.fluxus-engineering.com/). A pair-wise distance matrix

Table 1. Standard diversity indices for mtDNA analysis of Nigerian sheep breeds.

Indices	Balami	Uda	WAD	Yankasa
Number of gene copies	98	43	39	110
Number of haplotypes (h)	49	27	15	39
Number of loci	297	297	297	297
Number of polymorphic sites (S)	195	96	190	201
Sum of square frequency	0.0889	0.0622	0.1772	0.1425
Hyplotype diversity (Hd)	0.9205 ± 0.0219	0.9601 ± 0.0170	0.8522 ± 0.0611	0.8654 ± 0.0288
Mismatch observed mean	13.175	11.218	18.214	10.764
Mismatch observed variance	690.468	150.985	2078.648	642.036
Parameters of the spatial expansion assuming constant deme size				
Tau	19.213	0.689	0.945	0.594
Theta	5.784	6.267	1.481	2.288
M	0.425	938.614	8.815	1166.750

between mtDNA sequences were computed using the nucleotide p-distance (Nei and Kumar, 2000), and a neighbour-joining (NJ) tree constructed on the basis of these distances using the MEGA 3.0 software (Kumar, Tamura and Nei, 2004). A median joining network (Bandelt, Forster and Rohl, 1999) was drawn from haplotypes using the program Network 4.1.0.9 (www.fluxus-engineering.com). Indices of sequence variation and haplotype structure were calculated using the DnaSP 4.00 program (Rozas *et al.*, 2003) including nucleotide diversity (π), number of haplotypes (nh), haplotype diversity (Hd) and number of polymorphic sites (S). An analysis of molecular variance (AMOVA) was computed to test significant differences in mitochondrial diversity between Nigerian sheep breeds using ARLEQUIN 3.01 (Excoffier, Laval and Schneider, 2005).

Results

Table 1 shows values for standard diversity indices for the study of mtDNA of the Nigerian sheep. A total of 96 haplotypes were observed among the populations. Haplotypes 2, 3, 9, 12, 13, 14, 15, 16, 17, 18, 22, 23, 25, 31, 34, 36, 37 and 63 were shared among the different populations with haplotypes 2, 9, 12 and 15, common to all the populations. However, haplotype 2 had the highest distribution among the four populations studied (Tables 2 and 3). Number of polymorphic sites varied across the populations with the highest value in Yankasa (201) and the lowest in Uda (96). Gene diversity was high in all the populations. Values ranged from 0.9601 ± 0.0170 in Uda to 0.8522 ± 0.0611 in WAD. A variation in mismatch observed mean was noticed in this study, with WAD having the highest value of 18.214.

Parameters of spatial expansion assuming constant deme size is shown in Table 1. Tau ranged from 0.594 in Yankasa to 19.213 in Balami. However, Uda had the highest value of 6.267 for Theta, with the lowest value seen in WAD. Higher variation in M was also observed with values ranging from 0.425 in Balami to 9338.613 in Uda. The AMOVA is shown in Table 4. The AMOVA analysis revealed that 0.23 percent of the variation is found among populations compared with 99.77 percent variation found within populations. Population-specific F_{ST} indices are presented in Table 5. F_{ST} values are very low and range from 0.00133 in Uda to 0.00335 in WAD. The fixation index F_{ST} is 0.00226.

The estimation of population size change for Nigerian sheep breeds using pair-wise comparison is shown in Figure 2. In all the populations, a sharp variation for both observed and expected pair-wise differences was observed. The fluctuation was highest among Uda. Figure 3 shows the median joining network for the haplotypes observed among Nigerian sheep. The network shows a grouping of the haplotypes into two haplogroups. The unweighted pair group method analysis (UPGMA) tree of Nigerian sheep mtDNA sequences is shown in Figure 4. The tree shows that all the breeds originated from a common source. However, Yankasa diverged first. This was followed by WAD and lastly Balami and Uda, although separated but are more genetically closely related.

Discussion

Variation among all the standard diversity indices was observed across the four Nigerian sheep breeds studied.

Table 2. Haplotypes shared among populations.

	Balami	Uda	WAD
Uda	14 (2, 3, 9, 12, 14, 15, 17, 18, 22, 23, 25, 34, 36, 37)		
WAD	5 (2, 9, 12, 14, 15)	5 (2, 9, 12, 14, 15)	
Yankasa	14 (1, 2, 3, 9, 12, 13, 14, 15, 16, 18, 21, 31, 34, 37)	9 (2, 3, 9, 12, 15, 18, 34, 37)	6 (2, 9, 12, 14, 15, 63)

Table 3. Distribution of haplotypes among the populations studied.

Haplotype	Balami	Uda	WAD	Yankasa
1, 13	1	0	0	1
2	26	7	11	38
3	1	1	0	2
4–8, 10–11, 19–20, 24, 26–30, 32–33, 35, 38–49	1	0	0	0
9	6	3	3	11
12	5	4	2	3
13	2	0	0	1
14	3	1	1	3
15	4	3	2	5
16	2	0	0	4
17, 20, 25, 36	1	1	0	0
18	4	2	0	4
21	5	0	0	6
22	1	2	0	0
34	1	2	0	2
37	1	1	0	1
50–62	0	1	0	0
63	0	0	1	1
64–72	0	0	1	0
73–77, 79–89, 91–96	0	0	0	1
78	0	0	0	3
90	0	0	0	2

The highest number of polymorphic sites in Yankasa could be attributed to the fact that it is the most populous sheep breed in Nigeria spread across different agro-ecological zones of the country (Adebambo *et al.*, 2004). The mismatch distribution analyses and the genetic diversity analyses suggest that these breeds must have undergone relatively recent population expansion (Qing *et al.*, 2009). The values of haplotype and nucleotide diversities observed in this study are a little higher than haplotype diversity of 0.792 ± 0.37 and nucleotide diversity of 0.00392 ± 0.00046 observed by Wang *et al.* (2006) from analysis of mtDNA variation and matrilineal structure in blue sheep populations of Helan Mountain, China. However, the values of haplotype diversity are comparable to 0.857 ± 0.137 to 1.000 ± 0.052 reported by Sulaiman, Wu and Zhao (2011). Mohammadhashemi *et al.* (2010) also reported that sequence analysis of the mtDNA from Moghani breed with another Iranian sheep showed high genetic diversity with some Iranian sheep breeds. Pariset *et al.* (2011) observed that mtDNA analysis showed higher levels of sheep nucleotide diversity in the South-East, which was congruent with the proximity to the domestication centre. In a related study in goats, Benjelloun *et al.* (2011) reported very high haplotype diversity obtained for the Moroccan goats, and this, according to the same authors, could have resulted from the capture of a large part of the wild diversity during domestication.

Table 4. AMOVA analysis.

Source of variation	Df	Sum of squares	Variance components	Percentage of variation
Among population	3	1.543	0.00102	0.23
Within population	286	123.900	0.48910	99.77
Total	289	125.443	0.44993	

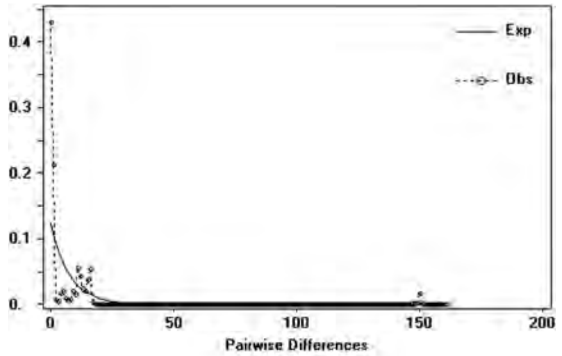
Table 5. Population specific F_{ST} indices.

Population	F_{ST}
Balami	0.00180
Uda	0.00133
WAD	0.00335
Yankasa	0.00274

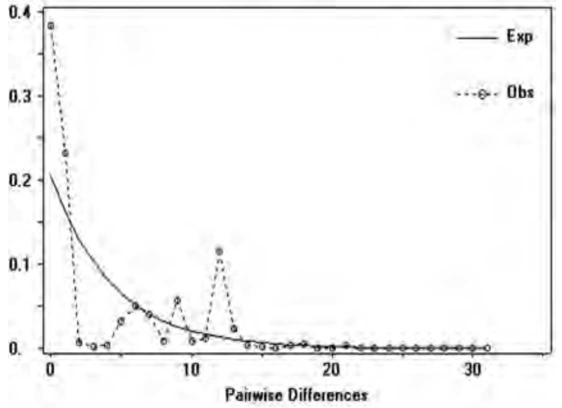
Fixation index F_{ST}: 0.00226.

The AMOVA showed that 0.23 percent of the genetic variation among Nigerian sheep breeds is attributed to among populations compared with 99.77 percent due to variation within populations. A higher variation within than among Nigerian sheep breeds suggests high levels of female-mediated gene flow (Tserenbataa *et al.*, 2004). More so, the results of pair-wise computations and AMOVA indicates that some breeds are differentiated relative to a random collection of genotypes and reflect differences in the spatial distribution of genetic variation (Wang *et al.*, 2006). Similar to these findings, Pariset *et al.* (2011) reported that the major mitochondrial variation was distributed within breeds (95.04 percent), while it was lower among regions (0.90 percent) and among breeds within regions (4.06 percent).

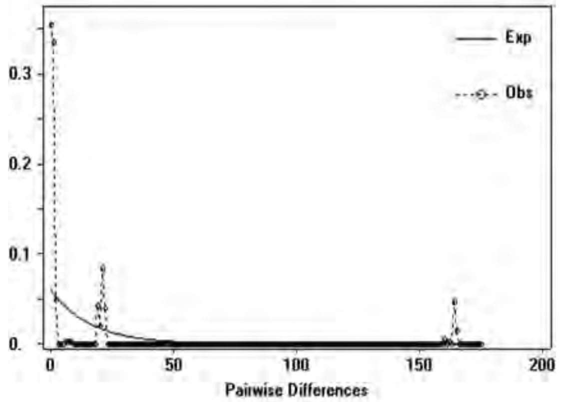
The genetic differentiation fixation index (F_{ST}) among the Nigerian sheep breeds was low. The highest F_{ST} value in Nigerian WAD sheep could be the results of its presence only in the southern part of the country. Reduced differentiation could be attributed to shrinkage of grazing area, indiscriminate cross-breeding/intermixing between breeds and lack of appropriate breeding and management policies. Although there are no strict breeding rules, geographical isolation between the investigated sheep from different regions has probably led to the moderate level of differentiation among them since genetic drift and natural selection are two main factors that give rise to genetic differentiation among populations (Qing *et al.*, 2009). The observed F_{ST} values indicate significant inbreeding from subdivision of the breeds. The degree of subdivision suggests gene flow between the breeds (Kantanen *et al.*, 1995). If gene flow is greater than one, it could play a uniform action of resisting the action of genetic drift and preventing differentiation between populations (Qing *et al.*, 2009). According to Gizaw *et al.* (2011), an important characteristic to note in genetic diversity in livestock populations is that the variation within a population is much larger than that between the populations. This is well exemplified in the study of Ethiopian sheep where the diversity between Ethiopian sheep populations accounted for only 4.6 percent of the overall genetic diversity (global F_{ST} value = 0.046 ±



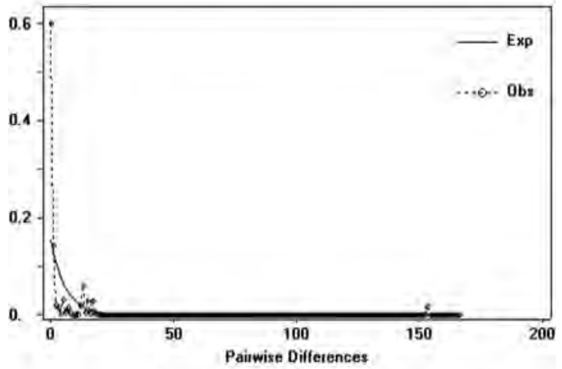
Balami



Uda



WAD



Yankasa

Figure 2. Estimation of population size changes for Nigerian sheep breeds.

0.004), the rest being accounted for by within-population variation. The variation in the number of haplotypes and gene copies analysed contributes to unravelling genetic diversity among Nigerian sheep breeds. Despite the high haplotype diversity observed in Uda, the higher number of polymorphic sites in Yankasa compared with other breeds is likely to have contributed to Yankasa's adaptation ability.

Out of the 96 haplotypes observed in this study, only 5 haplotypes are common to all the breeds with haplotype 2 having the highest frequency. This probably points to the existence of evolutionary relationship among them; and equally suggests evidence linking the four Nigerian sheep breeds to a common ancestor or a small number of founders. In a related study in buffalo, few haplotypes of South Kanara and Toda were found to be quite distinct from the commonly found haplotypes, indicating that these might have been ancestral to all the present-day haplotypes (Kathiravan *et al.*, 2011). Relatively divergent haplotypes within breeds and geographical locations suggests that gene flow has occurred on a regional scale at some time in the recent past and that the breeds have not been subdivided by long-term biogeographic barriers (Luikart and Allendorf, 1996). Similar mean haplotype diversity of 0.945 and mean nucleotide diversity and 0.013 from genetic diversity and structure of the West Balkan Pramenka sheep types as revealed by microsatellite and mtDNA analyses further support the results of this study (Cinkulov *et al.*, 2008). In a related study in goats, Vacca *et al.* (2010) reported that the animals showed a high genetic haplotype diversity, as 35 haplotypes were each represented by a single sequence and only a few haplotypes were shared among the animals, thereby lending credence to the findings of Naderi *et al.* (2007) that it is common to find haplotypes represented by one individual or shared by only a few subjects, because mtDNA variation is a more frequent component within breeds than between them. The significant differentiation in the haplotype frequencies among Nigerian sheep breeds suggest that little gene flow currently exist among the breeds (Luikart and Allendorf, 1996).

The median joining network separated the 96 haplotypes into two major haplogroups. The UPGMA tree separated the four Nigerian sheep breeds according to their geographical locations and population sizes in the country. Balami and Uda are northern breeds which are also fewer than WAD which is a southern breed compared with Yankasa with a wider geographical spread across the country. Evidence from the phylogenetic tree supports first divergence of Yankasa followed by WAD and later by Uda and Balami. However, Zhao *et al.* (2011) reported that F_S value was -13.17574 ($P = 0.00000$) for haplogroup A in Chinese large-fat-tailed sheep breeds, which suggested one expansion event in this population's demographic history. Analysis of mismatch distribution also revealed an almost multi-modal distribution of mtDNA *D-loop* for haplogroup B. F_S value was -6.39666 ($P = 0.00000$) for haplogroup B, which showed no population expansion and relatively stable population size because of no significant difference from neutrality.

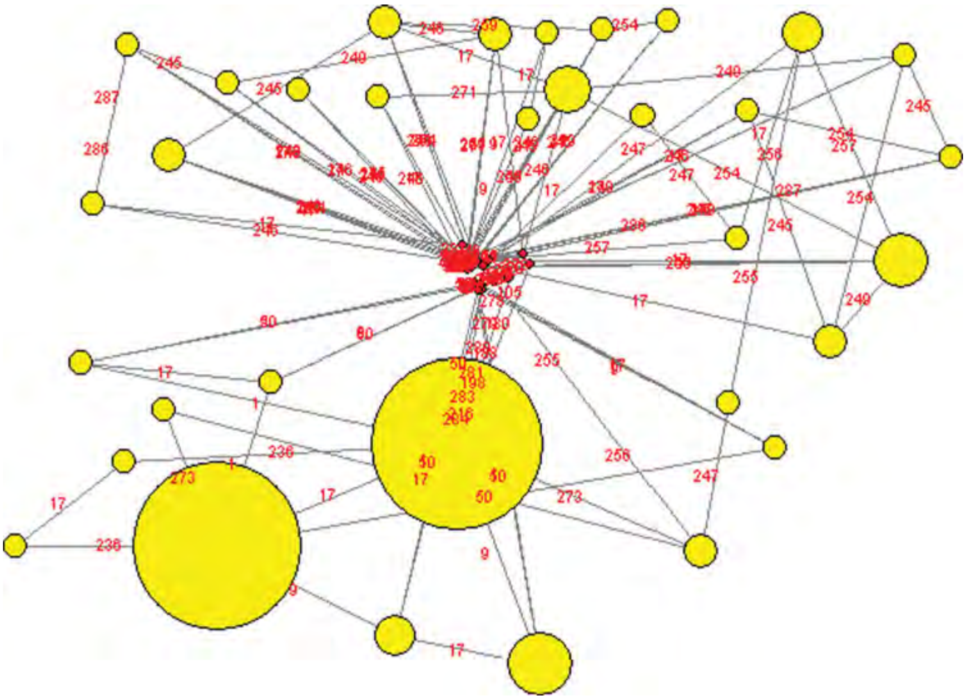


Figure 3. A median joining network for the haplotypes observed among Nigerian sheep. Circles represent haplotypes and have a size proportional to frequency. Mutational differences are shown on lines.

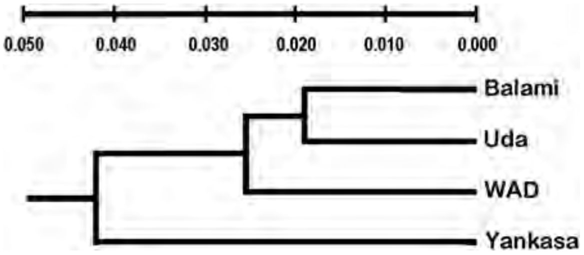


Figure 4. UPGMA tree of Nigerian sheep mtDNA sequences.

The present information could be used to strengthen the monitoring, characterization and conservation of animal genetic resources towards the sustainable rearing of the autochtonuous sheep breeds. However, further studies involving the use of endogenous retroviruses (Chessa *et al.*, 2009) as a new class of genetic markers, combined with existing knowledge from microsatellite (Agaviezor *et al.* accepted. Adebambo *et al.*, 2004) will help to unravel the history of domestication of Nigerian sheep.

Conclusions

Genetic diversity among Nigerian indigenous sheep breeds is eroding due to indiscriminate cross-breeding/intermixing between breeds, and lack of appropriate breeding and management policies. The highest number of polymorphic loci in Yankasa compared with other breeds suggests wider genetic variation that can be exploited in its improvement. In addition, the four Nigerian sheep breeds studied separated genetically based on their geographical locations and population sizes with a rough grouping of the northern breeds (Balami and Uda) and the southern breeds (WAD and Yankasa). The evolutionary divergence into distinct entities of Nigerian sheep breeds based on mtDNA *D-loop* sequence appear to closely follow their geographical distribution in Nigeria, and this could have implications for management, improvement and conservation strategies in Nigerian sheep.

Statement of Interest: The authors wish to state that there is no conflict of interest as regards this manuscript.

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Multifactorial discriminant analysis of morphological and heat-tolerant traits in indigenous, exotic and cross-bred turkeys in Nigeria

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Summary

This investigation explored the ability to distinguish the morphological and heat-tolerant traits of Nigerian indigenous, exotic and cross-bred turkeys using multivariate discriminant analysis. A total of 228 turkeys that were 20 weeks old were utilized in the study. The body parameters measured were body weight (BW), body length (BL), shank length (SL), thigh length (TL), keel length (KL), breast girth (BG), rectal temperature (RT), pulse rate (PR), respiratory rate (RR) and heat stress index (HI). Analysis of variance revealed that the exotic turkeys had significantly ($p < 0.05$) higher values than Nigerian indigenous and cross-bred turkeys in all the morphological traits with the exception of TL. However, the indigenous and cross-bred turkeys appeared to have more adaptive capability than the exotic ones based on their low HI. Sexual dimorphism was observed only in the morphological traits with male birds having significantly ($p < 0.05$) higher BW, BL, SL, TL and KL than that in females. However, the stepwise discriminant analysis revealed that BW, TL and HI were the most discriminating variables to separate the three genetic groups. The longest Mahalanobis distance was observed between the indigenous and exotic turkeys (36.68) while the shortest distance was recorded for the indigenous turkeys and their cross-bred counterparts (7.97). The canonical plot revealed the heterogeneity of the turkey populations as the birds clustered separately. In the nearest-neighbour discriminant analysis, 100.00, 98.73 and 96.43 percent of exotic, cross-bred and indigenous turkeys were correctly assigned into their source genetic groups. The present findings could aid the implementation of a conservation and improvement strategy of indigenous turkeys towards sustainable development of animal genetic resources.

Keywords: *adaptive trait, body measurement, discriminant analysis, Nigeria, turkey*

Résumé

Cette étude a examiné la capacité d'identifier les caractères morphologiques et de tolérance à la chaleur des dindes indigènes, exotiques et croisées au Nigéria en utilisant l'analyse multidimensionnelle discriminante. Au total, 228 dindes, âgées de 20 semaines, ont été utilisées pour cette recherche. Les paramètres utilisés ont été le poids corporel, la longueur du corps, du tarse, de la cuisse et du bréchet, la circonférence de la poitrine, la température rectale, la fréquence du pouls, la fréquence respiratoire et l'indice de contrainte thermique. L'analyse de la variance a révélé que les dindes exotiques présentaient des valeurs considérablement plus élevées ($p < 0{,}05$) par rapport aux dindes nigériennes indigènes et croisées pour tous les caractères morphologiques, à l'exception de la longueur de la cuisse. Cependant, la capacité adaptative des dindes indigènes et croisées, sur la base de leur indice de contrainte thermique modéré, semblait supérieure à celle des races exotiques. Le dimorphisme sexuel n'a été observé que dans les caractères morphologiques des mâles qui présentaient des valeurs plus élevées que les femelles pour le poids corporel, la longueur du corps, du tarse, de la cuisse et du bréchet. Toutefois, l'analyse discriminante progressive a révélé que le poids corporel, la longueur de la cuisse et l'indice de contrainte thermique étaient les variables les plus discriminantes dans la répartition des trois groupes génétiques. La distance de Mahalanobis la plus importante a été observée entre les dindes indigènes et exotiques (36,68) tandis que la plus courte a été enregistrée entre les dindes indigènes et leurs homologues croisés (7,97). Les graphiques canoniques ont indiqué l'hétérogénéité des populations de dindes lorsque les oiseaux se regroupaient séparément. Dans l'analyse discriminante de leur voisin le plus proche, 100 pour cent des dindes exotiques, 98,73 pour cent des croisées et 96,43 pour cent des indigènes ont été correctement attribués à leurs groupes génétiques d'origine. Les conclusions de l'étude pourraient contribuer à l'élaboration d'une stratégie de conservation et d'amélioration des dindes indigènes entraînant une mise en valeur durable des ressources zoogénétiques.

Mots-clés: *mesures anthropométriques, caractère adaptatif, analyse discriminante, dindes, Nigéria*

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Resumen

Este estudio examina la capacidad para distinguir los rasgos morfológicos y de tolerancia al calor en pavos autóctonos, exóticos y cruzados en Nigeria mediante el análisis discriminante multivariado. Un total de 228 pavos de 20 semanas de edad fueron utilizados en el estudio. Los parámetros corporales medidos fueron el peso corporal (BW), diámetro longitudinal (BL), longitud del tarso (SL), longitud del muslo (TL), longitud de quilla (KL), perímetro torácico (BG), temperatura rectal (RT), frecuencia del pulso (PR), frecuencia respiratoria (FR) y el índice de estrés térmico (HI). El análisis de la varianza reveló que los pavos exóticos mostraban valores significativamente ($p < 0{,}05$) mayores que los pavos autóctonos de Nigeria y que los cruzados para todos los rasgos morfológicos, con la excepción de la TL. Sin embargo, los pavos autóctonos y los cruzados parecían tener más capacidad de adaptación que los exóticos en base a valores de HI más bajos. El dimorfismo sexual se observó sólo en los caracteres morfológicos, donde los machos presentaron de forma significativa ($p < 0{,}05$) un mayor BW, BL, SL, TL y KL que en las hembras. Sin embargo, el análisis discriminante por pasos reveló que BW, TL y HI, fueron las variables más discriminantes a la hora de separar los tres grupos genéticos. La mayor distancia de Mahalanobis se observó entre los pavos autóctonos y exóticos (36,68), mientras que la distancia más corta se registró entre los pavos autóctonos y los cruzados (7,97). El diagrama canónico puso de manifiesto la heterogeneidad de las poblaciones de pavo, agrupando las aves por separado. En el nivel de asignación más cercano del análisis discriminante, el 100,00%, el 98,73 % y el 96,43 % de pavos exóticos, cruzados y autóctonos fueron asignados correctamente en sus grupos de origen genético. Los presentes hallazgos podrían ayudar a la implementación de una estrategia de conservación y mejora de los pavos autóctonos hacia el desarrollo sostenible de los recursos zoogenéticos.

Palabras clave: *medida corporal, rasgo adaptativo, análisis discriminante, pavo, Nigeria*

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Introduction

Characterization means the distillation of knowledge, which contributes to the reliable prediction of the genetic performance of an animal genetic resource (AnGR) in a defined environment and provides a basis for distinguishing different AnGR and for assessing available diversity. It involves a clear definition of the genetic attributes of an AnGR and the environments to which it is adapted or known to be partially or not adapted at all (Sponenberg *et al.*, 2000; Rege and Okeyo, 2010; Melesse and Negesse, 2011). The AnGR of poultry in West Africa are mainly represented by domestic indigenous chicken (*Gallus gallus domesticus*), guinea fowl (*Numida meleagris*), duck (*Cairina* sp.) and turkey (*Meleagris* gallopavo). With the rapid development of the poultry industry worldwide, especially in developing countries, importation of temperate-zone high-performance stocks to hot regions is on the rise (Melesse, 2011), and this has led to a threat of AnGR as indigenous birds are being excluded from the intensive production systems. One of the most difficult issues to deal with in the context of the management of AnGR is priority setting, both for conservation of endangered or potentially endangered populations or breeds and for breed improvement programmes (Zanetti, 2009). Managing breeds for a secure future tackles the challenges of maintaining AnGR in species and breeds of livestock and poultry (Sponenberg and Bixby, 2007). Indigenous birds are a vital reservoir of gene resources and their conservation has a technical role related to the future development of the productive system as well as a social-cultural role (Benabdeljelil and Arfaoui, 2001; Camacho-Escobar *et al.*, 2008; Cerolini *et al.*, 2010; Francesch, Villalba and Cartana, 2011). Breeding and selection strategies can therefore be exploited to achieve the best possible production in unfavourable environments.

Approximately 70 percent of the world’s rural poor depend on livestock as an important component of their livelihoods (Hoffman, 2010). Turkey production is both an important and a profitable agricultural industry, with a rising global demand for its products (Case, Miller and Wood, 2010). Local turkeys is about 1.05 million in Nigeria, being the smallest when compared with other poultry species such as chicken estimated to be 160 million, guinea fowl 8.3 million and ducks 1.7 million (FAOSTAT, 2011). However, scarce works deal with the characterization of indigenous turkeys in Nigeria. Because the genotypes required for the future are difficult to predict, characterization of indigenous turkey populations can make a major contribution to their effective long-term management and conservation. The first step in such characterization involves the use of morphological traits.

The mechanisms involved in the control of the morphology of a bird are too complex to be explained only under univariate analysis of variance because all related traits are biologically correlated owing to pleiotropy or linkage. Therefore, the univariate analysis does not take account of all the co-variation that exists between the traits. A multivariate approach might offer a better resolution. Multivariate discriminant analysis is currently being employed in evaluating genotypes based on growth, carcass parameters (Rosario *et al.*, 2008; Al-Atiyat, 2009), morphological variables (FAO, 2009; Yakubu and Ibrahim, 2011) and heat-tolerant traits (Chen *et al.*, 2004; Castanheira *et al.*, 2011). Although attempts have been made at characterizing chickens in Nigeria using the multivariate approach (Yakubu, Kuje and Okpeku, 2009; Yakubu *et al.*, 2010), there is paucity of information on the multivariate characterization of morphological and heat-tolerant traits for studying diversity in turkeys in

Nigeria. Therefore, the present investigation aimed at differentiating indigenous, cross-bred and exotic turkeys using multivariate discriminant analysis. This will assist in initiating a programme for the preservation of AnGR of indigenous turkeys in Nigeria.

Materials and methods

Study area

The research work was carried out at the Turkey Breeding Unit of the Teaching and Research Farm of the College of Animal Science and Livestock Production, University of Agriculture, Abeokuta, Ogun State, Nigeria. The environmental conditions of the study area have been previously described in Ilori *et al.* (2010).

Management of birds

A total of 228 poults consisting of 84 indigenous, 79 indigenous × exotic cross-breds and 65 exotic poults of both sexes (132 males and 96 females) were used. Nigerian indigenous turkeys are a population of birds that have become adapted to the Nigerian environment by some combination of genetic changes occurring over generations and environmentally induced developmental events reoccurring during each generation. The turkeys are reared mostly by the rural folks with little inputs from the owners. A large foundation stock of these indigenous stocks was established at the Poultry Breeding Unit. The exotic turkeys (Nicholas White), on the other hand, were obtained from Obasanjo Farm, the country representative of Nicholas white brand of Aviagen Turkey Ltd Lewisburg, West Virginia, USA. Parent stocks of these exotic turkeys are maintained also at the Poultry Breeding Unit. The male Nicholas White turkeys and the female indigenous turkeys were used to generate the cross-breds through artificial insemination. The poults were brooded in deep litter pens according to their genetic groups. All poults were wing-tagged for proper identification and subjected to the same management practices throughout the experimental period. The essence of rearing the turkeys in pens was to ensure appropriate management and monitoring of their performance. Commercial feeds were provided for the birds ad libitum. Starter mash containing 28 percent crude protein (CP), grower mash 24 percent CP and finisher mash 20 percent CP were fed to the birds from 0 to 6 weeks, 7 to 16 weeks and 17 to 20 weeks, respectively. Clean and cool water was supplied ad libitum. Necessary vaccinations against Newcastle, fowl pox and gumboro diseases as well as prophylactic antibiotics and anticoccidial drugs were administered to the birds.

Data collection

At 20 weeks of age, body weight (BW) (kg) and five morphometric traits (cm) namely the body length (BL) from the base of the comb to the base of the tail around the uropigial gland, the shank length (SL) from the hock joint to the tarsometarsus digit-3 joint, the thigh length (TL) between the hock joint and the pelvic joint, the keel length (KL) of the cartilaginous keel bone or metasternum and the breast girth (BG) were recorded. The heat-tolerant traits measured included rectal temperature (RT), pulse rate (PR) and respiratory rate (RR). The relationship between PR and RR together with their normal average values was used to derive heat stress index (HI). RT was measured by inserting a digital rectal thermometer into the rectum of the birds for 1 min after which the readings were taken. PR was measured by placing finger tips under wing vein and counting the number of beats per minute using a stopwatch while RR was determined for each bird by counting the movement of abdominal region or vent using a stopwatch. RT, PR and RR of all the birds were measured between the hours of 7.00 a.m. and 9.00 a.m. as well as between 1.00 p.m. and 3.00 p.m. at 20 weeks of age as described by Oladimeji *et al.* (1996).

Statistical analysis

Analysis of variance was performed to test the fixed effect of genotype and sex on morphological and heat-tolerant traits of turkeys. Means were separated using Duncan's multiple range test at 95 percent confidence interval. Multivariate analysis was conducted to investigate how similar or different the turkey populations are. Stepwise discriminant analysis of the ten traits using the STEPDISC procedure (SAS, 2010) indicated which variable contributed most to differentiation among the three genetic groups. Canonical discriminant analysis (CANDISC procedure) was performed to obtain canonical variables, canonical coefficients and Mahalanobis distances between the three populations based on the selected traits. The DISCRIM procedure (nearest-neighbour discriminant analysis) was used to find the percentage of correct assignment of each bird to its genetic group.

The linear model employed was

$$Y_{ij} = \mu + G_i + S_j + e_{ij}$$

where Y_{ij} is the observed variable, μ is the overall mean, G_i is the effect of genotype (i = indigenous, cross-bred, exotic), S_j is the effect of sex (j = male, female), e_{ij} is the random error terms such that e_{ij} are independent normally distributed random variables with $E(e_{ij}) = 0$ and $V(e_{ij}) = \sigma^2$.

Results

The means and standard deviations of the morphometric and heat-tolerant traits of the indigenous, cross-bred and exotic turkeys are presented in Table 1. The exotic turkeys had significantly ($p < 0.05$) higher mean values than the

Table 1. Descriptive statistics of the morphological and heat-tolerant traits of turkeys according to genotype and sex.

Trait	Indigenous		Exotic		Cross-bred		Male turkey		Female turkey	
	Mean	SD	Mean	SD	Mean	SD	Mean	SD	Mean	SD
BW	2.85^{c}	0.36	4.47^{a}	0.23	3.33^{b}	0.22	3.59^{a}	0.71	3.33^{b}	0.70
BL	38.93^{c}	2.24	48.44^{a}	3.18	44.66^{b}	1.10	44.31^{a}	4.80	42.68^{b}	3.89
SL	15.21^{c}	0.91	17.73^{a}	2.50	16.55^{b}	1.24	16.97^{a}	2.11	15.60^{b}	1.19
TL	18.44^{c}	1.40	21.01^{b}	2.22	22.68^{a}	1.09	21.06^{a}	2.20	20.07^{b}	2.56
KL	13.56^{c}	0.77	15.57^{a}	0.70	14.57^{b}	0.44	14.70^{a}	1.06	14.19^{b}	0.93
BG	39.75^{c}	2.65	53.59^{a}	4.29	44.95^{b}	1.08	45.85^{a}	6.54	45.01^{a}	5.86
RT	40.37^{b}	0.17	40.67^{a}	0.19	40.66^{a}	0.28	40.56^{a}	0.26	40.54^{a}	0.26
RR	34.75^{c}	6.70	51.05^{a}	7.57	36.78^{b}	2.37	40.68^{a}	9.37	39.30^{a}	8.75
PR	277.81^{c}	14.56	335.74^{a}	38.14	308.66^{b}	7.77	307.30^{a}	34.60	301.88^{a}	29.28
HI	0.815^{b}	0.16	0.998^{a}	0.18	0.776^{b}	0.06	0.859^{a}	0.17	0.845^{a}	0.16

BW: body weight, BL: body length, SL: shank length: TL: thigh length, KL: keel length, BG: breast girth, RT: rectal temperature, RR: respiratory rate, PR: pulse rate, HSI: heat stress index.

^{abc}Means within the same row having different superscripts differ significantly ($p < 0.05$) among the three genotypes.

^{ab}Means within the same row having different superscripts differ significantly ($p < 0.05$) between the two sexes.

indigenous and cross-breds in all the morphological traits with the exception of TL, which was significantly higher in cross-breds than in their parental populations. However, both the indigenous and cross-bred turkeys appeared to tolerate heat better than their exotic counterparts based on HI. Sexual dimorphism was observed in the morphological traits with males having significantly higher ($p < 0.05$) BW, BL, SL, TL and KL than females. However, the two sexes did not differ ($p > 0.05$) in the heat-tolerant traits.

The stepwise discriminant analysis indicated that eight out of the ten original traits were effective at detecting the differences among the three turkey populations. The eight traits showing a partial correlation above 10 percent are shown in Table 2. BW was the most discriminating variable followed by TL, HI, BG, RR, RT, SL and PR, respectively. The first three variables were included in the final model as they were more informative.

The canonical analysis carried out on the morphological and heat-tolerant variables (BW, TL and HI) identified two statistically significant ($p < 0.01$) canonical variables that accounted for 83.04 and 16.96 percent of the total variation (Table 3). The first canonical variable (CAN 1) was the linear combination of traits that best discriminates among the three genetic groups. BW and HI were highly correlated to CAN 1. The second canonical variable (CAN 2) was the next best linear combination, orthogonal to the first one. TL was highly associated with CAN 2. A bi-dimensional plot built with the two canonical variables illustrating the relationship between the three genetic groups is shown in Figure 1. The plot exhibited no significant overlap of any kind.

Table 3. Total canonical structure of the three turkey populations.

Traits	CAN 1	CAN 2
Body weight	0.98	0.20
Thigh length	0.22	0.96
Heat stress index	0.56	−0.24
Canonical correlation	0.93	0.76
Approximate standard error	0.009	0.028
Eigenvalue	6.522	1.332
Variance accounted for (%)	83.04	16.96
Cummulative variance (%)	83.04	100.00

The Mahalanobis distance between the indigenous and exotic turkeys (36.68) was longest while the shortest distance was recorded for the indigenous turkeys and their cross-bred counterparts (7.97). The distance between

Table 2. Summary of stepwise selection of traits.

Variables entered	Partial R^2	F-value	Pr > F	Wilks' Lambda	Pr < Lambda	Average squared canonical correlation	Pr > ASCC
BW	0.818	495.51	<0.0001	0.182	<0.0001	0.409	<0.0001
TL	0.572	147.23	<0.0001	0.078	<0.0001	0.688	<0.0001
HI	0.256	36.99	<0.0001	0.027	<0.0001	0.816	<0.0001
BG	0.221	31.00	<0.0001	0.048	<0.0001	0.725	<0.0001
RR	0.210	29.05	<0.0001	0.062	<0.0001	0.709	<0.0001
RT	0.168	21.95	<0.0001	0.040	<0.0001	0.760	<0.0001
SL	0.103	12.27	<0.0001	0.034	<0.0001	0.826	<0.0001
PR	0.102	12.27	<0.0001	0.036	<0.0001	0.773	<0.0001

BW: body weight, TL: thigh length, HSI: heat stress index, BG: breast girth, RR: respiratory rate, RT: rectal temperature, SL: shank length, PR: pulse rate.

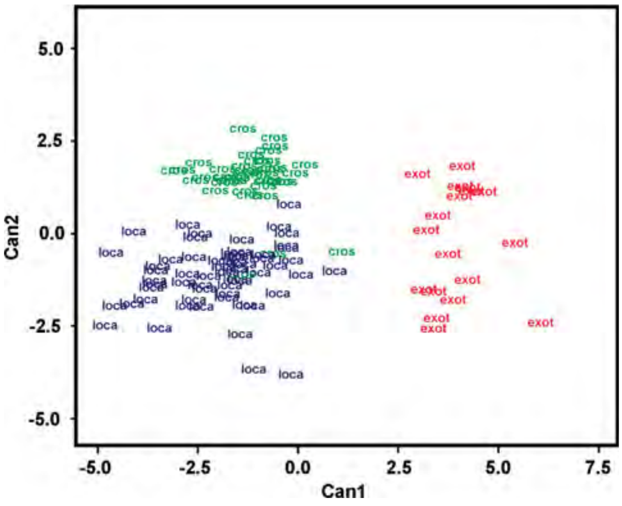

Figure 1. Canonical representation of the three turkey genetic groups. loca = indigenous turkeys, exot = exotic turkeys, cros = cross-bred turkeys.

the exotic turkeys and cross-breds (29.14) was intermediate. All pair-wise distances were significant ($p < 0.001$), demonstrating that differences between populations are important. However, local and cross-bred turkeys were closer to each other compared with their exotic counterparts.

In the nearest-neighbour discriminant analysis, 100.00 percent of exotic, 98.73 percent of cross-bred and 96.43 percent of indigenous turkeys (an average of 98.37 percent for the three populations) were correctly assigned into their genetic groups (Table 4).

Discussion

In the developed world, livestock recording schemes provide a continuous source of data for monitoring trends in the industry, including improved understanding of breeds and production systems. Unfortunately, such structures are not available in most developing countries (Rege and Okeyo, 2010). Therefore, the implementation of objective methodologies assessing the morphological and physiological parameters of birds is of major importance. While morphological differences can be mainly attributed to genetic differences in the present study, heat-tolerant traits are more likely to be affected by environmental influences. Each breed has a determined morpho-structure, an expression of its quantitative morpho-structure that responds to a particular environment to which it is adapted or being raised. The indigenous turkeys represented a pool of heterogeneous and unimproved individuals unlike their exotic counterparts that have undergone directional selection for high growth rate. However, the indigenous turkeys exhibited better adaptability in terms of heat-tolerant traits compared with their exotic counterparts. It is important to know the tolerant and adaptive capacity of various genetic groups as a technical basis for turkey exploration including the direction of cross-breeding programmes. Different phenotypic expression of a genotype in response to different environments has been reported (Kolmodin *et al.*, 2003). This is more so important because the most notable effect of selective breeding on physiology reduces the responsiveness to stress-evoking stimuli (i.e. environmental stress) as an adaptation to living in a biologically safe environment (Korte *et al.*, 2005). According to Dana *et al.* (2010), adaptation to the production environment was found as an important attribute of village chickens in Ethiopia, while Kohler-Rollefson, Rathore and Mathias (2009) reported that the ability to deal with thermal stress could provide a competitive advantage for indigenous breeds over their temperate counterparts in the event of climate change. The onset of air breathing has also been associated with the pattern of ossification of the uncinate processes in developing turkeys (Tickle and Codd, 2009), thereby giving an understanding of the skeletal changes during ontogeny and importance of developmental patterns. This might equally have an indirect influence on the adaptive capacity of birds. The better performance of cross-breds over the indigenous birds in body measurements portends hope for the genetic improvement of the native stock for improved productivity.

Table 4. Percent (%) of individual turkeys classified into three genetic groups.

Breed	Indigenous	Exotic	Cross-bred
Indigenous	96.43	0.00	3.57
Exotic	0.00	100.00	0.00
Cross-bred	1.27	0.00	98.73
Error level	0.036	0.000	0.013
Priors	0.333	0.333	0.333

The wide variations between the sexes might be connected with differences in growth rates, growth strategies, metabolic rates and reproductive strategies. According to Baeza *et al.* (2001), sexual dimorphism is attributable to the usual between-sex differential hormonal action, which invariably leads to differential growth rates. Similar findings had been reported by other workers (Blondel *et al.*, 2002; Yakubu, 2011).

Selecting the most important traits that explain the major part of the total phenotypic variability between turkey genotypes is a purposeful step towards selection. Variables of body skeleton sizes could be used as distinguishing variables or markers (Mulyono, Sartika and Nugraha, 2009) that can give an overview of specification of the homogeneity or heterogeneity of birds.

A considerable genetic variability was observed between the three genetic groups. The canonical analysis performed on the complete set of morphometric and heat-tolerant variables produced a grouping which was expected, judging from the univariate test. It showed a clear separation of the three genetic groups in the space created by the two canonical variables. Indigenous turkeys were more separated from their exotic counterparts. The Mahalanobis test established significant differences among the three genetic groups studied. Separate grouping especially of the indigenous and exotic turkeys is an indication that they have different morphometric traits as well as varying response to heat tolerance. This might be attributed to the difference in the geographical origin of the two genetic groups (the indigenous birds are more adaptable to the hot and humid tropical environment while the exotic birds were imported from the temperate region). According to Mulyono *et al.* (2009), differences of the origin distinguish the phenotypic response based on the potential for additive genes controlling the body measurements of each bird's genotype to the nature of growth, development and osteogenesis. The nearest-neighbour discriminant analysis revealed that a 98.37 percent correct classification of the samples of the three genetic groups can be achieved using a combination of BW, TL and HI variables. This affirmed the heterogeneity of the turkey populations. The present findings are in consonance with earlier reports on the use of discriminant analysis to separate birds of different genetic groups or ecotypes (Chen *et al.*, 2004; Abdelqader, Wollny and Gauly, 2008; Rosario *et al.*, 2008; Yakubu, Kaankuka and Ugbo, 2011).

Conclusions

The application of univariate and multivariate statistical methods enabled us to discriminate between the indigenous, exotic and cross-bred turkeys using morphometric and heat-tolerant traits. BW, TL and HI were found as the most discriminating variables in separating the birds. The Mahalanobis distances between the turkey populations were highly significant. The average 98.37 percent of correct assignments was relatively high, thereby justifying the methodology applied in separating the three genetic groups. However, geometric morphometry (shape analysis), molecular genetic analyses with diagnostic marker loci in addition to an increased sample size would be desirable in future research because these might increase the discriminant power and precision of the classification.

Statement of interest: The authors declare that there are no competing interests.

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Caracterización genética de los pequeños rumiantes saharauis con microsatélites de ADN

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Resumen

En los años setenta, gran parte del pueblo Saharaui tomó el camino del exilio estableciéndose como refugiados en los campos de Tindouf (Argelia). Con ellos se llevaron su medio de vida como pastores tradicionales, las razas de pequeños rumiantes que eran gran parte de su sustento. Casi tres décadas después, estas razas que han sufrido la guerra y el éxodo están en un serio peligro de extinción, en primer lugar por su situación y en segundo lugar por el desconocimiento científico sobre las mismas. En el presente trabajo, realizamos una caracterización genética de las razas ovinas Sidaun y Kerrian, así como de la raza caprina Buzguender, en los campos de refugiados Saharauis. Los resultados obtenidos indican que todas las razas mantienen un elevado nivel de diferenciación genética y no evidencian signos de migraciones de genes exóticos recientes. Esto es alentador ya que indica que aun hay tiempo de conservar estos recursos genéticos animales de elevado valor ecológico por su capacidad de supervivencia en el desierto.

Palabras clave: *Sahara occidental, microsatélites, distancia genética, conservación*

Summary

In the 1970s a large proportion of the people of Western Sahara went into exile, settling as refugees in camps in Tindouf, Algeria. They took with them their traditional pastoralist way of life and their breeds of small ruminants, which formed the main part of their diet. Almost three decades later, these breeds, having endured the war and the exodus, are in danger of extinction, firstly because of their situation, and secondly because of scientific ignorance about them. In the present paper, we develop a genetic characterization of the Sidaun and Kerrian breeds of sheep and the Buzguender breed of goats in the Saharawi refugee camps. The results indicate that all the breeds studied still have a high level of genetic differentiation and are not showing signs of recent exotic gene migrations. This is encouraging, for it indicates that we are in time to conserve these genotypes of high ecological value for their capacity to survive in the desert.

Keywords: *Western Sahara, microsatellites, genetic distance, conservation*

Résumé

Au cours des années 1970, une grande partie des populations du Sahara occidental ont émigré en masse et se sont installées, en tant que réfugiés, dans les terres de Tindouf (Algérie). Les réfugiés avaient emporté leurs moyens d'existence en tant que pasteurs traditionnels, leurs petits ruminants qui représentaient une part importante de leur alimentation. Presque 30 ans après, ces races, qui ont subi la guerre et l'exode, sont menacées d'extinction, d'abord en raison de leur situation et aussi à cause de l'ignorance scientifique qui les concerne. Cet article présente la caractérisation génétique des races de moutons Sidaun et Kerrian et de chèvres Buzguender réalisée dans les terres des réfugiés du peuple Saharoui. Les résultats indiquent que toutes les races analysées maintiennent encore un niveau élevé de différenciation génétique et qu'elles ne présentent pas de signes de migrations récentes de gènes exotiques. Il s'agit d'un résultat très positif car il montre qu'il est encore possible de conserver ces génotypes qui possèdent une grande valeur écologique en raison de leurs capacités de survie dans le désert.

Mots-clés: *Sahara occidental, microsatellites, distance génétique, conservation*

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1 Introducción

La descolonización del Sáhara por parte de España en los años 70 del siglo XX, que terminó en una apropiación del territorio por parte de Marruecos, obligó a cientos de miles de Saharauis a huir a la vecina Argelia como refugiados. Con ellos se llevaron sus animales domésticos, como principal patrimonio de un pueblo de tradición nómada y pastoril como el Saharaui.

Hoy, los campamentos de refugiados Saharauis se ubican en una meseta desértica llamada Hammada, teniendo como referencia más cercana la ciudad de Tindouf, al Suroeste de Argelia, en el territorio más árido e inhóspito del desierto

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Figura 1. a. Localización geográfica de los campamentos saharauis próximos a Tindouf (Argelia). b. Fotografía de uno de los campamentos saharauis (http://www.sadicum.org/campamentos/campamentos.htm).

del Sáhara (Figuras 1a, 1b). En estos campamentos viven cerca de 200.000 personas desde el año 1976.

Estos campamentos han tomado los nombres de provincias y ciudades de su tierra de origen: el Sáhara Occidental. Los campamentos de El Aaiun, Ausserd y Smara están situados más cerca de la ciudad argelina de Tindouf, mientras que el campamento de Dajla se ubica más alejado que los anteriores (Figura 1b). Están distribuidos de forma discontinua en el territorio, dependiendo de la existencia de pozos de agua potable en el lugar. La Hammada de Tindouf se caracteriza por la rigidez de su clima, con temperaturas muy oscilantes entre el día y la noche, que pueden superar los 50°–60°C en verano y hasta –1°C en invierno.

Otro factor adverso que dificulta la supervivencia en esta zona son los vientos sirocos y las tormentas de arena, muy violentas y secas. Debido a la escasez de agua y de vegetación, estos territorios no habían sido objeto de explotaciones agrícolas hasta el asentamiento en esta región del pueblo Saharaui.

Saharauis (‘gente del desierto’), es el nombre dado a las tribus nómadas y de pastoreo que tradicionalmente habitaban en el área costera occidental de África, llamada Sáhara. La población Saharaui era esencialmente nómada, pastores de camellos, cabras y ovejas en las llanuras bajas arenosas del Sáhara Occidental, dependientes de alimentos como la leche de camella, carne, dátiles, azúcar y pequeñas cantidades de cereales y legumbres. Se movilizaban dependiendo de la estacionalidad y sus rutas se basaban fundamentalmente en la localización de los pozos, abrevaderos y las lluvias. En 1960, bajo la colonización española, los Saharauis se hicieron más sedentarios.

La economía saharaui tradicional se ha basado en el pastoreo de razas locales fuertemente adaptadas a un medio tan hostil como es el desierto, aunque siempre planteándose como una economía de subsistencia, a través de pastores nómadas que han utilizaban como principal medio de desplazamiento el camello, llevando consigo sus rebaños de cabras y ovejas. La agricultura, poco extendida, se limitaba tradicionalmente al cultivo de productos como la cebada, generalmente en terrenos arcillosos de subsuelo húmedo. La pesca, por otro lado, ha constituido siempre uno de los grandes recursos para el país, desarrollándose una importante actividad pesquera en sus costas. En la actualidad, la única práctica de agricultura en los campamentos Saharahuis, dentro de su sistema de subsistencia autárquico, es el cultivo de cereales, especialmente la cebada, en los periodos y regiones en que las lluvias permiten la siembra.

Los recursos genéticos de pequeños rumiantes en el África subsahariana juegan un papel importante en el bienestar de las personas, especialmente en zonas con mayor escasez de recursos. Estos recursos genéticos, incluyendo ovejas y cabras, proporcionan sustento, ingresos en efectivo, vínculos socio-culturales y constituyen un seguro contra riesgos en ambientes frágiles y desfavorables, sobre todo en las zonas rurales (Fitzhugh *et al.*, 1992; Lebbie *et al.*, 1996; Ramsay *et al.*, 1984; Winrock International, 1992).

Atendiendo a la situación actual de los Saharauis como pueblo en éxodo, en los que todos los presupuestos y recursos disponibles se destinan a la supervivencia, hasta ahora se han realizado muy pocos estudios científicos sobre sus recursos genéticos animales, y por tanto, no han existido programas de conservación ni tan siquiera de caracterización de sus razas nacionales. Sólo debemos destacar aquí el trabajo de Schulz *et al.* (2010) sobre la caracterización genética del camello Saharaui o raza del Sahel.

En el seno de una colaboración entre técnicos españoles y saharauis se ha planteado en el presente trabajo una caracterización genética con marcadores microsatélites de las razas ovinas y caprinas que constituyen buena parte del patrimonio genético y del sustento del pueblo Saharaui refugiado en los campamentos de Tindouf.

1.2 Patrimonio genético saharaui

1.2.1 Las ovejas saharauis

La oveja Kerrian es muy resistente. Por su aspecto externo podría pensarse que pertenece al tronco merino y procede de la época de la presencia española en el Sáhara Occidental. Son animales no muy grandes, sus hembras son buenas productoras de leche y carne y su lana se utiliza para la confección de las viviendas de los campamentos Saharauis. Los cueros son más frágiles que los de los caprinos. Los de ovino se utilizan para confeccionar sandalias, almohadas y bolsas para el tabaco. Son de vellón blanco y a veces con manchas negras. Los machos tienen cuernos (Figura 2, derecha). La oveja Sidaun proviene de Mali, de Argelia y de Mauritania. Hay de capas blancas, blancas y negras y de color almendra. La raza Adiman, es más parecida a la Sidaun, pero es más robusta y tiene más pelaje, de mayor alzada que la Kerrian aunque tiene menos pelo y es menos resistente.

1.2.2 La cabra Buzguender

La cabra autóctona del Sáhara es la Buzguender, y se encuentra también en la frontera con Mauritania. Son negras, con mucho pelo, bajas de alzada, unos 80 cm, suelen tener perilla y algunas presentan mamellas (Figura 2, izquierda). Las orejas son medianas a grandes y caídas. En cuanto a los cuernos, los machos tienen cuernos en tirabuzón y las hembras en medio arco. Viven una media de 9 a 10 años. Se caracterizan por su gran resistencia a períodos sin agua, también al frío y a las enfermedades. Si ha habido buenos pastos paren un cabrito al inicio del invierno. Además de la carne y la leche, se utiliza el pelo, que se trenza y con el que se confeccionan las viviendas típicas de los campamentos saharauis. Las pieles se emplean para fabricar depósitos de agua y leche y para confeccionar sandalias. Otras razas caprinas africanas e incluso españolas tienen cada vez mayor implantación en el Sáhara y se están cruzando con las autóctonas, colocando a estas últimas en un mayor riesgo de desaparición.

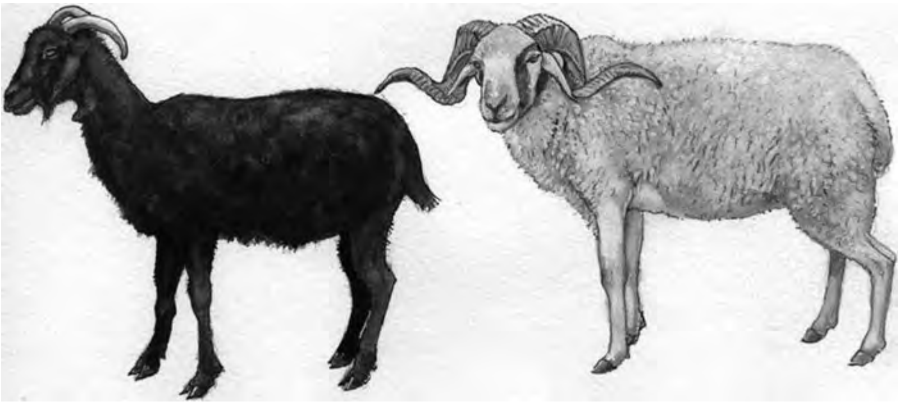

Figura 2. Grabado de las cabras (izquierda) y ovejas saharauis (derecha), realizado por D. Ángel Domínguez

2 Material y métodos

Este estudio es el resultado de una colaboración entre técnicos españoles y saharauis cuyo objetivo principal es la sensibilización de la situación actual de las razas autóctonas de ovinos y caprinos saharauis. Cuando los saharauis fueron desplazados por Marruecos de su territorio, llevaron con ellos sus razas de ovejas y cabras autóctonas, pero durante el tiempo transcurrido en los campamentos de refugiados, estos han ido desapareciendo debido en gran medida a una estrategia para disolver el patrimonio cultural saharaui, del que forman parte sus razas autóctonas, que consiste en el cruzamiento de las mismas con razas locales de Marruecos. Los pocos rebaños de ovejas que quedan, pertenecen a la República Árabe Saharaui Democrática, pero un pequeño número de animales está todavía en manos privadas que ante la imposibilidad de criar sus razas tradicionales, compran para la fiesta del cordero animales de otras razas de Mauritania o Mali. Esto dificulta en gran medida encontrar animales puros, sobre todo de ovinos. En el caso de los caprinos, los pocos animales puros que quedan están en manos de mujeres viudas de guerra que mantienen su raza tradicional.

Todas estas circunstancias han dificultado el disponer de un muestreo representativo de las razas locales saharauis en los campamentos de refugiados, y, aunque el número de muestras es escaso para un estudio de caracterización genética, este trabajo contribuirá al conocimiento de estas razas y servirá para despertar el interés por ellas antes de su desaparición total.

Se han analizado 21 muestras de pelo de la raza ovina Sidaun, 5 de la raza ovina Kerrian y 11 de la raza caprina Buzguender obtenidas en varios rebaños de los campamentos Saharauis de Tindouf (Argelia).

Se ha extraído el ADN de los bulbos pilosos de las muestras utilizando el método de Kawasaki (1990), y se han amplificado 31 microsatélites en las muestras de ovinos (Tabla 1) y 29 en la raza caprina Buzguender (Tabla 4) mediante la técnica de la Reacción en Cadena de la Polimerasa. Los microsatélites utilizados en ambas especies se han seleccionado siguiendo las recomendaciones de la FAO (Hoffman *et al.*, 2004) y

Tabla 1. Microsatélites tipificados, número de alelos detectados, número efectivo de alelos, heterocigosis esperada y observada, contenido de información polimórfica, y P-value en la raza ovina Sidaun.

Microsatélite	*Nº Alelos*	*Ne*	*He*	*Ho*	*PIC*	*P-value*
BM1818	10	6,68	0,875	0,833	0,833	**0,0091**
BM1824	4	3,53	0,734	0,905	0,664	**0,0321**
BM6506	5	1,82	0,463	0,450	0,427	0,5204
BM6526	9	4,85	0,813	0,810	0,773	0,2567
BM8125	3	2,17	0,553	0,762	0,478	0,0795
CSRD247	4	2,19	0,558	0,450	0,460	0,2219
CSSM66	9	5,73	0,846	0,905	0,804	0,1060
D5S2	5	2,90	0,673	0,316	0,614	**0,0008**
ETH10	2	1,27	0,215	0,238	0,188	1
ETH225	6	3,42	0,725	0,524	0,659	0,0522
HSC	11	7,67	0,891	0,810	0,856	0,1135
ILSTS011	7	3,42	0,725	0,714	0,675	0,7842
INRA035	6	4,41	0,792	0,810	0,737	0,9379
INRA063	8	5,41	0,836	0,800	0,791	**0,0364**
MAF209	7	3,00	0,683	0,619	0,616	0,3263
MAF214	4	2,59	0,628	0,667	0,537	1
MAF65	5	2,42	0,600	0,476	0,500	0,5604
McM527	7	3,77	0,753	0,762	0,696	0,1766
OarAE0129	5	3,19	0,704	0,500	0,625	**0,0013**
OarCP20	5	4,18	0,779	0,905	0,724	0,7507
OarCP34	6	3,47	0,729	0,714	0,660	0,6891
OarCP49	8	3,68	0,746	0,905	0,698	0,9837
OarFCB11	7	2,67	0,641	0,650	0,594	**0,0078**
OarFCB20	8	4,48	0,796	0,714	0,754	**0,0062**
OarFCB304	8	6,04	0,855	0,857	0,814	**0,0022**
OarFCB48	10	5,96	0,852	0,857	0,814	**0,0081**
RM006	6	5,07	0,822	0,857	0,775	0,7165
SPS115	3	2,93	0,675	0,524	0,585	**0,0297**
TGLA122	9	3,23	0,707	0,714	0,670	0,1657
TGLA126	9	7,35	0,885	0,476	0,849	**0,0001**
TGLA53	7	4,57	0,800	0,857	0,750	0,0973

Nº Alelos: Número de alelos. *Ne:* Número efectivo de alelos. *He:* Heterocigosis esperada. *Ho:* Heterocigosis observada. *PIC:* Contenido de información polimórfica. *P-value:* Valores de probabilidad obtenidos en la prueba de equilibrio Hardy-Weinberg realizada mediante un test exacto aplicando el método de Monte Carlo con 100 baterías de análisis y 5000 permutaciones por batería (se destacan en negrita los marcadores que no se encuentran en equilibrio Hardy-Weinberg, $p < 0,05$).

Tabla 2. Microsatélites tipificados, número de alelos detectados, número efectivo de alelos, heterocigosis esperada y observada, contenido de información polimórfica, y P-value en la raza ovina Kerrian.

Microsatélite	*Nº Alelos*	*Ne*	*He*	*Ho*	*PIC*	*P-value*
BM1818	2	2,00	0,600	0.333	0,375	1,0000
BM1824	3	2,63	0,689	1,000	0,548	0,4286
BM6506	3	2,63	0,689	0.600	0,548	0,6190
BM6526	4	3,33	0,778	0.600	0,645	0,1873
BM8125	4	2,78	0,711	1,000	0,581	0,4286
CSRD247	3	2,63	0,689	0.600	0,548	0,6190
CSSM66	6	5,00	0,889	1,000	0,772	1,0000
D5S2	3	2,91	0,750	0.250	0,582	0,1429
ETH10	1	1,00	0,000	0.000	0,000	–
ETH225	3	2,27	0,622	0.800	0,499	1,0000
HSC	6	4,17	0,844	1.000	0,730	1,0000
ILSTS011	5	3,57	0,800	1,000	0,676	**0,0000**
INRA35	5	3,57	0,800	0.600	0,676	0,4680
INRA63	6	5,00	0,889	0.800	0,772	0,1411
MAF209	5	2,50	0,667	0.600	0,570	0,6150
MAF214	3	2,38	0,644	0.800	0,492	0,6190
MAF65	3	2,27	0,622	0.400	0,499	0,2381
McM527	4	3,57	0,800	0.400	0,672	0,0603
OarAE0129	2	2,00	0,571	0.500	0,375	1,0000
OarCP20	4	3,85	0,822	1.000	0,692	**0,0286**
OarCP34	5	4,55	0,867	1.000	0,745	0,2990
OarCP49	4	3,33	0,778	0.800	0,645	0,6952
OarFCB11	6	5,00	0,889	1.000	0,772	**0,0000**
OarFCB20	5	3,85	0,822	0.600	0,701	0,0875
OarFCB304	5	4,17	0,844	0.800	0,720	0,3563
OarFCB48	4	2,78	0,711	0.800	0,581	0,2063
RM006	6	4,17	0,844	0.800	0,730	0,7915
SPS115	5	4,17	0,844	1,000	0,720	0,8486
TGLA122	3	1,85	0,511	0.400	0,410	0,3333
TGLA126	5	4,55	0,867	0.400	0,745	0,0583
TGLA53	6	5,00	0,889	1.000	0,772	1,0000

Nº Alelos: Número de alelos. *Ne:* Número efectivo de alelos. *He:* Heterocigosis esperada. *Ho:* Heterocigosis por recuento directo. *PIC:* Contenido de información polimórfica. *P-value:* Valores de probabilidad obtenidos en la prueba de equilibrio Hardy-Weinberg realizada mediante un test exacto aplicando el método de Monte Carlo con 100 baterías de análisis y 5000 permutaciones por batería (se destacan en negrita los marcadores que no se encuentran en equilibrio Hardy-Weinberg, $p < 0,05$).

han demostrado su utilidad en estudios de diversidad ovina y caprina en trabajos previos (Quiroz *et al.*, 2008; Lasagna *et al.*, 2011; Martínez *et al.*, 2006). La separación por tamaños de los fragmentos obtenidos se ha realizado mediante electroforesis en gel de poliacrilamida en un secuenciador automático ABI 377XL. Para el análisis de los fragmentos y la tipificación alélica se han utilizado los programas informáticos Genescan Analysis 3.1.2 y Genotyper 2.5.2 respectivamente. Se han calculado las frecuencias alélicas, las heterocigosis y el contenido de información polimórfica (PIC) de cada microsatélite mediante la aplicación Microsatellite Toolkit (Park, 2002). El número efectivo de alelos se ha calculado mediante el programa Fstat v. 2.9.3 (Goudet, 2001). Se ha realizado una prueba de equilibrio Hardy-Weinberg mediante el programa Genepop v. 3.1c (Raymond & Rousset, 1995), que aplica el test exacto de Fisher usando el método en cadena de Monte Carlo Markov (Guo & Thompson, 1992). Se ha calculado el valor de Fis (Weir & Cockerham, 1984) de cada población con un intervalo de confianza de 95% con 1000 permutaciones y 10 000 bootstraps mediante el programa Genetix v. 4.02 (Belkhir *et al.*, 2003).

3 Resultados y Discusión

3.1 Caracterización genética de las razas ovinas razas Kerrian y Sidaun

En la raza Sidaun, todos los microsatélites utilizados han resultado polimórficos, encontrándose un mínimo de 2 alelos en el microsatélite ETH10 y un máximo de 11 alelos para el marcador HSC (Tabla 1). El número efectivo de alelos mínimo se encuentra también en el marcador ETH10 (1,27) y el máximo en el marcador HSC (7,67). La heterocigosis esperada más alta se encuentra para el marcador HSC con un valor de 0,891 y la más baja para el ETH10 con un valor de 0,215. Los valores de heterocigosis observada oscilan entre un máximo de 0,905 para los marcadores BM1824, CSSM66, OarCP20 y OarCP49 y un mínimo de 0,238 para el locus ETH10. El valor de PIC más alto es el

Tabla 3. Número de muestras analizadas, número promedio de alelos, número efectivo de alelos medio, heterocigosis media esperada y observada para todos los microsatélites, y valores de Fis por población.

	N	*NA (SD)*	*Ne (SD)*	*He (SD)*	*Ho (SD)*	*Fis (IC 95%)*
SIDAUN	21	6,55 (2,28)	4,00 (1,62)	0,721 (0,025)	0,690 (0,018)	0,045 (−0,020 – 0,050)
KERRIAN	5	4,16 (1,37)	3,34 (1,08)	0,734 (0,031)	0,706 (0,037)	0,029 (−0,412 – 0,032)

N: Número de muestras analizadas. *NA:* Número promedio de alelos. *Ne:* Número efectivo de alelos medio. *He:* Heterocigosis media esperada. *Ho:* Heterocigosis media observada. *SD:* Desviación estándar; *IC:* Intervalo de confianza con 10 000 bootstraps.

del marcador HSC y el más bajo el del ETH10. Considerando que un valor de PIC superior a 0,50 indica que un marcador es muy informativo, se puede decir que 27 de los marcadores son muy informativos a la hora de detectar variabilidad genética en la raza ovina Sidaun. Destaca el marcador ETH10 por ser poco informativo y los tres marcadores restantes son medianamente informativos en esta población (valor de PIC entre 0,25 y 0,50). Los valores de probabilidad obtenidos en la prueba de equilibrio Hardy-Weinberg para todas las combinaciones locus/población muestran que once marcadores se desvían significativamente del equilibrio Hardy-Weinberg.

En cuanto a la raza ovina Kerrian, todos los microsatélites utilizados, excepto el ETH10, han resultado polimórficos encontrándose un mínimo de 2 alelos (BM1818 y OarAE0129) y un máximo de 6 (Tabla 2). El número efectivo de alelos oscila entre un mínimo de 1,85 y un máximo de 5,0. La heterocigosis esperada varía entre 0,511 y 0,889 y la observada entre 0,250 y 1,000. Veinticuatro de los marcadores han resultado muy informativos y tres microsatélites se desvían significativamente del equilibrio Hardy-Weinberg.

Los resultados de la raza Kerrian deben ser interpretados con cautela debido al escaso número de muestras analizadas de esta población. El promedio de alelos de la raza Sidaun y las heterocigosis medias en las dos razas ovinas (Tabla 3) son similares a los encontrados en otras poblaciones ovinas (Ceccobelli *et al.*, 2009; Glowatzki-Mullis *et al.*, 2009; Vega-Pla *et al.*, 2007; Quiroz *et al.*, 2008; Santos-Silva *et al.*, 2008). Tanto el promedio de alelos como los valores de heterocigosis indican que la raza Sidaun muestra una diversidad genética elevada. El valor de Fis no es significativamente diferente de cero en ninguna de las dos razas.

Con estos primeros resultados se conoce la situación genética de las razas y en base a ella, sería posible diseñar estrategias oportunas de conservación de estas poblaciones ovinas.

3.2 Caracterización genética de la raza caprina Buzguender

Sólo se han analizado once animales de la raza caprina Buzguender en el análisis de su diversidad genética, por lo que los resultados obtenidos deben ser interpretados con prudencia por no cumplir la muestra todos los requisitos de representatividad de la población. Todos los microsatélites utilizados han resultado polimórficos encontrándose un mínimo de 2 alelos (ETH225 y SPS115) y un máximo de 8 (Tabla 4). El número efectivo de alelos oscila entre un mínimo de 1,20 y un máximo de 6,54. La heterocigosis esperada varía entre 0,173 y 0,887 y la observada entre 0,182 y 0,909. 25 de los marcadores han resultado muy informativos (PIC superior a 0,5) y cuatro microsatélites se desvían significativamente del equilibrio Hardy-Weinberg ($p < 0,05$).

Tabla 4. Microsatélites tipificados, número de alelos detectados, número efectivo de alelos, heterocigosis esperada y observada, contenido de información polimórfica, y P-value en la raza caprina Buzguender.

Microsatélite	*Nº Alelos*	*Ne*	*He*	*Ho*	*PIC*	*P-value*
BM1329	5	3,41	0,740	0,636	0,666	0,5438
BM1818	7	2,95	0,693	0,636	0,635	0,3891
BM6506	7	6,21	0,879	0,909	0,818	0,9854
BM6526	8	5,26	0,848	0,909	0,786	1,0000
BM8125	6	4,75	0,827	0,818	0,759	0,7284
CRSM60	6	4,17	0,797	0,909	0,724	0,8297
CSRD247	4	3,90	0,779	0,727	0,696	0,2407
CSSM66	8	5,90	0,870	0,455	0,810	**0,0006**
ETH10	4	2,78	0,671	0,727	0,572	1,0000
ETH225	2	1,20	0,173	0,182	0,152	1,0000
HAUT27	5	3,97	0,784	0,727	0,706	0,4599
HSC	7	5,90	0,870	0,818	0,809	0,6104
ILSTS011	4	2,60	0,645	0,636	0,560	0,6806
ILSTS019	5	2,47	0,623	0,818	0,554	0,8890
INRA5	4	2,40	0,610	0,727	0,533	1,0000
INRA63	3	2,18	0,567	0,545	0,436	1,0000
MAF209	3	2,49	0,628	0,727	0,532	1,0000
MAF65	6	5,04	0,840	0,818	0,771	0,6701
McM527	4	3,10	0,710	0,364	0,615	**0,0280**
MM12	8	6,54	0,887	0,909	0,829	0,7910
OarFCB11	6	3,78	0,771	0,636	0,694	0,3702
OarFCB304	6	4,05	0,797	0,556	0,718	0,2404
OarFCB48	6	4,57	0,818	0,909	0,752	0,7612
SPS115	2	1,94	0,506	0,636	0,367	0,5542
SRCRSP23	7	4,84	0,831	0,727	0,765	0,1440
SRCRSP24	6	3,23	0,726	0,400	0,643	**0,0146**
SRCRSP5	5	4,32	0,805	0,455	0,731	**0,0048**
SRCRSP8	6	4,75	0,827	0,727	0,758	0,7670
TGLA122	4	1,62	0,403	0,455	0,362	1,0000

Nº Alelos: Número de alelos. *Ne:* Número efectivo de alelos. *He:* Heterocigosis esperada. *Ho:* Heterocigosis por recuento directo. *PIC:* Contenido de información polimórfica. *P-value:* Valores de probabilidad obtenidos en la prueba de equilibrio Hardy-Weinberg realizada mediante un test exacto aplicando el método de Monte Carlo con 100 baterías de análisis y 5000 permutaciones por batería (se destacan en negrita los marcadores que no se encuentran en equilibrio Hardy-Weinberg, $p < 0,05$).

Tabla 5. Número de muestras analizadas, número promedio de alelos, número efectivo de alelos medio, heterocigosis media esperada y observada para todos los microsatélites, y valores de Fis por población.

	N	*NA (SD)*	*Ne (SD)*	*He (SD)*	*Ho (SD)*	*Fis (IC 95%)*
BUZGUENDER	11	5,31 (1,69)	3,80 (1,43)	0,722 (0,030)	0,672 (0,026)	0,071 (−0,096 – 0,111)

N: Número de muestras analizadas. *NA:* Número promedio de alelos. *Ne:* Número efectivo de alelos medio. *He:* Heterocigosis media esperada. *Ho:* Heterocigosis media observada. *SD:* Desviación estándar; *IC:* Intervalo de confianza con 10 000 bootstraps.

El promedio de alelos y las heterocigosis medias en la cabra Buzguender (Tabla 5) son similares a los encontrados en otras poblaciones caprinas (Bruno-de-Sousa *et al.*, 2011; Cañón *et al.*, 2006; Martínez *et al.*, 2006; Martínez *et al.*, 2004; Martínez *et al.*, 2011). Tanto el promedio de alelos como los valores de heterocigosis indican que la raza Buzguender muestra una diversidad genética elevada. El valor de Fis no es significativamente diferente de cero.

Al igual que se ha comentado en el estudio sobre los ovinos, esta parte del trabajo es el primer paso para cualquier estrategia que se quiera abordar con respecto a la gestión de la raza caprina Buzguender. Se ha realizado la caracterización genética de la misma, aunque sería conveniente aumentar el tamaño de la muestra para que los resultados fueran más sólidos. Con estos primeros resultados se conoce la situación genética de la raza y en base a ella, sería posible diseñar estrategias oportunas de conservación de esta población caprina, la cual sigue manteniendo signos de diferenciación genética y aun se mantiene fuera de influencias exóticas relevantes.

4 Conclusiones

Las razas ovinas saharauis Sidaun y Kerrian y la caprina Buzguender muestran una diversidad genética similar a la encontrada en otras razas españolas, portuguesas y africanas, que permitiría la implementación de un programa de conservación genética de estos recursos zoogenéticos tan importantes para una población tan desfavorecida como es el pueblo saharaui.

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Characterization of Madras Red sheep in their breeding tract

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Summary

The Madras Red sheep, a native breed of Tamil Nadu in India, is known for its high-quality meat and skin. The present study was carried out in 652 flocks consisting of 16 173 sheep in 46 villages randomly selected from the breeding tract to characterize and evaluate Madras Red sheep under field conditions during the period from 2006 to 2009. The data on various sheep management practices viz. flock size, housing, feeding, breeding, disease, etc. were collected based on personal observation and information provided by the farmers. The body weight and different body measurements namely horn length, ear length, tail length, height at withers, chest girth, body girth, flank girth, elbow-pin length and poll–tail length were taken. The animals are found to be medium in size with well built body having a broad and deep chest. Most of the animals are red in colour which varied from tan to dark brown. The flock size varies from 20 to 50. The main breeding season is from July to September. In 62 percent of rams, the horns are medium sized and about 15–25 cm long. In about 4 percent of ewes, the horns are small and less than 15 cm. The ears are pendulous and the tail is medium in length. The mean body weights in age groups of 0–3, 3–6, 6–12 and >12 months of males were 9.20, 12.68, 14.31 and 24.33 kg, respectively, and they were 8.93, 13.08, 17.59 and 24.23 kg, respectively, in females. The animals have excellent feed conversion efficiency under extreme conditions with a high dressing percentage. Sheep farming forms a major source of livelihood for the farmers of the study area and the non-availability of good quality fodder was the major constraint in the farming system. The results of the present study revealed that there is a scope for increasing the productivity of this breed.

Keywords: *Madras Red sheep, breed characteristics, habitat, management practice*

Résumé

Les moutons Madras Red, une race indigène du Tamil Nadu, en Inde, sont connus pour la qualité élevée de leur viande et de leur peau. Cette étude a été réalisée sur 652 troupeaux constitués de 16 173 moutons de 46 villages choisis au hasard dans la zone d'élevage. Le but était de caractériser et d'évaluer les moutons Madras Red sur le terrain au cours de la période allant de 2006 à 2009. Les données sur les différentes pratiques de gestion des moutons, c'est-à-dire la taille du troupeau, la stabulation, l'affouragement, la sélection, les maladies, etc., ont été collectées sur la base des observations et des informations personnelles fournies par les agriculteurs. On a saisi les données sur le poids et d'autres mesures corporelles, comme la longueur des cornes, des oreilles et de la queue, la taille au garrot, la circonférence de la poitrine, du corps et du flanc, la distance entre le coude et la cheville et entre la tête et la queue. On a constaté que les animaux sont de taille moyenne, robustes et présentent une poitrine large et puissante. La couleur de la plupart des animaux est d'un rouge allant de fauve à brun foncé. La taille du troupeau varie entre 20 et 50 animaux. La principale période d'accouplement se situe entre les mois de juillet et de septembre. Les cornes de 62 pour cent des béliers sont petites et mesurent moins de 15 cm. Les oreilles retombent et la longueur de la queue est moyenne. Les poids corporels moyens dans les groupes d'âge allant de 0 à 3 mois, de 3 à 6 mois, de 6 à 12 mois et de plus de 12 mois sont respectivement de 9,20 kg, de 12,68 kg, de 14,31 kg et de 24,33 kg pour les mâles, et de 8,93 kg, de 13,08 kg, de 17,59 kg et de 24,23 kg respectivement pour les femelles. Les animaux présentent une grande capacité d'utilisation du fourrage dans les conditions extrêmes et un rendement élevé à l'abattage. L'élevage ovin représente une des sources principales des moyens d'existence des agriculteurs qui résident dans la zone à l'étude et le manque de disponibilité de fourrage de bonne qualité est la contrainte majeure du système agricole. Les résultats de cette étude ont indiqué qu'il existe des possibilités pour accroître la productivité de cette race.

Mots-clés: *moutons Red Madras, caractéristiques raciales, habitat, pratique de gestion*

Resumen

La oveja roja de Madrás, una raza autóctona de Tamil Nadu en la India, es conocida por la alta calidad de su carne y su piel. El presente estudio se llevó a cabo en 652 rebaños compuestos por 16.173 ovejas en 46 pueblos seleccionados al azar de las zonas de cría para caracterizar y evaluar la oveja roja de Madras en condiciones naturales durante el período comprendido entre 2006 y 2009. Los datos relativos a las prácticas de manejo, tamaño del rebaño, estabulación, mejora, enfermedades, etc., fueron recogidos en base a observaciones personales y a la información proporcionada por el propio ganadero. Fue tomado el peso corporal, así como diferentes medidas corporales, concretamente, la longitud de los cuernos, la longitud de la oreja, la longitud de la cola, la alzada a la cruz, el perímetro torácico, el perímetro corporal, perímetro de la ijada, longitud de pata desde el codo y entre la cabeza y la cola. Los animales a pesar de

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ser un tamaño mediano tienen un cuerpo bien proporcionado poseen un pecho ancho y profundo. La mayoría de los animales presenta capa de color rojo que varía desde el canela al castaño oscuro. El tamaño de rebaño oscila de 20 a 50 animales. La principal estación de cría va desde julio a septiembre. En el 62 percent de los carneros, los cuernos son de tamaño mediano y de una longitud que oscila entre los 15 y 25 cm. Alrededor del 4 percent de las ovejas presentan cuernos de pequeño tamaño, de menos de 15 centímetros de longitud. Las orejas son colgantes y la cola es de longitud media. El peso corporal medio de los grupos de edades comprendidas entre los 0 y 3, 3 y 6, 6 y 12 y más de 12 meses, en los machos, fue, respectivamente, de 9,20, 12,68, 14,31 y 24,33 kg., y de 8,93, 13,08, 17,59 y 24,23 kg., respectivamente, para las hembras. Los animales presentan una excelente eficiencia en conversión de alimento bajo condiciones extremas, con un elevado porcentaje de lana. La ganadería ovina es la principal fuente de ingresos de los ganaderos de la zona de estudio y la escasez de forraje de buena calidad es el principal obstáculo en el sistema de cría. Los resultados del presente estudio han revelado que existe margen para el aumento de la productividad de esta raza.

Palabras clave: *Oveja roja de Madrás, características raciales, hábitat, gestión práctica*

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Introduction

The Madras Red sheep is one of the most popular breeds found in southern peninsular region of India (Acharya, 1982). It is a medium-sized breed reared mainly for meat production in the northern regions of Tamil Nadu State in India. It is among the native sheep breeds of India recognized by the Indian Council of Agricultural Research (ICAR). Even though studies have been conducted on the morphological characteristics of the breed (Raman *et al.*, 2003), breeding and performance characters (Devendran, Cauveri and Gajendran, 2009; Sivakumar *et al.*, 2009; Balasubramanyam, Jaishankar and Sivaselvam 2010; Balasubramanyam and Kumarasamy, 2011), most of these reports were mainly based on animals maintained on the organized farms or in adopted farmers' flocks. These animals are reared for meat purpose. Information about this breed from its breeding tract is scanty. Therefore the present study was undertaken to characterize and evaluate Madras Red sheep under field conditions for their morphological characteristics and performance parameters.

Materials and methods

Study location

The home tracts of Madras Red sheep are Chennai, Tiruvallur, Kancheepuram, Villupuram districts and adjacent taluks of Vellore, Cuddalore and Thiruvannamalai districts of Tamil Nadu State (Figure 1). The present study was undertaken in 46 villages randomly selected from the above districts.

Data recording

A total of 652 flocks consisting of 16 173 sheep were covered to collect various information related to current status of the breed during the period from 2006 to 2009. Information on the climate viz. temperature, rainfall, humidity, etc. was collected from the Meteorological Department of the state. The data on various sheep management practices viz. flock size, housing, feeding, breeding, disease, etc. were collected based on personal observation and information provided by the farmers. The morphometric measurements were recorded at the early hours of the day before feeding. The body weight and different body measurements namely horn length, ear length, tail length, height at withers, chest girth, body girth, flank girth, elbow-pin length and poll–tail length were taken according to Singh and Mathur (1971) and the data collected from both sexes were analysed statistically (Harvey, 1990). The ages of the animals were determined based on the presence of teeth and information collected from the farmers.

Results and discussion

Native environment

This region is situated between 8°5″ and 13°2″ of northern latitude and 76.15° and 80.22° of eastern longitude. The geographical area of this region is 31 065 km^2 equivalent to 24 percent of the state area. These areas have a predominance of red and black soils while alluvial soil is found in some areas of Kancheepuram district. The climate is semi-arid tropical with four distinct seasons. The average temperature ranges between 28.2–38.9 °C (Max) and 19.5–24.8 °C (Min). Maximum humidity (percent) is observed during the period from October to January. Annual rainfall varies from 80 to 140 cm.

Status of breed in its breeding tract

According to the 18th livestock and poultry census carried out by the Department of Animal Husbandry and Dairying, Government of India in 2007, the population of sheep in Tamil Nadu was 7 990 587, their percentage of increase over previous census was 29.90 and density in the state was 43 per km^2.

Figure 1. Breeding tract of Madras Red sheep (shown in blue dots).

Community responsible for the development of the breed

Naicker and Pillai are the two communities responsible for the development of the breed in the native tract of Kancheepuram and Thiruvallur districts. The Pillai communities are traditional farmers doing sheep farming for many generations in this tract. Most of them own medium-sized flocks and do agriculture and sheep rearing. Both communities belong to most-backward classes. Very few sheep farmers belong to scheduled caste.

Utility

Madras Red sheep is a meat-type breed. The meat is liked by the local people as much goat meat. The milk produced by these animals is just sufficient to maintain their lambs, therefore has no commercial value. The manure has a good value for agricultural purpose. It is a common practice to retain the flocks in the field during the nights for manuring. The skin of an adult sheep fetches Rs. 100–150.

Management practices

Feeding

In Kancheepuram, Thiruvallur, Villlupuram and Thiruvannamalai districts, the animals are mainly reared on extensive grazing as no fodder is cultivated separately for feeding the sheep. Animals are also fed with different fodder tree leaves. Major fodder trees available are Katuvagai (*Albizia lebbek*), Banyan (*Ficus benghalensis*), Arasan (*Ficus religiosa*), Subabul (*Leucaena leucocephala*), Gliricidia (*Gliricidia maculata*), Poovarasu (*Thespesia populnea*), Kalyana Murungai (*Erythrina indica*) and Kodukapuli (*Inga dulce*). Non-specific shrubs are found growing wildly. *Cyperus L*, *Eichnocloa L* and Para grass are major native grasses and dried ground nut haulms are given as feed to the sheep especially in the villages of Villupuram, Kancheepuram and Tiruvallur districts. For young lambs, suckling along with grazing is followed.

Housing

Housing is provided only at nights in all the villages of Kancheepuram, Thiruvallur, Villupuram and Thiruvannamalai districts. The partition is made with dried thorny bushes and 'all open' type housing is seen in the villages of Kancheepuram and Thiruvallur districts. 'Half open' type housing made of palm tree leaves is seen in a very few villages in Kancheepuram and Thiruvallur districts. In Villupuram and Thiruvannamalai districts, it is a common practice that the sheep are kept overnight in the fields for manuring purpose. The flock is kept for a week in the field and partition is provided by dried thorns tied with bamboo sticks.

Flock size

The average flock size varies from village to village and from farmer to farmer. The size varies from 20 to 50. Most of the farmers group their animals and rear them as a single flock for convenience in management and grazing. Only a few farmers have single flocks. However, Raman *et al.* (2003) reported an average flock size of 85 animals ranging from 9 to 315. The flock consists of mostly breeding ewes (44.2 percent) and breedable replacement females (29 percent). The rams and male lambs are seen only in limited number. Even for 100 breedable ewes only one ram is used. In some of the villages only one ram is used for different flocks. The male lambs are disposed from 6 months onwards. The females are disposed in 60 months of their age. All the young female lambs born are retained every year.

Breeding

The ram is retained in the flock all through the day. Natural service is the only method of mating practiced in all the villages. The breeding season is mainly seen from July to September after the onset of south-west monsoon and the availability of fresh green grass. Mostly 70–80 percent of the animals are covered during this season and the lambing season starts in January and ends in March. The second breeding season is not prominent since the availability of grass and pasture is very limited in this period.

Physical characteristics

Most of the animals are red in colour. The intensity of colour varies from tan to dark brown. The survey revealed that 69 percent of the animals are in red, 19 percent in medium tan and 12 percent in dark tan. Some of them have white markings on the forehead, inner parts of thigh and lower abdomen. The head is straight in 97 percent of the animals and slightly convex in 3 percent. The rams have corrugated twisted horns. The data also revealed that 62 percent of the males have horns and 4 percent of the females are horned. In rams, the horns are medium sized and 15–25 cm long. In ewes, the horns are small and less than 15 cm. The ears are pendulous and 12–13 cm in length. The pendulous lobules called wattles are seen in 73 percent of the females and 69 percent of the males. The coat is hairy and never shorn. The tail is medium and 7–9 cm in length (Figures 2 and 3). The same was reported by Raman *et al.* (2003).

Figure 2. Madras Red ram.

Body weight

The data of body weights of different age groups are presented in Table 1. In the present study, the sex had a significant ($P < 0.05$) effect on the body weights of groups at 3–6 and 6–12 months of age; whereas no significant effect was observed for body weights of groups at 0–3 months and above 12 months of age. Raman *et al.* (2003) observed that the body weights were higher in males than females at 0–3 and 3–6 months of age, although not significant. However, a significantly higher weight in males than females was detected in animals of 12 months of age (Raman *et al.*, 2003).

Figure 3. Madras Red ewe.

Table 1. Average (±s.e.) body measurements (cm) and body weight (kg) in Madras Red sheep.

Age groups	0–3 months		>3–6 months		>6–12 months		Above 12 months	
	Male	Female	Male	Female	Male	Female	Male	Female
Body weight (kg)	9.20^a ± 0.13 (434)	8.93^a ± 0.11 (584)	12.68^a ± 0.15 (298)	13.08^b ± 0.14 (461)	14.31^a ± 0.15 (1837)	17.59^b ± 0.08 (4688)	24.33^a ± 0.39 (361)	24.23^a ± 0.04 (7510)
Body dimensions								
Horn length (cm)	1.94^a ± 0.14 (39)	2.71^b ± 0.48 (7)	2.80^a ± 0.53 (104)	2.58^a ± 0.36 (12)	9.47^a ± 0.84 (102)	5.65^b ± 0.39 (47)	30.00^a ± 1.50 (48)	7.39^b ± 0.69 (61)
Ear length (cm)	12.32^a ± 0.08 (434)	12.40^a ± 0.08 (584)	12.59^a ± 0.11 (298)	12.84^a ± 0.09 (461)	12.48^a ± 0.04 (1837)	13.18^a ± 0.03 (4688)	12.29^a ± 0.14 (361)	13.54^b ± 0.02 (7510)
Tail length (cm)	7.79^a ± 0.08 (434)	7.76^a ± 0.08 (584)	8.14^a ± 0.10 (298)	8.27^a ± 0.08 (461)	7.99^a ± 0.04 (1837)	8.69^a ± 0.03 (4688)	7.48^a ± 0.14 (361)	9.32^b ± 0.03 (7510)
Height at withers (cm)	51.05^a ± 0.28 (434)	50.25^a ± 0.25 (584)	55.16^a ± 0.36 (298)	55.80^b ± 0.29 (461)	57.24^a ± 0.21 (1837)	61.18^b ± 0.11 (4688)	63.13^a ± 0.57 (361)	66.82^b ± 0.05 (7510)
Chest girth (cm)	51.19^a ± 0.30 (434)	50.64^a ± 0.27 (584)	56.34^a ± 0.34 (298)	57.87^b ± 0.31 (461)	59.35^a ± 0.26 (1837)	64.32^b ± 0.13 (4688)	71.60^a ± 0.60 (361)	72.36^b ± 0.05 (7510)
Body girth (cm)	54.06^a ± 0.37 (434)	53.49^a ± 0.32 (584)	60.68^a ± 0.38 (298)	61.69^a ± 0.32 (461)	63.11^a ± 0.31 (1837)	68.49^b ± 0.15 (4688)	78.11^a ± 0.60 (361)	77.82^a ± 0.06 (7510)
Flank (cm)	50.38^a ± 0.36 (434)	49.88^a ± 0.34 (584)	56.87^a ± 0.39 (298)	57.76^a ± 0.32 (461)	57.53^a ± 0.29 (1837)	63.34^b ± 0.15 (4688)	67.88^a ± 0.60 (361)	71.54^b ± 0.06 (7510)
Elbow-pin length (cm)	42.22^a ± 0.31 (434)	41.14^a ± 0.25 (584)	45.97^a ± 0.34 (298)	46.97^a ± 0.27 (461)	46.31^a ± 0.23 (1837)	49.74^b ± 0.10 (4688)	59.91^a ± 0.54 (361)	54.87^b ± 0.05 (7510)
Poll–tail length (cm)	64.42^a ± 0.42 (434)	63.96^a ± 0.38 (584)	70.20^a ± 0.58 (298)	72.18^b ± 0.47 (461)	77.51^a ± 0.35 (1837)	84.92^b ± 0.19 (4688)	87.99^a ± 0.59 (361)	94.53^b ± 0.10 (7510)

The means bearing different superscripts under a particular age group differ significantly ($P < 0.05$).

Morphometric measurements

The morphometric measurements of Madras Red sheep such as horn length, ear length, tail length, height at withers, chest girth, body girth, flank length, elbow-to-pin length and poll-tail length are presented in Table 1. The sex had a significant ($P < 0.05$) effect on the horn, ear and tail lengths at above 12 months of age. In general, young lambs (0–3 months) were statistically similar for most of the morphometric traits. Significant differences were observed as the ages of animals advanced, indicating the variation in growth rate between male and female sheep. The body measurements at 0–3 and 3–6 months of age were higher than the values reported by Raman *et al.* (2003). The tail length and height at withers at 12 months of age were lower than the values observed by Raman *et al.* (2003).

Conclusions

The Madras Red sheep is medium sized, hairy sheep and well adapted to the local environmental conditions such as heat, cold, humidity, water scarcity and seasonal fluctuation in feed availability in terms of both quality and quantity as well as disease outbreaks. It shows excellent feed conversion efficiency under extreme conditions. The Madras Red sheep is preferred to the other breeds by local farmers because of their high dressing percentage (over 50 percent). The results of the present study also revealed that there is a scope for increasing the productivity of this breed.

Specific recommendations

Sheep farming forms a major source of livelihood for the farmers of the study area because of the increased demand for meat and low initial investments when compared with large animals. It attracts other marginal and landless farmers also to start a sheep farm. Even though the Madras Red sheep are generally maintained on grazing alone, their meat yield is as good as that of any other sheep breeds of the country. The non-availability of good quality fodder in the study area was the major constraint in the farming system, hence the farmers need to be educated on the importance of cultivating different fodder varieties for feeding sheep. The farmers are also to be trained on the scientific management practices such as de-worming, vaccination, castration, selection and breeding, etc. to increase the productivity of these sheep. Technical, extension and marketing support should be provided to the farmers so as to make sheep production a profitable enterprise for all sections of society irrespective of caste, creed, land holding, etc.

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Genetic diversity and bottleneck analysis of Konkan Kanyal goats

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Summary

Konkan Kanyal goats are medium-sized animals reared for meat purpose. They are predominantly black in colour with white markings in a specific pattern and are found in the Kudal, Sawantwadi, Dodamarg, Malvan and Vengurle Talukas of Sindhudurg district of Konkan region of Maharashtra state. The mean body weight ranges from 30 kg in adult females to 35 kg in males. The age at first kidding, kidding interval and twinning of these goats is 546 days, 240 days and 35 percent respectively. The average daily milk yield and lactation yield were found to be 0.6 and 69 kg, respectively. Characterization of Konkan Kanyal goats was carried out using a panel of 25 microsatellite markers. The genomic DNA of 50 unrelated goats was isolated and PCR amplified under standardized PCR conditions. The amplified DNA was used for genotyping by the automated DNA Sequencer ABI 3730. The analysis of data revealed that the effective number of alleles ranged from 1.17 to 8.94 and the number of observed alleles ranged from 5 to 19. A total of 255 alleles were observed with a mean of 10.2 alleles/locus. The observed heterozygosity ranged from 0.13 to 0.95, while the expected heterozygosity ranged from 0.14 to 0.89, indicating the heterogeneous nature of the population distributed in the breeding tract. The mean polymorphism content was 0.79. The qualitative graphical method based on the allele frequency spectra detected no shift in the frequency distribution of alleles and a normal L-shaped curve was observed where the alleles with the lowest frequencies were found to be most abundant. Based on the phenotypic and genetic variability, Konkan Kanyal goats appear to be distinct from other goats of Maharashtra state.

Keywords: *allele size, heterozygosity, microsatellite markers, polymorphism*

Résumé

Les chèvres Konkan Kanyal, de taille moyenne, sont élevées pour leur viande. Elles sont principalement de couleur noire avec des taches blanches ayant un motif caractéristique et vivent dans les unités administratives de Kudal, Sawantwadi, Dodamarg, Malvan et Vengurle du district de Sindhudurg sur la côte de Konkan dans l'État du Maharashtra. La moyenne de leur poids corporel varie entre 29,80 kg pour les femelles adultes et 35,26 kg pour les mâles. L'âge au premier agnelage et l'intervalle entre les agnelages sont respectivement de 546 jours et de 240 jours. Trente-cinq pour cent des naissances de ces chèvres sont gémellaires. On a constaté que le rendement moyen de lait par jour et la quantité de lait donnée au cours d'une lactation sont respectivement de 0,6 kg et de 69 kg. La caractérisation des chèvres Konkan Kanyal a été réalisée en utilisant un panel de vingt-cinq marqueurs microsatellites. L'ADN génomique de 50 chèvres sans liens de parenté a été isolé et amplifié selon des méthodes PCR standardisées. L'ADN amplifié a été utilisé pour le génotypage par le biais du séquenceur automatisé d'ADN ABI 3730. L'analyse des données a indiqué que le nombre réel d'allèles varie entre 1,17 et 8,94 et le nombre d'allèles observés entre 5 et 19. On a constaté au total 255 allèles avec une moyenne de 10,2 allèles par locus. L'hétérozygosité observée oscille entre 0,13 et 0,95 tandis que l'hétérozygosité prévue oscille entre 0,14 et 0,89, ce qui indique la nature hétérogène de la population dans la zone d'élevage. Le polymorphisme moyen est 0,79. La méthode graphique qualitative basée sur le spectre de fréquence allélique n'a décelé aucun changement dans la distribution de fréquence des allèles et l'on a observé une courbe en L normale où les allèles ayant les fréquences plus faibles étaient les plus abondants. Sur la base de la variabilité phénotypique et génétique, les chèvres Konkan Kanyal semblent se différencier des autres chèvres de l'État du Maharashtra.

Mots-clés: *taille des allèles, hétérozygosité, marqueurs microsatellites, polymorphisme*

Resumen

Las cabras Konkan Kanyal son animales de tamaño mediano criadas para la producción de carne. Presentan capa predominantemente de color negro con marcas blancas distribuidas siguiendo un patrón específico y se encuentran los distritos de Kudal, Sawantwadi, Dodamarg, Malvan y Vengurle Talukas de la región de Konkan, en el Estado de Maharashtra. El peso corporal medio es de 29,80 kg. en el caso de las hembras adultas y de 35,26 kg. en el caso de los machos. La edad al primer parto, el intervalo entre partos y los partos gemelares en estas cabras es a los 546 días, de 240 días y del 35 percent, respectivamente. La producción de leche media al día y por lactación es de 0,6 kg. y 69 kg., respectivamente. La caracterización de las cabras Konkan Kanyal se llevó a

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cabo utilizando un panel de veinte cinco marcadores de microsatélites. Fue aislado el ADN de 50 ejemplares no emparentados y amplificado mediante PCR bajo condiciones normalizadas de dicha técnica. La amplificación de ADN se utilizó para la determinación del genotipo por el secuenciador automático de ADN ABI 3730. El análisis de los datos reveló que el número efectivo de alelos oscilaba entre 1,17 y 8,94 y que el número de alelos observados oscilaba entre 5 y 19. Asimismo, se observó un total de 255 alelos, con una media de 10,2 alelos por locus. La heterocigosidad observada osciló entre 0,13 y 0,95, mientras que la heterocigosidad esperada osciló entre 0,14 y 0,89, lo que indica la naturaleza heterogénea de la población distribuida por la zona de cría. El contenido medio de polimorfismo fue de 0,79. El método gráfico cualitativo, basado en los espectros de frecuencia de los alelos, no detectó ningún cambio en la distribución de frecuencias de alelos y se observó una curva L normal cuando los alelos con las frecuencias más bajas resultaron ser más abundantes. Tomando como base la variabilidad fenotípica y genética, las cabras Konkan Kanyal parecen ser diferentes de otras poblaciones caprinas del Estado de Maharashtra.

Palabras clave: *tamaño del alelo, heterocigosidad, marcadores microsatélites, polimorfismo*

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Introduction

India possesses 21 recognized breeds of goats, which constitute 30 percent of the total goat population and the remaining 70 percent are non-descript with mixed features. These goat populations are distributed in different agro-climatic zones of the country. The diversity of goats in India is reflected by the fact that they have evolved and adapted under varied agro-climatic conditions, ranging from cold arctic (with −40 °C) to hot-humid tropical climate of coastal regions and dry-hot climate of Rajasthan (with 45 °C). The breeds are also diverse and specific in their performance traits such as production of the finest quality fibre by Pashmina goat, high prolificacy and quality meat in Black Bengal and the milk production of Jamunapari, Jakhrana, Barbari and Beetal goats. Among the non-descript goat populations Konkan Kanyal is one which is found in the Kudal, Sawantwadi, Dodamarg, Malvan and Vengurle Talukas of Sindhudurg district of Konkan region of Maharashtra state (Figure 1). About 11 800 goats exhibiting the Konkan Kanyal phenotype have been reported from Sindhudurg district. The flock size varied from 2 to over 100 but the proportion of Konkan Kanyal goats ranged from 14 to 68 percent (Verma *et al.*, 2011b). In a flock of Konkan Kanyal goats, the male–female ratio was 1:10. Natural service is practised to propagate the population. In the absence of true-type Konkan Kanyal buck, the mating takes place with the other type of buck. Since, Konkan Kanyal goats appeared phenotypically distinct from the Sangamneri and Osmanabadi goat breeds of Maharashtra, the characterization of these goats at phenotypic and genetic level is required. The Konkan Kanyal goats have been phenotypically characterized (Verma *et al.*, 2010) but no information is available on its genetic aspects. The present study was carried out to assess the genetic variability of Konkan Kanyal goats of Maharashtra.

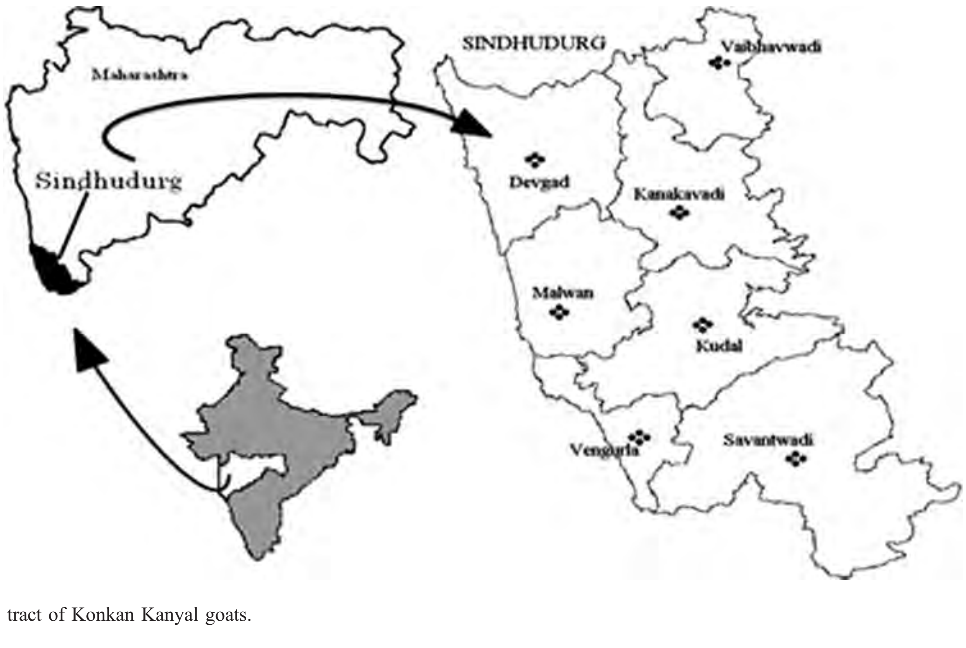

Figure 1. Breeding tract of Konkan Kanyal goats.

Materials and methods

DNA isolation

Blood samples of 50 animals belonging to 24 different flocks of Konkan Kanyal goat population were collected randomly from the breeding tract (Figure 1). Genomic DNA was isolated from these samples using a standard phenol-chloroform extraction method of Sambrook, Fritsch and Maniatis (1989). After testing the quality and quantity of the isolated DNA, the samples were used for amplification of microsatellite loci by the PCR method.

Microsatellite loci and PCR amplification

A battery of 25 microsatellite markers used to estimate different genetic parameters is given in Table 1. The panel of microsatellite markers used in this study has already been tested for genetic diversity estimation of Sirohi (Verma *et al.*, 2007), Changthangi (Priyanka *et al.*, 2010), Sangamneri (Verma *et al.*, 2011a), Kannaiadu (Dixit *et al.*, 2011) and Mehsana (Aggarwal *et al.*, 2007). Amplifications for the loci were performed in a 10 µl final reaction volume containing 50 ng of genomic DNA, 10 pm of each primer, 10 mM dNTPs, 0.5 U Taq polymerase and 10 × 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 for 1 min, extension for 45 s at 72 °C and final extension for 7 min at 72 °C. All the amplified products were separated by electrophoresis on 2 percent agarose gel. After ensuring the amplification on 2 percent agarose gel the PCR products were subjected to genotyping on automated DNA sequencer.

Statistical analysis

Microsatellite data on genotyping were analysed to estimate the observed number of alleles, the expected number of alleles, observed heterozygosity and expected heterozygosity using POPGEN 32 diversity analysis software. The test of the departure from Hardy–Weinberg proportions was performed using exact probability tests provided in GENEPOP. Within population inbreeding estimates (Fst) at microsatellite loci were estimated using F-STAT (version 2.9.3). Neighbour-Joining diagrams were constructed on genetic distances within individuals using the Nei's distance (Saitou and Nei, 1987) by the PHYLIP package.

To evaluate whether the Konkan Kanyal goat has experienced a recent bottleneck, different approaches were followed. In the first approach three different tests: sign test, standardized differences test and Wilcoxon sign-rank test were employed under infinite allele model (IAM), stepwise mutation model (SMM) and two-phase model (TPM). These were used for the test of departure from mutation drift equilibrium based on heterozygosity excess

Table 1. Genetic diversity and heterozygosity deficit in microsatellite loci.

Locus	Na	Ne	Ho	He	Fis	PIC	Gene diversity
ILSTS30	8.00	5.22	0.75	0.81	0.07	0.86	0.81
ILSTS033	11.00	3.68	0.73	0.73	0.004	0.80	0.73
ILSTS005	5.00	2.36	0.44	0.58	0.24	0.71	0.58
ILSTS065	11.00	1.50	0.24	0.33	0.28	0.54	0.33
ILSTS087	10.00	5.63	0.71	0.83	0.14	0.86	0.83
OarAE129	13.00	5.74	0.80	0.83	0.04	0.89	0.83
ETH225	12.00	4.04	0.64	0.76	0.15	0.84	0.76
ILSTS58	15.00	4.50	0.91	0.78	−0.16	0.82	0.78
ILSTS059	19.00	8.94	0.82	0.89	0.08	0.91	0.89
OARHH64	11.00	8.08	0.73	0.88	0.17	0.90	0.88
ILSTS008	6.00	3.33	0.93	0.70	−0.32	0.72	0.70
ILSTS019	8.00	3.81	0.53	0.74	0.28	0.84	0.74
ILSTS34	10.00	3.75	0.95	0.74	−0.29	0.81	0.73
ILSTS082	16.00	8.88	0.75	0.89	0.16	0.91	0.89
RM4	10.00	3.47	0.60	0.72	0.16	0.82	0.72
OarFCB304	15.00	4.13	0.66	0.76	0.13	0.86	0.76
OarFCB48	14.00	6.86	0.88	0.86	−0.02	0.91	0.86
OarJMP29	6.00	1.17	0.13	0.14	0.11	0.48	0.15
ILSTS029	7.00	2.10	0.48	0.53	0.08	0.71	0.53
ILSTS044	5.00	2.51	0.27	0.60	0.54	0.76	0.61
ILSTS049	7.00	3.13	0.71	0.68	−0.03	0.77	0.68
ILSTS002	6.00	5.05	0.80	0.81	0.01	0.85	0.81
RM088	13.00	2.92	0.91	0.66	−0.37	0.67	0.66
OMHC1	11.00	5.17	0.84	0.81	−0.03	0.87	0.81
ILSTS022	6.00	3.11	0.66	0.68	0.29	0.78	0.68
Mean	10.20	4.36	0.67	0.71	0.05	0.79	0.73

Na = observed number of alleles; Ne = effective number of alleles; He = expected heterozygosity; Ho = observed heterozygosity; PIC = polymorphic information content; Fis = within population inbreeding.

or deficiency. The second approach was used to visualize the allele frequency spectra. The microsatellite alleles were classified into 10 frequency classes, which allow checking whether the distribution followed the normal L-shaped curve, where the alleles with low frequencies (0.01–0.1) are the most abundant.

Result and discussion

Phenotypic attributes

Konkan Kanyal goats are predominantly black in colour with white markings in a specific pattern. The white markings are on the collar, lower jaw and/or ventral surface (Figure 2). The head bears bilateral strips extending from the ears to the base of the nostrils. The muzzle is white crescent type. The ears are black with white margins, flat, long, drooping. The legs are long, laterally black, and medially white from the knee to the fetlock joint. These goats are regular breeders and breed round the year. The mean body weights range from 30 kg in adult females to 35 kg in males. The age at first kidding, kidding interval and twinning of these goats is 546 days, 240 days and 35 percent respectively. The average daily milk yield and lactation yield was found to be 0.6 and 69 kg respectively (Verma *et al.*, 2011b).

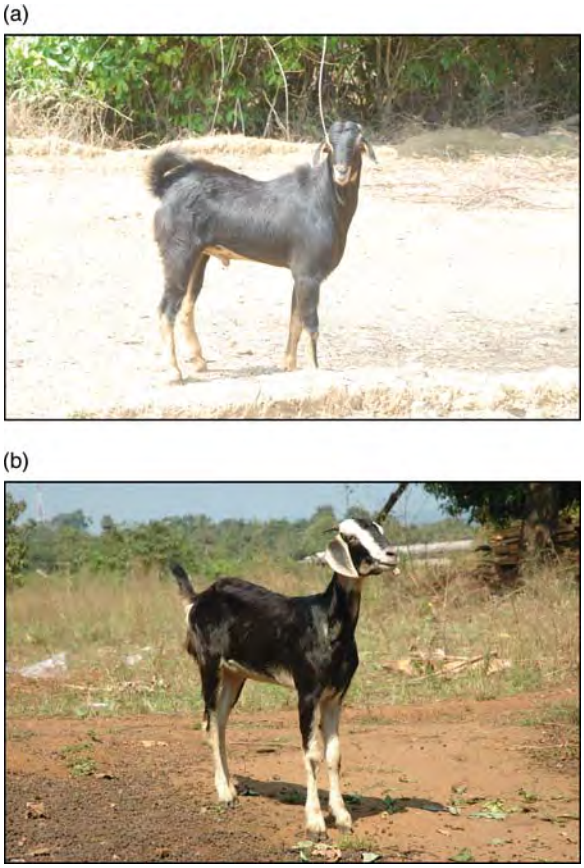

Figure 2. Konkan Kanyal male (A) and female (B).

Genetic variability

The genetic variability estimates in terms of the observed number of allele (Na), effective number of allele (Ne) and polymorphic information content (PIC), heterozygosities, within population inbreeding (Fis) and gene diversity are presented in Table 1. The effective number of alleles was less than the observed values across all the loci. The observed number of alleles varied from 5 (ILSTS08, ILSTS044) to 19 (ILSTS059) and a total of 255 alleles were observed with a mean of 10.2 alleles/locus which is higher than the Kannaiadu goat, Sangamneri and Osmanabadi goat breeds studied by Dixit *et al.* (2010), and than that of Sangamneri goat studied by Verma *et al.* (2011a). The effective number of alleles varied from 1.17 (OarJMP29) to 8.94 (ILSTS059) with a mean value of 4.36 which is higher than the Kannaiadu (4.22), Osmanabadi (3.25) and Sangamneri (3.30) studied by Dixit *et al.* (2010) and from Sangamneri (4.04) by Verma *et al.* (2011a). The mean polymorphism content was 0.79.

The mean observed and expected heterozygosities were found to be 0.67 and 0.71, respectively. The lowest observed heterozygosity value was 0.13 (OarJMP29) and the highest was 0.95 (ILSTS034). The expected heterozygosity ranged from 0.14 (OarJMP29) to 0.89 (ILSTS082 and ILSTS 059).

We utilized three tests viz: sign test (non-parametric), standardized differences test (parametric) and Wilcoxon test to test whether the Konkan Kanyal population is in mutation drift equilibrium. The estimated values obtained from these tests are given in Table 2. The sign test expected numbers of loci with heterozygosity excess were 14.97, 14.87 and 14.72 respectively whereas the observed numbers of loci with heterozygosity excess were 16, 9 and 3 for IAM (Kimura and Crow, 1964), TPM (Di Rienzo *et al.*, 1994) and SMM (Ohta and Kimura, 1973) respectively.

The difference between the expected and the observed heterozygosity excess was not significant in IAM and TPM, whereas this was significant for the heterozygote

Table 2. Different tests for null hypothesis for mutation drift equilibrium.

Test		**IAM**	**TPM**	**SMM**
Sign test	Expected no. of loci with He excess	14.97	14.87	14.72
	Observed no. of loci with He excess	16	9	3
	P-value	0.41	0.015	0.000
Standardized difference test	*P*-value	0.34	0.000***	0.000***
	T2-value	−0.38	−6.31	−16.93
Wilcoxon test	*P*-value (one tail for He excess)	0.80	0.98	1.00

*** = $P < 0.001$

deficiency in SMM showing lack of severe reduction in effective population size. The standardized difference test (statistic T_2) is equal to -0.38, -6.31 and -16.93 respectively for the IAM, TPM and SMM models in these goats. The values of TPM and SMM are less than 1.645 (value from table of normal distribution) and thus accept the null hypothesis of mutation-drift equilibrium. Similar results were obtained in the Wilcoxon sign rank test. The Mode Shift test allows to check whether the distribution followed the normal L-shaped curve depicted in the graph given below (Figure 3). Qualitative graphical methods based on the allele frequency spectra detected no shift in the frequency distribution of the alleles, where the alleles with the lowest frequencies (0.01–0.1) were found to be most abundant. This reflects that the population had not undergone bottleneck in recent past.

The study indicated the genetic variability using molecular markers in Konkan Kanyal goat population of Maharashtra state. The different measures of genetic variation such as Na, Ne and PIC showed that all of the studied loci were highly informative, indicating high polymorphism across the loci, thus suggesting suitability of these markers for the study of genetic diversity in goats. Suitability of these markers was further supported by the fact that the number of alleles for each marker was higher than the minimum number of alleles (four) recommended for microsatellite markers to be used in the estimation of genetic distance in order to reduce the standard error. The F-statistics were applied to know the extent of inbreeding and outbreeding in the population (Table 1). The Fis value provides the non-random union of gametes in the population, i.e. the mating among the individuals in the population which is related more than average relationship. More the Fis value, more the inbreeding. The negative values of Fis point towards outbreeding, i.e. mating of individuals who are less related than the average relationship of the population. The mean number of alleles observed over a range of loci in different populations is considered to be a reasonable indicator of genetic variation within the population. This population of goat showed low effective number of alleles than the observed number. This is due to very low frequency of most of the alleles at each locus and very few alleles might have contributed to the major part of the allelic frequency at each locus. Another appropriate measure of genetic variation within a population is gene diversity (Table 1). The overall mean of gene diversity (0.73) was higher than the value reported in Gohilwadi (0.68) goats for the same panel of microsatellite markers (Kumar *et al.*, 2009) and in Swiss goat breeds (0.58) for 20 microsatellite loci (Saitbekova *et al.*, 1999). The Konkan Kanyal goat population exhibited higher mean observed heterozygosity than Gohilwadi (Kumar *et al.*, 2009), Kutchi (Dixit *et al.*, 2008) and many other Asian goats but lower than that of Kanniadu breed of goat (Thilagam *et al.*, 2006). The genetic variation observed in the goats under study might be due to immigration of new gene, intermixing of different population and low selection pressure. The three tests (Sign test, Standardized difference test and Wilcoxon test) under the three models (IAM, TPM and SMM) for heterozygosity excess can detect the bottleneck for only a short duration of time after a bottleneck has been initiated. These are the quantitative tests that can detect bottleneck up to 50–250 generations. As discussed above, the null hypothesis of mutation-drift equilibrium was accepted, overall there was no serious recent genetic bottleneck in Konkan Kanyal goat population.

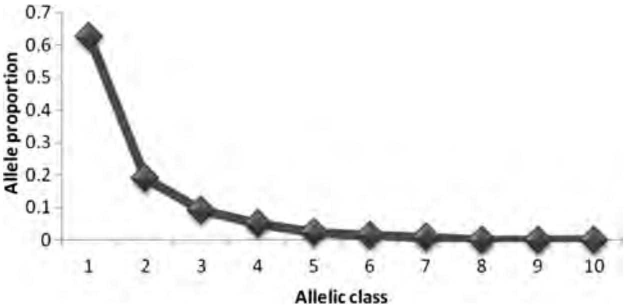

Figure 3. Mode shift analysis of Konkan Kanyal goat population.

Conclusion

There was substantial genetic variation and polymorphism across the studied loci in the Konkan Kanyal goats. This population was not in Hardy–Weinberg equilibrium at most of the studied loci. There may be receiving of new genetic material through unplanned mating. The fact that the Konkan Kanyal goat population has not undergone a genetic bottleneck is important for goat breeders and conservationists, as it suggests that any unique alleles present in this breed may not have been lost. Therefore, within breed diversity is actively maintained to enable these extensively managed stocks to adapt to future demands and conditions and there is ample scope for further improvement in its productivity through appropriate breeding strategies.

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Phenotypic characterization of Indian equine breeds: a comparative study

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Summary

Populations of the six equine breeds registered by the Indian National Bureau of Animal Genetic Resources have drastically decreased due to indiscriminate breeding and their low utilization. In this study, 15 biometric indices along with typical breed characteristics were recorded for 50 animals of each breed except Bhutia breed (35) for their phenotypic characterization. On the basis of their heights at wither, Kathiawari and Marwari breeds were grouped under "horse", while Zanskari, Manipuri, Bhutia and Spiti fell under "pony" breeds. Marwari was the tallest and significantly different from other breeds in most of the biometric indices. Spiti was the shortest breed among all the six horse and pony breeds. Sex-wise differences were also observed in some of the biometric indices in different breeds. In Marwari and Kathiawari breeds, both stallions and mares can rotate their ears at an angle of 180° making the ear tips meet in the centre, which is a typical characteristic of the two breeds. This report aims at providing reference data for identification and comparison of different breeds of equines in India with a view to raise awareness among animal geneticists and breeders for production of true to breed animals, conservation and better management of these precious genetic resources.

Keywords: *biometric, breed, characteristics, horse, phenotype, pony*

Résumé

Les populations des six races équines enregistrées par le Indian National Bureau of Animal Genetic Resources (Bureau national des ressources zoogénétiques) ont radicalement baissé en raison d'une sélection sans discernement et de la réduction de leur utilisation. Dans cette étude, on a enregistré, pour la caractérisation phénotypique, 15 indices biométriques, ainsi que les caractéristiques typiques raciales de 50 animaux pour chaque race, à l'exception de la race Bhutia (35). Sur la base de leur hauteur au garrot, les races Kathiawari et Marwari ont été classées comme "chevaux" tandis que les races Zanskari, Manipuri, Bhutia et Spiti ont été classées comme "poneys". La race Marwari est la plus grande et elle est considérablement différente par rapport aux autres races en ce qui concerne la plupart des indices biométriques. La race Spiti est la plus petite parmi toutes les six races de chevaux et de poneys. On a également constaté des diversités au niveau des sexes dans certains des indices biométriques de races différentes. Une caractéristique particulière des races Marwari et Kathiawari est que les étalons et les juments peuvent pivoter leurs oreilles de 180° de façon à en réunir les pointes. Ce rapport vise à fournir des données de référence pour l'identification et la comparaison des différentes races équines de l'Inde afin de sensibiliser les généticiens et les sélectionneurs en faveur de la production d'animaux de race pure, de la conservation et de l'amélioration de la gestion de ces ressources génétiques précieuses.

Mots-clés: *biométrique, race, caractéristiques, cheval, phénotype, poney*

Resumen

Las poblaciones de las seis razas equinas registradas por la Oficina Nacional India de Recursos Zoogenéticos han disminuido drásticamente a causa de la cría sin criterio y de su menor utilización. En este trabajo, se estudiaron 15 índices biométricos, junto con características raciales típicas, en 50 animales de cada raza, excepto en la raza Bhutia (35) para su caracterización fenotípica. En base a sus alzadas a la cruz, las razas Kathiawari y Marwari se clasificaron como "caballos", mientras que las razas Zanskari, Manipuri, Bhutia y Spiti se clasificaron como "ponis". La raza Marwari fue la de mayor alzada y la que era significativamente diferente a otras razas en la mayoría de los índices biométricos. La raza Spiti fue la que presentó una menor alzada entre las seis poblaciones de caballos y ponis estudiadas. Se observó un moderado dimorfismo sexual en algunos de los índices biométricos en las diferentes razas. En las razas Marwari y Kathiawari, tanto los sementales como las yeguas, pueden girar las orejas en un ángulo de 180°, quedando las puntas de las orejas en el centro, siendo una característica típica de estas dos razas. Este trabajo tiene como objetivo proporcionar información de referencia para la identificación y comparación de las distintas razas de équidos de la India, con el propósito de sensibilizar a genetistas y criadores acerca de la importancia de producir ejemplares típicos, de su conservación y para la mejora de la gestión de estos valiosos recursos genéticos.

Palabras clave: *biométrico, raza, características, caballo, fenotipo, poni*

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Introduction

India has a unique amalgamation of geographically distinct, six breeds of horses namely Marwari, Kathiawari, Bhutia, Spiti, Manipuri and Zanskari registered by the Indian National Bureau of Animal Genetic Resources (Kaura, 1961; Singhvi, 2001; Yadav, Ghei and Tandon, 2001; Anonymous, 2008; Singh, Pal and Gupta, 2009, 2010; Gupta, 2010). Kathiawari and Marwari are the horses of North-western plain region (Kachhiapatel, 2010), Spiti and Zanskari of high altitude temperate areas of the Northern Himalayan hills, while Bhutia and Manipuri of Eastern region. These area-specific horses are well adapted to different agro-climatic zones in India in their home tracts and have acquired certain unique characteristics which make them suitable to that particular zone. During the last five decades, overall population of the horses and animals true to breed in particular have decreased at an alarming rate due to indiscriminate breeding, poor availability of good quality stallions, their decreased demand and utility as well as poor health and management. Some of the equine breeds namely Zanskari, Manipuri, Bhutia and Spiti breeds are now endangered, as their populations are very limited (Gupta, Pal and Tandon, 2010; http://ahdhp.nic.in/chamurthi.pdf, Animal Husbandry Department, Arunachal Pradesh, http://www.e-pao.net/GP.asp?src=23..221011.oct11). Kathiawari breed also has been considered as an endangered breed as its population is <10 000 (Kachhiapatel, 2010). This has recently attracted the attention of the government institutions and stakeholders to adopt a strategic breeding plan and to conserve these breeds, as future requirement of these precious genetic resources is not known. Selection of true to breed stallions and mares on the basis of their phenotypic characteristics is quite important in the above endeavour.

Most of the early information on phenotypic characterization is confined mainly to Marwari, Kathiawari and Spiti breeds (Pundir *et al.*, 1997; Pundir, 2001, 2004; Singh, Yadav and Mehta, 2002a, b). Further detailed studies on high-quality phenotypes can also give direct insight into genetic quality of these highly structured populations. In the present genomic era, it is feasible to work on genotyping and sequencing with available robust tools and softwares; however, morphological studies require direct involvement with the animals including identification of animals true to breed and extensive work to record their phenotypic characteristics. The data generated will be helpful in correlating phenotypic traits with genetic parameters responsible for these complex traits. Many breed registries select animals on the basis of their morphology/utility/functions and work for the continuous improvement of those selected animals. Body shape, size and conformation are some of the pointers of utmost importance for selection of horses for breeding purposes. The acquisition of high-quality true to breed animals will be highly valuable as the future requirement of this animal power is not known.

The present study is an effort to phenotypically characterize all the Indian equine breeds together based on their different biometric indices and specific breed characters for selection and conservation of stallions and mares for breeding purpose by private breeders, to help the government departments to maintain good quality stallions for semen collection for artificial insemination (AI), and to facilitate their multiple uses by the horse owners viz in sale and purchase, for use as pack and transport animals as well as for the socio-economic development of their owners.

Materials and methods

Animals

Fifty adults at 3–6 years old, healthy, unrelated and true to breed equines of all the six breeds registered by the Indian National Bureau of Animal Genetic Resources (NBAGR) of the Indian Council of Agricultural Research (ICAR), Karnal, India (Table 1), except Bhutia (35), were selected on the basis of their morphological features in their home tracts from different parts of India. The selected animals either belonged to the government organizations or private equine breeders maintaining the animals for breeding purpose. Kathiawari equines were selected from the state government equine farms at Junagadh and Inaz, Police horses with Junagadh, Rajkot, Sundranagar as well as some private breeders in different parts of Kathiawar (Gujarat); Marwari equines from private breeders of Jodhpur, Pali, Marwar, Udaipur, Dundlod, Nawalgarh, Jalore, Nagore, Bikaner and Pushkar (Ajmer) in Rajasthan; Manipuri equines from Manipur Polo and Riding Club as well as

Table 1. Registration number of horse and pony breeds of India.

Sr. No.	Breed	Home tract	Accession number
1.	Bhutia	Sikkim and Arunachal Pradesh	INDIA_HORSE_2223_BHUTIA_07005
2.	Kathiawari	Gujarat	INDIA_HORSE_0400_KATHIAWARI_07002
3.	Manipuri	Manipur	INDIA_HORSE_1200_MANIPURI_07003
4.	Marwari	Rajasthan	INDIA_HORSE_1700_MARWARI_07001
5.	Spiti	Himachal Pradesh	INDIA_HORSE_0600_SPITI_07004
6.	Zanskari	Jammu and Kashmir	INDIA_HORSE_0700_ZANSKARI_07006

The above breeds of horse have been registered by National Bureau of Animal Genetics and Breeding (NBAGR), India (Anonymous, 2008).

from private breeders of nearby area in Imphal, Manipur; Zanskari horses from the two government farms namely Zanskari Equine Breeding Farm, Chuchot and Russian Marino Sheep Breeding Farm, Mathoo (Leh) and from private equine breeders of Zanskar valley, Ladakh; Bhutia equines from different local areas including Yumthang and Katao in Lachung, ITBP camps both at Dambong and Chunthang in Sikkim; and Spiti horses from the government livestock farm at Lari (Kaza) and private equine breeders from Lahaul and Spiti valley in Himachal Pradesh. Breeding tracts of all these breeds are presented in Figure 1. Efforts were made to select animals from different parts of their home tract to include adequate representatives of the breed. For phenotypic characterization, both biometric indices and some of the salient qualitative morphological characteristics of the breeds were recorded.

Biometric indices and breed characteristics

Fifteen biometric indices were recorded for phenotypic characterization of each breed viz., height at wither (HW), body length (BL), heart girth (HG), face length (FL), face width (FW), ear length (EL), ear width (EW), hoof length (HoL), hoof width (HoW), fore leg length (FLL), hind leg length (HLL), height at knee (HK), height at hock (HH), canon and pole. Animals of both sexes were included in this study. Coat colour, texture of hairs and the age of individual equine were also recorded. Besides these data, good quality photographs were also taken along with typical breed characteristics for their documentation.

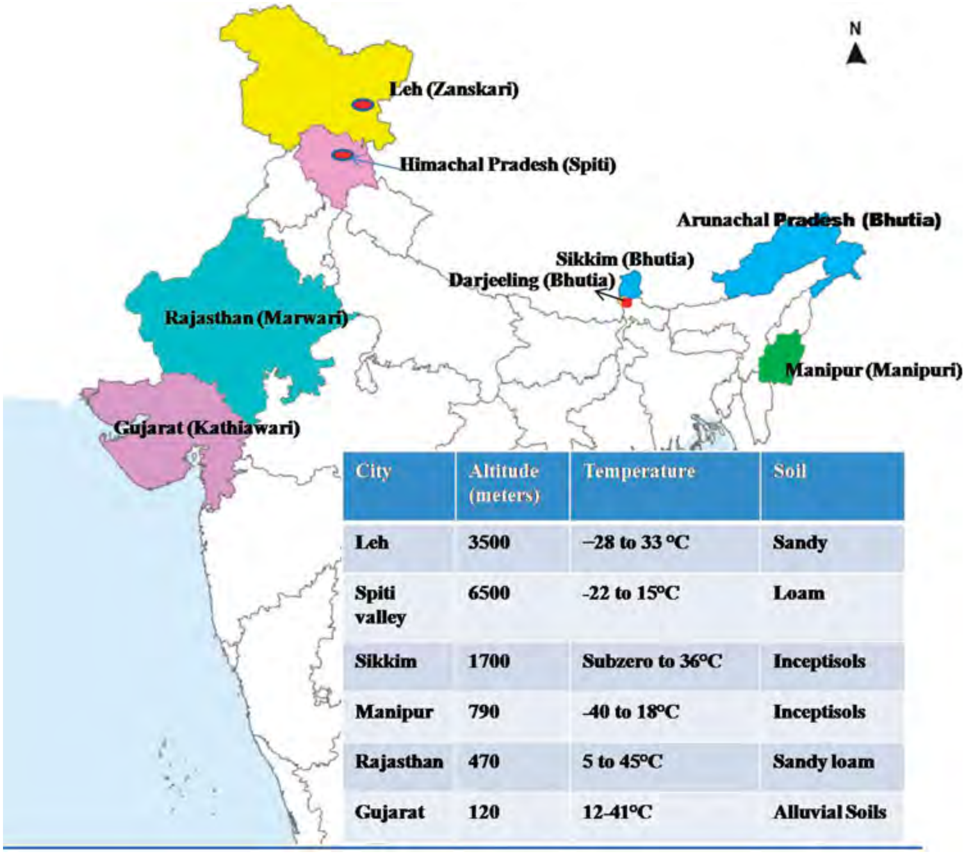
Statistical analysis

Physical characteristics and coat colour were expressed in percentage/frequency. Data on different body measurements was analysed by using standard statistical SPSS package (SPSS Inc., 1998).

Results and discussion

All the six breeds are well acclimatized to their geographical conditions over generations and have acquired certain unique traits such as stamina, sturdiness, endurance, adaptability to harsh climatic conditions, their speed, sure footedness, load carrying capacity on steep and narrow hilly terrains, disease resistance etc. This is the first report on the comparative phenotypic characteristics of all these registered equine breeds together based on their biometric indices and specific breed characteristics. Some of the representative animals of each breed are presented in Figure 2.

Marwari horses are quite heavy, smart, nice looking, tall, fast moving with high endurance capacity and thrive in



City	Altitude (meters)	Temperature	Soil
Leh	3500	–28 to 33 °C	Sandy
Spiti valley	6500	-22 to 15°C	Loam
Sikkim	1700	Subzero to 36°C	Inceptisols
Manipur	790	-40 to 18°C	Inceptisols
Rajasthan	470	5 to 45°C	Sandy loam
Gujarat	120	12-41°C	Alluvial Soils

Figure 1. Home tract of indigenous equine breeds in India.

Figure 2. Representative animals of all the six equine breeds in India.

sandy Thar desert (Rajasthan) where temperature is as high as 48–50 °C during summer but as low as −3 °C during winter. Kathiawari horses are also smart, good looking, hardy and sure footed, suitable for traversing the stony, rough and broken countryside in Kathiawar region, Gujarat. Similar observations to some extent have also been reported by Kachhiapatel (2010) and Zala (2010). Zanskari and Spiti horses belong to the Northern Himalayan terrains having cold climate and mountainous regions termed as cold desert. These breeds are quite adapted to very low temperature conditions (−20 to −40 °C) with low feed and fodder availability. Both breeds are slow moving but surefooted on difficult and steep terrains. They are very hard working animals with high stamina. Zanskari horses very seldom fall sick due probably to the neat and clean environment. Manipuri and Bhutia equines are also extremely tough, quick mover, sure-footed with high pack load and placid capable of extreme endurance.

Biometric characteristics

Comparison of biometric indices in different indigenous breeds

Ranges and mean values of the 15 biometric indices along with standard error of mean of all the six indigenous equine breeds are presented in Table 2. Out of the six indigenous equine breeds, Marwari and Kathiawari had mean HW equivalent to 150 cm or more while equines of Manipuri (129 cm), Spiti (124 cm), Zanskari (126 cm) and Bhutia (127 cm) breeds had their mean HW less than 150 cm. HW is an important biometric index mainly for categorizing equines under horse or pony category.

Table 2. Range, mean and standard error of mean (SEM) values of different biometric indices in Indian equine breeds (values in cm).

Indices/Breeds		Kathiawari ($N = 50$)	Marwari ($N = 66$)	Manipuri ($N = 50$)	Spiti ($N = 50$)	Zanskari ($N = 50$)	Bhutia ($N = 35$)
WH	Range	139–159	142–167	119–136	93–151	110–140	114–134
	Mean ± SEM	150.20d ± 0.87	155.42e ± 0.76	129.04c ± 0.88	123.54a ± 1.01	126.32b ± 0.87	126.94b,c ± 1.04
BL	Range	143–167	142–183	119–138	73–144	102–142	117–140
	Mean ± SEM	151.64c ± 1.20	156.62d ± 1.05	129.57b ± 1.21	116.32a ± 1.39	126.10b ± 1.197	129.06b ± 1.43
HG	Range	147–185	156–196	127–160	101–175	115–172	134–168
	Mean ± SEM	165.86c ± 1.53	174.03d ± 1.34	143.57a ± 1.54	148.14b ± 1.78	146.26b ± 1.53	149.51b ± 1.83
Canon	Range	23–29	24–31.5	–	–	13–19	20–25
	Mean ± SEM	26.70c ± 0.75	22.44b ± 0.66	–	–	16.06a ± 0.75	21.60b ± 0.89
EL	Range	10–13.5	11–18	13–17	12–18	11–15	11–16
	Mean ± SEM	11.73a ± 0.18	13.41b ± 0.16	14.87c ± 0.18	15.41d ± 0.21	13.12b ± 0.18	13.34b ± 0.21
EW	Range	6–19	7–13.5	8–16	5–8.5	8–11.5	8–12
	Mean ± SEM	9.32b ± 0.21	9.99c ± 0.18	12.83e ± 0.21	6.51a ± 0.24	10.02c ± 0.21	10.66d ± 0.25
FL	Range	55–70	54–75	51–65	38–67	42–61	47–59
	Mean ± SEM	64.58d ± 0.55	65.62d ± 0.48	58.18c ± 0.55	51.89a ± 0.64	53.72b ± 0.55	54.06b ± 0.65
FW	Range	17–22	15–22	19–22	11–20	13–18	16–19
	Mean ± SEM	19.28d ± 0.20	18.34c ± 0.18	20.20e ± 0.20	15.82a ± 0.23	15.54a ± 0.199	17.54b ± 0.24
FLL	Range	88–106	83–114	71–95	66–92	74–94	75–93
	Mean ± SEM	97.34c ± 0.74	99.35c ± 0.65	78.37a ± 0.75	78.03a ± 0.86	84.56b ± 0.74	85.91b ± 0.88
HH	Range	45–67	48–68	39–50	–	39–46	45–56
	Mean ± SEM	59.92c ± 0.37	60.58c ± 0.33	44.45a ± 0.38	–	43.45a ± 0.38	51.43b ± 0.45
HLL	Range	90–102	87–111	72–90	65–94	73–90	77–90
	Mean ± SEM	96.88c ± 0.51	98.83d ± 0.45	82.33b ± 0.51	79.45a ± 0.59	79.96a ± 0.51	83.60b ± 0.61
HoL	Range	10–14	10–14	–	–	8–13	11–14
	Mean ± SEM	11.49b ± 0.11	12.44c ± 0.10	–	–	10.35a ± 0.11	12.13c ± 0.14
HoW	Range	9–11	9–13	–	–	7–11	8.5–11
	Mean ± SEM	10.32c ± 0.09	11.39d ± 0.08	–	–	9.22a ± 0.09	9.80b ± 0.11
HK	Range	41–48	42–62	36–50	36–43	33–60	32–50
	Mean ± SEM	45.60a,b ± 2.72	47.23b ± 2.39	39.44a,b ± 2.75	39.05a,b ± 3.17	43.74a,b ± 2.72	37.83a ± 3.25
Pole	Range	4.5–12	6–10	13–17	9–14	8–15	9–13
	Mean ± SEM	7.20a ± 0.17	7.98b ± 0.15	14.40e ± 0.17	12.18d ± 0.20	12.45d ± 0.17	11.03c ± 0.20

Different alphabets given along with numerical values indicate significant ($P < 0.05$) differences between breeds in each row. – not recorded.

Horses less than 150 cm are grouped under pony category and those above 150 cm are considered as horses, while the International Federation for Equestrian Sports defines the official cut-off point at 148 cm without shoes and 149 cm with shoes (http://en.wikipedia.org/wiki/Pony). Among all the indigenous equine breeds studied, horses of both Marwari and Kathiawari breeds were around 150 cm or more in height and as such come under 'horse' breeds, while Zanskari, Spiti, Manipuri and Bhutia equids fall under 'pony' breeds. It was quite interesting to record that the average HW of the Kathiawari horses was around or less than 150 cm. If suitable breeding measures are not taken by the Gujarat Government or concerned breeders, this breed may be reclassified as a pony breed. Among both horse breeds, Marwari horses were significantly higher than Kathiawari horses. Singh, Yadav and Mehta (2002a, b) pointed out a lower HW of Kathiawari horses than that of Marwari horses, while Zala (2010) also described Kathiawari as a pony breed. Further, it was interesting to note that among all these breeds, animals of Marwari and Spiti breeds were observed to be significantly ($P < 0.05$) the tallest and the shortest, respectively.

Similar to HW, a very similar pattern was observed in the BL of all these breeds. Differences in HG were also significant ($P < 0.05$) between Kathiawari and Marwari breeds. HGs in Spiti, Zanskari and Bhutia animals were not significantly different from each other but they were significantly ($P < 0.05$) higher than that in Manipuri equines. Canon length of Kathiawari equids was significantly ($P < 0.05$) higher than that of Marwari, Zanskari and Bhutia breeds while Bhutia ponies had a longer canon than Zanskari ponies. Some of the features reported are in agreement with earlier observations (Pundir *et al.*, 1997; Pundir, 2001; Singh, Yadav and Mehta, 2002a, b).

EL and EW were recorded to be maximum and significantly ($P > 0.05$) higher in Spiti and Manipuri ponies than in the other four breeds. Further, EW of Spiti ponies was significantly ($P < 0.05$) the lowest compared with other horse and pony breeds. Among Kathiawari and Marwari horses, both these indices were significantly ($P < 0.05$) higher in Marwari animals.

FL is an important feature depicting animal grace. It also varied significantly ($P < 0.05$) among the breeds with a minimum in Spiti ponies and a maximum in Kathiawari animals. FLs of Kathiawari and Marwari animals were almost at par but FW was significantly ($P < 0.05$) higher in the former than in the latter, indicating that face of Kathiawari horse is broader than Marwari horse.

However, face of Manipuri ponies was the broadest among these breeds.

Both FLL and HLL were significantly ($P < 0.05$) higher in Marwari animals, but the lowest values were detected in Spiti ponies compared with other breeds. Similar to leg length, HH and knee height were maximum and significantly higher in Marwari animals than pony breeds. The HoL was observed to be maximum and significantly ($P < 0.05$) higher in both Marwari and Bhutia equines than in the remaining four breeds. However, the HoW was maximum and significantly ($P < 0.05$) higher in Marwari animals than pony breeds. Among all the breeds, pole (gap between ears) was significantly ($P < 0.05$) the lowest in the animals of Kathiawari breeds compared with other breeds. Maximum pole was observed in Manipuri breed.

Coat colour

Different coat colours were observed in all true to breed animals selected for this study irrespective of their sexes. In Marwari horses, bay (56 percent), chestnut (18 percent), grey (14 percent) and pie/skewbald (12 percent) were the prominent colours, while in Kathiawari, chestnut (40 percent) was the most prominent colour followed by bay (38 percent), grey (16 percent) and pie/skew bald (6 percent). In Spiti ponies, common coat colours were grey (32 percent), brown (28 percent), piebald (22 percent) and black (18 percent). In Spiti ponies, animals having black body with white patches were taken as piebald. In Zanskari ponies, grey was the most prominent coat colour (54 percent) followed by bay (26 percent) and black (20 percent). In Bhutia ponies, bay was the most common colour (69 percent) followed by chestnut (23 percent), grey and other colours (8 percent). In Manipuri breed, bay, chestnut, brown, grey and cream were quite common, but black and roan were extremely rare. Beside these, other colours (local names) such as palomino, cream, dun and pinto were also available.

In general, no particular colour trend was observed in animals of both sexes in all the breeds. Colour varies from region to region depending on breeder's choice. Some more information on other coat colours also has been given under breed characteristics.

Comparative biometric indices in mares and stallions of different equine breeds

Sex-wise evaluation of biometric indices in all six breeds indicated significant differences between and within some of the breeds (Table 3).

Both mares and stallions of Kathiawari and Marwari breeds were at par as far as HW was concerned. Spiti stallions (117.80 cm) were observed to be significantly ($P < 0.05$) the smallest compared with its mares and both sexes of other breeds. Similarly BL of Spiti stallions was significantly ($P < 0.05$) the smallest compared with its mares and both sexes of other breeds. Between the two horse breeds, Marwari mares were significantly ($P < 0.05$) higher in their BL than Kathiawari mares but no such difference was observed between their stallions. Further, BLs of Spiti and Zanskari mares were significantly ($P < 0.05$) higher than that of their stallions. HG of Spiti stallions was significantly ($P < 0.05$) lower than that of its mares. However, no such difference was observed between both sexes within other breeds.

The FLs of mares and stallions were at par within the breeds except Kathiawari horses in which FL of stallions was significantly ($P < 0.05$) higher than that of its mares. Among breeds, FL of Spiti mares was the smallest, while Manipuri mares and stallions had significantly ($P < 0.05$) higher FLs than both sexes of Zanskari, Bhutia and Spiti ponies but lower than that of Kathiawari and Marwari horses. FW also varied appreciably among all the breeds with a maximum in Manipuri mares and a minimum in Spiti stallions but no difference was observed between sexes within the breeds. EL was significantly ($P < 0.05$) lower only in Spiti stallions than its mares, while no such difference was observed between sexes within other breeds. EWs of both Kathiawari and Spiti stallions were significantly ($P < 0.05$) smaller than that of their mares, otherwise no such difference was observed between sexes within other breeds.

There was no significant difference in FLL and HLL between sexes of all the breeds except Marwari, in which HLL was significantly ($P < 0.05$) longer in stallions than mares. HH and canon length in Marwari mares were significantly ($P < 0.05$) higher than that in both sexes of other breeds but lower than its stallions. No difference was observed in both these traits between mares and stallions within other breeds. Similarly, no difference was observed in HoL, HoW and pole between mares and stallions within all the six breeds.

On the basis of all these biometric indices, Spiti pony appeared to be the smallest, while Marwari horse to be the robust among all the Indian horse and pony breeds. To date, little information is available on such aspects and these data will serve as a baseline data for future selection of animals for breeding purpose.

Breed characteristics of Indian horse and pony breeds

Every breed has its own typical characteristics which are unique to some extent for its identification and differentiation from other similar type of breeding animals. Some characters may be common or near about, indicating similarities among those breeds which can be solved by their evolutionary studies. Figures 3 and 4 present some of the salient characteristics of each breed.

Marwari horse

This breed has its origin in Marwar and Mewar region of Rajasthan. The breeding tract of Marwari breed is

Table 3. Sex-wise comparative mean values of various biometric indices in Indian equine breeds (values in cm ± SEM).

Breeds	Sex (no. of animals)	WH	BL	HG	Canon	EL	EW	FL	FW	FLL	HH	HLL	HoL	HoW	HK	Pole
Kathiawari	♂ ($N = 32$)	149.71c ± 1.119	150.78e ± 1.499	164.84c ± 1.919	26.66c ± 0.939	11.75a ± 0.220	9.82d ± 0.255	63.43c ± 0.674	19.09c,d ± 0.250	96.37c ± 0.937	59.62c,d ± 0.474	96.53c ± 0.644	11.42b ± 0.193	10.18b,c ± 0.164	45.18d ± 0.445	7.10a ± 0.226
	♀ ($N = 18$)	150.94c ± 1.492	153.17e,f ± 1.998	167.60c ± 2.559	26.78c ± 1.252	11.69a ± 0.293	8.41c ± 0.340	66.61d ± 0.898	19.61d,e ± 0.333	99.05c ± 1.250	60.44c,d ± 0.633	97.50c ± 0.859	11.61b,c ± 0.257	10.55c,d ± 0.219	45.94d ± 0.593	7.36a ± 0.301
Marwari	♂ ($N = 50$)	155.00c ± 0.895	157.26f ± 1.199	174.10d ± 1.535	20.39b ± 0.751	13.54b ± 0.176	10.14d ± 0.204	65.54c,d ± 0.539	18.16b,c ± 0.200	98.80c ± 0.750	60.98d ± 0.380	97.88c ± 0.515	12.36c ± 0.154	11.25e ± 0.131	46.88d,e ± 0.356	7.96a,b ± 0.181
	♀ ($N = 16$)	155.19c ± 1.582	153.25e,f ± 2.120	172.0c,d ± 2.714	27.44c ± 1.328	13.00b ± 0.311	9.65d ± 0.361	65.81c,d ± 0.953	19.12c,d ± 0.353	99.93c ± 1.326	58.50c ± 0.671	101.00d ± 0.911	11.90b,c ± 0.273	11.12d,e ± 0.232	47.93e ± 0629	8.50b ± 0.319
Manipuri	♂ ($N = 25$)	129.08b ± 1.292	129.96d ±1.731	143.33a,b ± 2.216	–	15.29d,e ± 0.254	13.12e ± 0.295	57.50b ± 0.778	20.20e ± 0.288	78.37a ± 1.082	43.62a ± 0548	81.50a,b ± 0.744	–	–	39.33b,c ± 0.514	14.68e ± 0.261
	♀ ($N = 25$)	129.04b ± 1.292	129.17c,d ± 1.731	143.75a,b ± 2.216	–	14.52c,d ± 0.254	12.56e ± 0.295	58.58b ± 0.778	20.12d,e ± 0.288	78.16a ± 1.082	45.12a ± 0.548	83.04b ± 0.744	–	–	39.47b,c ± 0.514	14.08e ± 0.216
Spiti	♂ ($N = 37$)	124.43b ± 1.119	117.31b ± 1.499	150.03c ± 1.919	–	15.53e ± 0.220	6.67b ± 0.255	51.62a ± 0.674	15.89a ± 0.250	77.90a ± 0.937	–	79.38a ± 0.712	–	–	38.96b,c ± 0.445	12.12d ± 0.221
	♀ ($N = 13$)	117.80a ± 2.830	110.00a ± 3.792	136.00a ± 4.856	–	14.60c,d ± 0.556	5.50a ± 0.646	53.60a ± 1.704	15.40a ± 0.632	78.80a ± 2.372	–	79.65a ± 0.921	–	–	39.60c ± 1.125	12.24d ± 0.213
Zanskari	♂ ($N = 22$)	125.18b ± 1.349	129.86d ± 1.808	148.50c ± 2.315	15.90a ± 1.132	13.36b ± 0.265	10.04d ± 0.308	53.63a ± 0.813	15.36a ± 0.301	83.90b ± 1.131	43.41a ± 0.600	79.77a ± 0.777	10.45a ± 0.232	9.27a ± 0.198	36.86a ± 0.536	12.38d ± 0.272
	♀ ($N = 28$)	127.21b ± 1.196	123.07b.c ± 1.602	144.50c ± 2.052	16.18a ± 1.004	12.92b ± 0.235	10.00d ± 0.273	53.78a ± 0.720	15.67a ± 0.267	85.07b ± 1.002	43.50a ± 0.532	80.10a ± 0.688	10.26a ± 0.206	9.17a ± 0.176	37.57a,b ± 0.476	12.50d ± 0.242
Bhutia	♂ ($N = 7$)	126.00b ± 2.392	128.57c,d ± 3.205	147.57c ± 4.104	22.14b ± 2.008	13.71b,c ± 0.470	10.57d ± 0.546	52.71a ± 1.440	17.85b ± 0.534	83.85b ± 2.004	51.71b ± 1.014	83.57b ± 1.377	11.64b,c ± 0.412	9.50a ± 0.351	37.85a,b,c ± 0.951	10.85c ± 0.483
	♀ ($N = 28$)	127.17b ± 1.196	129.18c,d ± 1.602	150.00c ± 2.052	21.46b ± 1.004	13.25b ± 0.235	10.67d ± 0.273	54.39a ± 0.720	17.46b ± 0.267	86.42b ± 1.002	51.35b ± 0.507	83.60b ± 0.688	12.25b,c ± 0.206	9.87a,b ± 0.176	37.82a,b,c ± 0.476	11.07c ± 0.242

Different alphabets given along with numerical values indicate significant ($P < 0.05$) differences due to breed and sex.
SEM = standard error of mean

Figure 3. Faces of Indian equine breeds showing typical breed characteristics.

Figure 4. Hind portions of Indian equine breeds showing typical characteristics.

Jodhpur, Udaipur, Jalore, Sanchor, Nagore, Pali, Sirohi, Barmer, Jaisalmer and Rajsamand districts of Rajasthan. These horses facially resemble Kathiawari breed probably due to mixing of Arabian blood. Some of the important features of this breed are as follows.

The animals of this breed have a majestic look with fine coat. Their average HW is commonly above 150 cm or 15 hands (range between 14 and 16 hands) with an average weight of healthy adults about 371 kg. Stallions are generally heavier than mares. These horses have proportional structure, well-developed neck and head, long back and body, low set tail and sickle-shaped hocks. Head is generally long with a medium muzzle. Face and neck of Marwari horses are longer than Kathiawari horses. Head joins the neck at an angle of about 45°. Forehead is flat and broad between eyes, and has a flat and long nasal bone. Eyes are large, round and widely apart. The ears are soft, about 10–15 cm long, curved, located at 90° axis and can rotate at 180° angle. Tips of ears are pointed and curved inward like a sickle. The tips of the ears meet or overlap each other when the animal rotates its ears. The ears are slightly larger among the mares compared with stallions. Mane is not very long. Chest is generally deep and medium. Wither is well defined. Shoulders are muscular and long. Canon bones are long and appear broad from side. Hock is broad, while fetlock is round and strong with short pastern. Hooves appear a little different, front ones oblong but hind ones round. The common colours of Marwari breed are bay, kumet (chestnut), surang (liver chestnut), bhanwar (black or dark brown), dane, skewbald, piebald and grey.

It takes much shorter time to train a Marwari horse than many other breeds. In long distance races, its endurance is amazing. Like Arab, it has surefooted and sound legs. It has an easy pace with a beautiful gait.

Kathiawari horse

The breeding tract of Kathiawari horses is Rajkot, Bhavnagar, Surendranagar, Junagadh and Amreli districts of Gujarat. This breed is also found in parts of Rajasthan adjoining Gujarat. This breed is believed to have evolved from the wild horses of Kathiawar of Gujarat state and Arabian horses which happened to land on sea shore after the crash of a ship in Arabian Sea (Kaura, 1961). Some of the salient characteristic features of this breed are as given below.

The Kathiawari horses are good looking, well built, intelligent and hardy animals. These animals measure about 13.5–14.5 hands in HW and weigh about 380 kg. Some selected animals also have HW more than 15 hands. Kathiawari horses have developed structure, well-developed neck and head, curved and short back and body but long mane. They also have prominent orbital fossa, concave back and nasal bone with broad face. Muzzle is small with big nostrils. Eyes are large (toad-like) and well set on sides of the forehead. Ears are small (10.0–13.5 cm), narrow, fine, located at 90° axis and can rotate at 180° angle. Tips of ears are pointed and curved inward like a sickle, and can meet or overlap each other when an animal rotates its ears. These animals have well-muscled thighs and shoulders. Neck is crested and stout with slopping shoulder and prominent wither. The main characteristic features are that these horses have sickle hocks. Quarters is strong and almost squash with long forearms. Hooves are generally round. Tail is set high and long. These animals are well known for pace and speed and can withstand both extreme cold and hot climates. The prevalent colours of this breed are mainly chestnut, bay, brown, piebald, skewbald and grey of all types. Some of these similar types of characteristics have also been reported by Ghanshyamji (2010) and Singh, Pal and Gupta (2010).

Bhutia pony

Bhutia ponies have their origin in India and their home tract includes Darjeeling, Arunachal Pradesh, Sikkim and Bhutan. They are popular in hilly regions for riding as well as pack purposes. They are similar to Spiti pony and Tibetan pony, as these breeds have been interbred for years.

The HW of Bhutia ponies is 13.0 to 13.2 hands and they weigh about 270 kg. They have a large head with a pronounced jaw and a straight profile. These ponies have a short neck, low withers, a straight back, sloping quarters and deep chest. Their shoulders are straight with long mane and a well-set tail. Their feet are fairly open at hoofs. These ponies can survive on much smaller and poor quality food rations than other ponies of its size. The prevailing colours are usually grey and iron grey, occasionally chestnut and roan.

They are well known especially due to the terrifying habit while moving they always keep to the extreme edge of a mountain path and generally one leg dangles over several hundred feet of nothingness. The reason for this is that the animals are used to carrying luggage on either side of their body, so they keep to the outside of a track to avoid bumping against the cliff wall on the inner side.

Spiti pony

The breeding tract of Spiti horses is Kaza subdivision of the Lahaul and Spiti district and the Yanthang area of the Kinnaur district of Himachal Pradesh in India. They are reared as pack animals at high altitudes in the Himalayan range.

Spiti ponies are smaller in HW at 129 cm, 100 cm BL, 148 cm HG and they weigh about 320 kg. Mane is long and has hairs of 25–40 cm in length. The body is solid, displaying an alert attitude. Face is convex, ears are erect and eyes are black. The tail is medium in length and straight. The common coat colours are grey, brown, black and piebald. These ponies are capable of tolerating extreme cold conditions very easily as their bodies are covered with thick, coarse and long hairs. The ponies are docile in temperament. Pundir (2004) has also reported similar ranges for height, BL and coat colours.

Generally, these ponies are hardy, surefooted animals, and used mainly for riding and as pack animals in cold hilly regions. Presently population of true to breed Spiti animal is less than 1000 (http://www.hplahaulspiti.nic.in/history.htm), which is much less than the European standards for declaring it as an endangered breed.

Manipuri pony

These animals are bred and found in the state of Manipur. Manipuri is considered to be a descendant of both the Mongolian wild horse and the Arab horse. Some of the common characteristics of this breed are as follows:

These ponies are well known for elegance, endurance and speed. The HW of Manipuri ponies is about 11–13 hands and body weight about 300 kg. These ponies have small-sized body with a fairly long face. Head is proportional and attractive with a straight profile. Ears are alert, small, pointed, pricked and slightly slant like an almond. The muzzle is broad with dilated nostrils. The body is compact with a broad chest but wither is not very prominent. The neck is muscular with coarse mane and slopping shoulders for better movement. The legs are proportionate to the body with strong knees and hocks. Pasterns possess a gradual and proportionate slope. Hooves are in proportion to the body and round, not too boxy while tail is highly set. In Manipuri pony, the predominant body colours are bay, chestnut, grey, skewbald type and brown but black and roan are extremely rare.

These ponies are extremely tough, sure-footed, placid capable of extreme endurance and mainly used for polo, ceremonial activities and routine pack animal. Presently, population of Manipuri pony is 1218 (http://www.e-pao.net/GP.asp?src=13..220411.apr11) and as such there is an urgent need to conserve this breed.

Zanskari pony

Zanskari ponies have their origin in the Great Himalayan range (India), namely in the high altitude Zanskar area of Ladakh region of Jammu and Kashmir state of India. These animals are bred in cold desert at high altitudes where temperature ranges from 20 to −40 °C. At present, only a few hundred ponies exist in the Zanskar and other valleys of Ladakh region. These ponies are known for their hardiness and ability to work at high altitudes.

The Zanskari pony is considered the hardiest among all the pony breeds and can work in the extremes of altitude and temperature. Physique of this pony seems to be very similar to the Spiti pony but it is more adaptable to higher altitude where they are used as work animals. Body hairs are fine, glossy and long. The HW of the animal is between 13.2 and 14.7 hands. Hair coat of Zanskari ponies is thick, rough and quite similar to that of Spiti ponies. Their body is compact and head is broad. The neck is well built and placed middle. The ratio of the HW to BL is 1:1. The animals have well built conformation. The face is long with length and width ratio of about 3:1. The nasal bone is flat or convex. The ocular fossa and pole are deep. The ears are larger in length than width. The eyes are bulging out, muzzle is strong and compact. The tail and mane are long. Tail commonly touches the ground. The common body colour is grey followed by bay and black (Gupta, Pal and Tandon, 2010).

Special mention is made of equines of this region for their exceptional ability to survive and perform under very harsh and unfavourable climatic conditions of their high altitude habitat (between 3000 and 5000 m above sea level). Since this is a breed of hilly region, they have very good stamina as pack animals. They are sure-footed animals when used in difficult terrains. Very seldom they fall sick. These ponies are known for their ability to work tirelessly and carry loads in high altitude regions. These animals are also used for riding and polo and for logistic support by Indian army in Ladakh region.

Indigenous Horse Society of India (http://www.horseindian.com) has defined some of the breed characteristics of five breeds but these are not fully defined and partial information has been provided for some of the breeds. The information presented in this article provides salient breed characteristics of all the six registered Indian horse and pony breeds along with their biometric indices which are quite useful for the selection of purebred animals.

Conclusions

In view of all biometric indices and breed characteristics, it is clear that Marwari and Kathiawari breeds can be differentiated on the basis of their FL, FWs, EL, EWs, HG, HoL, HoW and pole. Single biometric index is not sufficient to differentiate these breeds. More precisely, the face of Kathiawari is much wider than that of Marwari horse; nasal bone of Kathiawari was concave, while in the case of Marwari it was flat or convex. Some of the similarities include that horses of both Marwari and Kathiawari breeds can rotate their ear tips by 180°, leading the tips meet together at the open end. This breed characteristic is not available in any Indian pony breed.

Among pony breeds, Spiti ponies can be differentiated from other breeds on the basis of their HW, BL, EL, EW as well as FL, while pole, FL and muzzle of Manipuri pony can be used to differentiate this breed from other pony breeds. Manipuri breed is considered to be the original polo breed of the world. Although significant differences were observed in most of the biometric indices in all the pony breeds yet Spiti pony is quite similar to Zanskari pony in physical appearance, while Manipuri and Bhutia ponies appear very similar to each other. In general, it is not easy to differentiate these breeds from each other on the basis of a single biometric index as wide or overlapping ranges have been observed for most of the characteristics, but a set of indices can pin point such differences. Further, this study has generated baseline data on different measureable phenotypic traits and other qualitative traits to help in fixing breed standards of Indian horses and ponies and for adopting strategies for planned breeding and conservation of true to breed animals of each breed as populations of all the horse and pony breeds are less than the standard figures.

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Principal component analysis of cephalic morphology to classify some Pyrenean cattle

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Summary

Seven morphostructural traits namely head, face and skull widths and lengths and head depth of 300 cows belonging to seven different French and Spanish breeds were measured. The investigation aimed at grouping these cattle breeds according to their head conformation using principal component analysis. From the normalized varimax rotation, two principal components that accounted for 68.1 percent of the total variance were extracted. The first principal component, termed viscerocranium length component, had its loadings for face and head lengths and explained 49.9 percent of the generalized variance. Skull and head widths determined the second principal component, which contributed to 19.2 percent of the variance, and could be termed the component of the neurocranium width. There is a good deal of overlap between breeds although the Avileña breed shows an increasingly longer built skull in terms of face and skull lengths. The Blanca del Pallars breed appears significantly separated from alpine breeds but closely related to Gascon.

Keywords: *bovine, brachyceros, cranium, osteometry*

Résumé

On a mesuré sept caractères morphostructuraux (c'est-à-dire, largeur et longueur de la tête, de la face et du crâne, ainsi que profondeur de la tête) de 300 vaches appartenant à sept différentes races françaises et espagnoles. L'enquête visait à regrouper ces races de bovins selon la conformation de leur tête, en utilisant l'analyse en composantes principales. On a dégagé de la rotation varimax normalisée deux composantes principales qui représentaient 68,1 pour cent de la variance totale. La première composante principale, appelée composante de la longueur du viscérocrâne, qui mesurait la longueur de la face et de la tête, justifiait 49,9 pour cent de la variance généralisée. Les largeurs du crâne et de la tête ont défini la deuxième composante principale qui représentait 19,2 pour cent de la variance. On pourrait l'appeler la composante de la largeur du neurocrâne. Les races se chevauchent beaucoup, bien que la race Avileña présente la structure d'un crâne de plus en plus long sur le plan des longueurs de la tête et du crâne. La race Blanca del Pallars semble être sensiblement éloignée des races alpines, mais très proche de la race Gasconne.

Mots-clés: *bovin, brachyceros, crâne, ostéométrie*

Resumen

Se han medido siete caracteres morfoestructurales (anchura y longitud de la cabeza, de la cara y del cráneo, y la profundidad de la cabeza) a 300 vacas pertenecientes a siete razas francesas y españolas. El objetivo de la investigación estuvo centrado en el agrupamiento de estas razas de ganado de acuerdo a su conformación de la cabeza, utilizando análisis de componentes principales. De la rotación varimax normalizada, se extrajeron dos componentes principales que representaban el 68,1 percent de la variación total. El primer componente principal, denominado longitud *viscerocranium*, tenía peso específico para la longitud de la cara y de la cabeza, y explicaba el 49,9 percent de la varianza generalizada. La anchura del cráneo y de la cabeza determinó el segundo componente principal, lo que contribuía a un 19,2 percent de la varianza, y que podría denominarse como el componente anchura *neurocranium.* Existe un gran solapamiento entre las razas; aunque la Avileña muestra un cráneo cada vez más largo de acuerdo a la relación existente entre la longitud de la cara y la del cráneo. La raza Blanca del Pallars aparece muy separada del resto de las razas alpinas, pero cercana a la Gascón.

Palabras clave: *bovino, brachyceros, cráneo, osteometría*

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Introduction

Biological relationships among cattle breeds are studied for a variety of reasons (Kidd and Pirchner, 1971). For example, the relationships may reflect breed histories and thereby illuminate human migrations, they may identify breeds potentially useful in breeding programmes and they may aid in understanding domestication (Simon *et al.*, 2008). Historically, morphological studies, especially of the skull, were the major source of data used to characterize breeds (Kidd and Pirchner, 1971), but molecular genetics were recognized soon after their discovery to be another valuable source of data (Viana

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et al., 1998; Pariset *et al.*, 2010; Martín-Burriel *et al.*, 2011). Evolution of mammalian skeletal structure can be rapid and the changes profound, as illustrated by the morphological diversity of the cattle. There are several ways of trying to group the European cattle breeds: by role, geographically, by obvious external characteristics such as colour and horns, by genetic distance or by any of several hypotheses suggesting how the breeds might have evolved an diversified and in which general directions their ancestors migrated with the invaders and settlers of their country of origin (Porter, 1991; Čítek *et al.*, 2006; Achilli *et al.*, 2009). There is certain arbitrariness in such groupings and it depends, to some extent, on why the connections between the breeds are being sought (Porter, 1991). It has been traditionally stated that cattle breeds were distinguishable on the basis of suites of head measurements and considered that skull and face lengths and widths were most useful for their identification.

The objective of principal component analysis (PCA) is to account for the maximum portion of the variance present in the original set of variables with a minimum number of composite variables. It assumes that the unique variance represents a small portion of the total variance. The present investigation therefore explores the relationships among some cephalic dimensions in some bovine breeds using PCA with a view to reduce the number of body measurements required for genetic and breeding purposes. Rotation of principal components was through the transformation of the components to approximate a simple structure. PCA can be used with success when morphological characteristics are interdependent. This is to find the loadings that can explain the highest variation in the data set over the dependent variable. The resulting PC or loadings may decrease the dimension of the explanatory variables and break the possible dependence among explanatory variables (Yakubu and Ayoade, 2009).

To the present, skull morphometric studies within and among cattle breeds based on a relatively large number of specimens and employing multivariate analysis techniques have been limited. In addition, most of the craniological studies were based on measurements of very few skulls (Kidd and Pirchner, 1971) and from the studies of this type, no comparative one has been performed between the Pyrenean breeds. Therefore, the aim of the present study is to examine the skull differences between some Pyrenean breeds based on large samples as well as their intraspecific variability by means of multivariate analyses. This study therefore also considers the "Pyrenean bovine patchwork", with the special interest of conserving those breeds which are highly endangered, such as Blanca del Pallars.

Material and methods

Three hundred adult cows of known breeds were included in the study. Studied animals belonged to the following seven French and Spanish breeds: Avileña (AVI, $N = 9$), Blanca del Pallars (BLP, $N = 36$), Bruna dels Pirineus (BRU, $N = 193$), Gascon (GAS, $N = 7$), Pardo Alpina (PAL, $N = 19$), Parda de Montaña (PMU, $N = 19$) and Pyrenean (PIR, $N = 17$). Only adult specimens (at least M^3 erupted) were included in this study, because the developing skeleton undergoes large changes in size and proportions, which might limit the distinction between breeds. The Avileña is a black, long-horned draught-and-meat breed that belongs to the black Iberian group and it has many similarities with the so-called Celtic breeds, such as Welsh, Longhorn, Kerry, Camargue and Tortona while the Gascon is a wheaten or grey meat-and-draught breed and is long horned, a trait that is shared with the Podolian types in Italy and the Pyrenean is a blond breed that is straw coloured with pale shading on the underside and lower parts of extremities (Porter, 1991). The muzzle and the mucosae are pink (Sambraus, 1992). Its breed history could be traced back to Celtic cattle. The Bruna dels Pirineus, Pardo Alpina and Parda de Montaña belong to the so-called Alpine Swiss brown group having Swiss strains as their ancestor and are closely related to each other because of their same origin. They are mostly medium to dark brown with a pale back line and almost white around the muzzle. Muzzle and hooves are dark. Finally, the Blanca del Pallars is a fairly primitive pure white breed, the mucosae and hooves being dark. It is classified as a relic breed on the brink of extinction by the Food and Agriculture Organization of the United Nations, as only 33 breeding animals remain alive (2 bulls and 31 cows) and could represent the last vestiges of an ancient Podolian population introduced from France many years ago (unpublished data, 2011) which has been blanketed out of existence by successful alpine Swiss invaders. It is well managed and well adapted to the local Pyrenean hard terrain and climate.

In the present study, following the criteria described in the classical literature (Sánchez, 1984; Porter, 1991), cows were classified as belonging to the Alpine (BRU, PAL and PMU), Blonde (PIR), Iberian (AVI) and Podolian trunks (BLP and GAS). Seven basic measurements were taken following standard procedure and anatomical reference points described (Herrera and Luque, 2009) (Figures 1 and 2):

(1) Skull width.
(2) Head width.
(3) Face width.
(4) Skull length.
(5) Face length.
(6) Head length (V3 + V4).
(7) Head depth.

Only traditional measurements were included. Mandibular measurements were excluded. The cephalic measurements were taken with a slide gauge equipped with a scale. The measurements are in millimetres to the nearest 0.5 mm. All bones were measured by one of the authors (Pere-Miquel

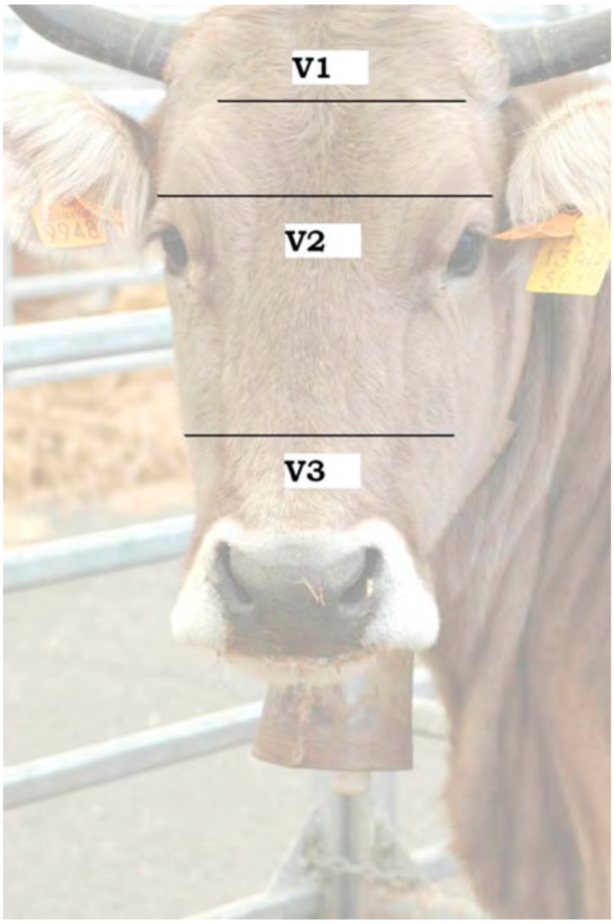

Figure 1. Anatomical reference points described (frontal view). V1, skull width; V2, head width; V3, face width.

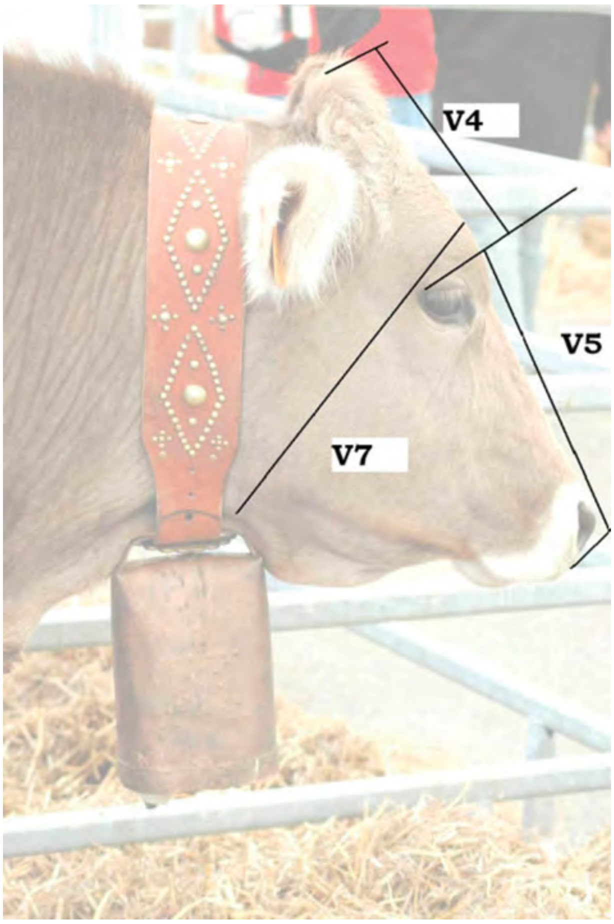

Figure 2. Anatomical reference points described (lateral view). V4, skull length; V5, ace length; V6, head length (V3 + V4); V7, head depth.

Parés) except for 28 Blanca del Pallars cows, which were measured by Ignasi Sinfreu, but since the measurements are defined anatomically, authors do not believe that this fact involved any systematic differences. No specimens had missing measurements. Ethical approval was considered not necessary as the study involved simple manipulations.

Standard statistics comprised mean, standard deviation and coefficient of variation (CV). Also, one-way analysis of variance (ANOVA) on each character was used to ascertain whether or not significant differences existed among breeds. Pearson's correlations were determined and those variables showing all absolute $r < 0.3$ were excluded from subsequent multivariate analysis. The Kaiser – Meyer – Olkin rule criterion was used to determine the number of components, i.e. relating only the components that have eigenvalue greater than 1. For further analysis, a varimax rotation was performed. The next method used in this study was principal components analysis using the correlation matrix. Finally, the standardized canonical coefficients, which represent the contribution of each variable to the discriminative function, were inspected in order to investigate the breed differences.

Statistical analyses were performed using the standard methods of Factor v. 7.00 software package (Lorenzo-Seva and Ferrando, 2006) and PAST (Hammer, Harper and Ryan, 2001). Data are available at the following address: peremiquelp@prodan.udl.cat.

Results and discussion

The analysed breeds differ differently in terms of all the studied parameters (Table 1). Breed variation, expressed by the CVs, is relatively high for some variables in some breeds. Although high CVs have been also reported in previous morphometric studies (Parés and Jordana, 2008) this general variability may be a feature of cattle and it should be taken into account when variables are selected for analysis. On average, the face of Avileña is shorter than those of the other breeds, being a clear brachyprosopic breed, and Blanca del Pallars has the widest skull but in general all measurements show an overlap in ranges. The tests reveal significant differences between breeds in all variables ($p \leq 0.05$), with the exception of head width ($p > 0.05$).

V4 (skull length) is excluded from subsequent analysis as it presents a Pearson's correlation coefficient lower than absolute 0.3. In the component analysis for the six remnant

Table 1. Descriptive statistics of features and significance differences.

	Skull width	Head width	Face width	Skull length	Face length	Head length	Head depth
AVI	18.18^{a}	23.10^{a}	16.49^{ab}	15.60^{abc}	28.92^{a***}	44.52^{a***}	37.50^{a*bcde}
	1.12	1.07	0.95	1.38	5.86	5.44	3.91
	6.1	4.6	5.7	8.8	20.2	12.2	10.4
BLP	19.49^{b*}	23.99^{a}	15.91^{a*}	15.76^{a*c}	37.18^{bc}	51.54^{b**d}	37.66^{ade}
	1.30	1.69	1.82	1.48	2.42	3.87	1.82
	6.6	7.0	11.4	9.3	6.5	7.5	4.8
BRU	18.76^{a}	23.65^{a}	16.98^{ab}	15.01^{ab*}	38.57^{bc}	53.58^{bcd}	35.19^{ab*cd**e***}
	1.20	1.26	1.06	1.32	3.18	2.79	2.20
	6.4	5.3	6.2	8.8	8.2	5.2	6.2
GAS	18.34^{a}	23.10^{a}	17.09^{ab}	14.29^{b***}	39.64^{bc}	53.93^{bcd}	38.01^{abce}
	0.71	0.58	0.70	1.07	1.83	2.30	2.09
	3.8	2.5	4.0	7.5	4.6	4.2	5.5
PAL	18.86^{a}	24.07^{a}	17.44^{b*}	16.67^{abc}	36.67^{b*}	53.34^{bcd}	35.06^{bc*de***}
	0.82	0.97	0.95	1.80	3.83	3.42	1.66
	4.3	4.0	5.4	10.7	10.4	6.4	4.7
PMU	19.22^{a}	24.16^{a}	17.26^{b*}	15.26^{abc}	40.35^{c}	55.61^{cd*}	38.77^{abcd}
	1.20	1.27	1.00	1.37	2.01	2.02	2.05
	6.2	5.2	5.8	8.9	4.9	3.6	5.2
PIR	18.57^{a}	23.18^{a}	17.04^{ab}	14.66^{ab**}	37.75^{bc}	52.41^{bc}	36.45^{abcde*}
	0.89	0.86	1.03	1.56	1.95	2.56	2.24
	4.8	3.7	6.0	10.6	5.1	4.8	6.1

Rows: (1) mean; (2) standard deviation; (3) CV.
Different letters in the same column differ significantly $*p \leq 0.05$, $**p \leq 0.01$, $***p \leq 0.001$.

variables, the estimate of sampling adequacy Kaiser – Meyer – Olkin reveals the proposition of the use in different biometric traits by underlying components (0.66888) and indicates a mediocre sampling adequacy. The determinant of the matrix is 0.05501523013747.

The PCA reveals that the percentage of total variance that best explained the data was summarized in the first two components (Table 2). The two analysed components of the PCA analysis reveal two components, the eigenvalues of which are bigger than 1.0. Eigenvalues for components I and II are 2.99 and 1.15, respectively. These components jointly explain 68.1 percent of the total variance formed by the six metric traits. After the varimax rotation is performed, each variable is given a load, reflecting the linkage of a variable with a given component. The highest loads (>0.7) in Table 3 are marked in bold and loadings lower than absolute 0.300 omitted. PCI is especially linked mostly with two traits out of six (Table 3) reflecting lengths: face and head lengths. PCI accounts for 49.9 percent of the total variation and is interpreted as a size component as suggested by the positive coefficients for almost all measurements. It indicates a proportional increase in the face length in relation to head length in all the breeds. PCI may be called the component of the viscerocranium length. PCII defines traits of width: skull and head widths. PCII may be called the component of the neurocranium width.

Table 2. Extraction of the three first principal components.

Principal component	Eigenvalue	Percentage of variance	Cumulative percentage of variance
1	2.99497	0.49916	0.49916
2	1.15296	0.19216	0.68132
3	0.79004	0.13167	

Table 3. Component loading matrix after varimax rotation.

Variable	PCI	PCII
Skull width		**0.787**
Head width		**0.852**
Face width	0.448	
Face length	**0.875**	
Head length	**1.028**	
Head depth		

The highest loads (> 0.7) are marked in bold and loadings lower than absolute 0.300 omitted.

The polygons of the plot (Figure 3) show a lack of distinct breed difference of skulls. The only apparent tendency is the slight shift to the right of the graph in case of the skulls of Avileña which shows an increasingly shorter built face and head. Due to the marked dispersion of points representing the skulls of the breeds, it may be stated that in terms of the structure of the skull the studied breeds do not constitute uniform groups. On the other hand, the second principal component does not contrast differences between skulls of cows of studied breeds. These observations are confirmed by ANOVA which shows that Avileña differs in terms of face ($F = 76.33$, $p < 0.0001$) and head length ($F = 69.99$, $p < 0.0001$). ANOVA conducted for PCI did show significant differences between Avileña and the others ($F = 283.9$, $p \leq 0.0001$) but as PCI – just connected with two parameters – explains less of half of the total variance, it is difficult to draw final conclusions.

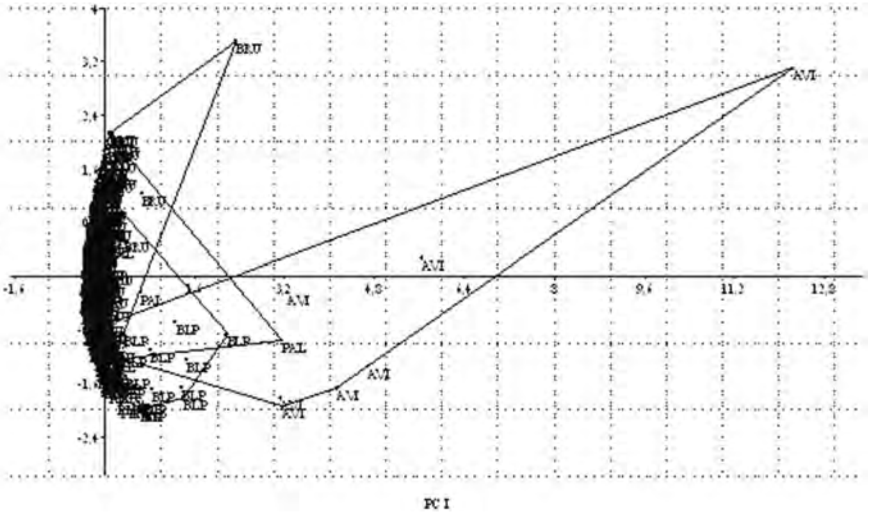

Figure 3. Principal component plot (PCI and PCII). Polygons enclose the breeds. Abbreviations are explained in the text.

ANOVA conducted for PCII shows highly significant differences in some breeds: between Avileña and Bruna dels Pirineus ($p \leq 0.05$), between Blanca del Pallars and Bruna dels Pirineus ($p \leq 0.0001$) and between Blanca del Pallars and Pardo Alpina ($p \leq 0.01$). Of special interest is the position of Blanca del Pallars, which appears clearly separated from alpine breeds such Bruna dels Pirineus and Pardo Alpina but closely related to Gascon. The relationship between Blanca del Pallars and Gascon, as revealed in this investigation, makes possible the claim that the former breed is very distinct from the alpine breeds, differing from the idea of Avellanet, Aranguren-Méndez and Jordana (2002), Jordana *et al.* (2010), and Marmi, Casas and Jordana (2005), although the Blanca del Pallars and the Bruna dels Pirineus are in the same area. One can attempt to identify Blanca del Pallars as a sphere of influence of what we call a "provincialism" in the "Podolian occupation". The Blanca del Pallars breed could have a certain relation with an ancient variety of a grey breed, similar to the extant "Gascon areole" or Mirandais (not studied here), as suggested by general morphological traits of both breeds (authors, 2011, *in press*). Historical, intense relationships have been demonstrated along both sides of Pyrenees (in the Middle Ages, Gascony was a principality in the southwest of France, linked to the ancient county of Pallars Sobirà, in the northeast of Spain). Considerable commerce and traffic must have existed between French and Spanish Pyrenees and this, with intermingling on common or adjacent mountain pastures (a current phenomenon in Pyrenees), must have led to some exchange of breeding stock. Thus, for these historical and geographical reasons, a transpyrenean relationship between Podolian breeds seems quite reasonable.

Finally, the discriminative function analysis indicates no significant differences among breeds ($F = 0.070$; d.f. = 503.14, 68; $P = 1$). Examination of the standardized canonical coefficients revealed that the variables that most contributed to the discrimination between breeds, in decreasing order, were face width and head depth (Table 4).

Table 4. CCA scores for the canonical correspondence analysis.

Variable	Axis 1	Axis 2
Head depth	−1.3931	−0.8586
Face length	−0.2890	1.6423
Skull width	−0.0816	0.1586
Head width	0.0352	0.1740
Head length	0.5867	−0.4971
Face width	1.7688	−0.3141

Our results contrast with the classification of the old zootechnical schools which based breed classification mostly on cranial measurements (Kidd and Pirchner, 1971). Nevertheless, our obtained tree appears to represent a more reasonable picture of the phylogenetic relationships, at least among Pyrenean cattle breeds. Now it would be of some interest to compare results of multivariate analyses of skull measurements from other relict Pyrenean breeds, such as Betizu, Lourdaise and Casta with the present results. But this will be only done if effective sampling is facilitated and collaborative transboundary scientific links are established.

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This research could not have succeeded without the help and support of many farmers who allowed the measurements of their animals. Authors wish to express their special gratitude to Ignasi Sinfreu Canturri, Fernando Blasi and Mercè Casals (Pallars Sobirà), and "Cal Puxica" (Berguedà) too, who all own the last cows of the near extinct Blanca del Pallars breed.

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The domestic livestock resources of Turkey: cattle local breeds and types and their conservation status

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Summary

Turkey's 10.6 million head of cattle comprise a rich array of native breeds and types but these are being increasingly eroded by the often indiscriminate use of exotic genotypes. 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 has been much modification of 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 remaining cattle genetic resources and their conservation status. Government is now aware of the danger of the 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: *indigenous farm animals, production systems, cross-breeding, risk status, extinction*

Résumé

En Turquie, les 10,6 millions de têtes de bétail comprennent une vaste gamme de races et de types indigènes qui, toutefois, subissent de plus en plus l'érosion en raison d'une utilisation souvent indiscriminée de génotypes exotiques. La structure de l'agriculture comporte que la plupart des fermes s'orientent principalement vers une agriculture de subsistance, sont de petite taille, élèvent peu d'animaux et ne fournissent que le minimum d'intrants. Les races indigènes ont évolué pour satisfaire ces conditions et sont convenablement adaptées au milieu naturel, à une nutrition inadéquate et déséquilibrée et aux stress provoqués par les maladies. Au cours des 80 dernières années, les modifications du pool de gènes naturel ont été nombreuses et plusieurs types de races distinctes sont en danger ou ont déjà disparu. Cet article décrit quelques-unes des principales ressources génétiques des bovins qui subsistent et leur état de conservation. Le gouvernement prend conscience à présent du danger de l'appauvrissement ou de la perte de cet aspect important de la biodiversité et a mis en place des programmes pour la conservation et la préservation de plusieurs races indigènes. Le gouvernement, les instituts de recherche et les producteurs devraient travailler conjointement pour assurer la préservation du pool de gènes local et sa contribution continue à la biodiversité et à une production animale durable.

Mots-clés: *animaux d'élevage indigènes, systèmes de production, croisement, état de danger, extinction*

Resumen

Los 10,6 millones de cabezas de ganado de Turquía comprenden un amplio abanico de razas y tipos; sin embargo, éstos están sufriendo una mayor erosión por el uso indiscriminado de genotipos foráneos. La estructura de la agricultura es tal que la mayoría de las explotaciones están orientadas a la subsistencia, de pequeño tamaño, manteniendo muy pocos animales y llevando a cabo una inversión mínima. Las razas autóctonas se han desarrollado para satisfacer estas condiciones y, en general, están muy bien adaptadas al medio en que se desarrollan, a una alimentación pobre y desequilibrada y a diferentes enfermedades. A lo largo de los últimos 80 años se han producido grandes modificaciones del acervo genético, motivo por el cual muchas de estas razas se encuentran en peligro de extinción o han llegado a extinguirse. Este trabajo describe algunas de los principales recursos genéticos de los animales domésticos que quedan y su estado conservación. Actualmente el gobierno es consciente del peligro de empobrecimiento o de la pérdida de esta importante parte de la biodiversidad y, para ello, ha puesto en marcha programas de conservación y preservación de varias razas autóctonas. Tanto el gobierno como los centros de investigación, así como los productores, deben trabajar conjuntamente para asegurar que el acervo genético local se mantenga, y poder contribuir así al desarrollo de la biodiversidad y a la producción sostenible del ganado.

Palabras clave: *animales indígenas de granja, sistemas de producción, cruzamientos, estado de riesgo, extinción*

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Introduction

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. What is not in dispute is that humpless *Bos taurus* is the only species of cattle – known as 'sigir' in Turkish – raised in Turkey (FAO/UNEP 2000). Several 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 cattle comprise six varieties but none is identified individually (MARA/FAO, 2001). An earlier publication on Turkish biological diversity identifies six types of cattle (Anon, 1987). A search of one authoritative source (Mason, 1996) brings to light several to many more breeds and types of livestock than the previous two sources. The European Association for Animal Production (EAAP, 2007) provides yet another view of the diversity of Turkey's domestic livestock. The breeds' database of the Food and Agriculture Organization lists 35 cattle although 15 of these are given as extinct (DAD-IS, 2010).

Cattle numbers have decreased steadily from 16.6 million head in 1980 to a little over 10.6 million head in 2009 (SIS, 2009). Production of milk and meat from cattle has remained relatively stable over the 30-year period from 1980 due mainly to changes in breed structure and the use of imported specialist dairy and beef breeds with milk yields per cow increasing by some 50 percent from 1 300 litres to almost 2 000 litres per lactation and carcass weights of slaughter cattle rising threefold from less than 60 kg to more than 180 kg (FAO, 2010). In spite of this, however, the contribution of cattle to the total output of animal products has declined because of 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 the importance of cattle in Turkey there has been a paucity of recent publications on the species in the international literature. Those that have been published include papers relating to animal health and disease (Cetinkaya *et al.*, 2003; Aslantas *et al.*, 2006; Temizel *et al.*, 2009), production on state farms (Ekerden and Ozkutuk, 1990), some aspects of the biochemistry of milk (Polat, Gencoglu and Turkmen, 2009; Gurcan, 2011) and reports of small-scale experiments on meat production (Ozluturk *et al.*, 2004; Unlu *et al.*, 2008; Yuksel *et al.*, 2009). The current paper aims to provide information on some of the main cattle populations of Turkey as well as some perceptions of their production and is one of a series (Wilson, Yilmaz and Ertugrul, 2011; Yilmaz, Ertugrul and Wilson, 2011a, 2011b) that will eventually cover all the nation's domestic animal species.

Cattle in the national and household economies

Products – meat, milk, eggs, wool and hides – from the livestock subsector in Turkey contributes 30 percent of total agricultural gross domestic product. Some 96 percent of the country's four million agricultural enterprises are mixed crop–livestock farms. About 65 percent of all farms keep some cattle but the average number per farm is less than four head. Farm sizes are less than 5 ha for 65 percent of holdings which accounts for only 22 percent of the agricultural land whereas the remaining 35 percent of holdings with an individual area of greater than 5 ha occupy 78 percent of the land. An overwhelming proportion of output is for subsistence use with any surplus usually being disposed of through middlemen because of the distance to markets. In spite of the small and fragmented nature of agriculture more than 45 percent of rural income derives directly from agriculture which is the key component of rural household livelihoods.

Poverty levels in Turkey are high. More than one-third of the population relies on the agricultural sector for employment and income generation. The family-owned and -managed farm is the basic unit of agricultural production and family members provide most of the farm labour. Household food security is very important to the impoverished populations of the rural and peri-urban areas and small-scale cattle farms contribute significantly to the nation's food supply and to local economies. Most cattle are still managed traditionally, rely mainly on extensive and low-quality grazing for their nutriments and receive very little in the way of veterinary care. The situation is exacerbated in winter as housing standards are low, feed is often of even poorer quality and cold and crowding produce stress that reduces tolerance to disease. The fragmented nature of traditional agriculture is often accepted as the norm and its sustainability and contribution to national welfare are neglected. Small-scale farms nonetheless contribute to human welfare (especially that of old and infirm people and children), are guardians of the common wealth and work, within their limits, to protect the soil, water and air and maintain and enhance biodiversity in addition to producing essential and often high-quality animal protein for the betterment of everyone. The income derived from small farms is not only used to buy additional items of food but also helps to pay for other and various items including health services, school fees, water and electricity and new assets.

In contrast to small holder subsistence farming, Turkey has a number of large-scale commercial farms including feedlots and several government and university experimental establishments.

Cattle breeds and types

Cattle have been an important part of the economy and in the lives of the people of Turkey for at least 10 000 years (Duru and De Cupere, 2003; Zeder, 2008). For many

Table 1. Origins, areas of distribution, morphological characteristics and products of some native cattle breeds of Turkey.

Trait	Breed/type (Turkish name in brackets)					
	Native Black (Yerli Kara)	**Eastern Anatolian Red (Dogu Anadolu Kirmizisi)**	**Native Southern Yellow (Yerli Sari, Cukurova, Dortyol, Siverek)**	**South Anatolian Red (Kilis (Bahcivan), Guney Anadolu Kirmizisi)**	**Turkish Grey, Anatolian Grey (Boz, Step, Plevne)**	**Zavot (Zavot)**
Origin of breed	Indigenous	Caucasian	Not known	Not known	Bulgaria	Caucasian
Main area of distribution	Central Anatolia	Eastern Anatolia	Southern provinces from Icel to Sanliurfa	Southern provinces from Icel to Sanliurfa	Thrace, South Marmara, North-western Turkey	Kars and Ardahan
Colour	Black	Basically red, varies from light to dark	Dark yellow to cinnamon red	Yellow to brown	Grey, light silver to dark ash	Light silver to light yellow
Horns	Both sexes horned	Both sexes horned	Both sexes horned (short black)	Both sexes horned (females shorter)	Male horned, female polled	Both sexes horned
Withers height, cm (♂, ♀)	100–110	115–125, 105–115	105–115 ♀	140–150, 125–135	123–128, 115–120	122–137, 102–130
Body length, cm (♂, ♀)	110–120	130–140, 115–125	110–120 ♀	135–145, 130–140	120–125, 110–115	127–164, 117–143
Adult weight, kg (♂, ♀)	200–300	350–450, 250–350	90–310 ♀	550–600, 350–450	350–450, 250–350	400–600, 270–450
Birth weight, kg (♂, ♀)	18–20, 17–19	20–22, 17–19	15–17, 12–14	25–27, 23–25	24–26, 22–24	24–36, 17–27
Products	Milk, meat	Milk, meat, draught	Milk, meat	Milk, meat	Meat, milk	Milk, meat
Carcass yield, percent	56	58	–	60	57	60
Average daily feedlot gain, g (♂, ♀)	700–900	800–1 000, 600–800	–	500–900	1 000–1 100 ♀	900–1 000, 700–850
Milk lactation yield, kg	1 000–1 100	900–1 000	600–650	1 500–2 500 (1 900)	1 000–1 200	2 300–3 300
Lactation length, days	240–260	200–220	180–200	200–250	210–230	275–300
Milk fat, %	4	3.5	3.6	3.2	3.9	3.5–4.5

Source: adapted from Anon (2004, 2009).

Figure 1. Native Black ('Yerli Kara') female.

Figure 3. East Anatolian Red ('Dogu Anadolu Kirmizisi') female.

millennia they have provided subsistence meat and milk to mainly small holder farmers yet only limited attention has been paid to this fact (Karakok, 2007). In these circumstances there has been little opportunity to improve individual performance. Even today in modern Turkey most cattle are kept in the traditional production systems and continue to be of a clear local type. Several native lines including Native Black ("Yerli Kara"), East Anatolian Red ("Dogu Anadolu Kirmizisi") and South Anatolian Red ("Kilis" or "Guneydogu Anadolu Kirmizisi") have been collectively nominated Anatolian native (Ertugrul, 1993; Mason, 1996). Distinct breeds and breed groups have been identified on morphological or regional grounds (Table 1) but cluster analysis and genetic distancing studies have shown that several to most of these are not distinctly separate (Ozbeyaz, Yildiz and Camdevsiren, 1999).

Native Black (Yerli Kara)

Found mainly in Inner or Central Anatolia the Native Black (Yerli Kara) or Anatolian Native Black (Anadolu Yerli Kara) is a *Bos brachyceros* type with a long narrow head (Figure 1). As its common name implies it is usually black (Mason, 1996), although other sources refer to it as the Anatolian Black Pied (Anadolu Siyah Alacasi) (DAD-IS, 2010). A conservation herd is maintained at the Central Livestock Research Institute at Lalahan some 30 km east of Ankara on the Anatolian Plateau. The breed has a herd book with 49 herds participating in a conservation programme in 1999 (FAO/DADIS, 2010). In 2002, the national population was estimated at between 100 000 and one million – down from five million in 1975 – but the breed was considered to be not at risk although numbers were expected to continue to decrease owing to crossbreeding. The breed is triple purpose for dairy, draught and meat and is able to 'withstand bad environmental conditions' (Anon, 1987).

East Anatolian Red (Dogu Anadolu Kirmizisi)

Originally descended from the Caucasian (Mason, 1996), the East Anatolian Red (Dogu Anadolu Kirmizisi) or Eastern Red (Anon, 1987) is found mainly in East Anatolia but has the widest distribution of all native breeds after the Native Black. The beast is a narrow-chested descendant of *Bos taurus brachyceros* (Figures 2–4). A conservation herd is maintained at the Eastern Anatolia

Figure 4. East Anatolian Red ('Dogu Anadolu Kirmizisi') group.

Figure 2. East Anatolian Red ('Dogu Anadolu Kirmizisi') male.

Figure 5. Native Southern Yellow ('Yerli Guney Sarisi') male.

Figure 6. Native Southern Yellow (‘Yerli Guney Sarisi’) female.

Figure 7. Native Southern Yellow (‘Yerli Guney Sarisi’) group.

Regional Research Station at Erzurum. The population of this type is now thought to be less than one million animals and is considered to be at risk. Recognized varieties of this type are the Cildir and the Gole (Mason, 1996; DAD-IS, 2010). The East Anatolian Red has been used in the development of the Turkish version of the Zavot (Aksoy, Kirmizibayrak and Saatci, 2006). The breed is primarily used for milk production.

Native Southern Yellow (Yerli Guney Sarisi)

Both Mason (1996) and (DAD-IS, 2010) list the Native Southern Yellow (Figures 5–7) with the former considering this to be a breed of historical importance. South Anatolian Red is sometimes used as a synonym for this type (Mason, 1996). Recognized varieties are Cukurova, Dortyol and Siverek. The Cukurova, originally from the Anatolian Black × Aleppo (=Damascus) is extinct (Mason, 1996) due mainly to cross-breeding with exotics,

Figure 8. South Anatolian Red (‘Kilis’) male.

Figure 9. South Anatolian Red (‘Kilis’) female.

Figure 10. South Anatolian Red (‘Kilis’) group.

Figure 11. Turkish Grey (‘Boz’) male.

Figure 12. Turkish Grey (‘Boz’) female.

Figure 13. Turkish Grey ('Boz') group.

the decreasing numbers of farmers and an inability to adapt to regions other than its centre of origin in the southeastern provinces bordering Syria and the Mediterranean (FAO/DADIS, 2010). The Dortyol is a small extinct variety said to be similar to the Baladi of Syria (Mason, 1996). Numbers of the Southern Yellow itself are said to be 20 000 and decreasing. This is mainly a dairy animal.

South Anatolian Red (Kilis, Guney Anadolu Kirmizisi)

This animal, mainly a dairy animal, sometimes known in English as the Southern Yellow-Red, is similar to the Damascus (Mason, 1996). The estimated population of 70 000 in 1990 decreased rapidly to less than 4 000 by the year 2000 and the breed is considered at risk. A short body, long narrow head and short or sometimes rudimentary horns are its characteristics (Figures 8–10). The type is well adapted to heat and is tolerant of parasites.

Turkish Grey (Boz)

Turkish Grey Steppe (Boz) cattle (Figures 11–13) probably originated from the Iskar or Bulgarian Grey Steppe in the middle of the nineteenth century. It is sometime also referred to as the Anatolian Steppe in English and Step and Plevne in Turkish (FAO/DADIS, 2010). This type is part of the general Grey Steppe group widespread in south-east Europe (Mason, 1996). The original descent of the group as a whole is probably from *Bos primigenius* (Save-Focus, 2005). The Turkish variety is a dual purpose meat and milk animal. Well adapted to harsh environmental conditions and able to survive on low-quality feed, the Boz nonetheless has poor reproductive performance. Numbers declined rapidly from about 930 000 head in 1975 to just over 20 000 head 30 years later.

Figure 14. Zavot ('Zavot') male.

Figure 15. Zavot ('Zavot') female.

Zavot (Zavot)

The Zavot is a composite of Simmental and Brown Swiss originally developed in the Russian Caucasus (Russian 'zavod' = factory, Mason, 1996). The Turkish Zavot (Figures 14 and 15) has been modified by infusions of the East Anatolian (Aksoy, Kirmizibayrak and Saatci, 2006). The home tract of the Zavot is Kars and Ardahan provinces of eastern Anatolia. In the late twentieth century the population was estimated at a maximum 10 000 animals and decreasing, down from 30 000 some ten years earlier (FAO/DADIS, 2010). Most Zavots are self-coloured grey and are well adapted to the local climate. In one experiment, 18-month-old steers fed for 162 days had a live weight of 348.5 kg, a hot carcass weight of 197.2 kg and a dressing percentage 56.5 (Aksoy, Kirmizibayrak and Saatci, 2006).

Other breeds

Several other breeds are noted but about which little, other than the name, is known. Among these are Anatolian Black

Table 2. Conservation status of Turkish cattle breeds.

Endangered (at risk)	Nearly extinct	Extinct
Native Black, East Anatolian Red, South Anatolian Red, Turkish Grey	Native Southern Yellow, Zavot	Aleppo, Caucasian, Cyprus, Cukurova, Diyarbakir, Dortyol, Eleskirt, Karaisali, Kalmuk (Black), Karacadag, Kirim (Leh), Kultak,[a] Malakan, Seferihisar, Urla

Note: [a]Kultak has possibly a remnant population in Gorum Province.
Source: Ertugrul *et al.,* 2010.

Table 3. Genetic material conservation status of Turkish cattle breeds in May 2011.

Breed	Institute and type of material							
	Genetic Engineering and Biotechnical Institute				Lalahan Livestock Central Research Institute			
	Embryo	Sperm	DNA	Cell	Embryo	Sperm	DNA	Cell
Native Black	–	–	54 animals	51 animals, 218 vials	86	25 animals, 6 886 straws	54 animals	–
East Anatolian Red	–	–	45 animals	45 animals, 450 vials	–	21 animals, 5 745 straws	45 animals	45 animals, 450 vials
Native Southern Yellow	–	–	51 animals	51 animals, 510 vials	–	16 animals, 515 straws	51 animals	51 animals, 510 vials
South Anatolian Red	–	–	50 animals	52 animals, 482 vials	–	27 animals, 976 straws	50 animals	–
Turkish Grey	–	–	54 animals	54 animals, 540 vials	32	25 animals, 896 straws	54 animals	54 animals, 540 vials
Zavot	–	–	19 animals	19 animals, 190 vials	–	12 animals, 12 250 straws	19 animals	19 animals, 190 vials

Source: Arat (2010).

Pied, Anatolian Brown, Antakli (also known as Lebanese) which is possibly a variety of the Damascus or a composite of Damascus and Baladi and is found around Hatay, Kurdi which is a mainly black animal that may be present in parts of the Kurdish area bordering on Iraq and Maras (FAO/DADIS, 2010). The Seferihisar is possibly equivalent to the Eskisehir of Izmir province in western Turkey and may be a composite of Simmental and Aleppo (Mason, 1996; FAO/DADIS, 2010) but is possibly extinct.

Genetic modification

It is evident from the foregoing section on breeds that there has long been an interchange – traditional and largely informal – of various types of livestock with neighbouring countries including especially Syria, Iraq and the countries of the Caucasus. In the early period of the Turkish Republic at the beginning of the 1920s government institutes and private individuals raised only native cattle breeds. In 1925, however, the first true exotics were imported from Austria and Hungary. An early outcome of this was the development of the Karacabey Brown (Karacabey Esmeri, Karacabey Montafon) – named after the State Farm where it was originally bred – from the local Plevne (Grey) Steppe cattle of northwest Turkey crossed with Austrian (Montafon) Brown Swiss (Felius, 1985). Now more commonly known as the Turkish Brown in English (Mason, 1996) it is also sometimes called the Cifteler and Karacabey Montafon in English and Karacabey Esmeri in Turkish (FAO/DADIS, 2010). The Eskisehir to which reference has been made in the preceding paragraph may be a varietal name for this type (Mason, 1996). The Karacabey is said to be a strong animal for meat and milk with good feed efficiency and resistance to ‘all climatic conditions’. Cows weigh 600 kg and have a milk yield of 4 330 kg – although 6 000 kg is possible – at 4 percent fat (Felius, 1985). Simmental cattle were also among the early imports and crossed with native cattle.

Concurrent with live animal imports, Turkey was one of the first countries to attempt to use biotechnology to improve livestock performance. Artificial insemination (AI) was first used in 1925 but lack of early success – conception rates were only 15–20 percent – resulted in the process being abandoned for many years (Ertugrul *et al.,* 1993).

Imports continued at a low level from 1925 up to 1958. In 1958, the World Council of Churches provided an eclectic mix of beef (Hereford and Aberdeen Angus), dairy (‘black and whites’ and Jersey) and dual-purpose breeds (Brown Swiss) to Turkey. From 1986, the number of incoming cattle was allowed to increase and it is believed as many as 150 000 head were imported over the next few years (Ertugrul, 1993). The commercial success of these imports both for meat and milk production is evident in increased carcass weights and lactation milk yields whereby a considerably reduced number of cattle produce annually for the nation as much meat and milk as far higher numbers of animals did in the past. This success has not been gained without cost, however, and the largely indiscriminate and even uncaring top crossing of exotics on native populations has resulted in drastic declines in the numbers of the latter and the total extinction of many types.

Conservation measures

In the mid-1990s the proportion of pure European cattle in Turkey’s national herd was about 13 percent and that of European × Native was in the region of 38 percent. Thus, less than half of the Turkish cattle population comprised animals of purely native origin. Cattle imports, crossbreeding programmes and a greater use of AI were not only responsible for a reduction in numbers but also the near disappearance of a number of breeds and the extinction of at least 15 breeds or types (Table 2). 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 cattle breeds.

The Scientific and Technological Research Council of Turkey (STRCT), Marmara Research Centre, Genetic

Engineering and Biotechnical Institute (GEBI), Gebze, Kocaeli, prepared a project titled the '*In Vitro* Conservation and Preliminary Molecular identification of some Turkish Domestic Animal Genetic Resources (TURKHAYGEN-I)' in 2005 (Arat, 2010). Consequent on several iterations the project was approved by 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, 2010).

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;
- 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.

An extensive bank of genetic material has been established for Native Black, East Anatolian Red, Native Southern Yellow, South Anatolian Red, Turkish Grey and Zavot cattle as a result of the project (Table 3). It is expected that this resource will be expanded for preservation, conservation and use of Turkey's native genetic resources in the future.

Conclusions

Biodiversity, including livestock biodiversity, is an indication of the genetic and economic wealth of a country. As a natural bridge between Europe and Asia, Turkey has been traversed by traders, travellers, treasure seekers and trespassers for thousands of years. The eclectic mix of species and breeds of domestic livestock within Turkey's boundaries is partially a result of these exchanges. The national patrimony has, however, been greatly diminished in the second half of the twentieth and the first decade of the twenty-first centuries where, indeed, it has not already been lost forever. New and possibly more productive breeds can provide more human food (but at greater cost) than native animals whose adaptation has been to survival rather than to output. 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 the safeguarding of the country's heritage. Livestock production will remain sustainable only if the nation's gene pool is 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 cattle are generally of low output but still constitute a fair proportion of the national herd. Efforts should continue to characterize and improve their productive traits alongside the use of exotic breeds with 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 cattle breeds of Turkey.

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Impacts of genetic drift and restricted gene flow in indigenous cattle breeds: evidence from the Jutland breed

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Summary

Indigenous cattle breeds represent a unique genetic resource, and understanding their variability, population structure and breeding units is important for their sustainable conservation. The endangered Jutland breed was widespread in Denmark in the eighteenth century, but decreased in population size following the introduction of modern farming. We investigated the impact of recent anthropogenic fragmentation of the breed by analysing 737-bp mitochondrial DNA and 23 microsatellites in 207 individuals. The results revealed the Jutland breed as a unique genetic entity with high levels of genetic diversity, and only limited introgression from other black-pied breeds. The data reflected the impacts of fragmentation and restricted gene flow in breeds with small segregated herds, and revealed the rapid differentiation of herds resulting from genetic drift. The application of a management strategy that conserves diversity and minimizes increase in inbreeding is important for the future conservation of the Jutland breed and other indigenous cattle breeds.

Keywords: *fragmentation, genetic diversity, indigenous cattle breeds, introgression*

Résumé

Les races de bétails indigènes representent une ressource génétique unique. Comprendre la variabilité génétique, la structure de la population et unités d'amelioration génétique est essentiel. La race Jutland, menacée aujourd'hui, était très répandue au Danemark durant le 18eme siècle avant de voir sa population décroitre suite a l'avènement des méthodes modernes d'agriculture. Nous avons etudiés l'impact de la fragmentation anthropogénique de cette race en analysant l'ADN mitochondrial (737-bp) et 23 microsatellites dans 207 individus. Les résultats dévoilent La race Jutland comme une entité génétique unique présentant une grande diversité, et montrent seulement une introgression limité d'autres races tachetés noires. Les données reflètent les impacts de la fragmentation et un flux de genes limite au sein des espèces avec de petits troupeaux issus d'une ségrégation et revèlent une differentiation rapide des troupeaux résultant de la dérive génétique. La mise en place d'une stratégie de management qui conserve la diversité et qui empêche les croisements est importante pour la conservation future de la race Jutland et des autres races de bétails indigènes.

Mots-clés: *la fragmentation, la diversité génétique, les races de bétail Indigènes, introgression*

Resumen

Las razas indígenas del ganado representan un fuente única de recurso genético, la comprensión de su variabilidad, estructura de población, y de sus unidades de cría son importantes factores para sus conservación sostenible. La raza de ganado en peligro de extinción de Jutlandia se encontraba muy dispersa en Dinamarca en el siglo XVIII, pero disminuyó e tamaño tras la introducción de la agricultura moderna. En este estudio, se investigó el impacto antropogénico en la fragmentación de la raza usando el análisis de 737 pares de bases del ADN mitocondrial y 23 microsatélites en 207 animales. Los resultados muestran que la raza en Jutlandia contiene una entidad genética única con altos niveles de diversidad genética, y limitada solamente por la introgresión de otras razas comunes de ganado. Los datos reflejan el impacto de la fragmentación y el flujo genético en razas restringidas y separadas en pequeños rebaños; y pone en manifiesto la rápida diferenciación de los rebaños como resultado de la deriva genética. La aplicación de una estrategia de gestión que conserve la diversidad y evite la mezcla de razas es importante para la futura conservación de la raza de Jutlandia y otras razas de ganado indígenas.

Palabras clave: *fragmentación, diversidad genética, razas de ganado Indígenas, introgression*

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Introduction

The diversity of domestic cattle reflects millennia of artificial breeding, selection and geographic separation, which have led to a broad spectrum of phenotypes (Hanotte *et al.*, 2002). Since the introduction of modern farming in the eighteenth century, an erosion of genetic diversity has taken place in livestock (Tapio *et al.*, 2006). A few high-performance cattle breeds have been utilized in the industrial farming system, where selective breeding and assisted reproduction have resulted in an overall loss of genetic variability (Kantanen *et al.*, 2000; Taberlet *et al.*, 2008).

The indigenous breeds are – in contrast to the highly selected commercial breeds – exposed to lower selection pressures. They have been subjected to local use and traditional husbandry management, and have – as a group – generally maintained a large pool of genetic variability, despite their small population sizes (Tapio *et al.*, 2006). As a consequence, there are high levels of phenotypic variation among indigenous breeds, a variety of adaptations to local environmental conditions and high fitness under natural conditions (Tapio *et al.*, 2006; Dalvit *et al.*, 2008). They represent a unique genetic resource, and can potentially contribute genetic diversity beneficial for meeting present and future breeding objectives (Sørensen, Sørensen and Berg, 2005; Toro, Fernández and Caballero, 2009). At present, a high number of indigenous breeds have low effective population sizes (N_e) and are listed as at risk by the Food and Agriculture Organization of the United Nations (FAO, 2007). Understanding the variability, genetic structure and breeding units of indigenous breeds is important for conserving them in the most sustainable way (Taberlet *et al.*, 2008; Toro, Fernández and Caballero, 2009).

In Denmark, the Danish livestock industry has focused on the commercial Holstein and Jersey breeds (Sørensen, Sørensen and Berg, 2005; Taberlet *et al.*, 2008). As a consequence, indigenous breeds such as the Red Danish, Agersoe Cattle and the Jutland breed have been neglected. These breeds have suffered significant declines in population sizes, prompting concern about their long-term genetic viability (Danish Ministry of Food, Fisheries and Agriculture, 2008).

One indigenous breed that has been maintained through the efforts of private collectors is the Jutland breed. It presumably originated from black- and grey-pied cattle and was widespread in Denmark in the eighteenth century, mainly on the Jutland peninsula (Kantanen *et al.*, 2000; Negrini *et al.*, 2007; Danish Ministry of Food, Fisheries and Agriculture, 2010; Withen *et al.*, 2011). Since then it has experienced a drastic decline in population size and is now classified as endangered (FAO, 2007). Estimated from unequal sex ratios (Hedrick, 2002, equation 6.6a), the effective population size of the Jutland breed was estimated at 40 out of a census size of ~350 individuals in 2007 (http://dad.fao.org). This is similar to the effective population size of commercial Danish breeds: Danish Holstein ($N_e = 49$), Danish Jersey ($N_e = 53$) and Danish Red ($N_e = 47$) (Sørensen, Sørensen and Berg, 2005). As these breeds have considerably larger population sizes of 560 000 to 3 700 000 individuals (Sørensen, Sørensen and Berg, 2005), they are not classified as endangered (http://iuncredlist.org).

Before the introduction of modern farming, the Jutland breed was used in both dairy and beef production under traditional usbandry management. In the eighteenth–twentieth century, there was a large export, of mainly steers, to the North German market (Danish Ministry of Food, Fisheries and Agriculture, 2010). In 1881, the first herd book was published and in 1950 part of the breed was crossed with black-pied cattle from Holland and Germany to form the Danish Black-Pied. A few private collectors continued to breed the original Jutland breed, and the breed currently consists of four main herds and a number of herds of smaller size, which have been separated for at least the last five decades without admixture from other breeds (S. Benzon, personal communication). A management strategy for the breed is currently being planned on the basis of the present survey.

We used 737-bp of the mitochondrial DNA (mtDNA) control region and 23 microsatellites to estimate genetic diversity and structuring within the Jutland breed. To elucidate the genetic relationship between the Jutland breed and breeds which may have been admixed with it, we included microsatellite data from the following six breeds: the German Black-Pied ($N_e = 172$) (H. Simianer, personal communication), Dutch Belted ($N_e = 136$), Dutch Friesian ($N_e = 225$), Groningen White-Head ($N_e = 149$), Meuse–Rhine–Yssel ($N_e = 689$) and the Danish Black-Pied ($N_e = 4$). Effective population sizes were estimated from unequal sex ratios (Hedrick, 2002, equation 6.6a) based on data from FAO's Domestic Animal Diversity Information System (http://dad.fao.org).

Materials and methods

Samples

Blood and tissue samples were collected between 1997 and 2007 from 207 registered Jutland breed animals. Four main herds were sampled: Kortegaard ($n = 21$), Vesterboelle ($n = 28$) and Westergaard ($n = 22$) all from Northern Jutland, and Oregaard from Funen ($n = 82$), in addition to 54 animals from smaller herds consisting of one to four animals, mainly from Jutland. The animals were selected to be as unrelated as possible (avoiding siblings and parent/offspring) according to the Danish Register for Livestock. Due to difficulties in amplifying mtDNA and microsatellites for a number of samples, not all animals were represented in every analysis.

Dr H. Lenstra from the European Cattle Genetic Consortium (ECGC) kindly provided microsatellite data from the Danish Black-Pied ($n = 44$), the German Black-Pied ($n = 20$) and four Dutch cattle breeds: Dutch Belted ($n = 24$), Dutch Friesian ($n = 34$), Groningen White-Head ($n = 25$) and the Meuse–Rhine–Yssel ($n = 39$). The ECGC dataset is based on 30 microsatellite loci, which are recommended by the International Society for Animal Genetics (ISAG) and FAO. The loci are unlinked and neutral, and widely used in genetic studies of cattle. All samples were collected in 1999. Unfortunately mitochondrial data were not available for these breeds.

In the following, we use *herds* to refer to the analysis of the four main herds. The term *breeds* is used in reference to the comparative analysis between the Jutland breed and the six black-pied breeds.

DNA extraction

DNA was extracted and purified from 100 μl blood or 20 mg tissue samples according to the DNeasy Blood & Tissue Kit (Qiagen) following the manufacturer's protocol and was stored at −20 °C in the laboratory.

MtDNA

The control region (d-loop) of the mtDNA was amplified in PCR using two flanking primers 5′-CTGCAGTCTCACCATCAACC-3′ (Loftus *et al.*, 1994) and 5′-AGAGTTAACAGGAAGGCTGG-3′ (Kim *et al.*, 2003). The amplification was performed in a 25 μl volume PCR containing 1 μl purified DNA, 1 × PCR buffer, 1.5 mM $MgCl_2$, 1 μM of each primer, 2 μM of each dNTP and 1 unit *Taq* polymerase (Thermo Scientific). The following cycling conditions were used: 2 min at 94 °C; 35 cycles of 1 min at 94 °C; 1 min at 57 °C; 1 min at 72 °C and a final extension for 10 min at 72 °C. PCR blanks were always included and remained negative throughout. Purification of PCR products was performed with *Invisorb Vacuum Manifold kit* (Invisorb) following the manufacturer's protocol. The PCR product was run on a 2 percent agarose-gel and verified afterwards.

Sequencing was performed using ABI Prism®BigDye Terminator version 3.1 Cycle Sequencing Kit (Applied Biosystems) in a 10 μl volume containing 1 μl DNA template and 10 μl HiFi. Two primer pairs were used in the sequencing 5′-CTGCAGTCTCACCATCAACC-3′ (Loftus *et al.*, 1994), 5′-CGAGATGTCTTATTTAAGAGG-3′ (Cymbron *et al.*, 1999), 5′-CGCTCCGGGCCCATAAACCG-3′ and 5′-GCCTGCGTTTATATATTGAC-3′ (Withen *et al.*, 2011). The fragments of 597 and 588-bp, respectively, overlapped resulting in a 737-bp sequence. Cycle sequencing products were purified prior to separation on a 5 percent denaturing polyacrylamide gel in an ABI Prism®377 DNA sequencer (Applied Biosystems) using the DyeEx 2.0 Spin kit (Qiagen).

The two mtDNA sequence fragments were assembled and edited in SEQUENCHER version 4.8 (Gene Code Cooperation) and for each individual a consensus sequence was composed using the bovine mtDNA reference sequence (Anderson *et al.*, 1982; accession no. NC_00156, GenBank). The sequences were aligned in SE-AL version 2.0a11 (Rambaut, 1996) and formatted in CLUSTALX version 2.0.7 (Larkin *et al.*, 2007).

Microsatellites

Thirty unlinked microsatellite loci were genotyped for each sample as recommended by the ISAG and FAO. StockMarks® Horse and Cattle Paternity PCR Typing Kit (Applied Biosystems) were used for 11 of the markers: *TGLA227* (18), *BM2113* (2), *TGLA53* (16), *ETH10* (5), *SPS115* (15), *TGLA126* (20), *TGLA122* (21), *INRA23* (12), *ETH3* (19), *ETH225* (9) and *BM1824* (1), numbers in parentheses indicate chromosome location (http://www.thearkdb.org/arkdb). The PCR was run, using 1 μl DNA template, according to the manufacturer's protocol with all 11 markers amplified in one PCR reaction (Supplementary Table S1). Sequencing was done on an ABI Prism®BigDye terminator version 3.1 Cycle Sequencing Kit (Applied Biosystems) in a 13 μl volume containing 1 μl DNA, 11.5 μl HiDi-formamid and 0.5 μl Rox500.

The remaining nineteen markers: *INRA063* (18), *INRA005* (12), *ILST005* (10), *HEL5* (21), *HEL1* (15), *INRA035* (16), *ETH152* (5), *HEL9* (8), *CSSM66* (14), *INRA032* (11), *HEL13* (11), *INRA037* (10), *BM1818* (23), *ILST006* (7), *MM12* (9), *CSRM60* (10), *ETH185* (17), *HAUT24* (22) and *HAUT27* (26) were amplified with QIAGEN® Multiplex PCR Kit (Qiagen) in six reactions with unique PCR conditions following the manufacturer's protocol using 1 μl DNA as the template. The reactions were combined in three groups and took place in 96-well microtitre plates with 1 μl DNA in 13 μl volume (Supplementary Table S1). All loci were sequenced on an ABI Prism®BigDye terminator version 3.1 Cycle Sequencing Kit (Applied Biosystems) in a 10 μl volume containing 2 μl DNA template, 7.5 μl HiDi-formamid and 0.5 μl Rox500. To be able to compare our data with the ECGC dataset, we standardized our microsatellite data to the ECGC data by including ECGC reference DNA in our sequencing and scoring our samples accordingly.

Statistical methods

Validation of microsatellite data

The microsatellite loci were checked for possible allelic stuttering, allele drop out and null alleles in MICRO–CHECKER version 2.2 (Van Oosterhout *et al.*, 2004), which resulted in elimination of the following seven loci: *TGLA227, TGLA122, INRA32, BM1818, INRA35, BM2113* and *ETH185*, yielding a total of 23 loci.

Genetic diversity

Quantification of mtDNA genetic variation was estimated in DNASP version 5.0 (Rozas *et al.*, 2003) as haplotype

(H) and nucleotide (π) diversity according to Nei (1987) along with Tajima (1989) to test for selection. Haplogroup relationship (T, T1, T2 and T3) for each sequence was determined according to Troy *et al.* (2001). JMODELTEST version 0.1.1 (Posada, 2008) was used to find the substitution model that best fitted the observed data based on the Akaike Information Criterion constrained to compute likelihood scores only for models available in ARLEQUIN version 3.11 (Excoffier, Laval and Schneider, 2005). A median-joining network (Bandelt, Foster and Röhl, 1999) was constructed in NETWORK version 4.5.1.6 (http://www.fluxus-engineering.com) using the default settings.

Basic microsatellite diversity indices; mean number of observed alleles (A_O), observed (H_O) and unbiased expected (UH_E) heterozygosities and numbers of private alleles (A_P), were estimated in GENALEX version 6.3 (Peakall and Smouse, 2006). Fixation indexes (f) and significant deviation from Hardy Weinberg Equilibrium (HWE) were estimated in GENODIVE version 2.0b17 (Meirmans and Van Tienderen, 2004), each tested for significance by 999 permutations. In GENEPOP version 3.4 (Raymond and Rousset, 1995) significant deviations from linkage equilibrium (LE), was estimated for each locus pair using Fishers Exact Test based on 10^4 batches with 10^5 de-memorizations and 10^5 permutations per batch resulting in standard error <0.03 followed by sequential Bonferroni correction to reduce type 1 errors.

Genetic differentiation

Haplotype differentiation, defined as Φ_{ST} (Weir and Cockerham, 1984), was estimated in ARLEQUIN applying Tamura and Nei's substitution model (Tamura and Nei, 1993). Genetic differentiation, defined as F_{ST} (Weir and Cockerham, 1984), based on microsatellite data was estimated in GENODIVE version 2.0b17, and tested for significance with 10^3 permutations followed by Bonferroni correction. Reynold's genetic distance (D_R) was estimated using ARLEQUIN with 10^3 permutations to test for significance. The results were visualized as a NeighborNet in SPLITSTREE version 4.10 (Huson and Bryant, 2006).

Genetic structure

Structuring was estimated in STRUCTURE version 2.2 (Pritchard, Stephens and Donnelly, 2000) based on an admixture model with no prior information. A burn-in of 10^4 iterations followed by an Markov Chain Monte Carlo (MCMC) of 10^5 iterations for each value of K (K = 1–12) was applied, with five repetitions for each K. The most likely number of clusters was determined following the delta-K method (Evanno, Regnaut and Goudet, 2005) in STRUCTURE HARVESTER version 0.56.3 (Earl, 2009). CLUMPP (Jakobsson and Rosenberg, 2007) was applied to permute membership matrices across replicates and generate a mean permuted matrix for a given value of K. The results were displayed using DISTRUCT (Rosenberg, 2004).

Assignment test was performed in GENALEX version 6.3 based on the "leave one out" option. The individual of interest was removed from the dataset prior to estimating the population genotype frequencies. The smaller herds were treated as unknown samples when assigned to populations and therefore not influencing the population genotype frequency estimates.

Gene flow

Pairwise gene flow rates were estimated in BAYESASS+ version 1.3 (Wilson and Rannala, 2003). The programme uses an MCMC algorithm to estimate recent gene flow assuming low levels of migration (<1/3 of the population total in each generation) and linkage equilibrium among loci. The method infers recent migration rates from the observed disequilibrium among genotypes in the population, generated by novel multi-locus genotypes introduced by migrants or individuals recently descended from migrants. BAYESASS+ may be applied to non-stationary populations that are far from HWE. We used a burn-in of 10^6 iterations followed by an MCMC of 4×10^6 iterations with a sampling frequency of 2×10^3. Delta values were set to 15 for allele frequency, migration rate and inbreeding level. To test for convergence, the programme was run with two different "seed" values (10 and 10^3). The results were examined in R ver. 2.12.2 (R Development Core Team, 2011) using the BOA package (Smith, 2007). Convergence was assumed when no significant difference was found between the mean of the first 10 percent of the chain and the mean of the last 50 percent (Geweke, 1992).

Results

Genetic diversity

The mtDNA analysis yielded 207 sequences of 737-bp (accession no. JQ234675–JQ234881). All haplotypes belong to the T3 haplogroup. There were 29 variable sites, resulting in 18 haplotypes. No sign of selection was detected (Table 1), which is consistent with expectations for this region (Anderson *et al.*, 1982; Tajima, 1989). Half of the haplotypes were shared among several herds with the most frequent found in 46 percent of the individuals (Figure 1). The overall haplotype diversity (H) was 0.72 and ranged from 0.17 in Westergaard to 0.81 in Kortegaard. The nucleotide diversity (π) was 0.0035 and varied from 0.0007 in Westergaard to 0.0043 in Vesterboelle (Table 1*a*).

The 23 microsatellite loci had 149 alleles in total, ranging from two alleles (*ILST005*) to 12 alleles (*TGLA53*) per locus. The observed heterozygosity (H_O) was 0.555–0.656 and mean number of alleles (A_O) was 4.6–4.8 per locus in the four herds, each having seven to eight unique

Table 1. Summary statistics of (*a*) the four main herds within the Jutland breed based on mtDNA and microsatellites and (*b*) the black-pied breeds based on microsatellites.

	mtDNA						Microsatellites					
	n	***H***	$\boldsymbol{H_P}$	***h***	**Π**	***D***	$\boldsymbol{A_O}$	$\boldsymbol{A_P}$	$\boldsymbol{H_O}$	$\boldsymbol{UH_E}$	***f***	***LE***
(*a*)												
Kortegaard	21	8	2	0.810 ± 0.065	0.0038 ± 0.0007	−1.52	4.8	7	0.656 ± 0.031	0.636 ± 0.026	−0.054	2*
Vesterboelle	28	7	2	0.704 ± 0.059	0.0043 ± 0.0006	−0.39	4.6	7	0.555 ± 0.036	0.525 ± 0.032	−0.083*	3*
Westergaard	22	2	–	0.173 ± 0.010	0.0007 ± 0.0004	−0.95	4.6	7	0.598 ± 0.041	0.568 ± 0.035	−0.036	1*
Oregaard	82	4	2	0.323 ± 0.063	0.0014 ± 0.0003	−0.62	4.7	8	0.605 ± 0.025	0.624 ± 0.025	0.018	6*
(*b*)												
Jutland breed	207	18	–	0.717 ± 0.025	0.0035 ± 0.0002	−1.44	6.5	8	0.611 ± 0.022	0.664 ± 0.022	0.055*	60*
Danish Black-Pied	44	–	–	–	–	–	5.7	1	0.608 ± 0.032	0.661 ± 0.029	0.060*	5*
German Black-Pied	20	–	–	–	–	–	5.6	3	0.722 ± 0.030	0.676 ± 0.027	−0.060	0
Dutch Belted	24	–	–	–	–	–	5.0	7	0.622 ± 0.039	0.631 ± 0.035	0.003	2*
Dutch Friesian	34	–	–	–	–	–	5.1	1	0.619 ± 0.034	0.649 ± 0.030	0.042	1*
Groningen White-Head	25	–	–	–	–	–	4.1	–	0.565 ± 0.038	0.562 ± 0.027	0.013	1*
Meuse–Rhine–Yssel	39	–	–	–	–	–	5.5	7	0.685 ± 0.027	0.683 ± 0.025	0.003	2*

MtDNA information based on 737 bp includes number of haplotypes (*H*), number of private haplotypes (H_P), haplotype diversity (*h*), nucleotide diversity (*π*) and Tajima's *D* (*D*). Information from the 23 microsatellite loci includes mean number of alleles (A_O), number of private alleles (A_P), observed heterozygosity (H_O), unbiased expected heterozygosity (UH_E), inbreeding coefficient (*f*) and number of significant pairwise linkage disequilibria (*LE*). *Indicates $p < 0.05$.

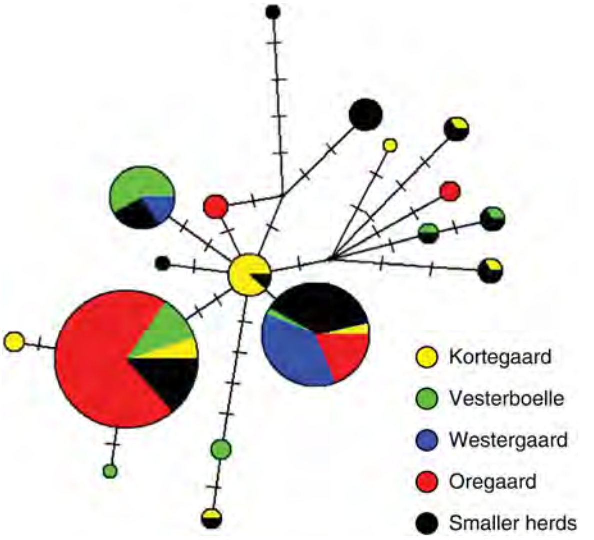

Figure 1. Median-joining network of the 18 mitochondrial haplotypes found in the Jutland breed. Each circle corresponds to a haplotype and the relative size of the circle represents the haplotype frequency. Substitutions are indicated with bars on the branches.

alleles (A_P). Vesterboelle showed a significant excess of heterozygotes compared to HWE (Table 1*a*). Non-random association among loci (*LE*) was found in all herds (Table 1*a*). The smaller herds had $LE = 48$, which resulted in $LE = 60$ in the Jutland breed (Table 1*b*).

The observed heterozygosity (H_O) was 0.611 for the Jutland breed and 0.565–0.722 for the other breeds with a mean number of alleles (A_O) of 6.5 and 4.1–5.7, respectively (Table 1*b*). Unique alleles ($A_P = 1–8$) were found in all breeds except for Groningen White-Head. Deviations from HWE were found in the Jutland breed and the Danish Black-Pied, which both showed an excess of homozygotes (Table 1*b*). Linkage disequilibrium ($LE = 1–5$) was found among pairs of loci in the Danish Black-Pied and all Dutch breeds. The Jutland breed had the highest amount ($LE = 60$) (Table 1*b*).

Genetic differentiation

All pairwise mtDNA Φ_{ST} comparisons among the herds revealed significant differentiation (Table 2*a*). Kortegaard and Vesterboelle were found to be the least differentiated, and Oregaard and Westergaard the most highly differentiated herds based on mtDNA. All pairwise microsatellite F_{ST} comparisons were also significant, but in contrast to the mtDNA data, the microsatellite data showed Kortegaard and Oregaard as the least differentiated herds, and Kortegaard and Vesterboelle as the most differentiated.

The genetic differentiation (F_{ST}) and genetic distance estimates (D_R) revealed significant genetic differentiation between herds and breeds (Table 2*b* and Figure 2*a*). All four herds were more closely related to the Danish and German Black-Pied than they were to each other. Overall, the Jutland breed was closely related to the Danish- and German Black-Pied breeds (Table 2*b* and Figure 2*b*).

Table 2. Pairwise estimates of genetic differentiation among (*a*) the four herds and (*b*) the Jutland breed and the black-pied breeds.

(*a*)	Herds	Kortegaard	Vesterboelle	Westergaard	Oregaard	
Herds	Kortegaard	–	0.162*	0.124*	0.079*	
	Vesterboelle	0.119*	–	0.160*	0.151*	
	Westergaard	0.338*	0.352*	–	0.116*	
	Oregaard	0.280*	0.337*	0.657*	–	
(*b*)	Herds/breed	Kortegaard	Vesterboelle	Westergaard	Oregaard	Jutland breed
Breeds	Danish Black-Pied	0.046*	0.100*	0.057*	0.053*	0.017*
	German Black-Pied	0.080*	0.134*	0.114*	0.086*	0.052*
	Dutch Belted	0.127*	0.183*	0.147*	0.114*	0.086*
	Dutch Friesian	0.108*	0.175*	0.136*	0.100*	0.080*
	Groningen White-Head	0.172*	0.230*	0.230*	0.162*	0.137*
	Meuse–Rhine–Yssel	0.102*	0.144*	0.107*	0.093*	0.066*

Values based on (*a*) pairwise comparisons of 737 bp mtDNA (Φ_{ST}) under the diagonal and 23 microsatellite loci (F_{ST}) above the diagonal and (*b*) 23 microsatellite loci (F_{ST}). All values from the microsatellite analysis are based on 10^3 permutations. *Indicates $p < 0.05$.

Genetic structure

Clear population structure was found among herds and among breeds (Figure 3). The distinction of the Jutland breed and the German and Dutch breeds was found throughout. The herds showed structure for lower values of K than the breeds. The most likely number of clusters was three ($\Delta K = 455$), which divided the samples into three groups: (1) Kortegaard, Oregaard and the smaller herds, (2) Vesterboelle and Westergaard and (3) the German and Dutch breeds. The Danish Black-Pied showed membership coefficients in all three groups (Figure 3).

The assignment test showed that the majority of individuals from the four main herds were assigned to their herd of origin (Table 3*a*). The smaller herds assigned primarily to Kortegaard, Vesterboelle and Oregaard (Table 3*a*). The majority of individuals from the breeds were assigned to their breed of origin, except for the Danish Black-Pied, where half of the individuals were assigned to the Jutland breed (Table 3*b*).

Gene flow

Gene flow among the herds (Table 4*a*) was high ($m > 0.10$) from Kortegaard to the smaller herds, from Vesterboelle to Oregaard, and from the smaller herds to Vesterboelle. All other gene flow rates were low ($m < 0.10$) among the herds.

Two gene flow rates were high ($m > 0.10$) among the breeds (Table 4*b*), from the Jutland breed to the Danish Black-Pied and from the Dutch Friesian to the German Black-Pied. Low gene flow rates ($m < 0.10$) were found among the rest of the breeds (Table 4*b*).

Discussion

Genetic diversity of the Jutland breed

This study reveals the Jutland breed as a highly structured breed that is significantly differentiated from other related breeds, which make it a valuable reserve of genetic variation for both the indigenous and commercial breeds.

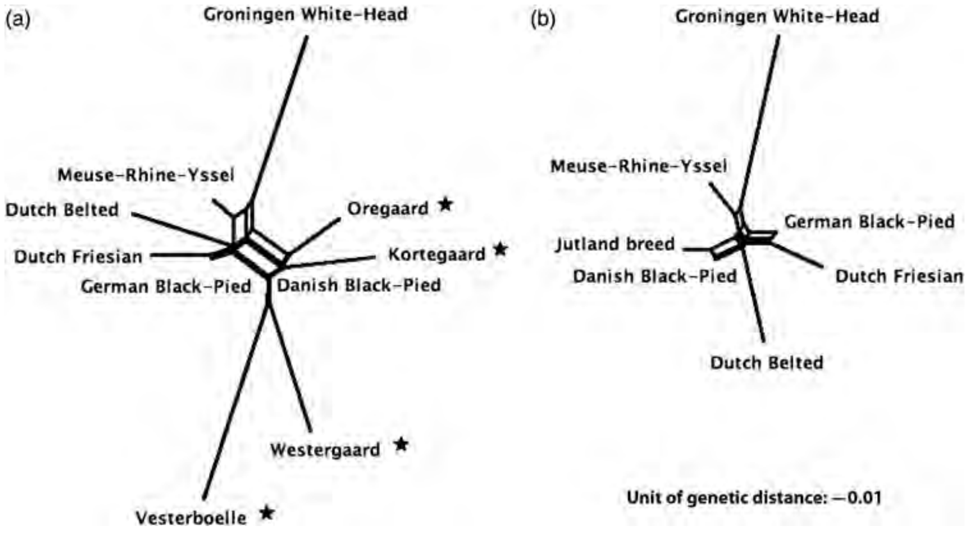

Figure 2. NeighborNets based on genetic distances (D_R) among (*a*) the four main Jutland breed herds (marked with a star) and the black-pied breeds, and (*b*) the entire Jutland breed and the black-pied breeds. The NeighborNets are based on 23 microsatellite loci.

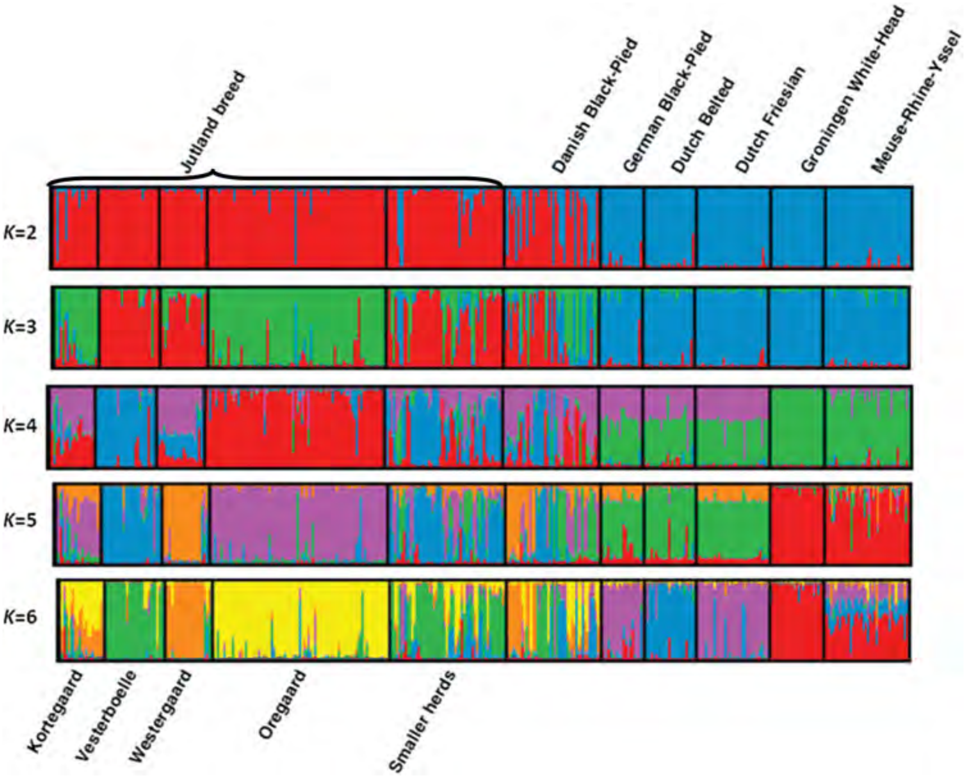

Figure 3. Estimated population structure among the Jutland breed herds and the black-pied breeds based on 23 microsatellite loci. Black vertical lines divide individuals into breeds, as indicated above the figure, and herds as indicated below the figure.

The Jutland breed has high genetic diversity (Table 1). All haplotypes belong to the common T3 haplogroup and most are shared among multiple herds (Figure 1). T3 is the most common haplogroup in Europe, and we found no evidence of introgression of breeds of the T, T1 or T2 haplogroups, which are more prevalent in the Middle East, Anatolia and Africa (Troy *et al.*, 2001).

The haplotype diversity is higher than that observed in other indigenous Danish breeds (Withen *et al.*, 2011). This corresponds well with their history of being widely used for local husbandry and not commercial selected breeding (Tapio *et al.*, 2006; Dalvit *et al.*, 2008). The level of genetic variation (H_O) is similar to that found in the Northern European black-pied breeds (Table 1); despite the Jutland breeds considerably lower effective population size as compared with the German and Dutch breeds. Different microsatellite loci have been applied to studies of genetic diversity in other cattle breeds, which makes direct comparisons of results complicated. However, based on data sets that have analysed a large number of same loci, the Jutland breed shows a level of genetic diversity comparable with the observed heterozygosity and mean allele number reported in other indigenous European cattle breeds (Kantanen *et al.*, 2000; Tapio *et al.*, 2006; Dalvit *et al.*, 2008; Withen *et al.*, 2011).

The small size of each herd – during at least the last five decades – is expected to lead to a reduction in genetic variation and an increase in levels of inbreeding (Reed and Frankham, 2003). Historically the herd sizes are expected to have been larger when the Jutland breed was widespread (Kantanen *et al.*, 2000; Negrini *et al.*, 2007; Withen *et al.*, 2011). We did not observe significant levels of inbreeding in Kortegaard, Westergaard and Oregaard. Unfortunately, we do not have historic data to address whether a change in inbreeding and genetic diversity has taken place. As of now, these three herds can be seen as stable.

Vesterboelle shows signs of out-breeding (Table 1*a*). This might in part be ascribed to introgression from a Dutch-born grey-pied bull of unknown origin, which has been used extensively in the breeding programme of this herd (Dalsgaard, 2001). Vesterboelle's small population size and the extensive introgression are expected to lead to deviations from HWE (Hedrick, 2002). The introgression has most likely led to the distinctness of the herd, based on microsatellite markers (Table 2*a* and *b*). Unfortunately, we did not have genetic samples from the grey-pied bull, so we can only speculate that the introgression might have led to the observed pattern. The bull's origin must be of a breed, which was not included in this analysis, as Vesterboelle is distinct from the analysed breeds (Table 2*b*; Figures 2*a* and 3).

The high haplotype diversity found in Kortegaard and Vesterboelle may be due to high diversity of the founder females. In contrast, the lower haplotype diversity observed in Westergaard and Oregaard suggests high relatedness among the founder females. This is most

Table 3. Assignment of individuals to (*a*) herds and (*b*) breeds. Rows represent the herd/breed of origin. Columns represent the herd/breed to which an individual is assigned.

(*a*)	Kortegaard	Vesterboelle	Westergaard	Oregaard
Kortegaard	19	0	1	1
Vesterboelle	1	26	0	1
Westergaard	1	2	18	1
Oregaard	2	0	0	80
Smaller herds	13	27	3	11

(*b*)	Jutland breed	Danish Black-Pied	German Black-Pied	Dutch Belted	Dutch Friesian	Groningen White-Head	Meuse–Rhine–Yssel
Jutland breed	148	54	3	1	1	0	0
Danish Black-Pied	19	21	1	2	1	0	0
German Black-Pied	0	3	11	0	4	0	2
Dutch Belted	0	0	0	22	1	0	1
Dutch Friesian	0	3	1	1	29	0	0
Groningen White-Head	0	0	0	0	0	23	2
Meuse–Rhine–Yssel	1	1	0	2	0	0	35

Assignment test are based on the “leave one out” option, where the individual of interest is removed from the dataset prior to estimating the population genotype frequencies.

pronounced in Westergaard, which showed very low levels of haplotype variation (Table 1*a*). The high number of haplotypes of low frequency was probably a remnant of a historically larger genetic diversity from a time when the breed was more abundant (Figure 1).

Impacts of restricted breeding

All results suggest the four main herds represent distinct units (Tables 1*a*, 2*a* and 4*a*; Figures 2*a* and 3). The contrast of low levels of linkage disequilibrium in each herd (0–2 percent) and high linkage disequilibrium in the Jutland breed (24 percent), with the smaller herds being the main contributor (16 percent), suggests the Wahlund effect (Wahlund, 1928) when grouping the herds (Table 1*b*). This is supported by the genetic distances among herds (Table 2*a*; Figure 2*a*), assignment of individuals almost exclusively to the herd of origin (Table 3*a*) and the clustering patterns (Figure 3). These findings correspond with the history of the breed, and the presumed separation of the four herds for at least the past 50 years, with only low levels of admixture (Table 3*a*).

The limited gene flow – among most of the herds – has resulted in genetic drift and resulting high level of differentiation among them (Table 4*a*) (Fernández, Toro and Caballero, 2008; Toro, Fernández and Caballero, 2009). This is well known from other small breeds (Kantanen *et al.*, 2000; Withen *et al.*, 2011). The high level of differentiation among herds (Figure 2*a*) may be due to a separation time longer than five decades (S. Benzon, personal communication).

The joint grouping of (1) Kortegaard and Oregaard and (2) Vesterboelle, Westergaard and a large number of individuals from the smaller herds could reflect the hierarchical structuring of the Jutland breed (Figure 3; $K = 3$). As the number of clusters increases it becomes evident that Vesterboelle, Westergaard and Oregaard are genetically distinct, whereas Kortegaard share genotypes with each of them (Figure 1; $K = 4$, 5, 6). In accordance with their history of originating from the main herds, the smaller herds represent the genetic diversity found in the four herds (Table 3*a*; Figures 1 and 3). Their resemblance to the German and Dutch breeds (Figure 3) and the unique haplotypes are most likely the result of minor introgression from these (Figure 1).

Genetic relationship among the black-pied breeds

Overall, the breeds are less differentiated than the herds (Table 2*b*) and have a higher level of gene flow (Table 4*b*), this is expected when accounting for genetic drift and differences in population size (Reed and Frankham, 2003). The Dutch breeds – and to a lesser extent the German Black-Pied – are distinct from the Jutland breed (Tables 2*b* and 4*c*; Figures 2*b* and 3*b*). Information on historic exchange of animals among the countries is limited; our results indicate that there has been limited exchange of animals between the breeds (Table 4*b*).

The putative origin of the Danish Black-Pied as a mix between the Jutland breed and black-pied cattle from Holland and Germany (Danish Ministry of Food, Fisheries and Agriculture, 2010) is supported by several of our analyses (Tables 3*b* and 4*b*; Figure 3), with the Jutland breed being by far the largest contributor (Tables 3*b* and 4*b*; Figure 3). All four herds have contributed almost equally with genetic material to the Danish Black-Pied breed (Table 2*b*; Figure 3), which is likely to have contributed to the observed Wahlund effect within this breed (Table 1*b*).

Management of a subdivided breed

The management of a subdivided breed, such as the Jutland breed, implies a compromise of two main factors: (1) maintenance of the highest possible levels of genetic

Table 4. Estimates of gene flow rates (*m*) among (*a*) the Jutland breed herds and (*b*) the black-pied breeds.

(*a*)	Kortegaard	Vesterboelle	Westergaard	Oregaard	Smaller herds
Kortegaard	*0.97* (*0.02*)	0.01 (0.01)	0.01 (0.01)	0.01 (0.01)	0.00 (0.01)
Vesterboelle	0.01 (0.01)	*0.68* (*0.01*)	0.01 (0.01)	0.01 (0.01)	*0.31* (*0.02*)
Westergaard	0.06 (0.02)	0.01 (0.01)	*0.88* (*0.03*)	0.01 (0.01)	0.05 (0.02)
Oregaard	0.01 (0.01)	*0.20* (*0.02*)	0.00 (0.00)	*0.79* (*0.02*)	0.00 (0.00)
Smaller herds	*0.22* (*0.02*)	0.00 (0.01)	0.00 (0.00)	0.01 (0.01)	*0.76* (*0.02*)

(*b*)	Jutland breed	Danish Black-Pied	German Black-Pied	Dutch Belted	Dutch Friesian	Groningen White-Head	Meuse–Rhine–Yssel
Jutland breed	*0.95* (*0.01*)	0.03 (0.01)	0.00 (0.00)	0.00 (0.00)	0.01 (0.01)	0.00 (0.00)	0.00 (0.00)
Danish Black-Pied	*0.19* (*0.03*)	*0.72* (*0.02*)	0.00 (0.01)	0.01 (0.02)	0.08 (0.02)	0.00 (0.01)	0.00 (0.01)
German Black-Pied	0.01 (0.01)	0.01 (0.01)	*0.68* (*0.02*)	0.01 (0.02)	*0.27* (*0.03*)	0.02 (0.02)	0.01 (0.01)
Dutch Belted	0.00 (0.01)	0.00 (0.01)	0.00 (0.01)	*0.98* (*0.02*)	0.00 (0.01)	0.00 (0.01)	0.00 (0.01)
Dutch Friesian	0.00 (0.00)	0.00 (0.00)	0.00 (0.00)	0.00 (0.00)	*0.99* (*0.01*)	0.00 (0.00)	0.00 (0.00)
Groningen White-Head	0.00 (0.01)	0.00 (0.01)	0.00 (0.00)	0.00 (0.01)	0.00 (0.01)	*0.98* (*0.02*)	0.01 (0.01)
Meuse–Rhine–Yssel	0.00 (0.01)	0.00 (0.00)	0.00 (0.00)	0.01 (0.01)	0.00 (0.01)	0.00 (0.01)	*0.98* (*0.02*)

Migration rates (*m*) into each population are shown with standard errors (SE) given in parentheses. Rows represent the population from which each individual was sampled, and columns represent the populations from which they migrated. Diagonal values represent the proportions of individuals derived from the source populations in each generation. Migration rates ≥0.10 are in italics.

diversity and (2) conservation of unique herd characteristics (Toro and Caballero, 2005). The two factors can be achieved if the four main herds are kept completely isolated. However, this will result in an increase in herd inbreeding levels, which can compromise their short-term survival (Reed and Frankham, 2003; Taberlet *et al.*, 2008). Alternatively, the herds could be united as one large breeding unit. The trade-off would be loss of genetic diversity, washing out singularity of the herds and a long-term decrease in effective population size (Toro and Caballero, 2005).

We propose a management strategy where the herds are managed separately, but with an increased amount of gene flow among them, to avoid further genetic drift. A minimum of one migrant per herd per generation has been shown to counteract the detrimental effects of genetic drift (Fernández, Toro and Caballero, 2008; Toro, Fernández and Caballero, 2009). To conserve the uniqueness of the Jutland breed, introgression from the German and Dutch Black-Pied breeds should be avoided.

Conclusion

Losses of indigenous cattle breeds are happening at a high rate worldwide, and FAO has recommended immediate action should be taken to conserve local cattle breeds and possible valuable genetic variation (FAO, 2007b). Our characterization of the indigenous Danish cattle breed; the Jutland breed, shows it to be a valuable reservoir of unique genetic variation. Our results further demonstrate the rapid diversification of the Jutland breed herds due to limited gene flow and genetic drift. The Jutland breed has experienced limited introgression from related Northern European black-pied breeds. We propose conserving the Jutland breed herds as separate breeding entities with moderate gene flow among the herds. This will assure conservation of the highest possible amount of genetic variation and fitness for future management of the Jutland breed.

Supplementary material

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

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Backyard poultry in Kabylie (Algeria): from an indigenous chicken to a local poultry breed?

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Summary

Backyard poultry is considered as a powerful tool for poverty alleviation. It is further promoted as a way of empowering women in communities where there is gender bias in poultry raising. The low-input systems involved are based on local breeds that are perfectly suited to their environment. However, socio-economic processes put local genetic resources under pressure, leading to the erosion of biodiversity. The present survey addresses this issue in the case of Kabylie, a mountainous coastal region of Algeria, through a survey conducted in 90 households raising poultry, a morpho-biometric description of 315 local chickens, and a performance evaluation of both growth and egg production in experimental semi-intensive conditions. The socio-economic profile of poultry smallholders in Kabylie reveals poor education and high diversification of agricultural assets and confirms gender bias in poultry keeping. The erosion of local genetic resources in chicken is found to be severe despite their cultural importance in Kabylie. From complementary surveys among experienced poultry keepers, the major original local type is postulated to consist of three varieties with black plumage (pure black, mottled and barred). The performance evaluation raised promising results, suggesting that exploiting the local breed could pursue some degree of improvement of low-input backyard systems. Finally, a strategy for a revival of the local breed through the support of the most involved smallholders is outlined in accordance with the information collected in the survey.

Keywords: *biodiversity, genetic resources, Kabylie, poultry, smallholder*

Résumé

L'élevage de volailles d'arrière-cour constitue un outil important de lutte contre la pauvreté. Il est en outre promu comme mode de renforcement de la position féminine dans une communauté, sous réserve de l'observation dans les faits du biais de genre classiquement rapporté dans le contrôle de cet élevage. Les systèmes à faible niveau d'intrant concernés sont basés sur des races locales rustiques, adaptées à leur environnement. Néanmoins, des processus socio-économiques mettent sous pression ces ressources génétiques locales, menant à une érosion de la biodiversité. La présente étude aborde cette problématique dans le cas de la Kabylie, région côtière montagneuse de l'Algérie, au travers d'une enquête auprès de 90 ménages élevant des poules, d'un relevé morpho-biométrique réalisé sur 315 sujets locaux ainsi qu'une évaluation des performances de ponte et de croissance dans des conditions semi-intensives expérimentales. Le profil socio-économique des petits éleveurs de poules en Kabylie révèle un faible niveau de formation, une grande diversification de l'outil agricole et confirme le biais de genre mentionné plus haut. Une érosion génétique sévère a été trouvée, en dépit de l'importance culturelle de la poule en Kabylie. Une enquête complémentaire auprès d'éleveurs expérimentés indique que trois variétés de plumages noirs (noir pur, caillouté, barré) sont considérées comme constituant les principaux types locaux d'origine. L'évaluation des performances a fourni des résultats prometteurs, suggérant qu'un certain degré d'amélioration des systèmes d'élevage d'arrière-cour pourrait être recherché sur base des types locaux. Finalement, en accord avec l'information recueillie dans cette enquête, une stratégie de revivification de la race locale au travers d'un soutien aux éleveurs les plus impliqués est brièvement proposée.

Mots-clés: *biodiversité, ressources génétiques, Kabylie, poule, petit éleveur*

Resumen

La cría de aves de traspatio es considerada como una poderosa herramienta para mitigar la pobreza. Además, es promovida como una forma de dotar de mayor poder a las mujeres en las comunidades donde existe una discriminación de género en la crianza de aves de corral. Los sistemas de bajos insumos en juego están basados en las razas locales, adaptadas a su entorno. Sin embargo, los diferentes procesos socioeconómicos acaecidos han sometido a presión los recursos genéticos locales, dando lugar a la erosión de la biodiversidad. El presente estudio aborda esta cuestión en el caso de Cabilia, una región montañosa de la costa de Argelia, a través de una encuesta realizada a 90 familias que crían aves de corral, una descripción morfométrica de 315 animales pertenecientes a poblaciones locales, y una evaluación del rendimiento relacionado con el crecimiento y la producción de huevos bajo condiciones experimentales semi-intensivas. El perfil socio-económico de los pequeños productores de aves de corral en Cabilia revela falta de educación y alta diversificación de los activos agrícolas, confirmando la discriminación de género en la tenencia de este tipo de aves. La erosión de los recursos genéticos locales relativos a las aves de corral es muy grave, a pesar de de la importancia cultural de éstos en Cabilia. Tomando como base encuestas complementarias, entre aquellos avicultores con mayor grado de experiencia, se presupone que el tipo original

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local más importante consta de tres variedades de plumaje negro (negro puro, moteado y barrado). El estudio de los rendimientos ha aportado prometedores resultados, indicando que la cría de razas locales puede dar pie a cierta mejora de los sistemas de traspatio de bajos insumos. Por último, de acuerdo con la información recogida a través de la encuesta, se esboza una estrategia para apoyar el restablecimiento de las razas locales, contando con el apoyo de la mayoría de los pequeños agricultores.

Palabras clave: *biodiversidad, recursos genéticos, Cabilia, ave de corral, pequeño agricultor*

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Introduction

Proteo-caloric malnutrition is a widespread consequence of poverty in developing countries, further compromising people's capability to step out of their condition. In this regard, backyard poultry can be an important tool in poverty alleviation, as eggs for home consumption are a low-cost protein source especially valuable for children's growth, or as it can provide additional income where markets are available (Mack, Hoffmann and Otte, 2005; Roothaert, Ssalongo and Fulgensio, 2011). In Algeria, as in other regions of the developing world, beyond this productive role, poultry moreover plays a pivotal role in the social sphere, being sacrificed at important occasions such as weddings and circumcision ceremonies or being offered to special guests (Moula *et al.*, 2009a; Raach-Moujahed, Moujahed and Haddad, 2011). Therefore, poultry can be considered as addressing the poverty problem in its multidimensional nature. The link between poultry and poverty alleviation is even more clearly expressed in the case of Kabylie where the poor are traditionally said to be "the one who does not even have a hen." Indeed, in contrast to larger animals such as ruminants or pigs, poultry is characterized by the low investment needed in backyard systems. Thus they often represent the first step in capitalization by poor people.

Unfortunately, the local breeds on which those low-input systems are based are presently endangered owing to the spread across rural areas of commercial hybrid strains from their initial intensive rearing spots. At present, half of the poultry breeds of known status are at risk of extinction (FAO, 2008). Poverty in itself is a basic explanation for this genetic erosion: backyard poultry breeders introduce highly productive and genetically uniform strains in their indigenous flocks according to a short-term gain strategy at the expense of sustainability (Anderson, 2003). Indeed, the lack of adaptation of these hybrid strains to the village raising practices induces a major risk to the present and future production system without realizing the expected profit. A more long-term-oriented strategy should consist of a progressive upgrading of the rearing systems, including the genetic improvement of the local breeds in accordance with the locally available inputs and environment control capacities and possible qualitative and cultural expectations. In this context, characterization of local breeds and assessment of their productive potential in their actual raising system as well as their response to an upgrading of this system is crucial. The present study aims at such an evaluation in Algeria.

Materials and methods

General structure of the study

Characteristics of backyard poultry raising were assessed in a sample of 30 villages of Basse-Kabylie, a mountainous costal region of Algeria about 200 km east of Algiers. The study villages were chosen in ten districts, spreading over the north (2), center (2), south (2), east (2) and west (2) of the region. The raising systems were first assessed through a socio-economic survey conducted in 3 households per village (90 households interviewed). Morpho-biometric characterization of 315 local chicken specimens was then completed. Finally, growth and laying performances were assessed in semi-intensive conditions for 111 chicks and 50 hens, respectively.

Socio-economic survey

Age, sex, education level, occupations and agricultural endowment of the respondent and the members of the household were recorded. Open questions related to poultry raising practices. Respondents were then asked about their motivations for chicken rearing in general and for the choice of the local breed in particular as well as for the use of the different products through three multiple-choice questions.

In the additional survey, 14 interviewees with over 50 years experience in poultry raising were asked an open question about their perception of a possible change in chicken genetic resources kept in their village (period, nature of the change, description of the former phenotypes).

Morpho-biometric characterization

Adult animals (>10 month) were exclusively used for the morpho-biometric characterization. The different body measurements were recorded in accordance with the FAO (1981) recommendations, by means of a digital balance (accuracy 1 g), an electronic sliding calliper (accuracy

0.01 mm) and a tape measure. The data collected were sex, body weight and reported age of the animal; thoracic girth; feathers type and colour; comb's type, length, height and colour; wattles' height and colour; tarsus length and diameter; wings' length; and the length and colour of the beak.

Egg production performance

Eggs collected in the different villages were put for natural incubation and hatching. Day 1 chicks were vaccinated against Marek's disease. The chicks were then kept in a brooder house and fed a commercial starter mix (22 percent crude protein, 2 700 kcal/kg metabolizable energy) ad libitum until 12 weeks of age. A commercial growth mix (18.9 percent crude protein, 2 700 kcal/kg metabolizable energy) was then given for the following weeks. Temperature and relative humidity were not kept constant but were recorded daily. Maximum temperature ranged between 24 and 32 °C and minimum temperature between 19 and 26 °C. Maximal relative humidity varied from 60 to more than 94 percent and minimal from 45 to 80 percent.

At week 18, a total of 60 hens were transferred to individual cages. Natural lighting duration was 12h15 at week 19 and was then increased by increments of 30 min per week till duration of 16h30 light per day at week 26. Ranges for maximal and minimal temperature as well as for maximal and minimal relative humidity were 12–31 °C, 6–14 °C, 75–96 and 50–83 percent, respectively. A laying hen feed mix (18.9 percent crude protein, 3 060 kcal/kg metabolizable energy) was given from week 20 (composition shown in Table 1). Ten animals died during the experiment, of unknown cause, as necropsies could not be carried out.

Table 1. Feed mix composition for starting, growth and laying.

Ingredients	**Mix**		
	Broiler starter	**Broiler**	**Layer hens**
Soy oil cake	32	30	20.0
Wheat	37	31	11.0
Corn	25	33	50.0
Soy oil	2.3	2.0	3.0
Calcium phosphate	1.5	1.8	1.0
Minerals (vitamins, micronutrients)[1]	1.1	1.0	1.0
Calcium carbonate	1.08	1.2	7.5
Methionine	0.02	0.2	0.1
Alfalfa	–	–	2.4
Beets molasse	–	–	1.5
Wheat middlings	–	–	2.5
Composition			
Metabolizable energy (kcal/kg)	2 870.00	2 950.00	3 060.40
Fat content (g/kg)	55.13	52.18	54.53
Lysine (g/kg)	12.45	8.46	11.28
Methionine (g/kg)	5.39	3.45	4.36
Calcium (g/kg)	9.5	38.0	10.00
Phosphorus (g/kg)	6.03	5.62	5.68
Dry matter (g/kg)	612.9	749.6	561.26
Crude protein (g/kg)	220	170	189.00

[1] Vitamin A 13 500 UI/kg, vitamin D_3 3.000 UI/kg, vitamin E 25 mg/kg, copper sulphate 15 mg/kg.

Laying records

Age and weight of the hens at the onset of laying were recorded. Laying was followed-up daily and individually for 52 weeks. Cumulative egg laying rate was assessed for two periods: from week 38 to 42 and from week 56 to 60.

Egg quality

Egg quality analysis was implemented at both above-mentioned periods by weekly collection of the first three eggs for each hen (1 500 eggs). Analysis was completed within a few hours after laying. Eggs were numbered and weighed to the nearest 0.01 g. Then, their length and width were measured by means of an electronic sliding calliper (accuracy 0.01 mm), so that an egg shape index could be calculated (ratio between length and width) (Moula *et al.*, 2010). The eggs were then broken with careful separation of yolk and albumen. The shell (including membranes) and yolks were weighed separately (accuracy 0.01 g). Albumen weight was determined by subtracting yolk and shell weights from total egg weight. The shell thickness was measured at three different random points in the equatorial shell zone using an electronic micrometre (accuracy 0.01 mm). The average of the three measures was used as a trait (Moula *et al.*, 2010).

Growth performance

A total of 160 eggs were put for natural incubation by 16 selected hens with acknowledged brooding ability. Hatching rate was recorded. The chicks ($n = 111$) were floor-bred on a sawdust litter in a same ventilated building (no air conditioning). Chicks were first put under a heating lamp and the room temperature was regulated manually according to chicks' behaviour. A continuous light regimen was adopted for the whole experiment period. Animals were fed ad libitum with a starter mix until the age of 14 days (22 percent crude protein, 2 870 kcal/kg metabolizable energy) and then passed to a tradition poultry mix (20 percent crude protein, 2 950 kcal/kg metabolizable energy) which was given ad libitum until slaughter (feed composition listed in Table 1).

Each animal was identified individually. After sexing at week 9, males and females were kept separated by a metallic net. Animals were weighed individually at week 0, 1, 4, 8, 12 and 16. The feed conversion index was assessed for the flocks by calculating the ratio between the total ingested food and total live weight gain.

Statistical analysis

All statistical analyses were performed with the SAS software (Statistical Analysis System, 2000).

Socio-economic and morpho-biometric surveys

Descriptive statistics were obtained for all socio-economic and morpho-biometric parameters. Answers to the multiple-choice questionnaire were analysed in terms of frequency of occurrence (citation rate).

Egg laying performance

Descriptive statistics (frequency, mean, standard deviation) were calculated for the following parameters: hatching rate, weight and age at onset of laying, laying rates, annual number of eggs laid per hen. Student's *t*-test was performed in order to compare data obtained for the two different laying periods (weeks 38–42 and weeks 56–60).

Growth performance

Mean body weight by sex was calculated for each week along with standard deviations. Growth was further described by the calculation of growth curve parameters according to the following Gompertz equation: $y = \alpha \times \exp(-\beta \times \exp(-\gamma \times t))$, where y is the weight of broiler (g); α is the asymptotic weight; β is the integrating constant; γ is the growth speed factor (maturation factor) and t is the time (Porter *et al.*, 2010). These parameters were estimated by non-linear regression using the Marquardt method in the Non-linear Models Procedure of SAS (2000). The age to inflexion, corresponding to the period when growth is maximum, was calculated using the formula: $T_i = (1/\gamma) \times \ln|\beta|$ (Porter *et al.*, 2010).

Results

Socio-economic characteristics of local poultry keepers

Median number of poultry by household was 11. Among the 90 respondents, 57 were men and 33 women. The men responding were effectively in charge of poultry keeping activities in only 17 households, poultry keeping being mainly a female occupation (81 percent of households). This means that 40 women involved in poultry keeping could not be directly interviewed because of the husband's intervention. In all households, women were housewives. Men's main occupation was agriculture in 37 percent of the households; 14 percent were civil servants, 9 percent were merchants and 7 percent were transporters. In 33 percent of households, men declared to be in a situation of unemployment. However, all households of the latter category did present agricultural occupations. Education level was globally low, especially in women; 64 percent of women were illiterate. Among men, 79 percent did not obtain the basic school certificate. Two noticeable exceptions were agronomists (university degree) that were employed as civil servants and were actually in charge of the poultry keeping activities in their household. For the complementary survey among experienced raisers, the median age of respondents was 69.5 years with a minimum at 60 and a maximum at 91.

Agricultural assets

Besides poultry keeping, 79 percent of households cultivate small plots. The major crops are cereals (wheat or barley) and some vegetables (tomatoes, beans, potatoes, onions, courgettes, etc.). Production is generally aimed at home consumption. Owing to the mountainous environment of Kabylie, fruit trees are a common agricultural capital owned by households. The most common trees are olive trees and fig trees, owned by 93 and 88 percent of interviewed households, respectively, but 94.5 percent of households also own other fruit trees such as apple, cherry, orange trees or even oaks (the acorns of which are both consumed by man and fed to animals). Beekeeping was practiced by 62 percent of the households. Fruit trees and beehives are both commonly situated on plots owned by other households, their tenure thus being independent of that of the land harbouring them. The other animals kept were sheep (86 percent), rabbits (64.5 percent), goats (44.5 percent), cattle (38 percent), turkeys (25.5 percent) and ducks (20 percent) (Table 2).

Table 2. Mean stocks by species and by sex in the surveyed households.

Species	% HH	Sex	Mean stock by HH ± SE	Lowest stock	Highest stock	CV (%)
Poultry	100.00	Male	2.57 ± 0.14	1	6	50.13
		Female	9.52 ± 0.46	2	21	45.41
Sheep	86.67	Male	3.08 ± 0.53	1	23	146.17
		Female	9.06 ± 0.87	2	42	84.70
Rabbit	64.44	Male	2.88 ± 0.53	1	23	133.76
		Female	9 ± 0.89	2	42	75.30
Goat	44.44	Male	1.82 ± 0.17	1	6	58.47
		Female	6.62 ± 0.65	2	21	62.16
Cattle	37.78	Male	2 ± 0.30	1	8	85.19
		Female	6.18 ± 0.97	1	28	91.71
Turkey	25.56	Male	3.13 ± 0.45	1	6	68.31
		Female	7.35 ± 1.21	2	23	78.99
Duck	20.00	Male	1.33 ± 0.11	1	2	36.38
		Female	4.17 ± 0.42	2	8	42.97

% HH: percentage of households holding a particular species; CV: coefficient of variation.

Motivational aspects and poultry genetic resources management

The major motivations cited for poultry keeping were egg production (58 percent), tradition (53 percent) and then meat production (52 percent) (Table 3). Rationale for the preference of keepers for the local chicken is presented in Table 3. The most cited reasons were the strong flavour of its meat (89 percent) and the resilience of the birds to harsh environment (73 percent). The ease of daily care was also commonly cited (65.5 percent).

The 14 experienced respondents, all raising poultry for more than 50 years, unanimously reported a noticeable change in the poultry genetic resources in their villages. The period at which they situate the beginning of this change is the early 1990s. The nature of the change discussed is a widening of phenotypic variability, a decrease in flock size and a loss in "quality" and flavour of both meat and eggs. All respondents described the original phenotypes as predominantly black with some white in the plumage (pure black, mottled or barred) and with blue or black legs. Ten of them also mentioned the partridge plumage along with the black and white varieties as the "true Kabyle chickens". Six persons also cited the blue plumage. The greater resistance to diseases (both digestive and respiratory) of the former Kabyle chicken is unanimously reported. Two persons from two different districts also mentioned the longer legs of the former varieties. White or yellow legs, as well as red plumage, were clearly associated by interviewees to the intrusion of exogenous genetics.

Raising systems

Housing and feeding

Data about raising practices are given in Table 4. Scavenging systems represented 21 percent of cases while semi-scavenging was encountered in the other 79 percent, meaning that poultry were kept sheltered at night. Shelters could be quite rudimentary and assembled from metal panels and wire netting or could be concrete constructions, often adjacent to the main habitation. Animals were mostly fed kitchen waste (98 percent). Cereals and mixes normally intended for use in complementary feeding for ruminants were seldom distributed to chickens for fattening before special celebrations (2 percent). The most common water sources for poultry were wells (48 percent) and tap water (43 percent).

Table 3. Motivational aspects related to local poultry keeping.

Objective of poultry keeping activity	Citation rate (%)	Reasons for preferring the local poultry	Citation rate (%)
Egg production	57.78	Taste of meat or eggs	88.89
Tradition	53.33	General resilience	73.33
Meat production	52.22	Ease of raising	65.56
Food security	7.78	Maternal behaviour	51.11
		Feather colour	44.44
		Resistance to diseases	38.89
		Longevity	21.11
		Price premium on markets	10.00
		Biodiversity conservation	2.22

Table 4. Poultry keeping system characteristics in Kabylie (citation rate in %).

Flock management		Feeding	
Semi-scavenging	78.89	Kitchen residue	97.78
Scavenging	21.11	Commercial feed	2.22
Main production purpose		Water	
Dual purpose	53.33	Wells	47.78
Egg production	33.33	Tap water	43.33
Meat production	13.33	Other[1]	8.89
Use of the products		Animals	Eggs
Reproduction		33.33	30.00
Self-consumption		42.22	56.67
Gift		8.88	11.11
Sale		12.22	2.22
Exchange		3.33	0.00

[1] Stream, spring, fountain, etc.

Use of poultry products

Uses were categorized separately for animals (live animals or meat) and eggs. For animals, home consumption was the first use mentioned (42 percent). Reproduction was also a common answer (33 percent). Less cited uses were commercialization (12 percent), gift (9 percent) and exchange (3 percent). For eggs' use, home consumption was more common than for meat (57 percent) while commercialization was less cited (2 percent) and exchange was not practiced. A price premium for local poultry products was stated by 10 percent of interviewees.

Morpho-biometric characterization

Feather colour and aspect

The different colours observed and their frequencies are reported in Table 5. The most common colours were black (17 percent), white (16 percent), gold (13 percent) and silver (11 percent). Other colours such as blue, grey, mottled, red, light brown, dark red, barred, partridge, dark brown, yellow, salmon and tan were less frequently encountered (between 1 and 8 percent). Globally, the population thus turned out to be highly heterogeneous. Males were mostly white or gold (20 percent of each colour), black or silver (14 percent of each colour). In females, black (19 percent) was more frequent than white plumage (12 percent). Naked necks were seldom observed with only 4 percent of cases in both sexes.

Table 5. Number (*n*) and percentages (%) of different feather colours and distribution in local chicken in Kabylie.

	Males		Females		Total	
	N	%	*N*	%	*N*	%
Feather colour						
Black	22	14.38	31	19.13	53	16.82
White	31	20.26	19	11.73	50	15.87
Golden	30	19.61	11	6.79	41	13.01
Silver	21	13.72	13	8.02	34	10.79
Light brown	5	3.27	21	12.96	26	8.25
Dark red	7	4.57	11	6.79	18	5.71
Dark brown	2	1.31	14	8.64	16	5.08
Barred	5	3.27	10	6.17	15	4.76
Blue	4	2.61	9	5.55	13	4.12
Red	8	5.23	2	1.23	10	3.17
White Columbian black	6	3.92	3	1.85	9	2.86
Grey	1	0.65	6	3.70	7	2.22
Mottled	4	2.61	2	1.23	6	1.90
Partridge	0	0	6	3.70	6	1.90
Yellow	3	1.96	1	0.62	4	1.27
Salmon	2	1.31	2	1.23	4	1.27
Tan	2	1.31	1	0.62	3	0.95
Total	153		162		315	
Feather distribution						
Normal	147	96.08	155	95.67	302	95.87
Naked neck	6	3.92	7	4.32	13	4.13
Total	153		162		315	

Type and colour of the comb and the wattles

Comb was mostly simple (93 percent) and red (84 percent) in both sexes. The wattles were in general of the same colour as the comb and had similar colour frequencies (Table 6).

Skin and legs colour

Skin was mostly white (44 percent) but also pink (22 percent) or yellow (28 percent). Black was rare (7 percent). Legs showed the same colours but with a higher frequency of yellow (37 percent).

Table 6. Number (*n*) and percentages (%) of different types and colours of the comb and the wattles in local chicken in Kabylie.

	Males		Females		Total	
	N	%	*N*	%	*N*	%
Comb type						
Simple	141	92.16	153	94.44	294	93.33
Double	8	5.22	8	4.93	16	5.08
Triple	4	2.61	1	0.62	5	1.59
Total	153		162		315	
Comb colour						
Red	138	90.20	126	77.77	264	83.81
Pink	13	8.50	25	15.43	38	12.06
Black	2	1.30	11	6.79	13	4.13
Total	153		162		315	
Wattles colour						
Red	150	98.04	134	82.72	284	90.16
Pink	2	1.31	16	9.88	18	5.71
Black	1	0.65	12	7.40	13	4.12
Total	153		162		315	

Weight and body measurements under traditional raising system

Results for body weight and measurements are presented in Table 7. Mean weight of females was 1 286 ± 326 g (minimum: 805 g; maximum: 2 754 g). Males were heavier with a mean weight of 1 646 ± 431 g (minimum: 1 060; maximum: 3 241 g). As for weight, all other body measurements were higher in males compared with females. Again, the population turned out to be very heterogeneous with coefficients of variation ranging from 6.8 to 65.3 percent.

Performances under experimental semi-intensive system

Egg production

Ten hens died during the experiment (16.7 percent mortality rate). The cause of this mortality has not been identified as necropsy could no be carried out. Table 8 shows the age and body weight at onset of laying, eggs number and annual laying rate. Mean age at onset was 189 days and mean body weight was 1 351 g. The hens laid a mean number of 163 eggs per year, with a laying rate of 44.6 percent. Values obtained for egg quality traits at each period are presented in Table 9. Laying rate showed a statistically significant decrease in the second period (44.68 vs 51.16 percent in the first period) while egg weight showed a statistically significant increase in this second period (54.32 ± 2.66 vs 50.23 ± 2.71 g in the first period). Egg component proportions did differ between periods.

Growth

Among the 160 eggs put for incubation, 111 hatched (hatching rate of 69.37 percent), and 43 males and 55 females were obtained. Mortality rate was 11.71 percent, distributed as follows: five chicks died on day 1, two at week 2, two at week 5 and one per week from week 9 to 12. At week 16, mean feed conversion index was 4.97. Mean weight at hatching was 33.00 ± 1.63 and 31.48 ± 2.10 g in males and females, respectively. At day 84, weights were 1 241.16 ± 160.62 g and 1 034.69 ± 84.38 for males and females, respectively. At day 112, these values were 1 605.56 ± 188.42 and 1 284.55 ± 102.41 g. Gompertz growth curves for males and females are presented in Figure 1 and estimated parameters are given in Table 10. Asymptotic weight (α) of males was superior to that of females (2 045.30 g vs 1 532.90 g) as was the constant of integration (β) (4.32 vs 4.09). The maturation rate (γ) was higher in females, who reached their inflexion weight sooner than males (50.28 vs 56.94 days).

Discussion

Socio-economic aspects

The present study showed a clear predominance of women in poultry raising activities in households of Kabylie. Such

Table 7. Body weight (g) and measurements (mm) according to sex and coefficient of variation in local Kabyle chicken.

	Male (n = 153)	Female (n = 162)	Total (n = 315)	CV (%)
Body weight	1 646.46 ± 431.25^{a}	1 286.48 ± 326.49^{b}	1 461.32 ± 420.90	28.80
Length of tarsus	87.20 ± 12.37^{a}	66.66 ± 4.76^{b}	76.64 ± 13.83	18.06
Length of wing	156.98 ± 12.37^{a}	144.79 ± 11.85^{b}	150.71 ± 13.43	8.91
Diameter of tarsus	15.39 ± 1.21^{a}	12.10 ± 1.25^{b}	13.70 ± 2.05	15.00
Thoracic perimeter	403.23 ± 25.23^{a}	374.95 ± 18.97^{b}	388.68 ± 26.33	6.77
Body length	417.04 ± 18.00^{a}	370.52 ± 17.70^{b}	393.12 ± 29.31	7.46
Comb height	33.25 ± 4.84^{a}	11.87 ± 4.61^{b}	22.26 ± 11.69	52.55
Beak length	34.40 ± 2.84^{a}	31.58 ± 2.06^{b}	32.95 ± 2.84	8.62
Comb length	69.49 ± 8.29^{a}	31.46 ± 3.32^{b}	49.93 ± 20.03	40.12
Wattles length	33.90 ± 3.67^{a}	7.92 ± 2.88^{b}	20.54 ± 13.41	65.28

^{a,b}: On a same line, different letters are assigned to values showing statistically significant differences between them ($p < 0.05$).
CV: coefficient of variation.

a gender bias has been reported in many other developing countries (Gueye, 2007; Keambou *et al.*, 2007; Ramdas, 2009). This bias is the rationale for the use of poultry-keeping programmes as a means of targeting women in poverty alleviation projects, an approach widely known as the "Bangladesh smallholder poultry model" (Jensen and Dolberg, 2003). As highlighted by Kitalyi (1998), the gender bias is not universally true and must be accordingly investigated as a precondition for the effectiveness of those programmes. Further attention must be paid to the fact that poultry keeping is neglected by men as long as it is oriented towards home consumption and does not bear any hope for profit. If cash earnings can be realized, men could then intervene in the management and selling decisions to the detriment of women (Gueye, Ndiaye and Branckaert, 1998). As a matter of fact, in Kabylie, larger semi-intensive or intensive poultry farms are mostly run by men. The monitoring of gender issues throughout the development of access of smallholders to the poultry markets is thus necessary. Upstream, the access to production factors, capital, credit and decision-making become pivotal gender questions if the development of this value chain is to benefit women. In the present survey, it has been difficult and sometimes impossible in many households to interview women directly despite their recognized role in poultry keeping in those households. This sheds light on the gender problem in this region and the many difficulties that would be encountered by projects designed to empower rural women.

A clear lack of education among poultry smallholders also appeared in the present survey. This lack should be addressed in any project aiming at improving poultry keeping practices and organizing producers. Indeed, education is a fundamental determinant of the ability of people to organize themselves and build the institutions needed for sustainable economic development. At present, basic scholarship is obligatory in Algeria but illiteracy remains a real problem in men and women in rural areas.

Chicken flocks owned by the sampled households were small, none of them exceeding 30. All households owned other agricultural assets such as animals, fruit trees, beehives or cropland. No clear grouping of households could be distinguished through principal component analysis and hierarchic classification (results not shown). Thereby, the households included in the survey appeared to be quite homogeneous regarding the diversity of agricultural occupations. In accordance with this global diversification of agricultural assets, attention should be paid to the change in factor allocation (mainly labour) ensuing from improvements in the raising system. For example, women are traditionally engaged in milking of cattle or goats, and may not be able to spend additional time on poultry raising or commercialization as men make

Table 8. Laying performance of local Kabyle hen under experimental semi-intensive conditions (n = 50)

	Mean	SD	Max	Min
BW at first egg (g)	1 351.00	100.24	1 521.00	1 150.00
Age at first egg (days)	188.72	16.96	214.00	159.00
Eggs layed per year	162.64	27.06	202.00	115.00
Annual laying rate (%)	44.56	7.49	55.34	31.51

SD: standard deviation; BW: body weight.

Table 9. Laying and egg quality parameters in local Kabyle hen under experimental semi-intensive conditions (n = 50).

	Mean ± SD		t-value	
	38–42 weeks	56–60 weeks		
Laying rate (%)	51.16 ± 10.97	44.68 ± 8.29	3.37	*
Egg weight (g)	50.23 ± 2.71	54.32 ± 2.66	7.71	***
Albumen weight (g)	29.01 ± 1.87	31.34 ± 1.86	6.27	***
Yolk weight (g)	15.36 ± 1.01	16.81 ± 1.30	6.20	***
Shell weight (g)	5.86 ± 0.59	6.18 ± 0.80	2.24	*
Albumen percentage (%)	57.73 ± 1.51	57.69 ± 1.78	0.13	ns
Yolk percentage (%)	30.59 ± 1.38	30.93 ± 1.86	1.05	ns
Shell percentage (%)	11.68 ± 1.08	11.38 ± 1.41	1.20	ns
Shell thickness (10^{-2} mm)	36.34 ± 2.40	35.04 ± 4.31	1.86	ns
Shape index^{1}	75.50 ± 1.99	74.85 ± 2.37	1.47	ns
Y:A ratio (%)	52.82 ± 3.71	53.53 ± 4.24	0.60	ns

^{1}: Egg length/width ×100.
Y:A: yolk-to-albumen ratio.
ns, *,***: $p > 0.05$, $p < 0.05$, $p < 0.0001$, respectively.

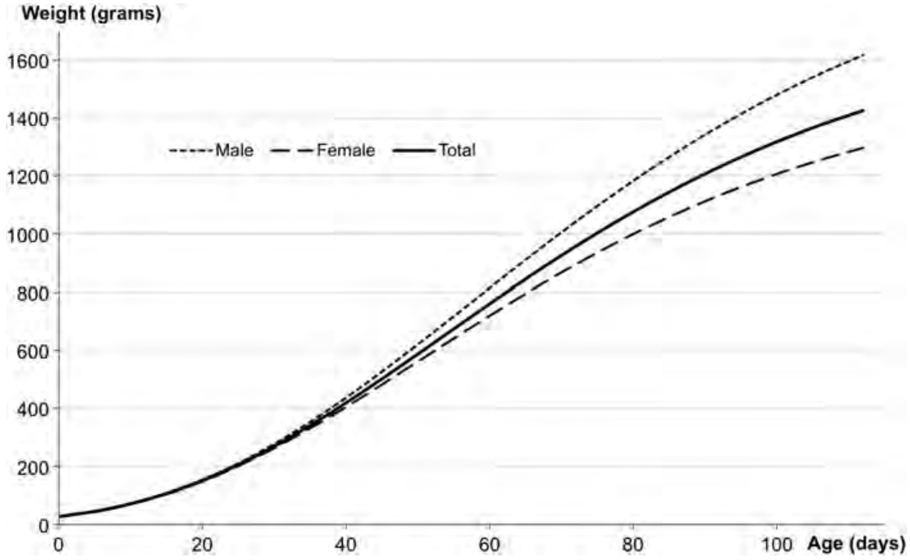

Figure 1. Gompertz growth curve parameters of local Kabyle chicken under experimental semi-intensive conditions.

decisions on the asset-diversification strategy of the household.

Motivations for poultry raising and indigenous genetic resources management

Poultry is primarily kept for home consumption of both eggs and meat. The fact that the tradition purpose comes as a frequent answer is interesting, showing the cultural and social importance of the simple owning of some hens in Kabylie. Reasons for preference for local chickens over commercial ones could be regarded as a first approximation of breeding goals. Resilience, ease of raising and flavour of eggs and meat are the principal motives. The first two statements fit into the general conception of poultry keeping as a low-investment, low-cost, low-risk and low-skill side activity. The great variety of phenotypes recorded through morpho-biometric descriptions might also point out a lack of management of genetic resources in accordance with the general tendency not to invest in poultry. The present erosion of these genetic resources can be estimated in this study from the percentage of black and blue legs in the total population, which barely attains 14 percent. Erosion can thus be considered as very advanced. Summing up the frequencies of the plumage colours cited as being those of the “true Kabyle chicken” by elders, a total of 29.5 percent is obtained. While black on its own is still relatively frequent (almost 17 percent), the barred, mottled, blue and partridge phenotypes hardly reach a combined frequency of 12.7 percent.

Table 10. Gompertz growth curve parameters of local Kabyle chicken under experimental semi-intensive conditions.

Sex	Gompertz curve’s parameter			
	α (g)	β	γ (day^{-1})	T (days)
Males	2 045.30	4.320	0.0257	56.94
Females	1 532.90	4.087	0.0280	50.28

Such an observation might be misleading about the true interest of local people in their poultry genetic resources. Indeed, an important share of respondents mentioned the colour of feathers to be a case for preference of the local chicken, which denotes cultural importance for the local type. However, this preference is apparently not strong enough to neutralize economic incentives for genetic resource wastage, as described below. Answers from experienced raisers tend to show that the Kabyle chicken previously had a well-standardized phenotype with a quite restricted number of different varieties.

The reported period of change corresponds to the rapid development of industrialized poultry farms in Algeria as a result of the general process of liberalization and privatization of economic activities under the Structural Adjustment Programme imposed by the International Monetary Fund in 1994. From this time onwards a double incentive led to erosion of local poultry genetic resources. First, even in rural villages, people gained access to low-cost eggs and poultry meat, which consequently reduced incentives for keeping large flocks at home in numerous households and especially in those that had the best access to markets. Then the culled layer hens from the industrialized sector were sold on markets and used by households to get an easy and rapid increase of egg production in their own flock.

It appears from the additional survey that in the past poultry raisers implemented some selection in order to increase egg production. The rapid increase obtained by crossbreeding was further reduced incentives for improvement of local chickens. Finally, the erosion process involves externalities linked to the quasi-public good nature of animal genetics (Roosen, Fadlaoui and Bertaglia, 2005).

Indeed, a reduction in the number of households keeping the local chicken resulted in a drastic cut in the local genetic pool, realized by a decrease in the number of local poultry eggs sold for hatching in village markets, as reported by some experienced raisers in the survey. This led to reduced access to local chickens by the poorest smallholders that needed them to increase their flocks and a strong incentive for "intensification"' of their flock by introducing culled birds from industrial strains.

Performance in an experimental semi-intensive system

Egg production

The mortality rate during this study was high, which could be ascribed to the inadequacy of housing in cages for local hens. However, Benabdeljelil, Lahbabi and Bordas (2003) reported higher mortality rates in a similar experience in Morocco, rearing cross-bred Egyptian Fayoumi × Leghorn and Mandarah × ISA hens in cages (26.7 and 19.3 percent, respectively). Onset of laying occurred at 189 days. Among local breeds of the Maghreb, this appears late compared with the Mandarah hen, an Egyptian breed, which starts laying at 139 days, as well as to the Moroccan local hen, which start laying at 174 days (Raach-Moujahed *et al.*, 2011). However, the present individual production of 163 eggs per year is higher than that of the different known local breeds of the Maghreb, namely the Dandarawi (Egypt, 128 eggs/year) and the Fayoumi (Egypt, 141 eggs/year) (Raach-Moujahed *et al.*, 2011), as well as Tunisian and Moroccan local hen (127 and 78 eggs per year, respectively) (Raach-Moujahed *et al.*, 2011). The decrease of production in the second period is in accordance with the known evolution of productive performance in commercial strains. The rate of laying commonly reaches a peak and then declines until the end of the production cycle. The egg weight of over 50 g represents a very good performance compared with other local hens of the region such as the Fayoumi (42–47 g) in Egypt (Hossary and Galal, 1995; Raach-Moujahed *et al.*, 2011) or the Large Baladi (38.5 g), the Bare-Neck (39.4 g) and the Betwil (38 g) in Sudan (Mohammed *et al.*, 2005). The yolk-to-albumen ratio (52.8 percent) is high compared with commercial strains. This is a known feature of local hens, and this ratio is usually negatively correlated to egg weight (Moula *et al.*, 2010). The increase in egg weight that was observed between the two periods represented an increase of both yolk and albumen, as also reported in the literature (Hartmann *et al.*, 2000; Silversides and Budgell, 2004). Thus the yolk-to-albumen ratio did not show a statistically significant difference between periods.

Growth

The hatching rate was low, being below 70 percent, whereas rates are considered normal at 80 percent (Sonaiya and Swan, 2004). The effects on growth of age, sex and their interaction were all highly significant ($p < 0.0001$). Two different growth curves are presented for males and females (Table 10), as sexual dimorphism is a known characteristic of chicken (Pedersen *et al.*, 2003). At 16 weeks, the body weight of the Kabyle chicken was satisfactory, being superior to those reported for local chickens in Tunisia by Bessadok, Khochilef and El Gazzah (2003). The feed conversion index was high (4.97) compared with values recommended for slow-growing quality broiler such as the French "Label Rouge" (Sauveur, 1997) but were in the same range as values reported for other local breeds such as the Ardennaise chicken in Belgium (Moula *et al.*, 2009b).

Conclusion

The local poultry genetic resources of Kabylie are shown here to be undergoing serious erosion. As advocated by Anderson and Centonze (2007), collective action for the conservation of animal genetic resources is only possible where those resources are central to people's livelihoods. This importance of the Kabyle chicken is shown here to have both economic and cultural elements, and the case of the Kabyle chicken is accordingly proposed to be manageable on the condition that the identified stakeholders get effective technical and organizational support. The constitution of a breed society might be proposed in this context. On a practical side, the revival of a local chicken breed might first focus on the black phenotypes. Pure black, barred and mottled individuals should then be included in a mixed genetic pool. The blue plumage individuals might also be included in this base population, according to an inclusive strategy for genetic diversity management. Beside this first consolidation phase, objectives of the rearing system should be clarified with the stakeholders, leading to the definition of breeding goals that should govern a sustained selection effort. In this context, the opportunity for some degree of semi-intensification should be carefully considered. Such systems would need differentiated markets, which could be envisaged if the reported price premium for local products is confirmed. Indeed, chicken is notably consumed at feasts in Kabyle tradition (New Year, first day of spring) and quality products could benefit from this traditional support. The present performance of the indigenous chicken appears to be competitive with other breeds and local types of the Maghreb. However, the primary interest of the testing conditions in this study was experimental. Semi-intensification on the field should be more gradual and would possibly involve less advanced forms.

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Supporting conservation of livestock biodiversity through multidisciplinary studies: a case study of the Yakutian cattle in Siberia, the far east of Russia

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Summary

The Society for Conservation Biology has highlighted the vital importance of social sciences in animal conservation. For farm animals, their close association with humans over many centuries makes it more sensible and necessary to incorporate social sciences and humanity studies into the conservation efforts. In this review, we report a multidisciplinary study for the conservation of a unique native cattle population, the Yakutian cattle, which are the last remnants of the Turano-Mongolian *Bos taurus* cattle from Siberia, the far east of Russia. These cattle, which are well adapted to the severe climate and environmental conditions in the northeast Siberian territory, are gaining popularity as a hardy, adapted and useful genetic resource, particularly when man is facing the challenge of global climate change. However, the population is categorized by the FAO as "rare and endangered". Our multidisciplinary collaborative study has proved to be successful through animal genetics, anthropology, geography, history, sociology and bio-art, and could be applied also in developing conservation programmes for other livestock, wild animals or plants.

Keywords: *bio-art, conservation, multidisciplinary studies, Yakutian cattle*

Résumé

La Société pour la biologie de la conservation a mis l'accent sur l'importance capitale des sciences sociales dans la conservation des animaux. Pour les animaux d'élevage, en raison des relations étroites entretenues pendant plusieurs siècles avec les êtres humains, il est encore plus logique et nécessaire d'intégrer les sciences humaines et sociales au sein des initiatives concernant leur conservation. Nous présentons dans ce rapport une étude multidisciplinaire sur la conservation d'une population unique de bovins locaux, les Yakut, qui sont les derniers descendants des bovins *Bos taurus* du type Turano-Mongolian de la Sibérie, l'Extrême-Orient russe. Ces bovins, qui sont bien adaptés aux conditions climatiques et environnementales rigides du territoire nord-oriental de la Sibérie, sont de plus en plus appréciés en tant que ressources génétiques résistantes, adaptées et utiles, surtout lorsqu'on est confronté au défi du changement climatique mondial. Cependant, la FAO a classé cette population comme «rare et menacée d'extinction». Notre étude multidisciplinaire et participative s'est avérée précieuse dans les domaines de la génétique animale, de l'anthropologie, de la géographie, de l'histoire, de la sociologie et du bio-art. Elle pourrait être également appliquée à l'élaboration des programmes de conservation pour d'autres animaux d'élevage, pour les animaux sauvages et pour les plantes.

Mots-clés: *bio-art, conservation, études multidisciplinaires, bovins Yakut*

Resumen

La sociedad para la Conservación biológica ha destacado la vital importancia de las ciencias sociales en la conservación animal. La estrecha vinculación con el ser humano de los animales de granja, a lo largo de muchos siglos, hace que sea mucho más razonable y necesaria la incorporación de las ciencias sociales y los estudios de la humanidad en los esfuerzos llevados a cabo en materia de conservación. En esta revisión, se presenta un estudio multidisciplinario para la conservación de una población única de ganado bovino autóctono, el Yakutian, que representa los últimos restos del bovino Turano-Mongolian *Bos taurus* de Siberia, en el Lejano Oriente de Rusia. Estos animales, bien adaptados a climas y condiciones medioambientales extremas del territorio del noroeste de Siberia, están ganando popularidad como recurso genético resistente, adaptado y útil, sobre todo en la medida en que el hombre se enfrenta al reto del cambio climático en todo el mundo. Sin embargo, la población está clasificada por la FAO como "poco común y en peligro de extinción". Nuestro estudio de colaboración multidisciplinaria ha demostrado tener éxito por medio de la combinación de la genética animal, la antropología, la geografía, la historia, la sociología y el bio-arte, y podría

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aplicarse también en el desarrollo de programas de conservación para otro tipo de ganado, para animales salvajes y para plantas silvestres.

Palabras clave: *bio-arte, conservación, estudios multidisciplinarios, ganado bovino Yakutian*

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Introduction

Farm animals, like wild animal species, are recognized as important genetic resources in the World Conservation Strategy (International Union for the Conservation of Nature and Natural Resources, 1980). They have played significant roles in the sectors of agriculture, economy, culture and religion in earlier and current societies. Nevertheless, different from wild animal species, farm animals have been deeply affected by human interference in the history of their development, particularly because of the industrialization of animal agriculture and the rising ubiquity of a few efficient and productive breeds during the second half of the twentieth century. These have led to dramatic reduction in the population sizes of a large number of breeds and even to the extinction of many breeds (e.g. Hall and Ruane, 1993; Felius, 1995; Li *et al.*, 2007; Oldenbroek, 2007). As a result, conservation of farm animal genetic resources becomes important not only for their biological role, but also for their economic, social and cultural values (e.g. Barker, 2001; Oldenbroek, 2007). Rare and endangered breeds have a high priority in conservation programmes because the genes and gene combinations they carry may be commercially applicable in the future (Hall and Ruane, 1993).

To prevent the erosion and the loss of farm animal genetic resources, great efforts have been undertaken by various institutions at global and regional levels during the decades since the 1960s when the conservation awareness for farm animals arose (Hodges, 2002). The Society for Conservation Biology has highlighted the vital importance of both natural and social sciences in conservation activities. In conservation work, social sciences can augment the motivation for application of biological sciences in new ways, for example, by documenting the sociocultural and spiritual value of biodiversity (Mascia *et al.*, 2003). Moreover, multidisciplinary collaborative studies have been advocated as an important yet little-studied strategy for effective conservation outreach, attracting new audiences, increasing awareness, introducing new perspectives and creating a dialogue among a wide range of people (Jacobson, Mcduff and Monroe, 2006, 2007). The close association between farm animals and humans over many centuries makes it necessary to incorporate social sciences and humanities studies into the conservation efforts that have been based mainly on biological science investigations.

The Yakutian cattle are the last native cattle population remaining in Siberia, Russia and are critically endangered (Dmitriev and Ernst, 1989; FAO, 2007). In this study, we report a multidisciplinary collaboration in the conservation of this cattle breed involving biological, social and art sciences. This multidisciplinary conservation practice has provided us, as well as domestic animal conservation organizations, with many insights that will be useful in developing strategies for working with other endangered populations of livestock, wild animals or even plants.

Breed history and description

The Yakutian cattle, which are the last remaining variety of the indigenous Siberian cattle (Dmitriev and Ernst, 1989; Scherf, 2000), are a unique population of the Turano-Mongolian type of *Bos taurus* in the northern territory of the Republic of Sakha of the Russian Federation (Figure 1*a*). They were bred pure until 1929 and their recent ancestors can be traced back to Siberian cattle which had wandered and migrated over centuries with other domestic animal species and the Yakutian people. This migration was northwards from the south, probably the Cis-Baikal region, to the middle Lena basin, the lower Vilyui and Aldan as early as in the thirteenth century before finally settling down in small fragmented villages beside the Yana River (Forsyth, 1992; Puzyrev *et al.*, 2003; Granberg, Partanen and Soini, 2006). However, in the vast territory of the Yakutia (the Republic of Sakha) they have been preserved pure only at the Leninski state farm in the Verkhoyansk district (see Kantanen *et al.*, 2009a).

Owing to the industrialization and modernization of animal production during the last century, as well as the privatization of the collective production systems from the early 1990s onwards, the Yakutian cattle only had 28 bulls and 525 cows in a total population of 1 212 heads at the 2007 census (Kantanen *et al.*, 2009a). Therefore, the breed has been categorized as “endangered”, as listed by the FAO (Felius, 1995; Scherf, 2000).

The physical constitution of Yakutian cattle is strong in general, characteristic of dual-purpose (milk and meat) animals (see Figure 1*b* and *c* and Table 1). They have the typical features of the Turano-Mongolian *Bos taurus* cattle (Dmitriev and Ernst, 1989; Felius, 1995) and have high adaptation to the extreme environment and climate of the sub-arctic region. They are capable of thriving on the poor feed of fodder plants native to the northern

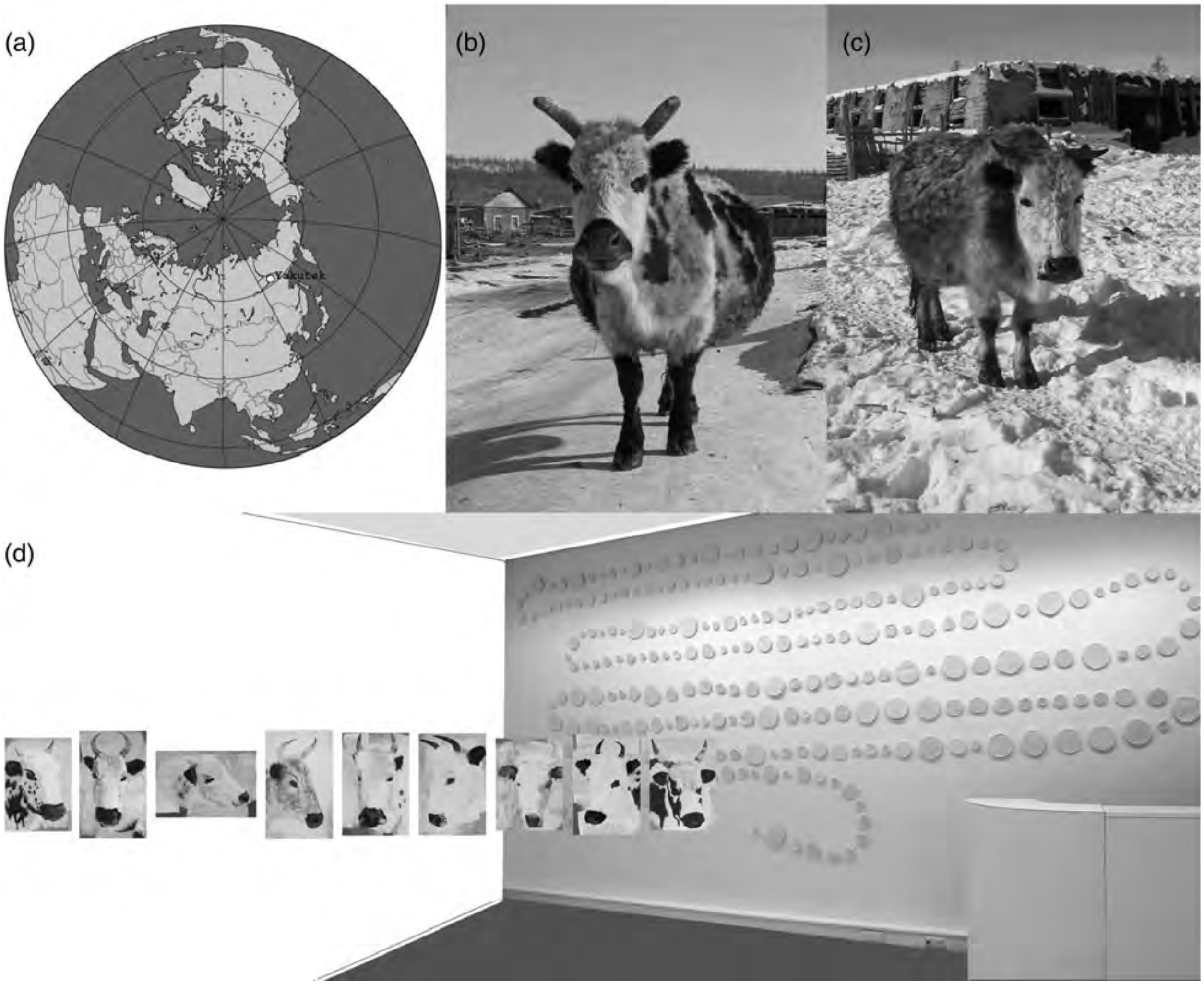

Figure 1. (a) Geographic origin of the Yakutian cattle; (b) a cow on the frozen land covered with snow, photo Anu Osva; (c) a cow standing on snow in the front of a cowshed built using manure, photo Anu Osva; (d) two artworks in the exhibition "*Yakutian Cattle – A Research Expedition to Siberia in 2000's*" by Anu Osva. Yakutian Cattle, nine portraits, 2007, oil on canvas, 60 × 55–65; Mother's Pearls, 2007, plaster, acrylic colour, about 25 m. The pearls, i.e. circles, represent nucleotides in a mitochondrial control region of the Yakutian cattle. In a multiple sequence alignment of mtDNA control region of Eurasian cattle (*Bos taurus*) breeds (see Kantanen *et al.*, 2009b), the nucleotide mutations are presented by pearls that reflect red light and the consensus nucleotides are represented by pearls that reflect green light.

environment. It has also been reported that the Yakutian cattle exhibit resistance to tuberculosis, leucosis and brucellosis (Scherf, 2000; Kantanen *et al.*, 2009a). In the northern villages of Sakha, it is not extremely unusual to find cows of more than 20 years. It is common that a Yakutian cow calves more than ten times during its life (see Kantanen *et al.*, 2009a). However, a modern dairy cow typically calves two to three times until the age of 4–5 years.

These phenotypic traits, on the one hand, resulted in a large-scale commercial crossbreeding between Yakutian cattle and imported breeds such as Khmologory and Simmental to obtain animals with both increased production efficiency and good adaptability (Li *et al.*, 2005). On the other hand, they have led to a dramatic population decrease of the native purebred Yakutian cattle (Scherf, 2000; Granberg, Partanen and Soini, 2006; Granberg, Kantanen and Soini, 2009). The factual official conservation programme, "The law to protect the genetic heritage of Yakutian cattle and use it", was initiated in the late 1990s and came into force in 2001 (Granberg, Partanen and Soini, 2006; Partanen and Kantanen, 2009). At present, a minimal viable population size for the safety of Yakutian cattle has been maintained, but many threats can be posed to their survival into the near future, and thus activities for their conservation are urgently needed.

Multidisciplinary collaborative study

Integrating social, economic and biological data into community-based conservation efforts has been urged over many years by conservationists (e.g. Western and Wright, 1994; Berkes, 2004; Chan *et al.*, 2007). Despite many efforts, this strategy has seldom been successfully practised in conservation projects because of the

Table 1. Phenotypic characteristics and adaptive traits of the Yakutian cattle.

Traits	Characteristics	Details	References
Production	Dual purpose (meat and milk); generally low milk production	(a) ca. 1000 kg of milk at 5.13% fat and 2000 kg of milk at 6.1–7.3% fat at best (b) Long productive period of even 12 years	Dmitriev and Ernst (1989), Scherf (2000), Kantanen *et al.* (2009a)
Reproductive	Long period	(a) Calve more than ten times	Dmitriev and Ernst (1989)
Adaptive	Adapted to the severe climatic and environmental conditions in the sub-arctic region	(a) Adapted to the long, dark and cold winter at the lowest −50 to 60 °C (b) Require less body maintenance energy in winter (c) Rapid growth and fattening in short summer (d) Adapted to feeding on poor quality fodder plants	Kantanen *et al.* (2009a), Granberg *et al.* (2006, 2009), Felius (1995), Kantanen (2010)
Physical constitution	Strong but small	(a) Cow: 107–115 cm in wither height and 350–400 kg in body weight (b) Bulls: on average 122 cm in height and 500–550 kg in weight (c) Deep, but rather narrow barrel and short firm legs (d) Wedge-shaped skull (e) Small and firm udders (f) The teats as well as the body are covered with thick hair (g) Multicoloured coat	Dmitriev and Ernst (1989), Scherf (2000), Felius (1995), Li *et al.* (2005, 2007)
Disease resistance	Not susceptible to diseases and maintain a healthy physical condition	(a) Tuberculosis (b) Leucosis (c) Brucellosis	Felius (1995), Li *et al.* (2005, 2007), Kantanen *et al.* (2009a)

complications of economic, social and biological perspectives, as well as the divergent philosophies and research styles of these disciplines (e.g. Terborgh and van Schaik, 2002). To our knowledge, this study on the Yakutian cattle by the Finnish research team (Granberg, Kantanen and Soini, 2009) is one of the very few interdisciplinary explorations of the dilemmas and unique solutions in the management of endangered farm animal genetic resources (see Table 2). Parallel to the genetic studies, the socio-economic and cultural values of this local breed and the demographic indicators of rural societies where the unique cattle have been traditionally raised were also investigated. In addition, earnest efforts were made to publicize the conservation value of the breed through the Bio-art exhibition, articles in newspapers and academic literature as well as the cover illustration in a scientific journal (see Table 2).

Genetic studies

By employing autosomal, mitochondrial and Y-chromosomal DNA markers, molecular and population genetic analyses identified the Yakutian cattle to be of a Near Eastern genetic origin (Li *et al.*, 2007; Kantanen *et al.*, 2009b; Li and Kantanen, 2010). Our studies presented genetic evidence for the particular patterns of the domestication process and demographic history of the breed from different genetic perspectives. Genetic distinctness of the Yakutian cattle breed has also been clearly characterized in an earlier study based on blood and milk protein polymorphism (Bannikova and Zubareva, 1995).

Social and humanities studies

In traditional societies, social and cultural aspects are closely connected to farm animal husbandry. The Yakutian cattle, which lived through the Russian transition, have witnessed the entire process of privatization of the sovkhozes and chaotic changes of agricultural structure as a whole (Granberg, Kantanen and Soini, 2009; Ovaska and Soini, 2011), and vice versa the privatization processes have largely affected the farming system of the Yakutian cattle. During the transition, the coexistence of collective and private production was the typical production type in cattle farming. The small-scale family-based production form prevailed in Yakut through the communist era. During transition such a subsidiary production relieved the shortage and poverty, and cattle production has been continued by many families as such. Also, some other families increased their cattle number in order to produce for the local market, and registered themselves as “fermers” (Russian expression for farmer) (Granberg, Kantanen and Soini, 2009; Ovaska and Soini, 2011).

In addition, the original Yakutian cattle have a major historical and ethnographic importance and are regarded as an important product of the national culture. The cattle are a living cultural heritage and property of the Yakutian people and a symbol or sign of the Yakutian history (e.g. Murdock, 1967). They are highly valued in maintaining the local traditions and retaining the people’s rituals. For example, massive slaughtering of cattle has been a

Table 2. Summary of the multidisciplinary study on conservation of the Yakutian cattle genetic resource.

Study subjects	Methods	Findings	References
Genetics	Autosomal, Y-chromosomal and mtDNA markers, blood and milk protein loci	(a) High level of intrapopulation homozygosity and interpopulation genetic differentiation from other Eurasian cattle populations (b) High number of private alleles (c) Unique Y-chromosomal haplotype and mtDNA haplogroup	Bannikova and Zubareva (1995), Li *et al.* (2005; 2007), Kantanen *et al.* (2009b), Tapio *et al.* (2010) Li and Kantanen (2010), Kantanen (2010)
Social and humanities	Farmer interview, anthropological investigation	(a) Are important in the social transition from collective or state to private enterprises in Russia (b) Contribute greatly to the maintenance of the economy in Yakut Republic (c) Have major historical and ethnographic importance (d) Are a living cultural heritage and property of the Yakutian people (e) Are a symbol or sign of Yakutian history	Murdock (1967), Puzyrev *et al.* (2003), Leete (2005), Granberg *et al.* (2006, 2009), Ovaska and Soini (2011)
Physiology and ecology	Anatomical, archaeological, geographical and field study	(a) Long intestines (b) Thicker hair coat than other cattle and thicker in winter than in summer (c) Good thermoregulation at low ambient temperatures (d) Have physical and/or chemical types of stress resistance (e) Are important in the grassland ecosystem restoration (f) Are important in the maintenance of ecological environments (g) Manure has been much valued as fertilizer in greenhouses and as insulation material for cowsheds	Ukhanov *et al.* (1990), Shumny *et al.* (1994), Popov (1996), Kushnir and Terletskiy (1997), Caro (2007), Jordan and Jordan-Bychkov (2001)
Bio-arts	Exhibition, cover pages for academic journal and book, and the media press e.g. newspaper	(a) Great aesthetic value (b) Increase public awareness about the conservation of domestic animals (c) Bring researchers and people with different backgrounds together to have a fruitful discussion	Joensuu (2007a, 2007b), Li *et al.* (2007), Granberg *et al.* (2009)

form of strong protest against the colonizers or the hegemonization of power in Yakut (Leete, 2005). The cattle are also very relevant in the legends of immigration of Yakutians to the north and have significant impact on fine arts, literature and motives of handcraft and decorations (Puzyrev *et al.*, 2003; Granberg, Kantanen and Soini, 2009).

Physiological and ecological studies

The extant Siberian fauna represents important sources for studying the influence of climatic changes on extinction of the big ice age mammals, for example, the mammoths. There is evidence that animal species in Siberia were all affected during the same period by climate changes and glacial retreat (e.g. Shumny, Kushnir and Tikhonov, 1994). There is now an opportunity, even from a global perspective, to study the ecological adaptation and the immunogenetic monitoring by investigating the contemporary animal species. Cattle, the traditional domesticated animal in Siberia, have adapted to the extreme arctic ambient conditions and are a good animal model for the studies.

The physiological characteristics of very long intestines (42 times of the length of the body) enable the Yakutian cattle to digest coarse forage. Comparative morphological and physiological investigations have revealed that the coat hair of the Yakutian cattle is on average three or four times thicker than that of the Simmental cattle and it is six times thicker in winter than in summer (see Ukhanov *et al.*, 1990). The basic mechanisms of thermoregulation at low ambient temperatures and their association with the physical and/or chemical types of stress resistance have been determined (e.g. Shumny, Kushnir and Tikhonov, 1994; Popov, 1996; Kushnir and Terletskiy, 1997). The animals can live solely on hay. Thus, the Yakutian cattle have had an important function in the past and will do so in the ongoing attempts to restore the rich grassland ecosystem and to maintain the ecological environment in Siberia (e.g. Caro, 2007). The cattle manure has been much valued as fertilizer in greenhouses and as insulation material for cowsheds (e.g. Jordan and Jordan-Bychkov, 2001; Granberg, Partanen and Soini, 2006).

Bio-arts

The work of artists is essential in the community-based conservation efforts to increase public awareness. The exhibition *Yakutian Cattle – A Research Expedition to Siberia in the 2000s* consisted of 17 artworks at the Gallery Katariina, one of the highly valued galleries in Helsinki, Finland. Afterwards the exhibition was presented in Kotka, Finland and in Stockholm, Sweden. We describe here two art works (Figure 1*d*), that is, Yakutian cattle in portraits and the construction "Mother's Pearls" on the opposite wall which is a representation of the genetic code in a specific mitochondrial DNA sequence unique to the Yakutian cattle. The portraits and "Mother's Pearls" refer to genetic history and identity of Yakutian cattle. On their faces they have it all, their genome, individual history and their moments of individual expression.

The exhibition raised questions about mankind's responsibility for domesticated animals, nature's strength and animals' adaptation to the environments. It moulds our perceptions about ourselves, and about life on the earth. It also makes us see, feel and experience the world differently. Particularly, the exhibition brought out a good discussion about the important roles of different disciplines such as genetics, ecology, physiology, humanities, aesthetics and ethics in preserving farm animals and saving biodiversity on the planet. The responses from the diverse group of visitors were overwhelmingly positive. The two articles in "*Maaseudun Tulevaisuus*" ("*The Rural Future*" in English), a newspaper with the third-largest readership in Finland, documented the exhibition and brought attention to the plight of the native cattle population more widely and with great profundity for the general public (Joensuu, 2007a, 2007b).

Besides these, the appearance of a Yakutian cow as a cover illustration of the scientific journal *Molecular Ecology* Vol. 16, No. 18 in the year of 2007 (see also http://www.blackwell-synergy.com/toc/mec/16/18) is expected to further increase the awareness about Yakutian cattle particularly among conservation biologists.

Conservation implications

We conclude by overviewing the recommendations that can be considered in the current and future conservation of the Yakutian cattle as follows:

(1) Because the population size has fluctuated widely in its history, the data that should be collected include the overall number, the number of breeding bulls and cows, number of subpopulations and trends in population size, so as to allow monitoring the changes in numbers on an ongoing basis.
(2) Since the cattle are of significant sociocultural, spiritual and anthropological value to the Yakutian people, an *in situ* conservation strategy should be prioritized with special emphasis on preserving such values.
(3) The Yakutian cattle experience suggests that the socio-diversity in terms of a coexistence of different types of public and private farms is a safeguard for farm animal biodiversity.
(4) Development of viable *ex situ* breeding programmes at a proper scale by emphasizing the phenotypic characteristics of the breed can create a long-term and sustainable conservation programme.
(5) As the production efficiency of the cattle is relatively low, added value by linking the breed maintenance with the Siberian natural or cultural tourism and farm visits can help to improve profitability and thus facilitate their conservation.
(6) An integration of Yakutian cattle conservation with conservation programmes for other species, for example, the Siberian landscape conservation and the conservation of Siberian Tiger, would be beneficial and effective.
(7) Cryopreservation of spermatozoa, oocytes and preferably embryos of animals is a viable method to conserve Yakutian cattle breed in Siberia.
(8) When kept as live animals or/and as frozen material, more than one location is needed, because natural disasters, accidents and changes in financial resources can result in instant loss of a stock, especially in Siberia (Patterson and Silversides, 2003).

Conclusions

In conclusion, this study has demonstrated the important roles of natural and social sciences and arts in conservation biology, which at its best should be an integrative and collaborative science. Our study promoted the collaboration between geneticists, social scientists/philosophers, artists and the public, and generated new opportunities for public discussion on and interaction with conservation biology. Although joint actions by arts, natural and social sciences are a new phenomenon in the conservation of farm animal resources, all the participants have been intrigued and found the collaboration beneficial. There is common agreement that interdisciplinary activities work towards better success in conservation efforts. Thus, the multidisciplinary collaborative study reported here has proven to be effective and successful. Similarly, the multidisciplinary collaborative study applied here can easily find its application in the conservation of genetic resources of other domestic animals, wild animals or even plants.

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Animal Genetic Resources, 2012, 50, 105. © Food and Agriculture Organization of the United Nations, 2012
doi:10.1017/S2078633612000045

ERRATUM

Preliminary analysis of microsatellite-based genetic diversity of goats in southern Nigeria – Erratum

M. Okpeku, S.O. Peters, M.O. Ozoje, O.A. Adebambo, B.O. Agaviezor, M.J. O'Neill and I.G. Imumorin

doi:10.1017/S207863361100035, published by Cambridge University Press, 1 December 2011

It is regretted that the originally published paper (Okpeku *et al.*, 2011) was not the authors' final amended version and contained incorrect figure captions. We apologize for this oversight and reproduce the correct figure captions here.

Figure 1. UPGMA dendrogram showing degree of diversity in Nigerian goats in southern Nigeria

Figure 2. UPGMA dendrogram showing degree of diversity among goat populations in southern Nigeria

Figure 3. West African Dwarf goat

Figure 4. Red Sokoto goat

Figure 5. Sahel goat

Reference

M. Okpeku, S.O. Peters, M.O. Ozoje, O.A. Adebambo, B.O. Agaviezor, M.J. O'Neill and I.G. Imumorin, 2011. Preliminary analysis of microsatellite-based genetic diversity of goats in southern Nigeria. *Anim. Genet. Resour.*, 49:33–41.

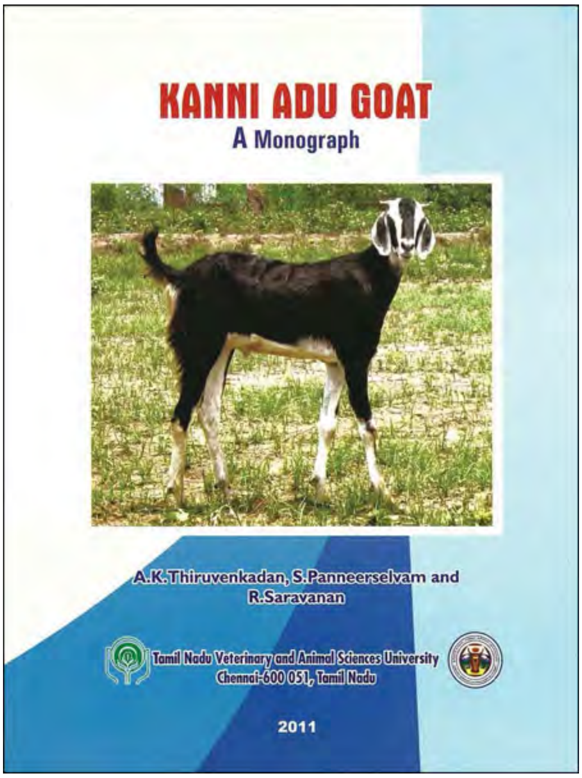
Animal Genetic Resources, 2012, 50, 107. © Food and Agriculture Organization of the United Nations, 2012

Recent Publication

Kanni Adu goat. A monograph

A.K. Thiruvenkadan, S. Panneerselvam and R. Saravanan
Tamil Nadu Veterinary and Animal Sciences University
Published in 2011, 85 pp.

doi:10.1017/S2078633612000203



The Kanni Adu goat is a meat-type goat found in southern Tamil Nadu, India. The monograph begins with a description of the Kanni Adu's breeding tract: covering topography, soil, climate, land use and vegetation. Further chapters provide descriptions of husbandry practices (feeding, housing and breeding); morphology; production and reproductive performance; cytogenetic, physiological and molecular characteristics; and mortality and disease prevalence. The authors conclude that the breed does not require immediate conservation measures, but that breed improvement programmes and other improvements to management should be considered. Options discussed include initiating an open nucleus breeding scheme, better monitoring of population trends, incentives for sustainable management, establishment of a breed society and a multi-stakeholder breed improvement committee, forage and range development programmes, training and awareness-raising on improved management practices, and improvements to marketing infrastructure.

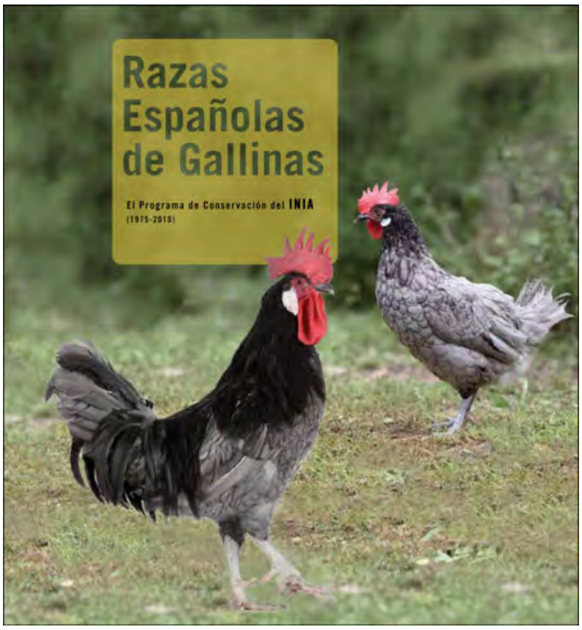
Animal Genetic Resources, 2012, 50, 108. © Food and Agriculture Organization of the United Nations, 2012

Recent Publication

Razas españolas de gallinas. El programa de conservación del INIA (1975–2010)

J.L. Campo Chavarri
Instituto Nacional de Investigación y Tecnología Agraria y Alimentaria
Published in 2010, 35 pp.
Available at www.inia.es/gcontrec/pub/CATALOGO_INIA_Gallinas_1290596384804.pdf

doi:10.1017/S2078633612000215



This publication provides an introduction to the chicken breeds included in the conservation programme of Spain's National Institute for Agricultural and Food Research and Technology. A short description of the work of the programme and its history is followed by a "catalogue" of the breeds. Information on history and origin of each breed, as well as on their phenotypic and genetic characteristics is presented. Each entry is illustrated with colour photographs showing hens, cocks and chicks.

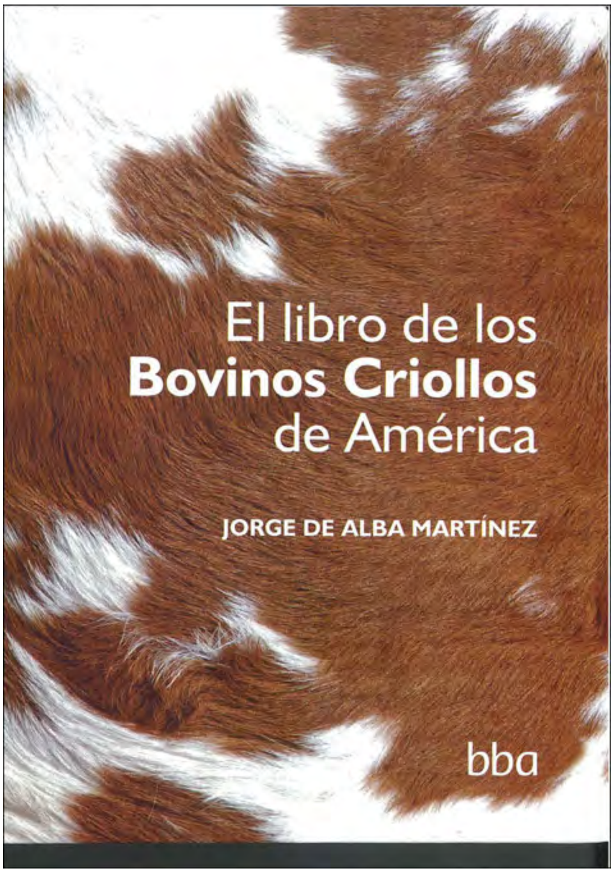
Animal Genetic Resources, 2012, 50, 109. © Food and Agriculture Organization of the United Nations, 2012

Recent Publication

El libro de los bovinos criollos de América

J. de Alba Martínez
Biblioteca Basica de Agricultura
Published in 2011, 444 pp.
ISBN: 9786077699118

doi:10.1017/S2078633612000227

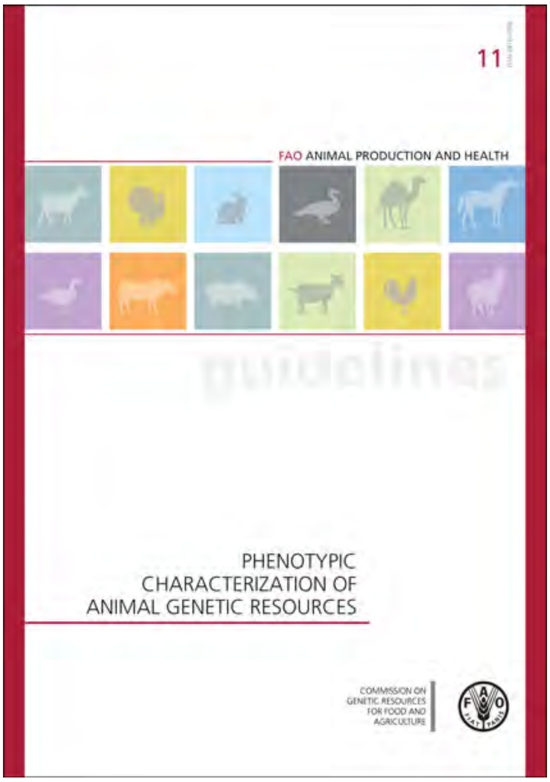


This book draws on Dr de Alba's 60 years of experience researching and promoting sustainable management of the Criollo cattle breeds of America. The story begins, more than five centuries ago, with the arrival of the continent's first cattle, brought across the Atlantic by Columbus on his second voyage to the New World. The book's first chapter describes this initial transoceanic transfer and the subsequent diffusion of cattle across the Caribbean and Central and South America. The next chapter presents a description of the many environmental challenges – including climatic extremes, parasites and high altitudes – that confronted cattle as they spread across the continent. The rest of the book features extensive descriptions of the characteristics, management and history of specific breeds or groups of breeds: the Blanco Orejinegro, tropical Criollo dairy cattle, the Romosinuano of Colombia, breeds of the Llanos grasslands of Colombia and Venezuela, Pantaneiro Criollos, Criollos of the Pampas, Criollos of the dry tropics, and Criollos of English- and Portuguese-speaking areas and of areas where Indo-American languages are spoken. In total, more than 20 breeds are described. Also included are a chapter on the physiology and genetics of lactation and another chapter that provides a detailed history of cattle in New Spain. The book is illustrated throughout with black and white photographs, and ends with an annex of colour photographs.

Animal Genetic Resources, 2012, 50, 110. © Food and Agriculture Organization of the United Nations, 2012

Recent Publication

Phenotypic characterization of animal genetic resources. Animal Production and Health Guidelines No. 11.



FAO
Published in 2012, 142 pp.
ISBN: 978-92-5-107199-1

doi:10.1017/S2078633612000239

This publication is the latest in FAO's series of guidelines prepared to support countries in their implementation of the Global Plan of Action for Animal Genetic Resources. It has been endorsed by the Commission on Genetic Resources for Food and Agriculture. It addresses Strategic Priority Area 1 of the Global Plan of Action – "Characterization, inventory and monitoring of trends and associated risks" and complements the recently published guidelines on molecular genetic characterization and on surveying and monitoring of animal genetic resources.

The objective is to provide advice on how to conduct a well-targeted and cost-effective phenotypic characterization study that contributes to the improvement of animal genetic resources management. An overview of the concepts and approaches that underpin phenotypic characterization is followed by practical guidance on planning and implementing field work, data management and data analysis. The annexes include lists of phenotypic variables for major livestock species, as well as a framework for recording data on breeds' production environments.

Animal Genetic Resources, 2012, 50, 111. © Food and Agriculture Organization of the United Nations, 2012

Recent Publication

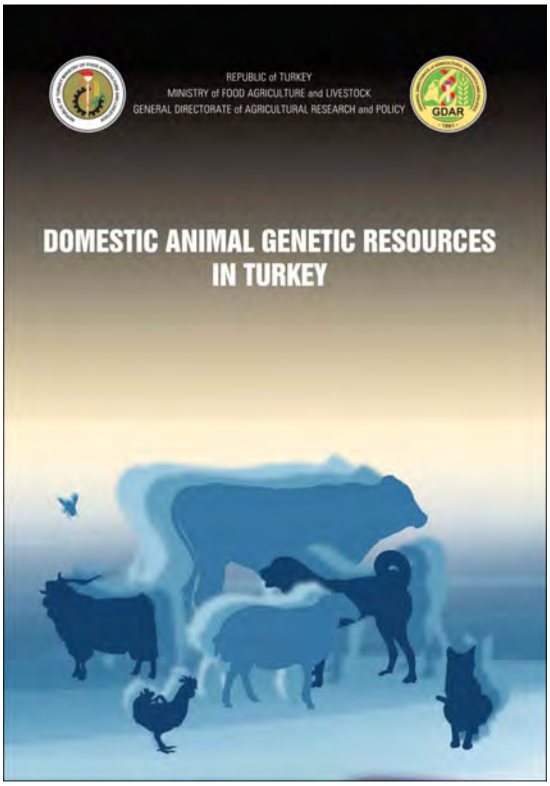
Domestic animal genetic resources in Turkey

General Directorate of Agricultural Research and Policy, Ministry of Food Agriculture and Livestock, Republic of Turkey
published in 2011, 112 pp.

Available at: http://www.tagem.gov.tr/pdf/english_AnGR.pdf (English version); http://www.tagem.gov.tr/yayin/tagem_ehgk_katalog.pdf (Turkish version)

doi:10.1017/S2078633612000240

This publication presents descriptions of Turkey's registered breeds of cattle, buffalo, sheep, goats, chickens, pigeons, rabbits, dogs, cats, bees and silkworms. For each breed, information is presented on its location within the country, main uses or purposes, appearance and other characteristics (environmental adaptations, etc.), body measurements, performance and management practices. Each entry is illustrated with a number of colour photographs. A short introductory chapter provides an overview of Turkey's work on the characterization, sustainable use and conservation of its animal genetic resources.



Animal Genetic Resources, 2012, 50, 112. © Food and Agriculture Organization of the United Nations, 2012

Recent Publication

Donner de la valeur ajoutée à la diversité du bétail: Commercialiser pour promouvoir les races locales et améliorer les moyens d'existence

LPP, LIFE Network, IUCN–WISP, FAO
Études FAO: Production et santé animales. Numéro 168
FAO
Published in 2011, 160 pp.
LPP, LIFE Network, IUCN–WISP et FAO. 2011.
Available at: http://www.fao.org/docrep/014/i1283f/i1283f.pdf

Añadiendo valor a la diversidad ganadera: Mercadotecnia para promover las razas autóctonas y los medios de subsistencia

LPP, LIFE Network, IUCN–WISP, FAO
Estudios FAO: Producción y Sanidad Animal, no. 168.
FAO
Published in 2011, 156 pp.
Available at: http://www.fao.org/docrep/014/i1283s/i1283s.pdf

doi:10.1017/S2078633612000252

Many local breeds and minor species are in decline because they cannot compete with high-yielding specialized breeds. Conserving these local breeds is important as many have unique traits, such as hardiness and disease resistance that are vital for the future of livestock production. One way to ensure the survival these breeds may be to sell their products in high-value specialized markets. This book presents eight examples of the use of such an approach. These case studies are grouped by the type of product: (i) wool and cashmere; (ii) meat and hides; and (iii) milk. They cover a range of species (Bactrian camel, dromedaries, goats, and sheep) and seven countries in Africa, Asia and Latin America. The case studies are followed by a final section that analyses lessons learned. It shows how livestock-keeping communities have kept local breeds in use, while enabling the people who raise them to improve their livelihood.

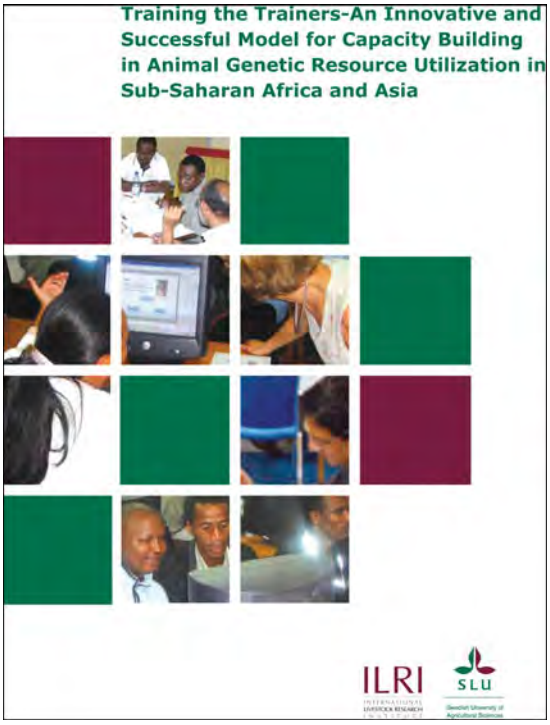
Although local breeds are suited to supplying niche markets – because of cultural factors and the unique characteristics of their products – some of these specificities (e.g. coloured wool) may hinder access to global mass markets. Such products need market development, diversification, market penetration and product development. The case studies describe various types of intervention that contribute to the addition of value – animal production, processing, and organizing and building value chains – with the main focus on processing and building value chains. The majority of the initiatives described involved a champion – a person or organization with a special interest in promoting the enterprise and making sure it worked. The book provides recommendations for those who are already in this business or who want to become involved. It makes nice reading with high degree of practicability.

Recent Publication

Training the trainers – an innovative and successful model for capacity building in animal genetic resource utilization in sub-Saharan Africa and Asia

J.M.K. Ojango, B. Malmfors, O. Mwai and J. Philipsson
International Livestock Research Institute
Published in 2011, 44 pp.
ISBN: 92-9146-271-3
Available at: http://cgspace.cgiar.org/bitstream/handle/10568/16393/ILRI_SLU_Report.pdfsequence=7

doi:10.1017/S2078633612000264



This report presents the activities and achievements of the project "Capacity Building for Sustainable Use of Animal Genetic Resources in Developing Countries", which was launched in 1999 by the International Livestock Research Institute (ILRI) in collaboration with the Swedish University of Agricultural Sciences and supported by the Swedish International Development Cooperation Agency (Sida). The project was based on a novel approach referred to as "training the trainers" primarily targeting university lecturers and researchers in developing countries who are actively involved in teaching and supervising research in animal breeding and genetics, the intention being that these individuals would reach out to a large number of students and colleagues in their home institutions.

The report presents the background and objectives of the project and details the main activities, including the planning phase (questionnaires, country visits and workshop), the organization of training courses and the development of a computer-based training resource on animal genetic resources (available at http://AGTR.ilri.cgiar.org and on CD from ILRI), and follow-up activities (questionnaires and workshops). A further section describes the outputs of the project, grouped according to their alignment with the agendas of the Consultative Group on International Agricultural Research, National Agricultural Research Systems and FAO. Short statements from some participants describing their experiences are also included. Finally, key lessons are summarized along with recommendations for future action.

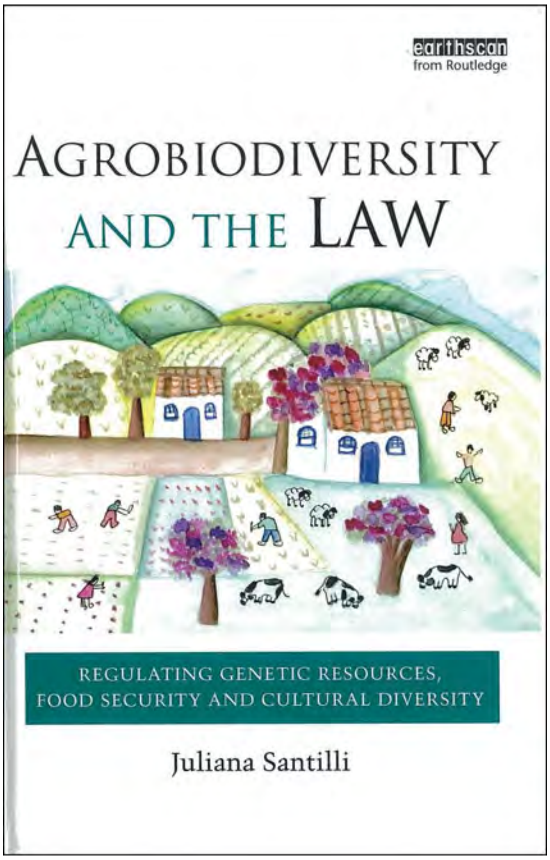
Animal Genetic Resources, 2012, 50, 114. © Food and Agriculture Organization of the United Nations, 2012

Recent Publication

Agrobiodiversity and the law

J. Santilli
Earthscan
Published in 2012, 348 pp.
ISBN: 978-1-84971-372-6 (hardback)
ISBN: 978-0-203-15525-7 (ebook)

doi:10.1017/S2078633612000276



This publication addresses the effects of national and international legal instruments on the management of agrobiodiversity. It begins by discussing the scope and definition of agrobiodiversity, concluding that it remains a "concept under construction". Chapters on food security and sustainability and on climate change, highlight the importance of agrobiodiversity to livelihoods and human wellbeing both currently and in the future. These scene-setting chapters are followed by a discussion of seed laws, featuring a number of examples from Latin American countries and Europe. A further chapter is dedicated to the UPOV system for the protection of intellectual property rights over plant varieties. This is followed by discussions of the international regime for access and benefit sharing in the plant genetic resources sector, options for the implementation of the International Treaty on Plant Genetic Resources for Food and Agriculture at the National level, and the issue of farmers' rights. Animal genetic resources then have their own dedicated chapter. After noting that there is generally very little awareness among policy makers on the importance of conserving livestock genetic diversity, this chapter provides an overview of the roles and values of animal genetic resources, their risk status and the threats they face. It also summarizes the main findings of FAO's report on 'The State of the World's Animal Genetic Resources for Food and Agriculture' and of various recent studies on the legal framework for the management of animal genetic resources. It concludes with a discussion on the issue of livestock keepers' rights. Returning to the wider field of agrobiodiversity, the book ends with chapters on the open source software movement, cultural heritage law, protected areas and geographical indications.

Animal Genetic Resources, 2012, 50, 115–116. © Food and Agriculture Organization of the United Nations, 2012

Recent Publication

The land we graze: a synthesis of case studies about how pastoralists' organizations defend their land rights

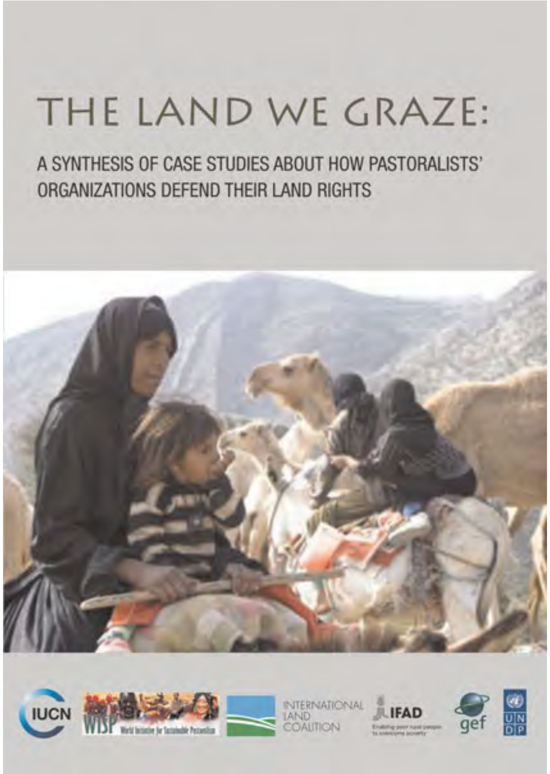
International Union for Conservation of Nature – Eastern and Southern Africa Regional Office
Published in 2011, 48 pp.
ISBN: 978-2-8317-1344-1
Available at: http://cmsdata.iucn.org/downloads/land_rights_publication_english_web.pdf (English version); http://cmsdata.iucn.org/downloads/land_rights_publication_french_web_version.pdf (French version); http://cmsdata.iucn.org/downloads/land_rights_publication_spanish_web_version.pdf (Spanish version)

doi:10.1017/S2078633612000288

This report, based on 21 case studies from 17 countries in four continents, aims at identifying elements that contribute to the success of pastoralists' in their efforts to secure land rights and resources. It begins by presenting an overview of the specific characteristics of pastoral land tenure. The case studies are then introduced, starting with a description of the political, legal and institutional settings, and how these have changed in recent years. Key issues

NOS TERRES DE PATURAGE:

UNE SYNTHESE D'ETUDES DE CAS SUR COMMENT LES ORGANISATIONS PASTORALES DEFENDENT LEURS DROITS FONCIERS



THE LAND WE GRAZE:

A SYNTHESIS OF CASE STUDIES ABOUT HOW PASTORALISTS' ORGANIZATIONS DEFEND THEIR LAND RIGHTS

LA TIERRA QUE PACEMOS:

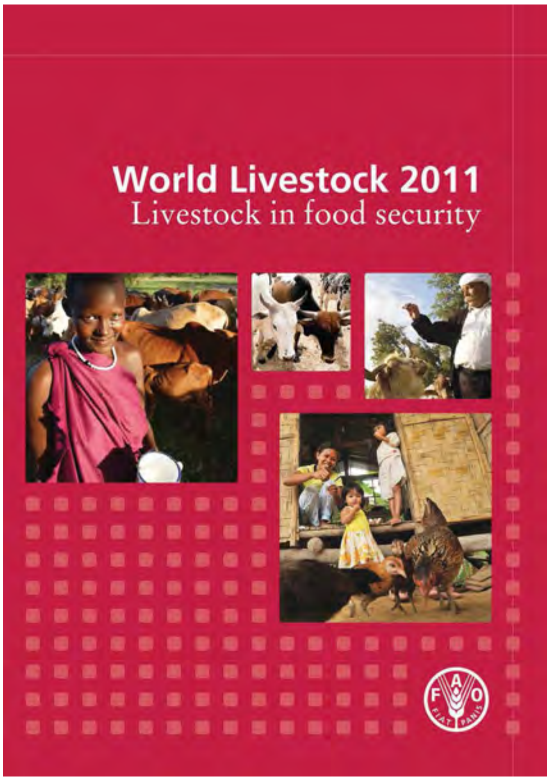
UNA SÍNTESIS DE CASOS DE ESTUDIO SOBRE CÓMO DEFIENDEN LAS ORGANIZACIONES DE PASTORES SUS DERECHOS SOBRE LA TIERRA such as competition for resources, marginalization of pastoral groups, inequality and discrimination within pastoral groups and legal issues (lack of legislation on pastoral land rights, tensions between formal and customary law, and problems in the implementation of existing laws) are summarized. The objectives of the study were to answer the following questions:

1. What are the rules, conditions and formalities that define access to the resources?
2. Who is making decisions on their management?
3. Who has control over land and use rights?
4. Are there commonalities regarding the policies on pastoralist land use and difficulties and conflicts pastoralists are confronted with?

These questions are addressed in an analytical section that focuses on law and institutions, property rights, political and economic development. The success stories of how pastoralists have been able (partially or fully) to improve the recognition and assertion of their rights are then presented. Basic elements underpinning success are identified and described (education, capacity building, awareness; participation, representation and organization; networking and cooperation, etc.). This is followed by a discussion on the processes of asserting rights (legal claims and advocacy) and of formalizing pastoral rights and institutions. Finally, a number of recommendations are put forward. The intended target audience is broad, and includes pastoralists themselves and their organizations, civil society organizations, policy-makers and governmental agencies.

Animal Genetic Resources, 2012, 50, 117. © Food and Agriculture Organization of the United Nations, 2012

Recent Publication



World livestock 2011. Livestock in food security

A. McLeod (ed.)
FAO
Published in 2011, 115 pp.
ISBN: 978-92-5-107013-0
Available at: http://www.fao.org/docrep/014/i2373e/i2373e00.htm

doi:10.1017/S207863361200029X

This book aims at providing a more comprehensive description of livestock's role in global food security than has been presented in any previous publication. It addresses the topic from three perspectives: first, the overall role of livestock in human nutrition and food supply; second, examples of the contribution of livestock to food security in three different human populations; and third, prospects for meeting future demand for livestock products. The first chapter begins with discussions of how food security is defined and measured, the role of livestock-derived food in the human diet, trends in food supplies, the roles of livestock in crop production (draught power and manure), livestock and the "food balance" (amount of livestock-derived protein produced relative to the amount of human edible protein used in its production) and livestock, and the stability of the food supply (livestock's role as a buffer against shocks to food production systems, including disruptions associated with climate change). The book recognizes that food security involves not only food production but also ensuring access to food for all. It therefore examines the various means by which livestock increase their owners' ability to access food via the provision of different kinds of "capital" – financial (providing cash income), human (providing means to meet educational and medical needs) and social (building networks and relationships that can be drawn upon in times of need). Further subsections deal with gender aspects of access to food, economic factors affecting choice of livestock-source foods and the role of marketing. The human populations that provide the focus for the second chapter of the book are "livestock dependent societies" (with Mongolia as a case study), small-scale mixed farmers (with a case study from Nepal) and city populations. The final chapter addresses both the question of how to produce enough food (including an assessment of future demand and a discussion on how to reduce waste) and the need to build resilience into livestock production systems. Animal genetic resources issues are acknowledged both in the discussion of niche market production as a potential source of income for small-scale livestock keepers and with regard to the need for animals that are able to cope with future challenges such as climate change and pressures on feed supplies.

Animal Genetic Resources, 2012, 50, 119–121. © Food and Agriculture Organization of the United Nations, 2012
doi:10.1017/S2078633612000306

Instructions for contributors

Animal Genetic Resources is a trilingual journal, published three times per year online (http://journals.cambridge.org/AGR) and in print. Main papers are published in English, French or Spanish, with a summary in all three languages. The journal has been published since 1983, and all back issues are available at http://dad.fao.org/cgi-bin/EfabisWeb.cgi?sid=−1,refcat_50000044.

The journal encourages submissions from all over the world. Authors who are not fluent in any of the three accepted languages are encouraged to seek assistance in this regard before submitting their manuscripts.

Mission statement

The journal provides an international forum for the publication of papers related to the management of animal genetic resources for food and agriculture (AnGR). It covers the following areas: phenotypic and molecular characterization; surveying and monitoring; development (genetic improvement); sustainable use; conservation; capacity-building in livestock keeper and pastoralist communities; and policies and institutions.

The editors welcome all papers addressing the topics above. Papers related to breeds and technologies contributing to the sustainable management of the world's medium-to-low input production systems, which account for the largest area of land involved in livestock production and for a major part of production from livestock, are of a particular interest.

The journal supports the implementation of the Global Plan of Action for Animal Genetic Resources, the internationally agreed framework for the management of AnGR and the Convention on Biological Diversity.

Disclaimer

Views expressed in the papers published in Animal Genetic Resources represent the opinions of the author(s) and do not necessarily reflect the policies of FAO or the views of the editors or the institutions with which the authors are affiliated.

Peer review

Manuscripts submitted for publication in Animal Genetic Resources undergo full peer review by two referees. The suitability of manuscripts is judged by the reviewers and editors, and the editors' decision on a paper is final.

Categories of papers

Research papers – Findings of work related to the management of AnGR will be considered for publication in AGRI. Authors are encouraged to include relevant high-quality photographs in their manuscripts. If photographs illustrate animals, they should be shown in the primary production environment to which they are adapted.

Review papers – Unsolicited papers reviewing country-level, regional or global developments in one or more aspects of AnGR management will be considered for publication. These papers may include state-of-the-art reviews of specific fields in AnGR management.

Position papers – Invited papers on topical issues will be published when the editors consider there to be such a requirement.

Other published material – Readers are encouraged to send the following items by e-mail to AnGR-Journal@fao.org:

- book reviews or proposals
- conclusions and recommendations arising from relevant meetings, workshops and conferences
- announcements of training courses and major national, regional and international events

Originality and copyright

To be considered for publication in the journal, a manuscript must not have been published previously, nor be under review for publication elsewhere. (Previously published figures may be used sparingly in reviews, provided that permission has been obtained as appropriate.) Prior to publication, an authorization and copyright transfer agreement form must be signed and returned to the publishers by the lead or corresponding author of a manuscript (corresponding authors sign on behalf of any co-authors). The form will be sent to the lead or corresponding author together with the proof of the paper for publication.

Authorship

Papers with multiple authors are reviewed with the assumption that all authors have contributed materially to the research reported, have approved the submitted manuscript, and concur with its submission. A contribution includes the conception and design of the project, the performance of experiments and/or the analysis and interpretation of data. Authors should have made a substantial intellectual contribution to the drafting or critical revision of the manuscript.

Manuscript submission

All manuscripts must be submitted online at http://journals.cambridge.org/AGR. No page charges are required from the author.

Receipt of your manuscript will be acknowledged, a manuscript reference number assigned and the manuscript will be sent out for review. You should quote your manuscript reference number in all subsequent correspondence.

The following instructions must be followed carefully (see *Manuscript preparation and style* for further details):

- Manuscripts may be submitted in English, French or Spanish. If your manuscript is written in French or Spanish, it should include a summary and keywords in that language as well as in English. All published articles will feature a summary in English, French and Spanish. It would be appreciated if, wherever possible, authors could supply a summary in all three languages, as this reduces the need for translating services and therefore expedites processing of the manuscript.
- The preferred file format for submission is Microsoft Word. Word Perfect or other word-processor files are not acceptable. Tables should be included within the same file but at the end of the document. Placeholders should be used within the text to indicate their positioning.
- Figures must be submitted as separate files, and at to-be-published resolution (see Manuscript preparation and style for further details).
- A cover letter should be provided as a separate file. The letter should indicate the category under which the manuscript is submitted (see Appendix 1) and provide the details of the corresponding author (telephone number, fax number and e-mail address).
- Filenames should indicate the name of the first author of the paper, either in full or abbreviated.
- Printed copies of the manuscript, tables and figures are not required and should not be sent.

Please note that correspondence regarding submitted and revised manuscripts will take place with the corresponding author only.

Manuscript preparation and style

The manuscript should be formatted with line spacing set to "double". Pages should be numbered sequentially beginning with the title page. Margins should be at least 2.5 cm on all sides. The font should be set to Arial.

Authors and affiliations – Names and affiliations of authors should be presented as follows:

E.C. Quispe[1], T.C. Rodríguez[2], L.R. Iñiguez[3] and J.P. Mueller[4]

[1]Universidad Nacional de Huancavelica, Huancavelica, Perú; [2]Universidad Mayor de San Andrés, La Paz, Bolivia; [3]Cochabamba, Bolivia; [4]Instituto Nacional de Tecnología Agropecuaria, Bariloche, Argentina

Correspondence to: E.C. Quispe, Universidad Nacional de Huancavelica, Huancavelica, Perú. E-mail: edgarquispe62@yahoo.com

A ***Running Head*** of up to 50 characters should be provided on the title page.

The ***Summary*** should be unstructured (i.e., no sub-headings) but must provide the reader with a self-contained summary of the paper. It should include a brief introduction to the paper, the method, the key findings and the conclusions. The summary should be no longer than 210 words in English and 250 words in French and Spanish. A list of three to five keywords or terms for indexing should follow the summary and be separated by commas. The summary and keywords should be provided in the same language as the manuscript as well as in English.

The ***Body of the manuscript*** should begin on page 3 and a new page should be used for the References. The lines of text must be numbered and the manuscript structured with consecutively numbered headers and sub-headers (e.g. 1., 1.1, 1.1.1 etc). However, it is important to *avoid cross-referencing using these numbers*, as the editorial office will remove numbering and apply heading styles in the final version.

Research papers should additionally include the following headers: ***Materials and Methods***; ***Results***; ***Discussion***; ***Conclusions***.

The ***Maximum length*** of the body of the manuscript should not exceed 10 journal pages (approx. 8 500 words). Short communications should not exceed 1 journal page (approx. 750 words or, when an image is included, 550 words).

Tables should be numbered consecutively as they are cited in the text (Table 1, 2 etc.). Each table should be on a separate page (at the end of the document) with the number and heading above and any notes below the table.

Figures should be numbered consecutively as they are cited in the text (Figure 1, 2, etc). Use italic letters for parts a, b, c, etc. Legends must be provided for each figure. If applicable, figures should be supplied as either TIFF or EPS files, preferably at the approximate size in which they are to be reproduced. Line artwork should be supplied in black and white mode at a resolution of 1 200 dpi; combination artwork (line/tone) at a resolution of 800 dpi; black and white halftone artwork should be saved in "grayscale" mode at a resolution of 300 dpi; colour halftone artwork should be saved in CMYK mode at a resolution of 400 dpi. All necessary permissions must be obtained.

Abbreviations and SI units – The use of abbreviations, except those that are widely used, is strongly discouraged. They should be used only if they improve comprehension of the manuscript. Acronyms should be spelled out at first mention. Metric system (SI) units should be used.

Acknowledgements

In this section authors should acknowledge any support from granting agencies and other sources for the work reported in their paper. The contribution of individuals who assisted with the research but are not included as authors of the paper may also be acknowledged in this section.

The Acknowledgements should be placed after the main body of the text before the references. If there are no Acknowledgements, the title should be inserted followed by "None".

Statement of interest

A conflict of interest exists when an author has interests that might inappropriately influence his or her judgement, even if that judgement is not influenced. Because of this, authors must disclose potentially conflicting interests so that others can make judgements about such effects. At the time of manuscript submission, authors should disclose any financial arrangements or connections they may have that are pertinent to the submitted manuscript and that may be perceived as potentially biasing their paper. Non-financial interests that could be relevant in this context should also be disclosed. If no relevant interests exist, this should be stated. This requirement applies to all the authors of a paper and to all categories of papers.

References

Every reference cited in the text should be included in the reference list and every entry in the reference list should have been mentioned in the text at least once. References should be ordered first alphabetically by the first author's surname, and then by year.

Examples:

1 *Reference in a periodical*:
    Köhler-Rollefson, I. 1992. The camel breeds of India in social and historical perspective. *Animal Genetic Resources Information* 10: 53–64.
2 *When there is more than one author*:
    Matos, C.A.P., Thomas, D.L., Gianola, D., Tempelman, R.J. & Young, L.D. 1997. Genetic analysis of discrete reproductive traits in sheep using linear and non-linear models: 1. Estimation of genetic parameters, *Journal of Animal Science* 75: 76–87.
3 *For a book or an* ad hoc *publication, e.g., reports, theses*:
    FAO, 2007. Global Plan of Action for Animal Genetic Resources and the Interlaken Declaration. Food and Agriculture Organization of the United Nations, Rome, Italy (available at http://www.fao.org/docrep/010/a1404e/a1404e00.htm).
    van der Werf, J., Graser, H-U., Frankham, R. & Gondro, C. (eds.) 2009. Adaptation and fitness in animal populations. evolutionary and breeding perspectives on genetic resources management. Springer.
4 *For an article in the proceedings of a meeting*:
    Abad, M., Arrigo, J., Gibbons, A., Lanari, M.R., Morris, G. & Taddeo, H. 2002. Breeding scheme for Angora goat production in North Patagonia. Proceedings 7th World Congress on Genetics Applied to Livestock Production, 19-23 August 2002, Montpellier, France, 12–14.
5 *Information hosted on a web site*:
    FAO. 2010. Domestic Animal Diversity Information System, http://www.fao.org/dad-is/, Food and Agriculture Organization of the United Nations, Rome, Italy.

For a work that has been accepted for publication but not yet published, "In press" should be written in place of the year of publication. Do not insert an expected year of publication.

Supplementary online material

The online platform gives authors the opportunity to include data that would be impossible or impractical to include in the printed version. Authors may include tables and figures as well as data such as videos, 3-D structures/images, extensive datasets and any other supplementary material not suitable for print duplication. All supplementary material must be submitted with the original manuscript. Supplementary data should be referred to in the text with the prefix "S" (e.g. Supplementary Table S1, Supplementary Figure S1). Supplementary files will not be copyedited but will be published as supplied. The electronic publication of this material needs to be approved by the editors. The manuscript must be able to stand alone without the supplementary material (for the benefit of readers with access to the hard copy only).

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Manuscripts submitted to the journal will be reviewed by two external reviewers and evaluated by one of the editors. If the editors deem that a paper is not relevant for this journal or is unlikely to be reviewed favourably, it may be returned to the author after initial review by the editors. This rapid rejection process enables the author to submit the work promptly for publication elsewhere. Manuscripts may also be rejected by the editors if they do not comply with the recommendations for preparation of manuscripts. Every effort will be made to provide authors with a review decision within six weeks of receipt of the manuscript. If the editors request revisions to a manuscript before publication, a maximum of one month shall be allowed for such revisions to be implemented.

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The publisher reserves the right to copyedit manuscripts to ensure that grammar and spelling are consistent with the style of the journal. The corresponding author will receive page proofs for final proofreading. These should be checked and returned within two days of receipt. The publisher reserves the right to charge authors for excessive correction of non-typographical errors.

Animal Genetic Resources, 2012, 50, 123–125. © Food and Agriculture Organization of the United Nations, 2012
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Instructions pour les auteurs

Animal Genetic Resources/Resources génétiques animales/ Recursos genéticos animales est un journal trilingue, publié trois fois par an en ligne (http://journals.cambridge.org/AGR) et en version imprimée. Les articles principaux sont publiés en anglais, français ou espagnol avec un résumé dans les trois langues. Le journal est publié depuis 1983 et tous les anciens numéros sont disponibles à l'adresse électronique http://dad.fao.org/cgi-bin/EfabisWeb.cgi?sid=-1,refcat_50000044.

On encourage la présentation d'articles provenant du monde entier à publier dans le journal. Les auteurs qui ne parlent aucune des trois langues admises sont encouragés à chercher de l'aide à cet égard avant de présenter leurs manuscrits.

Déclaration de mission

Le journal fait office de forum international pour la publication d'articles concernant la gestion des ressources zoogénétiques pour l'alimentation et l'agriculture. Il aborde en particulier les thèmes suivants: la caractérisation phénotypique et moléculaire; les enquêtes et le suivi; la mise en valeur (amélioration génétique); l'utilisation durable; la conservation; le renforcement des capacités au sein des communautés d'éleveurs et de pasteurs; et les politiques et les institutions.

Les éditeurs accueillent favorablement tous les articles abordant les thèmes indiqués ci-dessus. Un intérêt particulier sera attribué aux articles concernant les races et les technologies en faveur de la gestion durable des systèmes de production extensive ou semi-intensive dans le monde, qui représentent la plus grande partie des terres consacrées à l'élevage et une partie considérable de la production provenant de l'élevage.

Le journal soutient la mise en œuvre du Plan d'action mondial pour les ressources zoogénétiques, le cadre internationalement convenu en matière de gestion des ressources animales et la Convention sur la diversité biologique.

Déni de responsabilité

Les opinions exprimées dans les articles publiés dans Animal Genetic Resources/Resources génétiques animales/Recursos genéticos animales sont celles du/des auteur(s) et ne reflètent pas nécessairement les politiques de la FAO ou les opinions des éditeurs ou des institutions pour lesquelles ils travaillent.

Révision par les pairs

Deux experts s'occuperont de la révision complète des manuscrits présentés pour la publication dans Animal Genetic Resources/Resources génétiques animales/Recursos genéticos animales. L'opportunité ou non de publier un manuscrit sera jugée par les réviseurs et par les éditeurs, et la décision finale sur l'article appartient aux éditeurs.

Types d'articles

Articles de recherche – Seront prises en considération pour leur publication sur AGR les études sur la gestion des ressources animales. On encourage les auteurs à envoyer des photographies de haute qualité avec les manuscrits. S'il s'agit de photographies d'animaux, il faudra montrer les races en question dans leur milieu naturel de production.

Révisions – Occasionnellement, des articles contenant une révision aux niveaux national, régional ou mondial des développements d'un ou de plusieurs aspects se rapportant à la gestion des ressources animales seront pris en considération. Ces articles pourront inclure les mises à jour des différents domaines de la gestion des ressources animales.

Articles spécifiques – Ponctuellement, des articles sur des thèmes spécifiques pourront être demandés pour la publication lorsque les éditeurs le jugeront nécessaire.

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- la révision ou la proposition de livres
- les conclusions et les recommandations résultant de réunions, d'ateliers et de conférences importants
- les informations sur des cours de formation et sur les principaux événements régionaux, nationaux et internationaux.

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Pour que le manuscrit soit considéré pour la publication dans le journal, il faut qu'il n'ait pas été publié auparavant, ni qu'il soit en cours de révision pour la publication dans d'autres ouvrages. (Les chiffres publiés auparavant peuvent s'utiliser avec parcimonie dans les révisions, à condition d'en avoir obtenu l'autorisation.) Avant la publication, il faut que l'auteur principal du manuscrit signe et renvoie aux éditeurs le formulaire d'autorisation et d'accord de transfert des droits d'auteur (les auteurs principaux signent au nom de tous les co-auteurs). Le formulaire sera envoyé à l'auteur principal avec l'épreuve de l'article pour la publication.

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Les articles écrits par plusieurs auteurs sont révisés en présumant que tous les auteurs ont matériellement participé à la recherche signalée, ont approuvé le manuscrit présenté et approuvent sa présentation. Leur contribution comprend la conception et la création du projet, la performance d'expériences et/ ou l'analyse et l'interprétation des données. Les auteurs devront avoir apporté une contribution intellectuelle considérable à la rédaction et à la révision critique du manuscrit.

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- Le format de fichier préféré pour la présentation est Microsoft Word. Word Perfect ou d'autres fichiers de traitement de texte ne sont pas acceptés. Les tableaux seront inclus au même fichier, mais à la fin du document. Les paramètres fictifs seront utilisés dans le texte pour indiquer leur positionnement.
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- Les fichiers indiqueront le nom de l'auteur principal de l'article, soit en entier soit abrégé.
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Les manuscrits se présenteront à «double» interligne. Toutes les pages seront numérotées à commencer de la page du titre. Les marges seront d'au moins 2,5 cm pour tous les côtés. La police de caractère sera Arial.

Auteurs et institutions pour lesquelles ils travaillent – Les noms des auteurs et les institutions pour lesquelles ils travaillent se présenteront comme indiqué ci-après:

E.C. Quispe[1], T.C. Rodríguez[2], L.R. Iñiguez[3] et J.P. Mueller[4]

[1]Universidad Nacional de Huancavelica, Huancavelica, Perú; [2]Universidad Mayor de San Andrés, La Paz, Bolivia; [3]Cochabamba, Bolivia; [4]Instituto Nacional de Tecnología Agropecuaria, Bariloche, Argentina

Correspondance à envoyer à: E.C. Quispe, Universidad Nacional de Huancavelica, Huancavelica, Perú. Adresse électronique: edgarquispe62@yahoo.com

Sur la première page du manuscrit, on indiquera le ***titre de l'article*** qui ne devra pas dépasser les 50 caractères.

Le ***résumé*** ne sera pas structuré (c'est-à-dire, sans sous-titres), mais devra fournir au lecteur une brève description de l'article. Il inclura une introduction succincte à l'article, la méthode utilisée, les résultats principaux et les conclusions. Le résumé ne dépassera pas les 210 mots en anglais et les 250 mots en français et en espagnol. Une liste de mots clés ou de termes (entre trois et cinq) pour le sommaire suivra le résumé et les mots-clés seront séparés par des virgules. Le résumé et les mots-clés se présenteront dans la même langue du manuscrit ainsi qu'en anglais.

Le ***corps du manuscrit*** commencera à la page 3 et une nouvelle page sera utilisée pour les références. Les lignes du texte seront numérotées, le manuscrit sera structuré et tous les titres et les sous-titres seront numérotés (par exemple, 1, 1.1, 1.1.1, etc.). Il est toutefois important *d'éviter les références croisées avec ces numéros* car le bureau d'édition enlèvera la numérotation et appliquera des styles de titre dans la version finale.

Les articles de recherche devront en outre inclure les titres suivants: ***Matériels et méthodes; Résultats; Débat; Conclusions.***

La ***longueur maximale*** du corps du manuscrit ne dépassera pas les 10 pages du journal (environ 8 500 mots). Les communications brèves ne dépasseront pas 1 page (environ 750 mots ou, s'il y a également une image, 550 mots).

Les ***tableaux*** seront tous numérotés en suivant l'ordre d'apparition dans le texte (tableau 1, 2 etc.). Chaque tableau sera sur une page séparée (à la fin du document) avec le numéro et le titre au-dessus du tableau et d'éventuelles notes au-dessous.

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Abréviations et unités SI – L'utilisation des abréviations, à part celles qui sont largement employées, est vivement déconseillée. Elles ne seront utilisées que si elles améliorent la compréhension du manuscrit. Les sigles s'écriront en entier la première fois qu'elles sont employées. Il faudra utiliser les unités du système métrique (SI).

Remerciements

Dans cette section, les auteurs remercieront pour tout appui reçu des institutions et d'autres sources de soutien pour le travail inscrit dans leur article. On peut ajouter également dans cette section la contribution d'autres particuliers ayant aidé dans le travail de recherche, mais n'étant pas inclus en tant qu'auteurs.

Les remerciements seront placés après le corps principal du texte avant les références. En cas d'absence de remerciements, le titre sera toutefois écrit et suivi par l'indication «aucun remerciement».

Déclaration d'intérêts

On est en présence d'un conflit d'intérêts lorsqu'un auteur a des intérêts qui pourraient influencer de façon inappropriée son jugement, même si ce jugement n'est pas en fait influencé. Pour cette raison, les auteurs doivent révéler les conflits d'intérêts potentiels pour que d'autres puissent juger de ces effets. Au moment de la présentation du manuscrit, les auteurs révéleront tout arrangement ou rapport financier pertinent avec le manuscrit présenté et qui pourrait être perçu comme pouvant porter un préjudice potentiel à l'article. Les auteurs révéleront également les intérêts non financiers qui pourraient être pertinents dans ce contexte. Il faudra également déclarer l'absence d'intérêts pertinents. Cette obligation s'applique à tous les auteurs d'un article et à toutes les catégories d'articles.

Références

Toute référence présente dans le texte devra apparaître sur la liste des références, et chaque entrée de la liste aura été citée au moins une fois dans le texte. Les références iront en ordre alphabétique du nom de l'auteur, suivi de l'année.

Exemples:

1 *Référence sur une revue:*
   Köhler-Rollefson, I. 1992. The camel breeds of India in social and historical perspective. *Animal Genetic Resources Information* 10: 53–64.

2 *Lorsqu'il s'agit de plus d'un auteur*:
   Matos, C.A.P., Thomas, D.L., Gianola, D., Tempelman, R. J. et Young, L.D. 1997. Genetic analysis of discrete reproductive traits in sheep using linear and non-linear models: 1. Estimation of genetic parameters, *Journal of Animal Science* 75: 76–87.

3 *Dans le cas d'un livre ou d'une publication ad hoc, par exemple, un rapport, une thèse:*
   FAO, 2007. Plan mondial d'action pour les ressources zoogénétiques et la Déclaration d'Interlaken. Organisation des Nations Unies pour l'alimentation et l'agriculture, Rome, Italie (disponible à l'adresse électronique http://www.fao.org/docrep/010/a1404f/a1404f00.htm).
   van der Werf, J., Graser, H-U., Frankham, R. et Gondro, C. (éds.) 2009. Adaptation and fitness in animal populations. Evolutionary and breeding perspectives on genetic resources management. Springer.

4 *S'il s'agit d'un acte d'une réunion*:
   Abad, M., Arrigo, J., Gibbons, A., Lanari, M.R., Morris, G. et Taddeo, H. 2002. Breeding scheme for Angora goat production in North Patagonia. Actes du Septième congrès mondial sur l'application de la génétique à l'élevage, 19-23 août 2002, Montpellier, France, 12–14.

5 *Dans le cas d'informations hébergées sur un site Web:*
   FAO. 2010. Domestic Animal Diversity Information System, http://www.fao.org/dad-is/, Organisation des Nations Unies pour l'alimentation et l'agriculture, Rome, Italie.

Dans le cas d'un travail ayant été accepté pour la publication, mais n'ayant pas encore été publié, on écrira «sous presse» à la place de l'année de la publication. Il ne faudra pas écrire l'année prévue de la publication.

Documentation supplémentaire en ligne

La plate-forme en ligne donne la possibilité aux auteurs d'ajouter des données qui seraient autrement impossibles ou pas pratiques à inclure à la version imprimée. Les auteurs pourront inclure des tableaux et des figures ainsi que des données comme des vidéos, des images/structures en trois dimensions, des ensembles de données très détaillées et d'autres matériels supplémentaires ne convenant pas à la reproduction sur papier. Tout le matériel supplémentaire se présentera avec le manuscrit original. Les données supplémentaires seront indiquées dans le texte par le préfixe «S» (par exemple, tableau supplémentaire S1, figure supplémentaire S1). Les fichiers supplémentaires ne seront pas révisés et seront publiés tels que reçus. Les éditeurs devront approuver la publication électronique de ce matériel. Le manuscrit devra être autonome et se suffire à lui-même, sans le matériel supplémentaire (dans l'intérêt des lecteurs ayant uniquement accès à la copie papier).

Processus d'examen

Les manuscrits présentés au journal seront examinés par deux réviseurs externes et évalués par un des éditeurs. Si les éditeurs considèrent que l'article n'est pas pertinent avec ce journal ou que l'examen ne sera pas favorable, l'article pourra être renvoyé à l'auteur après l'examen initial des éditeurs. Ce processus de refus rapide permet à l'auteur de présenter immédiatement son travail ailleurs pour publication. Les manuscrits seront également refusés par les éditeurs s'ils ne sont pas conformes aux recommandations prévues pour leur préparation. Tous les efforts seront faits pour communiquer aux auteurs la décision de l'examen dans un délai de six semaines après la réception du manuscrit. Si les éditeurs demandent des révisions au manuscrit avant sa publication, on accordera un délai maximum d'un mois pour ces révisions.

Epreuves

L'éditeur se réserve le droit de réviser les manuscrits pour veiller à ce que la grammaire et l'orthographe soient cohérentes avec le style du journal. L'auteur principal recevra les épreuves en page pour la correction. Ces épreuves seront contrôlées et renvoyées dans un délai de deux jours après la réception. L'éditeur se réserve le droit de charger les auteurs en cas de correction excessive d'erreurs non typographiques.

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Instrucciones para los autores

Animal Genetic Resources/Resources génétiques animales/ Recursos genéticos animales es una revista trilingüe, publicada tres veces al año electrónicamente en internet (http://journals.cambridge.org/AGR) y de forma impresa. Los principales trabajos son publicados en inglés, francés y español, con resúmenes en estos tres idiomas. La revista viene siendo publicada desde el año 1983 y todas las ediciones pasadas están disponibles en el enlace: http://dad.fao.org/cgi-bin/EfabisWeb.cgi?sid=-1,refcat_50000044

La revista invita a la presentación de trabajos desde cualquier parte del mundo. Aquellos autores que no posean un nivel elevado en alguno de las tres lenguas aceptadas, les solicitamos que busquen la ayuda necesaria en este sentido antes de remitirnos sus manuscritos.

Misión

La revista proporciona un foro internacional para la publicación de trabajos relacionados con la gestión de los recursos genéticos animales para la alimentación y la agricultura (AnGR). En concreto, se tratan las siguientes áreas: caracterización fenotípica y molecular; sondeo y seguimiento; desarrollo (mejora genética); utilización sostenible; desarrollo de las capacidades de los ganaderos y las comunidades de pastores; y políticas e instituciones.

Los editores aceptan todos los trabajos enviados que traten sobre los temas mencionados anteriormente. Trabajos relativos a razas y tecnologías que contribuyan a la gestión sostenible de los sistemas de producción con ingresos medios y bajos en el mundo, que comprenden la mayor parte de las tierras dedicadas a la producción ganadera y la mayor parte de la producción del ganado, que son los que ostentan mayor grado de interés.

La revista apoya la implementación del Plan de Acción Mundial sobre los Recursos Zoogenéticos, el marco de trabajo acordado para la gestión de los AnGR y el Convenio sobre la Biodiversidad.

Descargo de responsabilidad

Los puntos de vista expresados en los trabajos publicados en Animal Genetic Resources/Resources génétiques animales/ Recursos genéticos animales son solamente las opiniones del autor o autores y, por tanto, no reflejan necesariamente las políticas de la FAO o los puntos de vista de los editores o de las instituciones a las que dichos autores pertenecen.

Evaluación de expertos

Los manuscritos enviados para su publicación en Animal Genetic Resources/Resources génétiques animales/Recursos genéticos animales serán estudiados minuciosamente por parte de dos críticos externos. Lo ideal es que los manuscritos sean evaluados por los críticos externos y por los editores, recayendo la decisión final acerca de los mismos sobre los editores.

Categorías de los trabajos

Trabajos sobre investigación – Se tomarán en consideración para su publicación en Recursos genéticos animales los trabajos relacionados con la gestión de los AnGR. Se invita a los autores a incluir las fotografías de alta calidad pertinentes relativas al trabajo presentado en sus manuscritos. Si las fotografías ilustran animales, éstas deben mostrar el entorno de producción primario al que estos animales se han adaptado.

Trabajos de revisión – Se podrán tomar en consideración ocasionalmente aquellos trabajos que presenten una revisión del desarrollo a nivel de nacional, regional o mundial en uno o más aspectos de la gestión de los AnGR. Estos trabajos podrán incluir las revisiones del estado actual de campos específicos de la gestión de los AnGR.

***Artículos específicos* –** Los artículos relacionados con los temas de la revista serán publicados cuando los editores lo consideren oportuno.

***Otros trabajos publicados*:** Se invita a los lectores a enviar la siguiente información a la dirección de correo electrónico: AnGR-Journal@fao.org

- Revisiones o propuestas de libros.
- Conclusiones y recomendaciones resultantes de reuniones, talleres y conferencias relevantes.
- Anuncios de cursos de capacitación y eventos a nivel nacional, regional o internacional.

Originalidad y copyright

Para poder ser publicado en la revista Recursos genéticos animales, el manuscrito deberá no haber sido publicado previamente o estar bajo estudio para ser publicado. (Los datos que hayan sido publicados previamente podrán ser usados en la revista con precaución y siempre y cuando se obtenga el permiso necesario). Antes de la publicación, el autor del manuscrito deberá firmar y entregar, en su nombre y en el de los co-autores, una autorización y un formulario de consentimiento de transferencia a la editorial. Este formulario se enviará al autor junto con la prueba del artículo a publicar.

Autoría

Los artículos que tengan múltiples autores serán revisados bajo el supuesto de que todos los autores han contribuido a la investigación descrita en el artículo y aprueban tanto el artículo en su totalidad como el envío y la publicación de éste. Contribución al trabajo presentado supone la concepción y el diseño del proyecto, los resultados de los experimentos y/o el análisis e interpretación de los datos. Los autores deberán haber contribuido sustancialmente al borrador o a la revisión de dicho trabajo.

Presentación del Manuscrito

Todos los manuscritos deberán enviarse online, y sin coste alguno para el autor, a través de la página Web: http://journals.cambridge.org/AGR.

Posteriormente al envío del manuscrito, se mandará acuse de recibo junto con un número de referencia y el manuscrito será presentado para ser estudiado. Para toda correspondencia relacionada con el manuscrito, se deberá incluir el número de referencia mencionado.

Se deberán seguir las siguientes instrucciones (para más información, ir a la sección "Preparación y estilo de manuscrito"):

- Los manuscritos se presentarán en ingles, francés o español. Si el manuscrito está escrito en francés o español se deberá incluir un resumen, así como palabras clave en el mismo idioma además del inglés. Todos los artículos publicados presentarán un resumen en inglés, francés y español. Se agradecerá el envío del resumen en los tres idiomas con objeto de reducir gastos de traducción y acelerar el proceso del manuscrito.
- El formato deseado de documento para la presentación es Microsoft Word. No se aceptarán manuscritos enviados en Word Perfect u otros procesadores de texto. Los cuadros se incluirán al final del documento, siguiendo el orden indicado por los marcadores de posición dentro del texto.
- Las figuras deberán presentarse en documentos separados con una resolución apropiada (Para más información ver "Preparación y estilo de manuscrito").
- Se deberá presentar una carta de presentación en un documento por separado. La carta deberá indicar la categoría bajo la que el manuscrito se presenta (Ver apéndice 1) y los datos del autor (número de teléfono, fax, y dirección de correo electrónico).
- Los nombres de los archivos enviados deberán indicar el nombre completo o abreviado del autor principal.
- No se requiere ni deberá enviarse copia en papel del manuscrito, de los cuadros o de las figuras.

Tenga en cuenta que toda correspondencia en relación con los manuscritos presentados y analizados se hará exclusivamente con el autor principal.

Preparación y estilo del manuscrito

El formato del manuscrito deberá tener un espaciamiento doble entre líneas. Las páginas deberán estar numeradas, siendo la página número uno la que lleva el título del artículo. Los márgenes de las páginas deberán tener al menos 2.5 cm. en todas sus caras. La letra debe ser estilo "Arial".

Autores y afiliaciones – Los nombres y afiliaciones de los autores deberán presentarse en el formato siguiente:

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El título abreviado tendrá un máximo de 50 caracteres y aparecerá en la página 1 del manuscrito.

El ***resumen*** no deberá tener estructura o subtítulos y deberá proporcionar al lector una sinopsis que sea independiente del documento. Deberá incluir una breve introducción, la metodología usada, los resultados obtenidos y las conclusiones. El resumen no deberá exceder de 210 palabras en inglés y 250 palabras en francés y español. El resumen deberá ser seguido de tres a cinco palabras clave separadas por una coma. Tanto el resumen como las palabras clave se escribirán en el mismo idioma del manuscrito además del inglés.

El ***texto principal del manuscrito*** deberá empezar en la página número 3 y las referencias deberán comenzar en una página nueva. Las líneas de texto deberán estar numeradas y el manuscrito estructurado con encabezamientos numerados consecutivamente (eje. 1., 1.1, 1.1.1 etc.). Es importante evitar el uso de referencias cruzadas cuando se use la numeración de los encabezamientos, en cuyo caso la editorial eliminará la numeración y aplicará los estilos de encabezamiento en la versión final.

Adicionalmente, los trabajos de investigación deben incluir los siguientes encabezamientos: ***Materiales y métodos, Resultados, Discusión y Conclusiones***.

La ***extensión máxima*** del texto principal del manuscrito no deberá exceder de 10 páginas (8.500 palabras aprox.). En caso de que el texto sea corto, éste no deberá exceder de una página (750 palabras ó 500 palabras si se incluye una imagen).

Los Cuadros deberán ser numerados consecutivamente tal y como están citados en el texto (Cuadro 1, 2 etc.). Cada cuadro deberá aparecer en una página distinta (al final del documento) con la numeración y título arriba y las anotaciones o comentarios debajo del mismo.

Las figuras se numerarán consecutivamente tal y como están citadas en el texto del documento (Figura 1, 2, etc.). Se deberán usar caracteres en cursiva para apartados a, b, c, etc. Cada figura deberá incluir una leyenda. En caso que corresponda, las figuras se deberán enviar en archivos con formato TIFF o EPS, preferiblemente con el mismo tamaño con el que serán reproducidos o publicados. Las ilustraciones o material gráfico deberán enviarse en blanco y negro con una resolución de 1200 dpi; las combinaciones de material gráfico con una resolución de 800 dpi; el material gráfico en modelo de semitono en blanco y negro deberá guardarse bajo el modo "escala de grises" con una resolución de 300 dpi; el material gráfico en modelo de semitono a color se guardará bajo modo "CMYK" con una resolución de 400 dpi. Se deberán obtener todos los permisos necesarios.

Abreviaturas y el sistema internacional de unidades (SI) – No se recomienda el uso de abreviaturas excepto aquellas extensamente utilizadas. Las abreviaturas deberán usarse sólo en caso de que mejoren la comprensión del manuscrito. Los acrónimos deberán ser escritos en palabras completas la primera vez que se mencionen. Se usarán las medidas del sistema métrico internacional (SI).

Lista de agradecimientos

En esta sección el autor deberá hacer mención a la ayuda económica recibida, por parte de las agencias de financiación u otras fuentes, para la realización del trabajo documentado en el manuscrito. También se podrán incluir, en esta sección, los agradecimientos a las personas que contribuyeron a la investigación pero que no aparecen como autores.

La lista de agradecimientos deberá aparecer después del texto principal antes de las referencias. En caso de que no haya agradecimientos, la palabra "ninguno" seguirá al encabezamiento "Lista de agradecimientos".

Declaración de interés

Existe conflicto de intereses cuando un autor tiene intereses que pudieran influir de forma inapropiada en su opinión o juicio, incluso si su opinión no ha sido finalmente influenciada. Por esta razón, los autores deberán revelar conflictos de intereses potenciales de forma que se pueda evaluar sobre sus efectos. En el momento en que se envíe el manuscrito, los autores deberán revelar cualquier acuerdo o conexiones económicas que puedan tener, que sean pertinentes al manuscrito enviado y que puedan ser percibidas como potencial amenaza a la imparcialidad del documento. También deberán declararse los intereses no-financieros que pudieran ser relevantes en este contexto. En caso de que no haya intereses relevantes, deberá también indicarse. Este requerimiento será aplicable a todos autores del documento y a todas las categorías de documentos.

Referencias

Toda referencia presente en el texto deberá aparecer en la lista de referencias y, de la misma manera, cada referencia de la lista deberá haber sido citada por lo menos una vez en el texto. Las referencias deben ir en orden alfabético del apellido del autor, seguido por el año.

Ejemplos:

1. *Ejemplo en el caso de una referencia de una revista*:
   Köhler-Rollefson, I. 1992. The camel breeds of India in social and historical perspective. *Animal Genetic Resources Information* 10: 53–64.
2. *Cuando se trate de más de un autor*:
   Matos, C.A.P., Thomas, D.L., Gianola, D., Tempelman, R. J. & Young, L.D. 1997. Genetic analysis of discrete reproductive traits in sheep using linear and non-linear models: 1. Estimation of genetic parameters, *Journal of Animal Science* 75: 76–87.
3. *En el caso de un libro o de una publicación ad hoc, por ejemplo informes, tesis, etc.*
   FAO, 2007. Global Plan of Action for Animal Genetic Resources and the Interlaken Declaration. Food and Agriculture Organization of the United Nations, Rome, Italy (available at http://www.fao.org/docrep/010/a1404e/a1404e00.htm).
   Van der Werf, J., Graser, H-U., Frankham, R. & Gondro, C. (eds.) 2009. Adaptation and fitness in animal populations. evolutionary and breeding perspectives on genetic resources management. Springer.
4. *Cuando se trate de un artículo dentro de las actas de una reunión*:
   Abad, M., Arrigo, J., Gibbons, A., Lanari, M.R., Morris, G. & Taddeo, H. 2002. Breeding scheme for Angora goat production in North Patagonia. Proceedings 7th World Congress on Genetics Applied to Livestock Production, 19-23 August 2002, Montpellier, France, 12–14.
5. *Cuando la información contenida en el artículo haya sido obtenida o derive de un sitio Web*:
   FAO. 2010. Domestic Animal Diversity Information System, http://www.fao.org/dad-is/, Food and Agriculture Organization of the United Nations, Rome, Italy.

En caso de trabajos que hayan sido aceptados para publicación pero que no hayan sido todavía publicados, se deberá escribir "en prensa" en lugar del año de publicación. No deberá indicarse el año estimado de publicación.

Material suplementario online

La plataforma online ofrece a los autores la oportunidad de incluir datos que serían imposibles o impracticables de incluir en la versión impresa de la revista. Los autores podrán incluir cuadros y figuras, así como videos, imágenes 3-D, grandes bases de datos o cualquier material adicional que no se pueda imprimir. Todo material suplementario deberá ser enviado con el manuscrito original. Los datos suplementarios deberán referirse en el texto del documento con el prefijo "S" (ej. Cuadro suplementario S1, Figura suplementaria S1). Los archivos suplementarios o adicionales no serán editados ni corregidos, y serán publicados tal y como se envíen. La publicación electrónica del material suplementario necesitará ser aprobada por los editores. Por otra parte, el manuscrito deberá ser autónomo sin el material suplementario (en beneficio de los lectores que sólo tengan acceso a la copia impresa).

El proceso de revisión

Los manuscritos enviados a la revista serán estudiados por dos críticos externos y evaluados por uno de los editores. Si los editores consideran que un documento no es relevante para la revista o que tiene pocas posibilidades de tener una buena evaluación, podrá ser devuelto al autor después de la primera revisión por parte de los editores. Este proceso de rechazo rápido facilita al autor enviar su trabajo para publicación a otros medios. Los manuscritos también podrán ser rechazados por los editores si no se ajustan a las recomendaciones de preparación de manuscritos. Se hará todo lo posible por informar a los autores sobre la revisión dentro del plazo de seis semanas tras la recepción del manuscrito. Si los editores requieren revisiones de un manuscrito antes de su publicación, se dará un máximo de un mes para que dicha revisión se haga efectiva.

Pruebas

La editorial se reserva el derecho a corregir manuscritos con objeto de asegurar que la gramática y la ortografía van en consonancia con el estilo de la revista. El autor recibirá pruebas de página para su última corrección. Las pruebas de página deberán ser revisadas y restituidas por el autor dentro de dos días después de su recepción. La editorial se reserva el derecho de cobrar una cantidad a los autores en caso de excesiva corrección de errores no tipográficos.

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