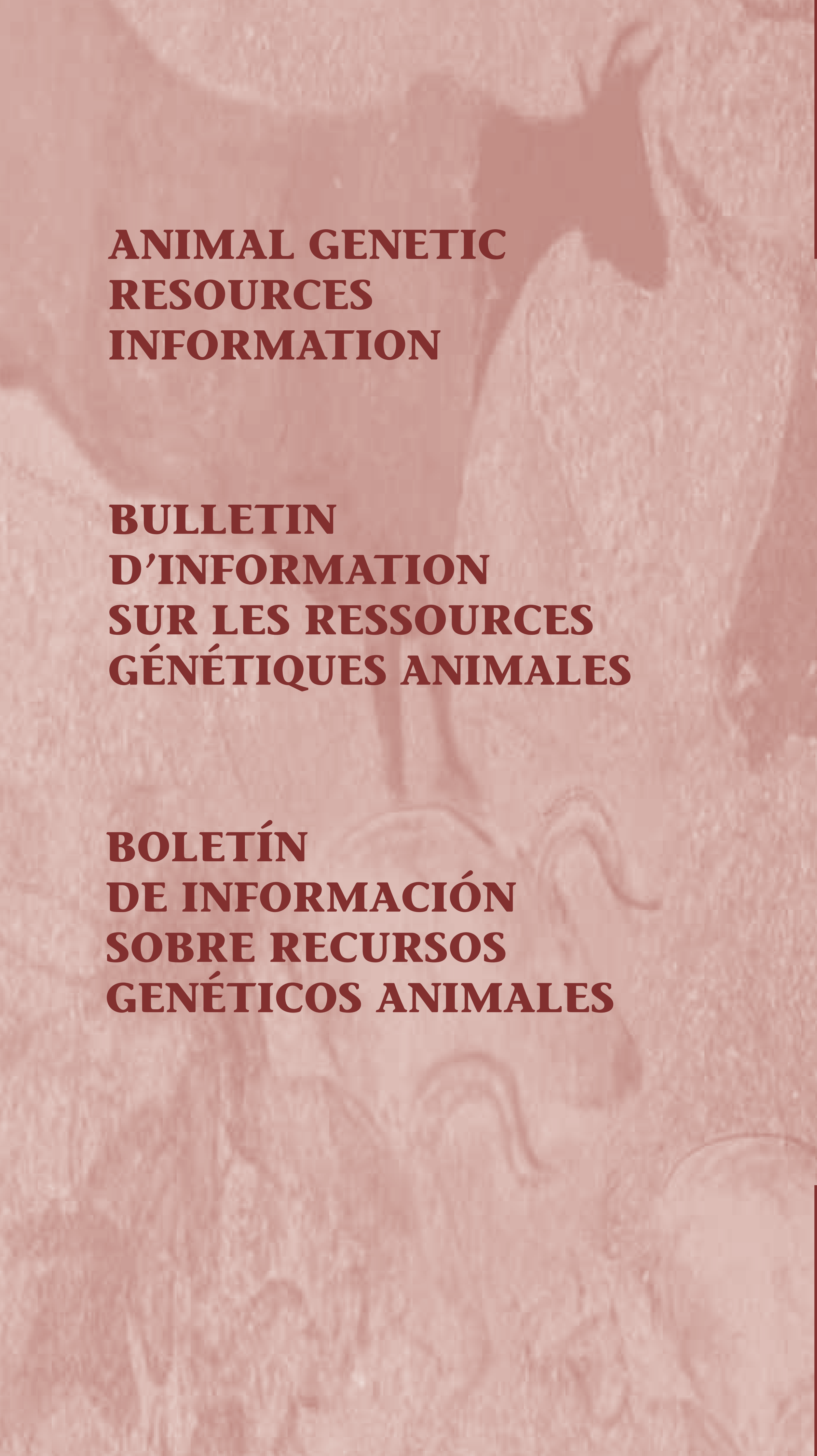

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ANIMAL GENETIC RESOURCES INFORMATION

BULLETIN D'INFORMATION SUR LES RESSOURCES GÉNÉTIQUES ANIMALES

BOLETÍN DE INFORMACIÓN SOBRE RECURSOS GENÉTICOS ANIMALES

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Editorial – The 5th session of the Intergovernmental Technical Working Group on Animal Genetic Resources for Food and Agriculture. Recommendations and advices

The Fifth Session of the Intergovernmental Technical Working Group on Animal Genetic Resources for Food and Agriculture took place in Rome in January 2009. This first meeting of the Working Group following the Interlaken Conference represented an important opportunity to foster momentum in the implementation of the *Global Plan of Action for Animal Genetic Resources*. The positive outcomes of the meeting, and the spirit of collaboration that characterized the discussions, were therefore very much to be welcomed. The Report of the Session[1] contains clear recommendations and advice to the Commission on Genetic Resources for Food and Agriculture, in particular on the design and elements of a Funding Strategy for the *Global Plan of Action* and on a process for evaluating progress in implementation.

A key objective for the immediate future is to translate the Strategic Priorities of the *Global Plan* into effective plans for action at country level. The Working Group recommended that the Commission welcome the *Draft guidelines to assist the preparation of national strategies and action plans for animal genetic resources for food and agriculture* presented to the meeting by the FAO Secretariat, and that it request FAO to finalize and publish these guidelines. Preparation of a National Strategy and Action Plan will help countries to decide on how to achieve more effective utilization of their animal genetic resources, taking national circumstances and priorities, including the availability of human and financial resources, fully into account. It will provide a means to better engage diverse interests within the livestock sector and to enhance understanding among policy-makers and the general public of the importance of animal genetic resources, the multiple roles and values of livestock, and the need to maintain the genetic diversity that will enable adaptation to changing conditions.

The Working Group also recommended that the Commission reaffirm the relevance of the establishment of country-based early warning and response systems for animal genetic resources as part of broader national strategies for the management of these resources, taking into account national circumstances and the relevant Strategic Priorities and Actions of the *Global Plan of Action*. The Working Group stressed the importance of national back-up storage systems for animal genetic resources and recommended that the Commission encourage countries to establish such systems, if they have not done so already.

The Working Group recommended that the Commission acknowledge the important contributions of small-scale livestock keepers, particularly in developing countries, as custodians of much of the world's animal genetic resources. It stressed the importance of capacity-building to support the improvement of local and multi-functional breeds in low- and medium-input production systems, and institutional support to address the particular needs of such systems, while ensuring respect for the knowledge, innovations and practices of indigenous and local communities, and the application of relevant national legislation and international agreements. It also recommended that the Commission note the need for countries to take into account the contributions of small-scale livestock keepers and promote their full and effective participation in the implementation of the *Global Plan of Action*; in the preparation and implementation of National Strategies and Action Plans for Animal Genetic Resources; and as appropriate, food security, poverty alleviation and livelihood security policies and programmes.

A two-pronged approach to reporting on progress in the implementation of the *Global Plan of Action* was discussed a) Reporting by countries, regions, FAO and other organizations on the process of implementation of the *Global Plan of Action*; and b) Reporting by countries on the status and trends of animal genetic resources which will also help to assess the actual impact of the implementation of the *Global Plan of Action*. For the first type of report, the Working Group recommended that the Commission adopt a

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[1] All ITWG 5 documents are available at: *http://www.fao.org/ag/againfo/programmes/en/genetics/angrvent-5th-docs.html*

progress reporting interval of four years. With regard to status and trends reports on animal genetic resources, the Working Group recommended that the Commission request FAO to prepare synthesis reports based on data and information provided by countries through DAD-IS, and make these reports available to the Commission at each of its regular sessions. In this regard, the Working Group stressed the need for regular updating of national data and information on animal genetic resources, and the importance of providing financial and technical support for developing countries to assist them in updating their data and information.

The Editors

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

La Cinquième session du Groupe de travail technique intergouvernemental sur les ressources zoogénétiques pour l'alimentation et l'agriculture a eu lieu à Rome en janvier 2009. Après la Conférence d'Interlaken, cette première réunion du Groupe de travail a représenté une importante occasion pour promouvoir la réalisation du *Plan d'action mondial sur les ressources zoogénétiques*. Les résultats positifs de la réunion, ainsi que l'esprit de collaboration qui a caractérisé les discussions, ont été hautement appréciés. Le rapport de la réunion[1] contient des recommandations et conseils précis pour la Commission sur les ressources génétiques pour l'alimentation et l'agriculture, et en particulier sur le concept et les éléments pour une Stratégie de financement de la mise en oeuvre du *Plan d'action mondial* et sur le processus d'évaluation des progrès obtenus dans la mise en oeuvre.

L'objectif principal pour le futur immédiat est la conversion des Priorités stratégiques du *Plan Mondial* en plans effectifs d'action au niveau national. Le Groupe de travail a recommandé que la Commission adopte l'ébauche des *Directives pour la préparation des stratégies nationales et des plans d'action sur les ressources zoogénétiques pour l'alimentation et l'agriculture* présentée lors de la réunion par le Secrétariat de la FAO, et que l'on sollicite de la FAO la finalisation et publication de ces directives. La préparation d'une Stratégie nationale et un Plan d'action aideront les pays à décider comment obtenir une utilisation plus effective de leurs ressources zoogénétiques tout en tenant compte pleinement des circonstances et des priorités au niveau national, y compris la disponibilité de ressources humaines et financières. De cette façon on mettra à disposition un outil pour faciliter un meilleur accord entre les différentes parties qui existent dans le domaine de l'élevage et une meilleure compréhension parmi les législateurs et le public sur l'importance des ressources zoogénétiques, les différents rôles et valeurs de l'élevage, ainsi que la nécessité de conserver la diversité génétique pour permettre son adaptation aux conditions changeantes.

Le Groupe de travail a aussi recommandé que la Commission reconfirme l'importance d'établir au niveau national des systèmes d'alerte et d'intervention rapide pour les ressources zoogénétiques à l'intérieur d'autres stratégies nationales plus larges pour la gestion de ces ressources, tout en considérant les circonstances nationales et l'importance des Priorités et des actions stratégiques du *Plan d'action mondial*. Le Groupe de travail a souligné l'importance des systèmes nationaux de sauvegarde pour les ressources zoogénétiques et a recommandé à la Commission d'encourager les pays pour qu'ils établissent ce type de systèmes s'ils ne l'ont pas encore fait.

Le Groupe de travail a recommandé que la Commission reconnaisse l'importance de la contribution des petits éleveurs, en particulier dans les pays en voie de développement, en tant que gardiens de la plus grande partie des ressources zoogénétiques existante dans le monde. On a souligné l'importance du renforcement des capacités de réalisation pour soutenir l'amélioration des races locales et multi fonctionnelles dans des systèmes de moyen et faible apport, ainsi que le soutien des institutions pour résoudre les besoins spécifiques de ces systèmes, tout en respectant les connaissances, les innovations et les pratiques des communautés indigènes et locales et l'application de la législation nationale appropriée et des accords internationaux. Il a également recommandé que la Commission note le besoin des pays à prendre en considération les contributions des petits propriétaires et à favoriser leur pleine et effective participation dans la réalisation du *Plan d'action mondial*; dans la préparation et réalisation des Plans nationaux de

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[1] Tous les documents ITWG 5 sont disponibles sur: *http://www.fao.org/ag/againfo/programmes/en/genetics/angrvent-5th-docs.html*

stratégie et d'action pour les ressources zoogénétiques; et, si nécessaire, dans les programmes et les politiques de sécurité alimentaire, atténuation de la pauvreté et sécurité des moyens d'existence.

On a discuté d'une double approche pour informer sur l'état de réalisation du *Plan d'action mondial*: a) rapports par pays, régions, de la FAO et des autres organisations sur l'état de la réalisation du *Plan d'action mondial;* et b) rapports par pays sur la situation et tendance des ressources zoogénétiques qui aideront à évaluer l'impact actuel de la réalisation du *Plan mondial d'action*. Pour le premier type de rapport le Groupe de travail a recommandé que la Commission adopte la présentation des rapports sur l'avancement du travail avec un intervalle de quatre ans. En ce qui concerne les rapports sur la situation et tendance des ressources zoogénétiques, le Groupe de travail a recommandé que la Commission sollicite de la FAO la préparation de rapports synthétiques basés sur les données et l'information fournis par les pays à travers DAD-IS et que ces rapports soient accessibles à la Commission lors de chacune de ses réunions ordinaires. A ce sujet, le Groupe de travail a souligné le besoin d'une mise à jour régulière des données et des informations nationales sur les ressources zoogénétiques, ainsi que l'importance de fournir une aide financière et technique aux pays en voie de développement pour les aider dans la mise à jour de leurs données et informations.

Les Editeurs

Quinta reunión del Grupo de Trabajo Técnico Intergubernamental sobre los Recursos Zoogenéticos para la Alimentación y la Agricultura

La Quinta reunión del Grupo de Trabajo Técnico Intergubernamental sobre los Recursos Zoogenéticos para la Alimentación y la Agricultura tuvo lugar en Roma en enero del 2009. Tras la Conferencia de Interlaken, esta primera reunión del Grupo de Trabajo ha representado una ocasión importante para fomentar la realización del *Plan de Acción Mundial sobre los Recursos Zoogenéticos*. Los resultados positivos de la reunión[1], así como el espíritu de colaboración que caracterizaron las discusiones, fueron muy apreciados. El informe de la reunión contiene claras recomendaciones y consejos para la Comisión sobre Recursos Genéticos para la Alimentación y la Agricultura, en particular, sobre el diseño y los elementos para una Estrategia de financiación para el *Plan de Acción Mundial*, y sobre el proceso de evaluación de los progresos obtenidos en su realización.

El objetivo principal para el futuro inmediato es la conversión de las Prioridades Estratégicas del *Plan de Acción Mundial* en planes efectivos de acción a nivel nacional. El Grupo de Trabajo recomendó que la Comisión adoptara el borrador de las *Líneas guía para la preparación de estrategias nacionales y planes de acción sobre los recursos zoogenéticos para la alimentación y la agricultura* presentado a la reunión por la Secretaría de la FAO, y que se solicitara a la FAO que finalicen y publiquen estas líneas guía. La preparación de una Estrategia Nacional y un Plan de Acción ayudará a los países a decidir cómo conseguir una utilización más efectiva de sus recursos zoogenéticos, teniendo en cuenta plenamente las circunstancias y prioridades nacionales, incluida la disponibilidad de recursos humanos y financieros. De esta forma, se proporcionara un medio para alcanzar un mejor compromiso entre los distintos intereses dentro del sector ganadero y un mayor entendimiento entre los legisladores y el público sobre la importancia de los recursos zoogenéticos, las múltiples líneas de conducta y valores de la ganadería, así como la necesidad de mantener la diversidad genética que permitirá la adaptación a las condiciones cambiantes.

El Grupo de Trabajo también recomendó que la Comisión reafirmara la importancia del establecimiento a nivel nacional de sistemas de alerta y respuesta rápidas para los recursos zoogenéticos como parte de las más amplias estrategias nacionales para la gestión de estos recursos, teniendo en cuenta las circunstancias nacionales y la importancia de las Prioridades y Acciones Estratégicas del *Plan de Acción Mundial*. El Grupo de Trabajo subrayó la importancia de los sistemas nacionales de salvaguardia de los datos sobre recursos zoogenéticos y recomendó a la Comisión alentar a los países para que establezcan este tipo de sistemas en caso de que no lo hayan hecho todavía.

El Grupo de Trabajo recomendó que la Comisión reconociera la importante contribución de los pequeños agricultores, en particular de los países en vía de desarrollo, en cuanto guardianes de la mayor parte de los recursos zoogenéticos existentes en el mundo. Se subrayó la importancia de reforzar las capacidades para apoyar la mejora de las razas locales y multi funcionales en sistemas de baja y media producción, y el apoyo institucional para resolver las necesidades particulares de esos sistemas, manteniendo el respeto por los conocimientos, innovaciones y prácticas de las comunidades indígenas y locales, y el uso de la legislación nacional relevante y de los acuerdos internacionales. También recomendó que la Comisión tomara nota de la necesidad de los países de tener en cuenta las contribuciones de los pequeños propietarios ganaderos y promoviera su plena y efectiva participación en la realización del *Plan de Acción Mundial*; en la preparación y realización de los Planes Nacionales de Estrategia y Acción para los Recursos Zoogenéticos; y, cuando sea necesario, en los programas y políticas de

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[1] Todos los documentos de ITWG 5 están disponibles en: *http://www.fao.org/ag/againfo/programmes/en/genetics/angrvent-5th-docs.html*

seguridad alimentaria, alivio de la pobreza y seguridad de sustento.

Se discutió sobre un doble enfoque para informar acerca del estado de realización del *Plan de Acción Mundial*: a) Informes por países, regiones, de la FAO y otras organizaciones sobre el estado de realización del *Plan de Acción Mundial*, y b) Informes por países sobre la situación y tendencia de los recursos zoogenéticos que ayudará a evaluar el impacto actual de la realización del *Plan de Acción Mundial.* Para el primer tipo de informe, el Grupo de Trabajo recomendó que la Comisión adoptara la presentación de informes sobre el avance del trabajo a intervalos de cuatro años. En cuanto a los informes sobre la situación y tendencia de los recursos zoogenéticos, el Grupo de Trabajo recomendó que la Comisión solicitara a la FAO la preparación de informes sintéticos basados en los datos y la información proporcionada por los países a través de DAD-IS y que estos informes fueran accesibles a la Comisión durante cada una de sus reuniones ordinarias. A este respecto, el Grupo de Trabajo subrayó la necesidad de una actualización continúa de los datos e informaciones nacionales sobre recursos zoogenéticos, así como la importancia de proveer ayuda financiera y técnica a los países en vía de desarrollo para apoyarles en la actualización de sus datos e informaciones.

Los Editores

Basic demographic data – a prerequisite for effective management of animal genetic resources

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Summary

Demographic data describe the size, structure and distribution of livestock populations and how these change over time. They are fundamental to determining the risk status of breed populations both on a national and a global scale. Currently, no population data are available for 36 percent of the breeds recorded in the Domestic Animal Diversity Information System (DAD-IS), and for many other breeds data are updated so infrequently that monitoring trends in risk status is difficult or impossible. Data on the geographical distribution of breeds are also generally inadequate. A baseline survey of the breed population needs to be followed by periodic monitoring. The required frequency of the monitoring activities will depend on the generation interval of the species in question. Data may be collected via breed-level censuses or surveys, or estimated based on species level data. It is important that national decision-making takes account of the global demographics of the breed; a classification system distinguishing breeds present only in one country from those present in several countries has been developed. Much remains to be done to improve the availability of demographic data. Moreover, methods need to be developed that account for the risks of genetic erosion associated with indiscriminate cross-breeding. A further key requirement is the development of methods for representative sampling of national animal populations to allow estimates of their total population size and other demographic data to be obtained in a cost-effective manner.

Résumé

Les données démographiques indiquent la taille, la structure et la distribution des populations domestiques et comment elles changent dans le temps. Ces données sont fondamentales pour déterminer la situation de risque des races au niveau national et mondial. Actuellement il n'existe aucune donnée de population pour 36% des races enregistrées dans le Système d'Information sur la Diversité des Animaux Domestiques (DAD-IS), et dans la plupart des autres cas les données sont mise à jour avec si peu de fréquence qu'il est difficile et même impossible de suivre la situation de risque et la tendance. Très souvent aussi les données sur la distribution géographique des races ne sont pas appropriée. Une enquête de base sur les populations a besoin d'un suivi continu. La fréquence nécessaire pour faire le suivi des activités dépendra de l'intervalle entre générations des espèces à l'étude. Les données doivent être saisies à travers les recensements par races ou les enquêtes, ou aussi à travers les estimations basées sur les données au niveau des espèces. Il est important que les législateurs au niveau national tiennent compte de la démographie mondiale de la race. Un système de classement a été mis au point qui détermine les races présentes seulement dans un pays de celles qui se trouvent dans différents pays. Il reste encore beaucoup à faire pour améliorer la disponibilité des données démographiques. Cependant, il est nécessaire de développer des méthodes qui valorisent les risques de l'érosion génétique associés aux croisements sans contrôle. Il est aussi important de développer des méthodes représentatives d'échantillonnage des populations animales au niveau national afin de permettre l'évaluation de la taille totale des populations et des autres données démographiques qui peuvent s'obtenir en forme de coût effectif.

Resumen

Los datos demográficos describen el tamaño, estructura y distribución de las poblaciones ganaderas y cómo éstas cambian en el tiempo. Estos datos son fundamentales para determinar la situación de riesgo de las razas tanto a nivel nacional como a escala mundial. Actualmente no existen datos sobre población para el 36% de las razas registradas en el Sistema de Información sobre Diversidad de Animales Domésticos (DAD-IS), y para muchas otras razas los datos se actualizan con tan poca frecuencia que resulta difícil e incluso imposible monitorear la situación de riesgo y tendencia. También los datos sobre la distribución geográfica de las razas resultan a menudo inadecuados. Una encuesta de base sobre las poblaciones necesita un seguimiento y monitoreo periódico. La frecuencia requerida para monitorear las actividades dependerá del intervalo entre generaciones de las especies en cuestión. Los datos deben recogerse a través de los censos por razas o de las encuestas, o también por estimaciones basadas sobre datos a nivel de especies. Es importante que los legisladores nacionales tengan en cuenta la demografía mundial de la raza; se ha puesto a punto un sistema de clasificación que distingue las razas presentes solo en un país de las que se encuentran en diversos países. Todavía queda mucho por hacer para mejorar la disponibilidad de los datos demográficos. Sin embargo, es necesario desarrollar métodos que valoren los riesgos de la erosión genética asociada a los cruces indiscriminados. Otra necesidad importante es el desarrollo de métodos representativos de muestreo de las poblaciones animales a nivel nacional para permitir las estimaciones del tamaño total de las poblaciones y otros datos demográficos que puedan ser obtenidos en forma de costo efectivo.

Key words: *National strategies, Effective population size, Population trends, Geographical distribution, Risk status, Management.*

Introduction

Demographic data describe the size, structure and distribution of livestock populations and how these change over time. They are fundamental to effective decision-making in animal genetic resources (AnGR) management, for example to address the question of whether a breed should be targeted for conservation or whether breeding strategies need to be adapted in order to avoid the loss of within-breed genetic diversity. The *Global Plan of Action for Animal Genetic Resources,* adopted by 109 countries at the first International Technical Conference on Animal Genetic Resources, held in Interlaken, Switzerland in 2007, and endorsed by the FAO Conference, highlights "*characterization, inventory and monitoring of trends and associated risks*" as one of its four Strategic Priority Areas (FAO 2007a).

The main focus of this paper is on the use of demographic data to inform strategic planning of the management of breed populations at national level, and in particular the basic decision as to whether a breed should be included in a conservation programme (Figure 1). However, they are also important for decision-making at supra-national level and for planning of breed conservation and development on a more local scale.

Use of Demographic Data for Planning National Strategies for the Management of AnGR

In the context of national planning, one of the main factors to be considered is the risk status of the breeds under consideration – essentially an indication of the likelihood that the breeds will become extinct if no remedial action is taken. Clearly, risk status is linked to the size of the population – small populations are at greater risk of being wiped out by a disastrous event and will be more rapidly threatened by a downward trend. The preferred measure for the determination of risk status is the effective population size (N_e) (FAO, 1992; Gandini *et al*., 2004). This allows the rate of inbreeding, and hence the loss of genetic diversity within the population, to be inferred. Calculating N_e requires that data on the size of both the female and the male breeding populations are available.

In addition to the effective size of the population, risk status depends on population trends. Predicting future population trends and fluctuations, and hence the size of the population at a given point in the future, is difficult given the number of factors involved. Nonetheless, current trends in the size of the population need to be monitored. A downward trend, particularly a rapid downward trend, should serve as a warning, and (unless the potential loss of the breed is accepted) as a call to action.

A further important consideration for determining risk status is the geographical distribution of the population. Of particular importance is the extent to which a breed population is restricted to a limited geographical area. The more concentrated the population is in spatial terms, the greater the risk that all the animals, or a large proportion of them, will be affected by a localized disaster such as a disease epidemic. Data on breeds' geographical distribution are important for a number of reasons in addition to

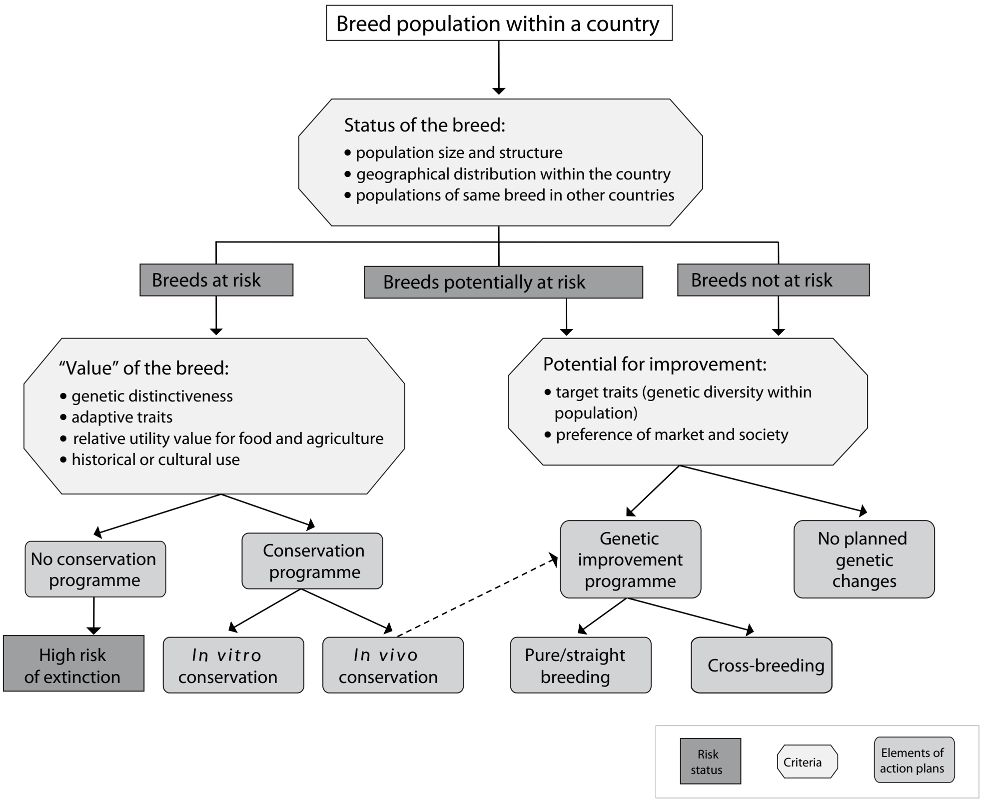

Figure 1. Information required to design management strategies. Source: (FAO, 2007b).

assessing risk. They facilitate further, more in depth, studies; they allow more effective planning for, and response to, emergencies that threaten genetic diversity; and, particularly if georeferenced, they allow breed data to be related to environmental and socio-economic datasets and hence more elaborate and comprehensive analysis (FAO/WAAP, 2008).

Finally, national-level assessment of risk status, and consequent decisions regarding conservation measures, need to be considered in the context of the demography of the breed on an international scale. A breed that has unthreatened populations in other countries is likely to be a lower priority for conservation efforts.

Determining risk status is, of course, only one aspect of the decision as to whether a conservation programme should be undertaken for a particular breed – genetic distinctiveness, adaptive traits, relative utility for food and agriculture, and historical or cultural factors need to be considered (Figure 1). Nonetheless, without basic demographic data, decision-makers will be at a loss.

Collecting Demographic Data

The above discussion has illustrated the importance of obtaining basic demographic data and the need to document changes and trends. This requires a baseline survey followed by periodic monitoring. Monitoring should be conducted at least once per generation of the species, particularly for breeds classified as at risk or potentially at risk. This requires (monitoring) surveys at intervals of about eight years for horses and donkeys, five years for cattle, buffalo, sheep and goats, three years for pigs, and two years for poultry species. Monitoring may be required more frequently depending on the reproductive technology employed for each species and breed. Thus the reproductive technology generally employed in the respective breed populations should be recorded. Monitoring should serve as the basis for national early warning.

Various methods may be employed to determine the total populations size, and these need to be documented (see Box 1). Analysis of data entered into the Domestic Animal Diversity Information System (DAD-IS)[1] by countries' National Coordinators[2] revealed that 87 percent of entries are based on a census or survey at breed level, while

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

[2] National Coordinators for the Management of Animal Genetic Resources are officially appointed by the relevant authorities in each country.

Box 1. Methods to determine total population size (FAO 1998).

Census at species level: census was conducted by species and not by breed; knowledge (or an estimate) of the proportion of the total population of a species that is made up of a particular breed can be used to estimate the population size of that breed.

Census at breed level: population figures were obtained by breed in a regular census. Censuses usually cover the whole country or include representative samples of farms.

Survey at breed level: survey was carried out in a certain area only to estimate the population size of the breed in its distribution area.

Survey at species level: survey carried out at species level from which breed population sizes were obtained. In general surveys include more detail in the type of data collected but are usually not country-wide. Data extrapolation is needed.

Estimate: the population size is not really known but can be figured out on the basis of experience or last census.

11 percent are estimates based on a census at species level (e.g. a national agricultural census). However, for 36 percent of all breeds reported to DAD-IS, National Coordinators were unable to estimate the total population size. Moreover, population data for many of the breed population have been only reported for a single year or have not been updated regularly, making it difficult or impossible to monitor trends.

Agricultural censuses are conducted regularly by most countries (FAO, 2005). Some countries also carry out more specific national livestock censuses. At present, however, most national censuses do not contain breed-level data. Incorporating breed-level questions within such censuses is potentially an important means to improve the availability of breed demographic data. The 2006 National Livestock Census of Pakistan is an example of a census that collected breed-level data (for cattle, buffaloes, sheep and goats; data for horses, mules and asses were collected only at the species level) (Government of Pakistan, 2006). In the absence of breed-level data, a species-level census can nonetheless be the basis for a rough estimate of breed population size (see Box 1).

The smaller the breed population, the easier it will usually be to provide an accurate estimate of its total size. These are the populations for which higher accuracy is more important, as they may be at risk of extinction. For these populations more detailed surveys might be required.

Characterization at the molecular genetic level may be undertaken to explore genetic diversity within and between populations, and to determine genetic relationships among them. In the absence of comprehensive breed characterization data and documentation of the origin of breeding populations, molecular marker information may provide the most easily obtainable estimates of genetic diversity within and between a given set of populations.

The International Dimension

As noted above, conservation decisions need to be considered in the light of the status of the breed on an international scale rather than merely based on national level data. A basic requirement is to distinguish breeds that are present in more than one country from those present in only one country. A classification based on this distinction was developed during the preparation of *The State of the World's Animal Genetic Resources for Food and Agriculture* (see Box 2). Identifying transboundary breed populations enables coordination between countries planning conservation programmes. Regional transboundary breeds are found in substantial numbers in most regions of the world; conservation measures for these breeds should be planned at regional or subregional level.

Box 2. Local versus transboundary breeds.

Local breeds: breeds that occur only in one country.

Transboundary breeds: breeds that occur in more than one country. These are further differentiated into:

- Regional transboundary breeds:
  transboundary breeds that occur only in one of the seven SoW-AnGR regions[3].
- International transboundary breeds:
  transboundary breeds that occur in more than one region.

Conclusions

Despite the importance of demographic data to decision-making in AnGR management, much remains to be done to fill the gaps and to address the priorities identified in the *Global Plan of Action*. For many breeds, no population data are available. For many others, trends in risk status cannot be adequately monitored because data are updated so infrequently. Within-country geographical distribution of breed populations – important for planning many aspects of AnGR management – is poorly recorded. Once collected, demographic data need to be made available to those who need them – hence the importance of information systems for AnGR. Improved demographic data need to be complemented by improved data on the phenotypic and molecular characteristics of the breeds' in question and on their uses and roles in the production systems where they are kept. These data also need to be made widely available to the relevant stakeholders.

At the international level, linking national breed populations with a common gene pool across countries has helped to provide a more realistic assessment of breeds' risk status. However, regional and global cooperation in the conservation and sustainable utilization of AnGR would benefit greatly if more comprehensive demographic data were available and used in the planning of management strategies.

In addition to addressing the problem of missing population data, other weaknesses of current systems for monitoring genetic erosion need to be overcome. A major problem is the lack of measures that capture genetic dilution caused by indiscriminate crossbreeding – a problem that is considered by many experts to be a major threat to AnGR diversity. At the same time, there are many nondescript local populations for which it is unclear whether they form (relatively) homogenous groups that can be distinguished from neighbouring populations. Molecular characterization studies help to unravel such relationships, but need to be better coordinated and the results better combined.

A final point to emphasize is the need for the development of methods for representative sampling of national animal populations to estimate their total population size and other demographic data in a cost-effective manner.

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[3] Regions defined for the purpose of the SoW-AnGR report: Africa, Asia, Europe and the Caucasus, Latin America and the Caribbean, the Near and Middle East, North America and the Southwest Pacific.

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Production environment recording

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Summary

Improved understanding of the adaptation of livestock breeds to their production environments is important for many decisions in the field of AnGR management, ranging from genetic improvement to conservation. However, adaptation is complex and difficult to measure. One approach to this problem is to characterize adaptation indirectly by describing the production environments in which a breed has been kept over time, and to which it has probably become adapted. Comprehensive and comparable descriptions of the production environments in which animals are kept are also needed to make meaningful evaluations of performance data and to enable comparative analysis of the performance of different breeds. To address these requirements and in accordance with the *Global Plan of Action for Animal Genetic Resources*, it has been proposed that a recognized set of "*production environment descriptors*" should be established and used throughout the world as a common framework for describing breeds' production environments. An important aspect of the process will be the georeferencing of breed distributions, which will allow them to be linked to a range of existing georeferenced data sets (e.g. climatic data). The link between a breed and a specific production environment may offer a basis for the development of a niche market; examples in include the Bresse chicken of France and the Abondance and Tarentaise cattle breeds of the northern Alps. Such niche markets represent important opportunities for keeping traditional breeds in use.

Résumé

Améliorer nos connaissances sur l'adaptation des races domestiques à leur milieu de production est important pour de nombreuses raisons dans le domaine de la gestion des AnGR, qui va de l'amélioration génétique à la conservation. Cependant, l'adaptation est complexe et difficile à mesurer. Une approche à ce problème est la caractérisation de l'adaptation indirectement, à travers la description des milieux de production dans lesquels une race se trouve et auxquels elle a dû probablement s'adapter. Il est aussi nécessaire d'avoir des descriptions compréhensibles et comparables des milieux de production dans lesquels les animaux se sont trouvés pour réaliser une évaluation des données de performance et permettre l'analyse de comparaison des performances des différentes races. Pour atteindre ces objectifs, et en accord avec le Plan Mondial d'Action pour les Ressources Zoogénétiques, il a été proposé qu'un ensemble reconnu de « *descripteurs des milieux de production* » soit établi et utilisé dans le monde comme cadre commun de travail pour la description des milieux de production des races. Un aspect important du processus sera la saisie des références géographiques de la distribution de la race, ce qui permettra de la mettre en relation avec un ensemble de données déjà existantes et référencées (p.e. données climatiques). La relation entre une race et un milieu spécifique de production peut offrir une base pour le développement d'un marché de niche, comme c'est le cas du poulet Bresse français et les races bovines Abondance et Tarentaise du Nord des Alpes. Ces marchés de niche représentent des occasions importantes qui permettent de conserver les races traditionnelles.

Resumen

Mejorar los conocimientos sobre la adaptación de las razas domésticas a sus medios de producción es importante por muchas razones en el campo de la gestión de los AnGR, que va desde la mejora genética a la conservación. Sin embargo, la adaptación es compleja y difícil de medir. Un enfoque a este problema es la caracterización de la adaptación indirectamente a través de la descripción de los medios de producción en los que una raza se ha encontrado y a los que probablemente se ha tenido que adaptar. También son necesarias las descripciones comprensibles y comparables de los medios de producción en los que los animales han estado para realizar evaluaciones de los datos de rendimiento y permitir los análisis de comparación de los rendimientos de las distintas razas. Para alcanzar estos requisitos y de acuerdo con el Plan Mundial de Acción para los Recursos Zoogenéticos, se ha propuesto que un conjunto reconocido de « *descriptores de medios de producción* » sea establecido e utilizado en todo el mundo como marco común de trabajo para la descripción de los medios de producción de las razas. Un aspecto importante del proceso será referenciar geográficamente la distribución de la raza, lo que permitirá relacionarla con un conjunto de datos ya existentes y georeferenciados (por ej. datos climáticos). La relación entre una raza y un medio específico de producción puede ofrecer una base para el desarrollo de un nicho de mercado, como los ejemplos que incluyen el pollo Bresse francés y las razas de vacuno Abondance y Tarentaise del norte de los Alpes. Estos nichos de mercado representan oportunidades muy importantes que permiten mantener a las razas tradicionales.

Key words*: Adaptation, Production Environment Descriptors (PEDs), Georeferencing, Surveys.*

Introduction

Livestock animal genetic resources (AnGR) have been domesticated throughout the world to meet local or regional needs. Animals have been selected by farmers for their particular characteristics or cultural value whilst they were also adapting genetically to local conditions, diseases, available feeds, climate, predators and many other persistent variables imposed by the local environment. Improved understanding of the adaptation of livestock breeds to their production environments is important for many decisions in the field of AnGR management ranging from genetic improvement to conservation. However, adaptation is complex and difficult to measure. One approach to this problem is to characterize adaptation indirectly by describing the production environments in which a breed has been kept over time, and to which it has probably become adapted. Comprehensive and comparable descriptions of the production environments in which animals are kept are also vital to make meaningful evaluations of performance data and to enable comparative analysis of the performance of different breeds.

Data Requirements

To address these requirements and in accordance with the *Global Plan of Action for Animal Genetic Resources* (FAO, 2007a), it has been proposed that a recognized set of "*production environment descriptors*" (PEDs) should be established and used throughout the world as a common framework for describing breeds' production environments. It is intended that such a framework be used as the basis for the inclusion of more detailed production environment data within FAO's Domestic Animal Diversity Information System (DAD-IS at: *http://www.fao.org/dad-is/*). A meeting held in Armidale, Australia in 1998 made a first attempt to devise a PEDS framework, and developed a worksheet or questionnaire for the purposes of collecting PEDs data (FAO, 1998). At a follow-up meeting held in Caprarola, Italy in 2008 the previous work was reviewed and further developed (FAO, 2008). According to the framework devised at the latter meeting, a breed's production environment is divided into two main domains, the management environment and the natural environment. These domains are further broken down into a hierarchy of criteria (see Figure 1). Measures were defined to describe each criterion.

Many developing countries have very little capacity to collect and analyse production environment variables. However, most of the measures required for the natural environment domain are now available on global high resolution maps with the exception of the distribution of diseases and parasites. If breed distributions were georeferenced it would be possible to overlay them with these mapped data sets, which could allow far more comprehensive description and analysis of the breeds' production environments. Georeferencing of breed distributions should therefore be given high priority.

Data Collection

Surveys will be organized differently depending on the institutional background. In developed countries, where commercial and conservation farms keep registers of individual animals and their pedigrees, structured surveys can be used to collect

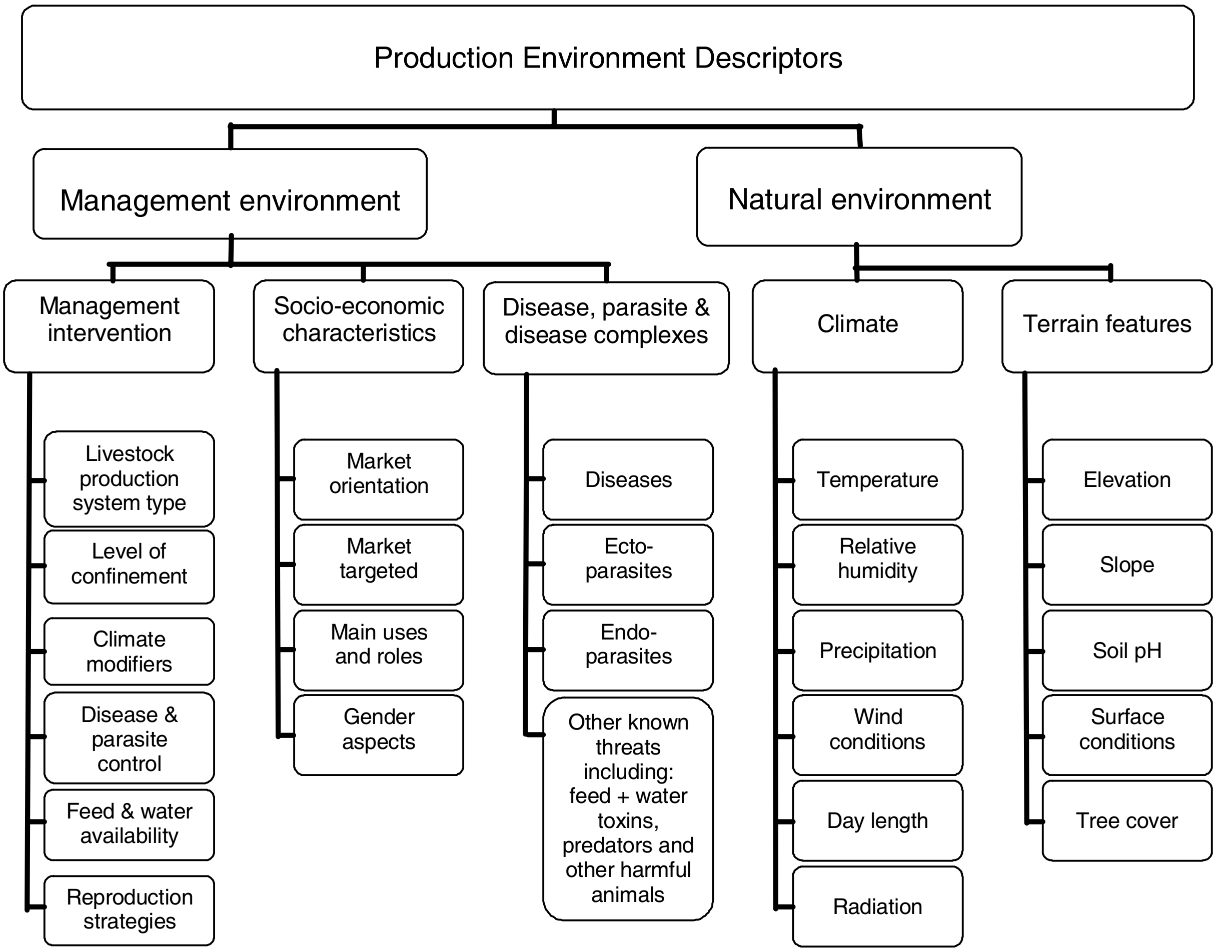

Figure 1. Production environment descriptors for characterization of animal genetic resources.

information on production systems and the environment. The procedure should take advantage of current data collection systems and additional costs should be quite limited.

In countries where such data are not regularly recorded, specific surveys need to be set up. For traditional communities in pastoral and farming production systems, participatory surveys and structured interviews can be used to generate data on breeding objectives, breed and trait preferences and production system constraints. In the context of traditional breeds, these descriptions give insights into the multitude of functions and services that breeds provide for their keepers. Statistical sampling procedures can be applied to study localities, farms and individual animals once the sampling framework is defined.

In situations where limited documented information on breed identification and characteristics is available, extensive exploratory surveys may be necessary. However, exploratory surveys have limitations; the facts generated are highly subject to the biases of questionnaire respondents. Thus, steps need to be taken to ground-truth and cross-check findings using complementary procedures such as key-informant interviews, focus-group discussions and reporting-back sessions with respondent communities. Consequently, these surveys become demanding in terms of time, skilled personnel and financial resources. This has been observed, for example, in livestock breed surveys in Zimbabwe and Ethiopia. (FAO, 2007b).

Use of Production Environment Descriptions for AnGR Management - an Example

Due to their adaptation to specific environments, local breeds may have considerable value for niche production. Verrier *et al.* (2005) provide two examples where nice markets have been successfully established by connecting natural constraints with specific features of local breeds. The creation of niche markets is supported in France by a certificate, the Appellation d'Origine Contrôlée (AOC = controlled term of origin). The Bresse AOC chicken is raised only in the Bresse geographical area as defined by law to promote product quality throughout the production process. For the AOC, a geographical district has to be defined and characterized by specific features of the natural conditions and production system, which cannot be found in another geographical area. Another example provided is AOC cheese production from Abondance and Tarentaise cattle breeds on high-altitude pastures of the northern Alps. These two breeds show some adaptation and functional traits of interest for the mountain farming system and the use of high-altitude pastures.

The efficiency of these systems and their dynamics do not depend only on the traits of the breeds but also on the organization of farmers and producers. A clear genetic strategy is needed, including on-farm performance recording and an emphasis on adaptation and functional traits in the selection goal. In harsh environments, such as mountain regions, particular attention should be given to adaptation to the local environment. The ability of local breeds to produce in such conditions, due to their rusticity and their productivity in relation to the environment, should be fully evaluated.

Niche products are appealing because they may combine, at a local level, dynamic breed conservation and economic profitability. Niche products are generally more expensive than standard products, and their success will depend on the buying power of consumers. Thus, niche products appear to present a very good opportunity to preserve local breeds in a favourable economic context such as may be found in developed countries. Niche products may not be so easy to develop in developing countries. Cultural practices are also key factors in the successful development of niche products.

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Community-based management of farm animal genetic resources in practice: framework for focal goats in two rural communities in Southern Benin

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Summary

This paper describes and analyses the process of implementing participatory community-based management (CBM) towards sustainable management of goat genetic resources in two rural communities in Southern Benin from November 2005 to February 2007. The process started with the selection of the communities. This was followed by a participatory situation analysis, identification of problems and of possible solutions, and the provision of relevant information and training to interested farmers. It was facilitated by a multidisciplinary research team composed of a specialist in livestock production systems, a socio-economist and an agronomist. The interaction between the research team and the farmers aimed to develop and implement community led strategies towards better management and conservation of the local resources of goat. The approach adopted to facilitate the creation of representative, accountable and legal local institutions and the efforts made in ensuring their empowerment are described. It has been shown that once local people recognise the benefits of such community-based activities and are offered the relevant information and technical support, they can organize themselves effectively and take appropriate actions to better manage and conserve their local resources. The interactive nature of this approach allows its rapid adjustment to different local conditions and thus its replication elsewhere.

Résumé

Cette étude décrit et analyse le processus d’élaboration et de mise en œuvre de mécanismes pour une gestion à base communautaire des ressources génétiques caprines dans deux communautés rurales au sud du Bénin. La première étape de cette recherche-action initiée en Novembre 2005 par une équipe pluridisciplinaire composée d’un spécialiste des systèmes de productions animales, d’un socio-économiste et d’un agronome est la sélection des communautés. Elle a été suivie par un diagnostic participatif des conditions actuelles d’utilisation des ressources caprines locales, par l’identification des contraintes et des solutions possibles, par des échanges d’informations pertinentes entre communautés rurales et chercheurs et par l’organisation de séances de sensibilisation et de formation à l’intention des éleveurs. Les résultats ont montré que lorsque les communautés locales sont informées du danger que représente la perte de la diversité génétique animale pour leur bien-être social, culturel et économique, et qu’elles bénéficient d’un appui technique adéquat, elles peuvent s’organiser de manière efficace et développer des stratégies appropriées pour mieux gérer et conserver leurs ressources zoogénétiques locales.

Resumen

Este estudio describe y analiza el proceso de elaboración y puesta en marcha de mecanismos para una gestión con base comunitaria de los recursos zoogenéticos caprinos en dos comunidades rurales en el sur de Benín. La primera etapa de esta acción-investigación inició en noviembre 2005 con la selección de las comunidades por parte de un equipo pluridisciplinario compuesto pour un especialista en sistemas de producción animal, un socioeconómico y un agrónomo. A esta etapa siguió un diagnóstico participativo sobre las condiciones actuales de utilización de los recursos locales en caprinos, una identificación de las limitaciones y de las posibles soluciones utilizando los intercambios de informaciones pertinentes entre las comunidades rurales y los investigadores y la formación de ganaderos. Los resultandos han mostrado que cuando las comunidades locales están informadas del peligro que representa la pérdida de diversidad genética animal para el bienestar social, cultural y económico, y si se les proporciona apoyo técnico adecuado, pueden organizarse de forma eficaz y desarrollar estrategias apropiadas para una mejor gestión y conservación de sus recursos zoogenéticos locales.

Key words: *Community-based management, Goat, Improvement program, Participatory research, Open-nucleus breeding scheme.*

Introduction

The increasing recognition that conservation of natural resources is unlikely to be sustainable over the long term unless the local communities whose lives depend upon these resources are actively involved and their needs considered (Campbell and Vainio-Mattila, 2003; Mascia *et al.*, 2003; Chan *et al.*, 2007) has resulted in the development of a new conservation paradigm of 'community-based natural resource management' (CBNRM). CBNRM asserts the principle of management of natural resources by, for, and with local communities (Western and Wright, 1994) and recognizes that local people have sophisticated knowledge of local ecological and social conditions that can be effectively used to manage natural resources (Berkes *et al.*, 2000).

The concept of community-based management of farm animal genetic resources (CBMFAnGR) builds on principles of CBNRM. It refers to a system of FAnGR and ecosystem management in which the livestock keepers organize themselves and play a central role in identifying their FAnGR and in implementing all activities related its conservation and sustainable use (Rege, 2001). Effective participation of the communities and their empowerment are determinants for the success of a CBNRM program (Little, 1994; Ghimire and Pimbert, 1997; Berkes, 2004) and appropriate legal and self-reliant local institutions are necessary for its sustainability (Ostrom, 1990; Brett, 2003). The same is true of any livestock genetic improvement program (Kahi *et al.*, 2005; Kosgey *et al.*, 2006). It is also argued that '*Open Nucleus Breeding Schemes*' (ONBS) could be an appropriate strategy for genetic improvement and conservation of animal genetic resources under smallholder production systems (Kiwuwa, 1992; Mueller *et al.*, 2002; Olivier *et al.*, 2002). The thrusts of the action research described in this paper are to:

- Empower, organize and enhance the capacity of local communities to sustainably use and manage their small ruminants.
- Create a legal and financial framework that supports community-based initiatives.

Materials and Methods

The methodology applied in this study is an iterative approach adapted from Sultana and Thompson (2003). It includes 4 major steps (Figure 1) and a lot of small steps within each major step.

Selection of communities

For the purpose of this study, the definition of community has been restricted to that of a village. Two communes, Come and Toffo (Figure 2) were selected because of the relatively high proportion of poverty in their populations. According to WFP (1998), about 24% of the population in Come and 26% in Toffo live below the poverty threshold. Come is located in the fishery area about 60 kilometers west of Cotonou, the economic capital of Benin, whereas Toffo is located about 80 kilometers north west of Cotonou. An initial assessment was carried out in November 2005 to select in each commune, a representative village out of four pre-selected. Village leaders were first contacted by a representative of the local agricultural extension service in Come and by a research and development agent of the National Agricultural Research Institute in Toffo.

Following an initial expression of interest by the village leaders, a meeting with local resource persons was arranged in each village. These resource persons were identified and informed together by the research team and the local authorities. The following topics were discussed during the meeting: the species of livestock kept in the community, their importance, priority species

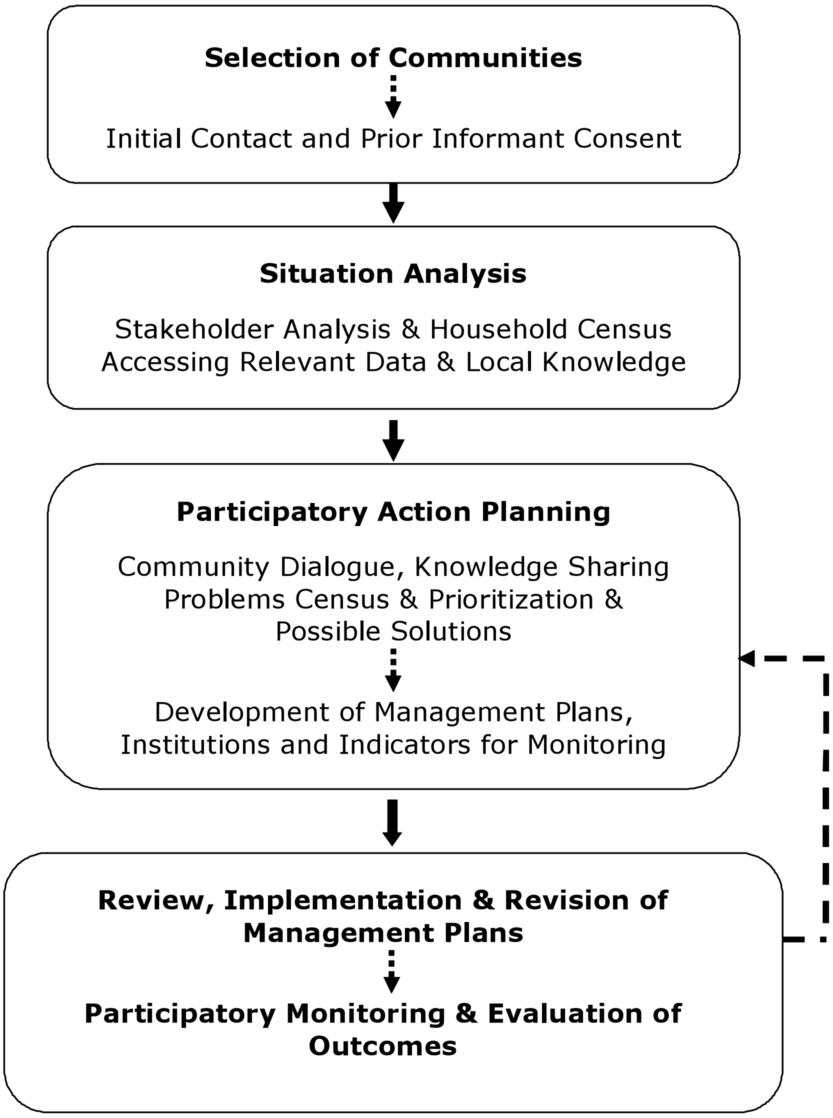

Figure 1. Methodological approach.

for eventual research action and the existence of any previous community based initiatives. Subsequently, the village of Ouedeme-Pedah in Come and the village of Gbede in Toffo were selected based on following criteria:

- Relative importance of small ruminants.
- Accessibility in all seasons.
- Pristineness: locations where no previous long-term research projects had been conducted and that were not connected to national research institutions.
- Interest of village leaders in participation.

The field work team consisted of a specialist in livestock production systems, a socio-economist and an agronomist. This team was reinforced in each research location by a livestock technician and a private veterinarian. In Gbede, the technician was a research assistant from the National Agricultural Research Institute, whereas the technician in Ouedeme-Pedah was a livestock extension officer. Together with the veterinarians, they provided the institutional support and acted as facilitators.

Initial village meeting and socio-economic studies

In each village selected, local leaders were asked to arrange for a village meeting where the research team provided the participants with all information related to the project, its objectives and benefits. The

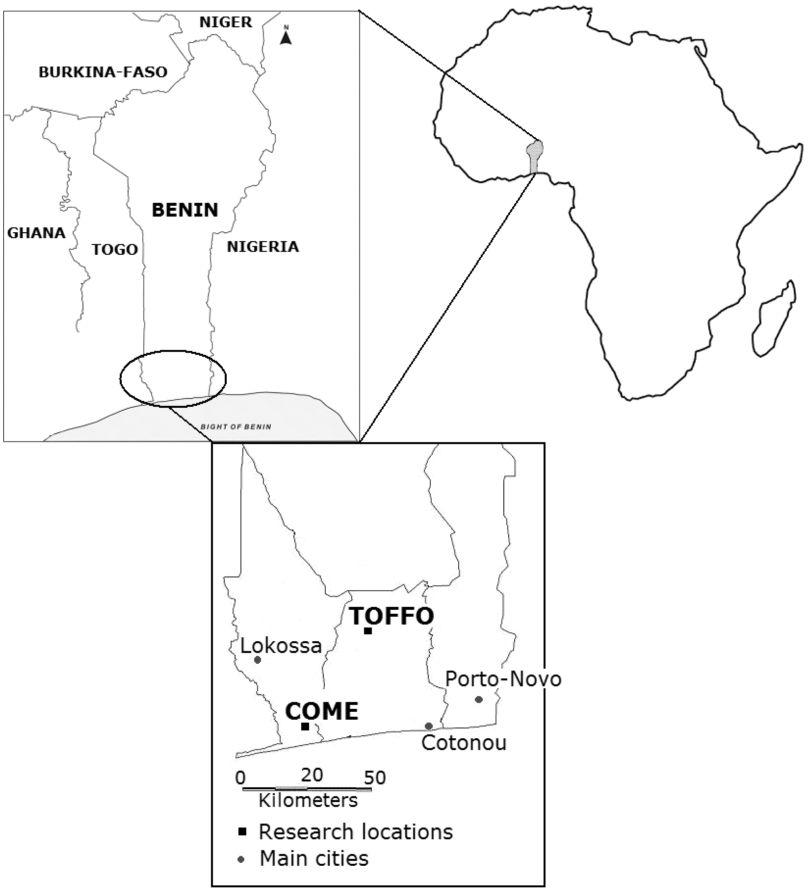

Figure 2. Research locations in southern Benin.

'*Prior Informed Consent*' (PIC) was obtained from the communities and was followed by the situation analysis which encompassed several socio-economic studies. It started with a participatory village social and resource mapping and seasonal calendar. Transect walks were done with community members to consider the geographical boundaries of the communities, their natural resources and related issues. One of the main concerns of the research project was to ensure that in each village, the socio-economic conditions and the concerns of the most vulnerable people keeping livestock were understood and taken into account during the development of the CBM framework. Therefore, three key informants were identified in each village based on their level of participation during the resource mapping and on their knowledge of the village for a participatory wealth rank exercise. A list of household heads living in the village was obtained from the chief of the village and was updated together with the key informants. Each key informant was interviewed separately. He was first asked about his own perception of wealth and poverty. Then he was asked to sort cards containing the name of the head of households into pile representing the wealth status of each household according to the method described by Grandin (1988). More detailed surveys of a random sample households stratified by wealth classes was done to find out more about their sources of income and the contribution of different livestock species to their livelihoods. Focus group discussions and in depth interviews in randomly selected households were carried out to understand the ownership patterns of small ruminants, to record owners' local technical knowledge, their perceptions of constraints and their traits preferences.

Participatory planning

Following the socio-economic studies, feedback meetings were held in each village in December 2005 to share information, to discuss and validate

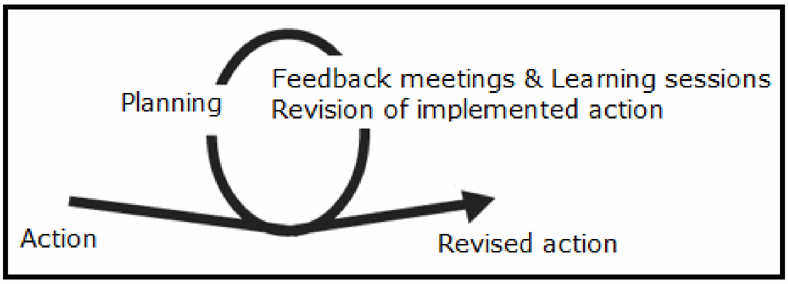

Figure 3. Management plan implementation loop.

the findings of the socio-economic studies and to mobilize communities towards CBM action planning. An interim planning team was elected and was responsible for the timing and organization of the next planning meetings. During subsequent village meetings and workshops, participants discussed, ranked and decided on key problems, determined causes and effects and proposed possible solutions. In each village, the interim planning team was assisted by a trained community development facilitator who was charged with the responsibilities of facilitating and supporting group development processes to reach the maturity and performance stages. This was achieved initially through supporting the facilitation of meetings and group dynamics, training and support in leadership skills, record keeping, and training in other areas of group development as well as providing specific technical support and linking groups with service providers. Various participatory tools such as brainstorming, ranking, problem and solution games, process diagrams, matrices and visualization techniques (for a review see Waters-Bayer and Bayer, 1994; Catley, 1999) were used.

Review, implementation and revision of management plan

This phase was overlapping with the participatory planning phase and involved regular facilitated feedback meetings and interactive learning sessions. In an iterative way (Figure 3), implemented actions were discussed, revised and the overall management plan readjusted accordingly.

Results and Discussion

Community mobilization and exchange of knowledge

Initial investigations during baseline surveys indicated that the communities in Gbede and Ouedeme-Pedah were suspicious about outsiders, government and NGO led development initiatives. This implies that a few local leaders would prevail in most community decisions. Therefore, at the first village meeting, the research team was successful in avoiding the risk of raising financial expectations by discussing short-term and long term benefits of the research project. It has been observed that some community members, mainly local ‘elites’ lost interest in participating in the research activities when the communities were told they would not be getting any handout of money but only facilitation and training.

Through the different steps of the mobilization phase, the research team was successful in gradually convincing the participants that the research project was for their own benefit. The different participatory rural appraisal techniques used in this process were helpful in entering the communities, in getting to know the people and the natural resources (including farm animal resources), in establishing relationships with the communities, in collecting and sharing information, in building mutual trust and in improving the understanding of the different sources of livelihood. First and foremost the participatory village resource mapping exercises (Figures 4 and 5) revealed that people have a valuable knowledge of the natural resources, including domestic animal resources and forage plants available in their environment.

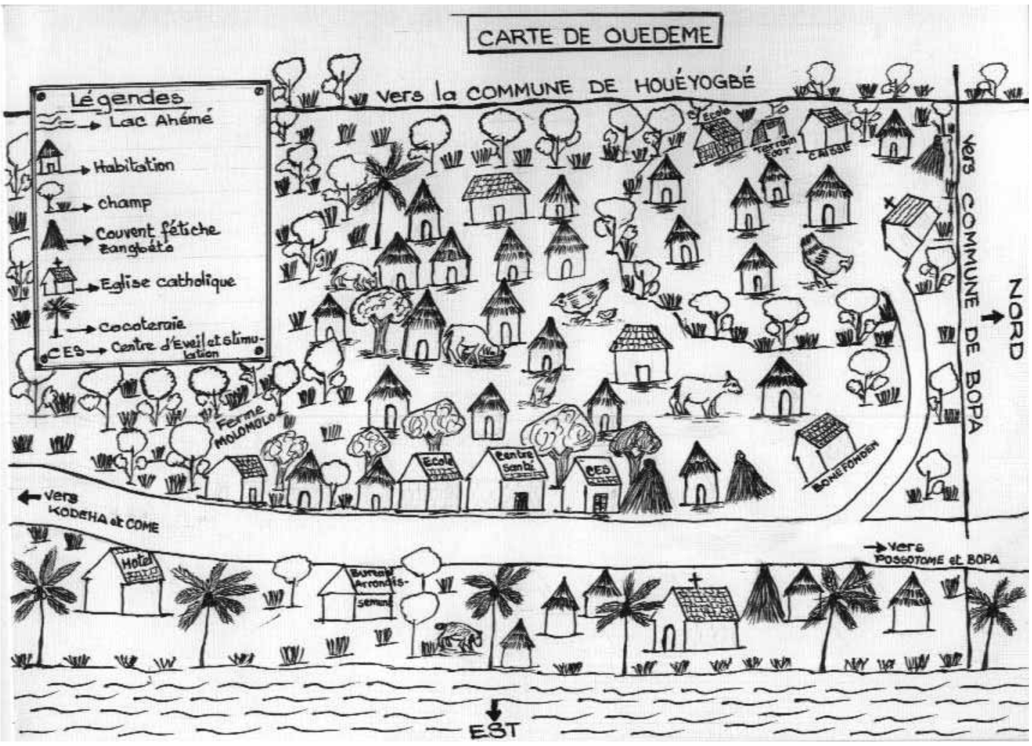

Figure 4. Sketch map village of Ouedeme-Pedah as drawn by community members.

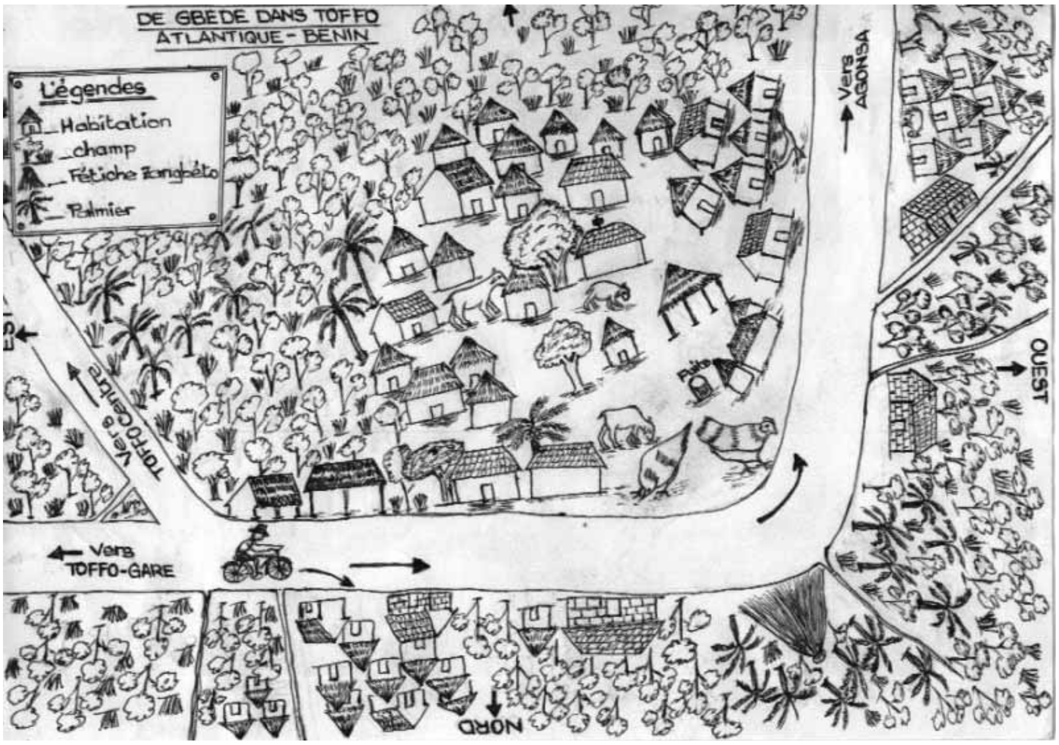

Figure 5. Sketch map village of Gbede as drawn by community members.

Table 1. Indicators of wealth in village Ouedeme-Pedah.

Criteria	Wealth classes		
	Rich	Medium	Poor
House and type of roof	Large houses with concrete walls; sheet-metal or tile-roofing; cemented floor	Houses in banco/clay walls; sheet-metal or tile-roofing; cemented or mud floor	Houses in banco/clay walls; straw roofing and mud floor
Number of fishing gears owned	4 and more	2-3	1
Transport means	4 and more dugout canoes; motorcycle and bicycle	2 dugout canoes, motorcycle or bicycle	1 dugout canoe
Agricultural land holdings	5 ha and more	1-3 ha	≤ 1ha; landless; sharecropping
Livestock owned	Large number of pig, goats, chicken, grass cutter	Pig, goats and chicken	Few goats and chicken
Labour employment	Employ labour	Employ labour but at lesser extent than the better-offs	Household members are casual workers and husband migrates during raining season to find non-fishing work
Education of children	Children attend school regularly	Children attend school irregularly	Interruption schooling of children
Financial status	Can borrow to other households	Can take a loan	Cannot take a loan
Other	Receive high social and political consideration	Use rarely basic medical services	Face food shortages; do not use basic medical services

Rare natural vegetation encountered in Ouedeme-Pedah are baobab trees (*Adansonia digitata*), iroko trees (*Chlorophora excelsa*) and bushes of mangroves (*Avicennia germinans* L.) in the most humid areas whereas planted vegetation included neem trees (*Azadirachta indica*), eucalyptus (*Eucalyptus camaldulensis*), acacia (*Cacia africana*) and coconut trees (*Cocos nucifera*). In Gbede, planted teak trees (*Oldfieldia africana*) and oil palms (*Elaeis guineensis*) predominate. The *Pedah* people are the dominant ethnic group in Ouedeme-Pedah and they live primarily on small-scale fishing and subsistence agriculture. The *Aizo* people dominate in Gbede. Agriculture is their major economic activity. The main food crops grown in both villages are maize, cassava and beans. Similar beliefs and religious practices were observed among both communities.

Key informants in both villages divided households in three wealth classes: rich, medium and poor households. Out of a total of 47 households ranked in Ouedeme-Pedah, 45% were ranked poor, 34% medium and 21% rich. Similar figures (46%, 35% and 19% respectively) were obtained in Gbede for a total of 66 households. Table 1 shows the characteristics of each wealth group as described by informants in Ouedeme-Pedah. Irrespective of the village and irrespective of the wealth group, chickens followed by goats and sheep were the most kept important livestock species. In Ouedeme-Pedah, pigs were also kept by some households. However, despite the predominance of chickens over goats, the latter species was selected in the two communities as priority species for the purpose of the intended CBM research action.

The village goat surveys generated interesting information about breed perception, trait preferences and production constraints (Dossa *et al.*, 2007). Apart from the introduced goat types from

Table 2. Outcomes of the consolidated analysis of goat production problems in Gbede and Ouedeme-Pedah.

Constraint	Cause	Effect	Solution	Level of application
Lack of appropriate housing	• Lack of knowledge on improved housing	• High losses and mortality rates due to: - Lack of protection of animals against bad weather conditions and contagious diseases - Missing to identify and to treat sick animals - Consumption of poisonous plants and dirty water by wandering animals - Road accident - Theft - Destruction of crops • Tethering during cropping seasons leading to malnutrition	• Farmer training in improved goat housing • Construction of improved goat houses	Both individual and community
Disease outbreaks	• High costs of veterinary services on individual basis • Difficulty to stock up on veterinary drugs for routine treatments • Lack of regular vaccination against epidemic diseases • Lack of regular control of internal and external parasites • Lack of appropriate housing =>close contact with infected free roaming goats • Poor hygiene • Poor nutrition	• High mortality rates • Small herd sizes with born-in herd bucks, very few village bucks • High risk of inbreeding and delays in conception • Kids grow slowly • Very few goats to sell year-round • Reduced profitability	• Farmer's training in improved management practices • Adoption of improved housing for animals • Adoption of Improved health through - Training on basic animal healthcare and hygiene - Establishment of a Drug-box at village level - Organization by the village committee of regular and collective vaccination against PPR, - Organization by the village committee of regular and collective control of internal parasites - Strict regulation of the introduction of imported animals into the village • Castration of unwanted and poor quality male goats • Adoption of improved nutrition • [1]Purchase and rotation of a village buck among participating herds • [1]Purchase by the village committee and use of Burdizzo castrator to castrate unwanted or/and poor quality male goats	Both individual and community
Feed shortage	• Seasonal fluctuation in feed availability • Lack knowledge on rational uses of available feed resources	• Poor or unbalanced nutrition • Weak animals open to infections from bacteria or/and parasites • Slow kid growth and bad body condition	• Farmer training in - Improved nutrition - Improved cut and carried feeding system - Rational use of crop residues and agro-by-products	Community

[1]Mentioned in Gbede only.

Table 3. Outcomes of the consolidated solution analysis in Gbede and Ouedeme-Pedah.

Village	Solution/Action	Purpose	Alternative	Political/ social impact	Technical/ economic aspect
Both Gbede and Ouedeme-Pedah	Adoption of improved housing	• Enable better management of individual herd • Reduce mortalities due to contagious agents and to non diseases related factors • Reduce morbidity rates due to sarcoptic mange • Reduce conflicts between farmers inherent to the free-roaming system	None	Individual participant farmers as well as community will benefit	Need training and demonstration from resource persons
	Strategic use of anthelmintics and wilting of cut and carried forage before feeding	• Elimination of the internal parasites burden • Increase feed conversion by the animals	None	Individual participant farmers as well as community will benefit	Need technical assistance from specialized staff
	Organization of annual collective vaccination program against PPR	• Reduce mortalities due to PPR	Individual action against PPR	Individual participant as well as community will benefit: increase ability of participants to work together and enhance social cohesion	Need technical assistance from specialized staff
	Adoption of improved feeding	• Reduce malnutrition, abortion and pre-weaning mortalities rates	None	Individual participant will benefit	Need training and demonstration from resource persons
	Strict regulation of introduction of imported animals into the village	• Conservation of local goat through avoidance of indiscriminate crossbreeding • Reduction of risks of introduction of imported diseases and infectious agents	None	Individual participant as well as community will benefit: increase ability of farmers to work together and enhance social cohesion	Need advices from resource persons
	Castration of unwanted/ poor quality male	• Reduce risk of inbreeding and make better use of the best performing village bucks	Individual control of mating	Individual participant as well as community will benefit	Need technical assistance and training from specialized staff

(To be continued…..)

(... continued).

Village	Solution/Action	Purpose	Alternative	Political/ social impact	Technical/ economic aspect
Gbede	• Training of two (02) farmers appointed by the community as local castrator in the use of the Burdizzo castrator • Commitment of participants to share the expenditure for the purchase of a Burdizzo castrator and two (2) communal bucks of local breed for breeding purposes • Rotation of the communal bucks among participating herds. After a year of service, the communal bucks will be sold and renewed	• Reduce risk of inbreeding and make better use of the best performing village bucks	• Individual control of reproduction • Surgical removal of testicles (traditionally used castration method)	• Individual participant as well as community will benefit	• Need technical assistance and training from specialized staff
	• Training of two (02) farmers appointed by the community as Village Animal Health Workers and establishment of a village based drug box	• Trained farmers provide general advice on health and husbandry and basic animal health services to other farmers in the same village	• Individual contact with the Private vet which are far away from the village and not easily reachable	• Individual participant as well as community will benefit: increase ability of farmers to work together and enhance social cohesion	• Need technical assistance from specialized and resource persons/ Need financial support from micro-credit institutions or NGOs
Ouedeme-Pedah	• Establishment of a village based drug and feedstuff store supplied by a private veterinarian but collectively managed by the community	• Close and permanent contact with the veterinary services • Reduction of transport costs	• Individual contact with the Private veterinary services which are located at about 20 km far away from the village and not easily reachable	• Individual participant as well as community will benefit: increase ability of farmers to work together and enhance social cohesion	• Need continuous monitoring of the private veterinarian

Table 4. Indicators and participatory monitoring arrangements agreed through CBM workshops in Gbede and Ouedeme-Pedah.

Village	Indicator/output	Type of monitoring	Responsibility
Both	• Adoption by participants of improved management practices including regular vaccination against PPR and anthelmintic treatment • Decrease in disease incidence and mortality rate in participating herds • Increase growth rate of animals in participating herds • Decrease rate of abortion in participating herds • Increase in number of marketable animals in participating herds • Increase in overall herd productivity in participating herds • Adoption by participants in the Community-based management program of a participatory recording system • Adoption of the Burdizzo castrator • Castration of undesired/low performing males intervene 3-4 months of age	• Regular meeting and training sessions on different aspects of small ruminant husbandry practices and on recording system throughout a year: Application of the "Farmer Field School" approach	• Village committees with the assistance of the specialized staff and resource persons
Gbede only	• Effective rotation of the communal purchased bucks among participant herds	• Only farmers who confine their animals and adopt improved management practices can receive the buck. The buck can stay in a herd for a maximum of 30 days and should then pass to another herd. No specific performance recording was planned.	• The village committee should ensure the effectiveness of the rotation system. After a year of service, the communal bucks will be sold and new one bought

northern Benin and from neighboring Sahelian countries, owners of goats in both villages clearly distinguished two varieties of goat native to southern Benin: the markedly dwarf and the short legged but non-dwarf. Although farmers perceived the markedly dwarf goat as more prolific and more resistant to disease than the short legged but non-dwarf, they considered that its growth is slower and it fetched relative lower prices on the market. Group discussions with elders in both villages revealed that the markedly dwarf goat was the most common goat variety encountered some decades ago. However, it has been progressively replaced by the non-dwarf goat and currently represented less than 2% of the breeding female goats counted in both villages. Communities also have a good knowledge of the seasonal occurrence of the major goat health problems and some valuable ethno-veterinary medicine practices. A number of locally available fodder resources are considered by farmers to have anthelmintic properties. The most promising plants include *Fagara zanthoxyloidès*, *Morinda lucida*, *Moringa oleifera*, *Newbouldia leavis* and *Spondias mombin*.

Planning with communities

During consecutive village meetings and workshops, the key problems, their causes and effects, the possible solutions and remedial actions and sets of criteria for assessing these actions were developed by each community. The results were very similar in the two villages (Tables 2, 3 and 4). In each village, the interim planning team worked out the timing, resources needed and the persons or institution(s) which would be responsible for ensuring implementation of each action. The interim planning team presented the first draft of the management plan to the wider community through village meetings. During this process the plan was discussed, additional issues were raised and the revisions took place. In the two villages, alongside CBM development activities, short term initiatives to improve productivity such as construction of improved goat housing, vaccination against Pests of Small Ruminants (PPR) and the adoption of other animal health control measures were taken up. These collective activities were done with the technical support of the research team and were aimed at motivating people to implement long-term and rational initiatives for better management of the goat resources.

Creation of local institutions towards CBM

Structure and legal framework

The intensive and long-term facilitation process was extremely helpful in preventing some local or village elites to dominate the decision-making and in giving voices to marginalised members of the communities, especially women. In each village, a CBM committee was elected to replace the interim planning team. In most cases, members of the interim planning team were appointed to the CBM committee which were made up of seven democratically-elected members in Gbede and of twelve in Ouedeme-Pedah, including a Chair, Vice-Chair, Secretary, Treasurer and Vice Treasurer. They are responsible for the planning, the implementing, the co-ordination and monitoring of the collective activities which have been agreed by the community at general meetings. The elected committees must maintain bank accounts and financial records, report on performance to the community, organize and manage community meetings.

Once the management plan was formally agreed, the research project team maintained regular contacts with the elected CBM committees and provided the technical support agreed to under the plan. By then in each village, the CBM committee had started to draft self-imposed rules and regulations. The final self-imposed rules and codes of conduct were validated during a village workshop. As an important rule in both communities, the introduction of animals of any non-local genotype for breeding purposes is banned. In addition, the introduction of any breeding animal in the village must be subject to authorisation by the CBM executive committee. This authorization will be granted only when the animal is declared by the local veterinary officer to be clear of any infectious disease. Mechanisms were laid down for the enforcement of these rules. Membership was open to any villager who was committed to the objectives of the CBM group and its rules and regulations.

Institutional formalization

Institutionalization of a community-based organization (CBO) towards management and/or conservation of natural resources includes its creation, but also its legalization with reference both to the local and national level (World Bank, 1999). In Benin, to be legally recognized, a CBO must go through a process to involve relevant agencies which are under legislation charged to administer the management of local communities. These are the Ministry of Agriculture Livestock and Fisheries (MAEP) and the Ministry of Decentralisation and Local Communities (MDCL). Upon reaching agreement with the community on the rules and regulations, the formalization process was begun by sending the CBM documents to the municipalities of Come and Toffo, which are decentralized institutions representative of the MDCL at local level. The two CBM groups soon received notification of their legalisation.

Financial framework

During the participatory phase, the research team consistently emphasized local initiatives and self-reliance. In response, the communities mobilized their own funding through cost-sharing to implement the first developed community management improvement initiatives such as the installation of a small animal feed store in Ouedeme-Pedah, and the purchase of a Burdizzo castrator and of two bucks for breeding purposes in Gbede. In addition, in both villages the CBM groups have established initial registration fees and monthly subscriptions that all members can afford. Each CBM group has opened an account at a local credit and saving institution.

Experiences have shown that the dependence of CBOs on external donor funding has often led to lack of sustainability (Platteau and Abraham, 2002) while for its long term viability, a CBO needs to have a secure and sustainable funding base from the beginning. It has also been argued that in poor communities, local contributions are usually not sufficient (Swantz, 1997; Kleemeier, 2000). To complement the membership fees, the need to generate monetary resources within both communities through income generating activities that will add value to the communities' core activities has been acknowledged. It has been recognized that the process in which community-based organizations engage to stimulate or maintain business activity is generally a cost-effective and community-empowering process which can yield tangible benefits for participating communities (Binns and Nel, 1999). However, it has been argued that some communities, for instance the poor, often do not have the financial resources to initiate theses activities and that any newly developed local institution concerned with the conservation of natural resources requires some external financial inputs at least in the short term to gain internal legitimacy and acceptance at both village and regional levels (World Bank, 1999). In addition, it is widely agreed that time is required for newly developed institutions to be tested, reviewed and adapted by their members before internal legitimacy can be achieved. Therefore, although income accruing from better management of goat constitutes an undeniable incentive to maintain participation in the CBM groups, each CBM group also received from the research project a community-empowerment fund of 200 000 FCFA (1 euro = 655.957 FCFA).

Participation of women and poorer people

The participatory approach used was also very successful in involving women in the whole process from the outset and in ensuring gender equity. Women have actively attended all the meetings and have participated in all planning and decision-making forums. The confidence and competence they have gained through their active participation in the planning and decision-making process have empowered these women to take a greater role within their community. They were well represented in both CBM groups as a whole, and in the CBM executive committees as shown in figure 6.

In Gbede, it is worth noting that in the elected CBM executive committee, the Treasurer, Vice Treasurer and auditors were women. In order words, they were responsible for the management of the community financial resources. The communities' decision to elect women to these positions was probably based upon their belief that the women would be more transparent, prudent, reliable and honest in handling the community money. Research has found that female representation and effective participation in a peasant committee enhances the committee's performance (Molians, 1998).

The participation of poorer people was also effective in both CBM groups as illustrated in figure 7, and has proved successful in impeding the better-off community members from dominating the decision-making process.

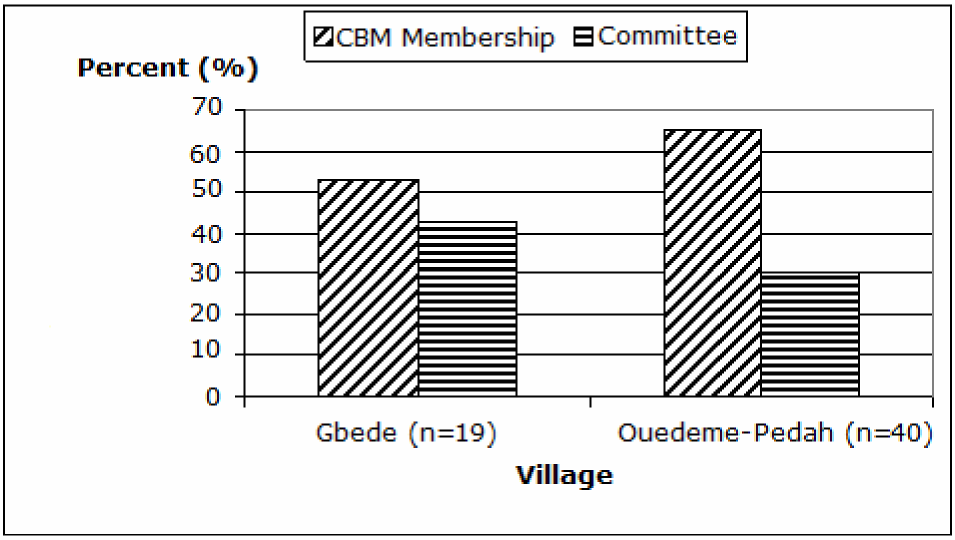

Figure 6. Representation of female people in CBM groups and in executive committees.

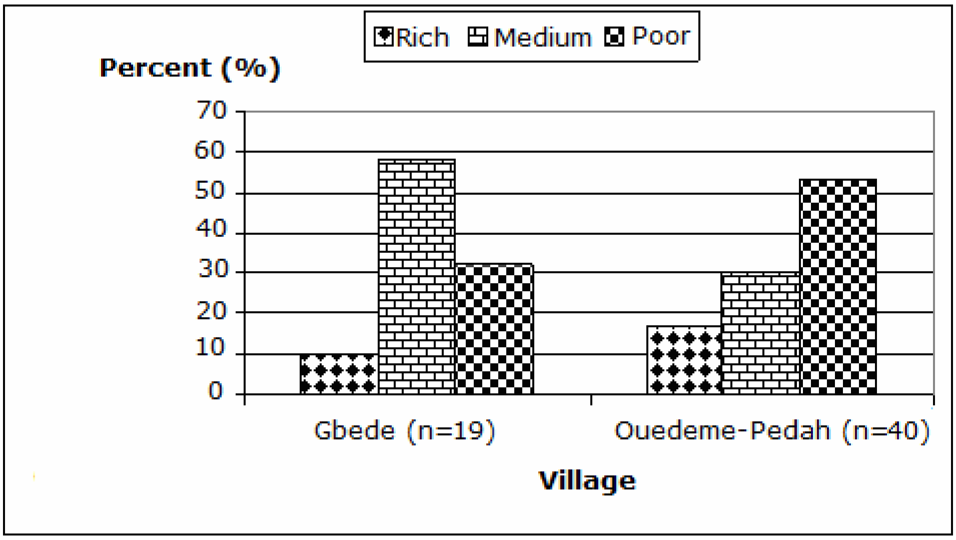

Figure 7. Participation of different wealth classes in CBM groups.

Training and capacity building

Two general training and demonstration sessions were initiated and organized in each community close to the beginning of the CBM process. The objective was to improve goat farmers' management skills as identified by farmers themselves at the early stages of the participatory planning process.

Each training session lasted a full day. Although these sessions covered all general aspects of goat keeping, emphasis was put on improved housing, feeding and disease control. The training sessions were facilitated by the research team, but the lead trainer was a successful farmer identified by community members themselves. The number of participants ranged from 17 to 25 in Gbede and from 23 to 37 in Ouedeme-Pedah. This 'farmer-expert' training approach was inspired by the well-known Livestock Farmer Field School (Minjauw, 2001). Although there has been yet no formal survey to measure the adoption by participants of the improved management techniques discussed during these sessions, a growing interest has been observed among community members. For example, actions were taken and 19 participant herds of goats in Gbede and 40 in Ouedeme-Pedah were successfully vaccinated against PPR and treated against internal and external parasites. For both disease preventive measures, a nil coverage rate was reported for the

Table 5. Chronology of events in planning and implementing CBM actions.

Date	Event
07 – 09 November 2005	First formal contact with selected communities and PIC
Situation analysis	
10 – 28 November 2005	▪ Wealth ranking with key informant ▪ Household census (socio-economic studies) ▪ Participatory village resource and social mapping ▪ Focus group discussions
Participatory planning for CBM actions	
December 2005	▪ Village meetings to validate PRA results and to agree on the major goat problems ▪ Election of the interim planning committee
January – September 2006	▪ Elaboration of the by-laws rules and regulations by the interim planning committee ▪ Meetings to validate village by-laws rules and regulations ▪ Election of village CBM committee
November 2006	▪ CBM committee members received training in team-building, goal setting, program planning, community problem-solving, conflict resolution and finance ▪ Finalization and validation by community members of CBM code of conduct document
December 2006 – February 2007	▪ Communities discussed with research team the feasibility, concepts, aims, benefits, legal and genetic aspects of a potential community-based genetic improvement program
January 2007	▪ Village CBM documents finalized and sent to the decentralized representation of Ministry of decentralization and local communities
Implementation of plans and monitoring	
December 2005	▪ Facilitated “Farmer’s expert” training workshops in improved goat housing and in improved goat nutrition
March 2006	▪ Vaccination against Pest of small ruminant and treatment against internal parasites and mange
April 2006	▪ Purchase of a Burdizzo castrator and castration training of two community members in Gbede ▪ Purchase of two (02) communal bucks in Gbede ▪ In commitment with a private veterinarian a small shop of veterinary products and animal feed was established in Ouedeme-Pedah
From May 2006 – ongoing	▪ Individual follow-up of CBM participant herds and recording of performance in each village
January 2007	▪ Two representatives of each community received training in community animal health services ▪ Each CBM group received a development fund of 200.000 FCFA
February 2007	▪ Vaccination against Pest of small ruminant and treatment against internal parasites and mange

previous year by the veterinarians in both communities. Likewise, increased adoption of improved housing and use of a Burdizzo castrator has been observed in both communities. The assumption is that continuous increased adoption could be achieved through further Livestock Farmer Field School sessions. In Gbede, two community members were designed by the community to assist the veterinarian during operations of castration in order to learn and to be able to perform the same operations later within the community. Furthermore, in response to the need to reinforce the community leadership skills and to promote interdependent leadership practices, supplemental advisory services and training in meeting-related activities such as team building, goal setting, program planning and community problem solving in conflict resolution and finance were provided to each CBM committee. The five day training program was designed by instructors from a local NGO who have expertise in leadership development, group dynamics, conflict management, problem solving, communication, managing change and community development. In addition, two people (a woman and a man) were appointed in each community by members to receive further training in animal health. The six day training in community animal health services was provided in both communities by a training team composed of a chief veterinarian and a technician, and will be repeated every three months.

Monitoring of implementation of planned activities

Table 5 shows the chronology of events in planning and implementing CBM actions. Implementation was facilitated through regular meetings of community members and planned interactive learning sessions. During the planning phase, community members identified some indicators for monitoring the outcomes of the CBM process. However, because of the lack of a well-established recording system in both communities, no formal monitoring of herd could take place. Therefore, at the outset of May 2006, a one-year participatory follow-up of individual herds of participants in the CBM program was implemented in both communities. Its main objective was to facilitate the establishment of a participatory recording system. For this purpose an enumerator was recruited and trained for each community. Animals in each herd were identified using a collar. Collars were previously used by farmers just to define ownership. For recording purposes, each animal was given an identification number which was printed on a piece of wood with hot iron. The piece of wood was then added to the collar and attached to the neck of the animal. Wood is a locally available material and does not create any cost to the farmer.

Therefore, it is expected that this method of identification will be easily adopted by farmers and will facilitate the establishment of a suitable recording system. Each community was provided with two scales. The pursued objective was to familiarize individual farmers with some basic recording tasks such as weighing a new born kid and animals before sale. In addition, an enumerator was recruited in each community and trained in recording. He is based in the village and visits each herd every two-week. He records from each CBM participant, the events that have occurred in the herd since his last visit and weights the animals. He also provides farmers with advice on management issues.

Towards a community-based genetic improvement program

In both communities, various factors have been identified that constrain the development of effective genetic improvement programs. These factors include the small sizes of the herd and the lack of proper management practices (recording, feeding, housing and disease control). During the planning process, farmers in both communities have developed initiatives to overcome these constraints and to achieve increases in productivity in the short term while creating favorable conditions for genetic improvement. One of these conditions is the increased number of participating herds. As stressed by Olivier *et al*. (2002), when a farmer has one or two animals as occurs now in both communities, knowing the performance of an individual animal becomes relevant only when related to the performance of all other animals in the village. Similarly, Van der Werf (2000) argues that in larger populations, consisting of a larger group of farmers, there is more opportunity to exploit the existing variation among animals, thus creating more potential for genetic improvement.

Further participatory planning meetings were held with both communities. During these meetings, the concepts, aims and benefits and the legal and genetic aspects of each genetic improvement scheme as well as their feasibility were discussed with participants. In both communities, the principles of

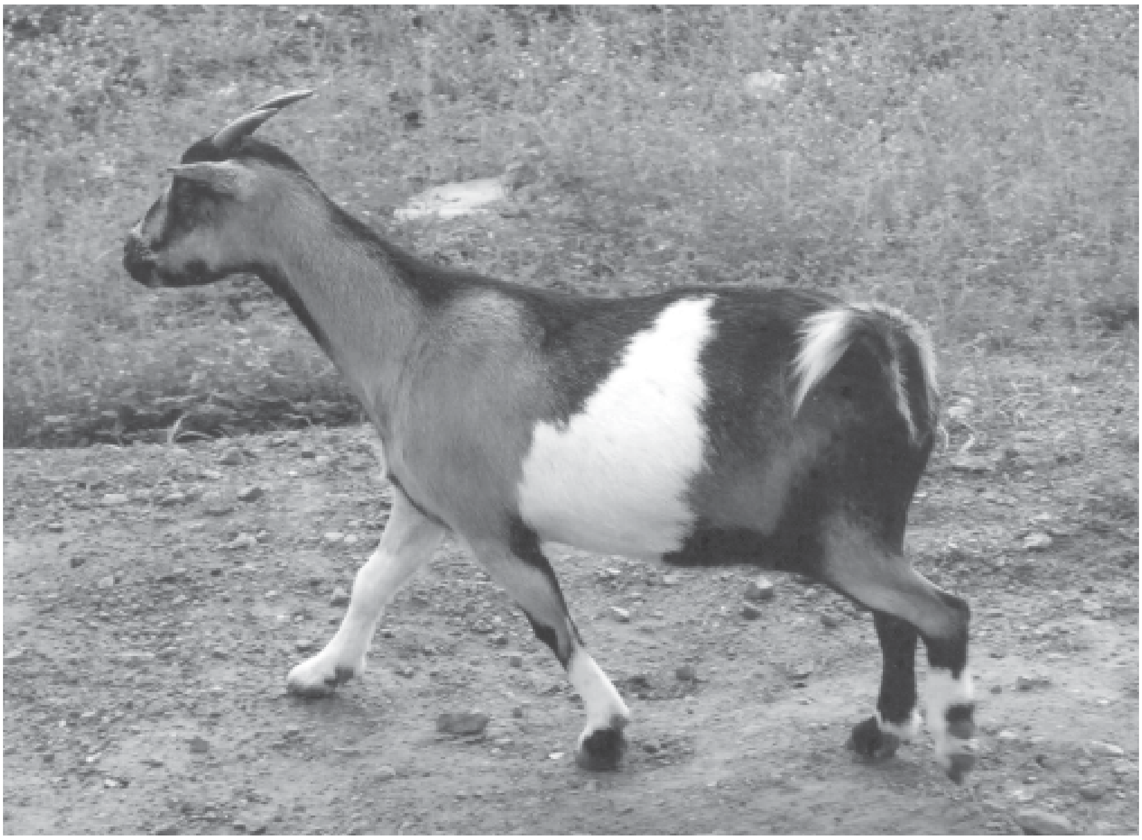

Figure 8. Short-legged but not dwarf goat, Southern Benin.

Figure 9. Dwarf goat, Southern Benin.

open nucleus breeding system (ONBS) has received wide acceptance. Each participant farmer has agreed to contribute the top performing females of his herd to the initial breeding herd.

The one-year screening of individual participants' herds has started in both communities aims to identify the best 50 females and 2-4 males. Height at withers, dam's litter size at birth, individual weight at birth and at six months of age were identified as initial selection criteria. However, these potential donors will not be housed in a central station but will be maintained in their respective herds of origin and a temporary contract will be signed between the CBM program and the individual farmer. The selected top 50 females will be mated with the top 2 males and the best performing offspring purchased by the CBM program to create the village nucleus. This nucleus will be located on land provided by the community and will be managed by the CBM executive committee with the support of a livestock technician acting as a nucleus manager. He will be responsible for performance recording and will be paid with the community funds. As agreed by participants in both communities, only male animals born in the village nucleus should be used in the participating herds whereas transfer of females will occur in both directions between the nucleus and the participating herds. This two-way gene transfer will allow genetic improvements made in the main population to be incorporated into the nucleus and vice-versa. Research by Mueller and James (1983) suggests that when 25 to 50% of the nucleus parents are selected in the base population (participating herds), the rate of increase of inbreeding in the nucleus is minimized and longer-term gains are maximized. In Gbede, farmers suggested replacing the bucks and the poorly performing females in the nucleus herd annually. Mating of relatives will be minimized by avoiding son-dam, daughter-sire and full-sib mating.

Generally, morphological traits including height at withers have higher heritability rate than fitness traits (Falconer and Mackay, 1996). Odubote (1996) obtained heritability estimates of 0.35 and 0.32 for litter size in West African Dwarf goats (Figure 8 and 9) from sire and sire-dam groups respectively. Since West African goats are already prolific (Wilson, 1991), selection for litter size would likely lead to higher incidence of multiple births. Likewise, Bosso *et al*. (2007) reported heritability estimates of 0.5, 0.32 for weight at birth and at weaning respectively. Starting from the results of these previous studies, a great response to selection based on these community-suggested traits can be expected if farmers adopt appropriate management techniques (i.e. improved feeding, disease control, etc.).

Broek van den and Gbégo (1994) recorded a fertility rate of 1.3 and a prolificacy rate of 1.8 in village goats herds kept in balanced nutritional conditions in Southern Benin. However they reported a relatively high yearling kid mortality rate of 27% due to unidentified epidemic disease. With improved disease control, a yearling survival rate of 85% can be an achievable objective in the village nucleus herd and would allow each doe to produce 2 kids per year (1.3* 1.8 *0.85). Annually, there will be a total of 100 yearling animals in the nucleus herd (50 males and 50 females). The top 2 males (4%) should be retained in the nucleus, the next 10 - 15 (20 to 30%) best males made available as breeding males in participant herds and the remaining 66-74% culled. The best 25% of the female animals could be retained annually in the nucleus for breeding purposes, and the 75% remaining culled.

The importance of the adoption of improved management practices by farmers for the success of the program can not be overemphasized. Further selection criteria could be identified and integrated later into the improvement program. The financial implications of such program have been discussed with farmers. The need for technical and financial assistance to create and operate the nucleus at least at the implementation phase of the program has been stressed by the farmers. However, the financial sustainability of the program will depend on the readiness of farmers to pay for the improved bucks they will receive from the breed improvement program.

Further relevant institutional, management and financial issues need to be discussed with the communities and a full proposal developed before the establishment of the outlined program.

Conclusion

The process outlined in this paper was effective in mobilizing in a short duration of time, collective interest and resources towards better management of local goat resources in both research villages. Central to the success of the ongoing Community-based management process are:

- The communities have recognized that their goat resources which contribute to diversification of their sources of income and sustain their livelihoods are vulnerable to mismanagement.

- The communities have perceived the tangible and immediate benefits from the ongoing research activities.
- The participatory research methodology used in this study has proved successful in turning the process into local capacity building and empowerment exercises: by giving the community a forum for the exchange of knowledge and experiences, and for analyzing their problems and finding solutions. By providing them with relevant information and training and by helping them in framing rules and regulations, the research program has enabled local people to discover and enhance their own potential in developing strategies and institutions towards better management of their goat resources.

In both communities, there have been preliminary discussions about possibilities for implementation of a community-based genetic improvement program. Farmers have shown strong interest in establishing an open nucleus breeding program with a central nucleus which would provide participant herds with local bucks of high genetic potential. However, to ensure the success of the implementation of such a genetic program, further discussions and institutional innovations are required. Also, with the adoption by farmers of improved general management practices being of paramount importance, further investigations are planned to scientifically validate the local knowledge of farmers on fodder resources and on ethno-veterinary practices through systematic on-farm experiments and to plan for participatory cost-effective technologies (improved feeding and control of diseases).

After more than twelve months of intensive interaction with the two communities, it can be argued that given some time for consolidation, and continued institutional and technical support, the two newly created CBM groups are highly likely to become self-reliant, socially and economically viable and to generate widely replicable results.

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List of Acronyms

- CBM FAnGR: Community-Based Management of Farm Animal Genetic Resources.
- CBM: Community-Based Management.
- CBNRM: Community-Based of Natural Resources Management.
- CBO: Community-Based Organization.
- FAnGR: Farm Animal Genetic Resources.
- FCFA: Francs de la Communauté Financière Africaine.
- MAEP: Ministère de l'Agriculture, de l'Elevage et de la Pêche.
- MDLC: Ministère de la Décentralisation et des Communautés Locales.
- NGO: Non Governmental Organization.
- ONBS: Open Nucleus Breeding Scheme.
- PIC: Prior Informed Consent.
- PPR: Pest of Small Ruminants.

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South African developed meat type goats: A forgotten animal genetic resource?

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Summary

There are mainly three locally developed meat type goat breeds in South Africa namely the South African Boer goat, the Savanna and the Kalahari Red. In order to maintain the characteristics of these breeds and to ensure that their unique traits are not lost through continuous selection and cross-breeding, it has become important to revisit current breed standards and introduce genetic characterization to obtain genetic diversity parameters. Both the Boer goat and Savanna breeds have established breeders associations while a breeders club was founded for the Kalahari Red goats. These associations have set breed standards and the breeds' morphometric traits have recently been described. The differences in morphometric traits among the breeds are fairly insignificant. Preliminary data on genetic diversity report heterozygosity values above 50% for each of the three breeds and they can be distinguished as separate breeds based on genotyping results with eighteen ISAG recommended microsatellite markers. There is however a need for a genetic characterization of both meat type and indigenous goats to ensure sufficient diversity within the breeds for long term conservation of the unique genetic resource.

Resumé

Il y a en gros trois races de chèvres à viande développées en Afrique du Sud, à savoir la chèvre Boer sud-africaine, la Savanna et la Kalahari Rouge. Afin de conserver les caractéristiques de ces races et de faire en sorte que leurs traits uniques ne se perdent pas au cours des sélections et croisements continus, il est devenu nécessaire de revoir les normes des races actuelles et d'introduire des caractéristiques génétiques pour obtenir des paramètres de diversité génétique. La race de chèvre Boer et la Savanna ont des associations d'éleveurs établies, tandis qu'un club d'éleveurs a été créé pour les Kalahari Rouge. Ces associations ont des normes raciales bien définies et les traits morpho-métriques des races ont été décrits récemment. Les différences dans les traits morpho-métriques des races sont négligeables. Les données préliminaires sur la diversité génétique révèlent des valeurs hétérozygotes de plus de 50% pour chacune des trois races et elles peuvent être distinguées comme des races séparées en se basant sur les résultats génotypiques avec dix-huit marqueurs microsatellites recommandés par l'ISAG. Cependant, il faut faire une caractérisation génétique des deux types de viande et des chèvres indigènes pour garantir une diversité suffisante dans les races afin de conserver à long terme cette unique ressource génétique.

Resumen

Existen mayormente tres razas de cabras de carne en Sud Africa, la cabra Boer sudafricana, la Savanna y la Kalahari Roja. Con el fin de conservar las características de estas razas y conseguir que sus rasgos únicos no se pierdan a lo largo de selecciones y cruces continuos, se ha hecho necesario revisar las normas de las razas actuales e introducir características genéticas para obtener parámetros de diversidad genética. Las razas de cabra Boer y Savanna poseen asociaciones de ganaderos, mientras que un club de ganaderos ha sido creado para la Kalahari Roja. Estas asociaciones tienen normas bien definidas para las razas y los rasgos morfométricos han sido descritos recientemente. Las diferencias en los rasgos morfométricos entre las razas no son importantes. Los datos preliminares sobre la diversidad genética revelan valores de heterocigosis de más del 50% para cada una de las tres razas y pueden diferenciarse como razas separadas en base a los resultados genotípicos con dieciocho marcadores microsatelitares recomendados por ISAG. Sin embargo, hay que hacer una caracterización genética de dos tipos de carne y de cabras indígenas para garantizar una diversidad suficiente entre las razas con el fin de conservar a largo plazo este recurso genético único.

Key words: *Meat type, Phenotypic, Genetic characteristics, Utilization, Conservation.*

Introduction

South Africa has a goat population of approximately 6.6 million of which 64% are kept and/or commercially farmed within the rural areas (Coetzee, 1998). The primary goat breeds consist of Angora for mohair production, three meat type goat breeds namely the South African Boer goat, the Savanna and the Kalahari Red and a number of indigenous types that are primarily classified according to the geographical area in which they reside. Apart from the Angora goats, these breeds are all believed to originate from indigenous types, which had migrated to Southern Africa by 2500 BC, due to increasing desertification of the southern regions of the Sahara (Maree and Plug, 1993). The local Khoisan shepherds travelled southwards from Northern Botswana down to the Orange River and later followed two additional routes to reach the Southern and Western Cape. One of the earliest references to the presence of goats in the Northern Cape was made by the missionary, J. Burrow, who described the goats kept by the local people as "*handsome goats, speckled like the leopard*" (Campbell, 2003). These goats, also referred to as '*skilder*' goats or speckled goats, were most likely the resource, which led to the development of the current meat type goats.

These locally developed breeds have been subjected to artificial selection for improved production and growth. Although this has led to improved performance in the breeds, the question arises if specific genetic characteristics could be compromised by continuous selection for improvement of growth and meat characteristics. Often these breeds and our indigenous types are marketed as having special adaptive characteristics; local types often survive tick borne diseases better than commercial types (Malan, 2000; Erasmus, 2000).

According to some authors, true indigenous goat breeds in South Africa have been virtually cross-bred to extinction due to the development of the meat type goats such as the Boer goat (Campbell, 1995). Some researchers and farmers believe that the pure 'unimproved' indigenous goats possess important economic traits (including viability, good mothering ability, disease resistance and resistance against ticks), which should not be disregarded (Campbell, 1995; Van der Walt, 200, personal communication).

Recently a strategy for the conservation and utilization of South African genetic animal resources, including goat genetic resources, has been formulated. This policy aims at facilitating poverty alleviation through the strategic management of genetic resources, thereby improving the livelihoods of farmers and rural communities. The characterization and evaluation of genetic resources is one of the proposed ways in which this goal could be attained (National Department of Agriculture: Genetic resource management, 2008).

In order to maintain the characteristics of these locally developed breeds and ensure that their unique traits are not lost through continuous selection and cross-breeding, it has become important to revisit current breed standards and introduce genetic characterization to obtain genetic diversity parameters.

The objective of this paper was therefore to review the potential of locally developed meat type goats as a genetic resource with reference to their phenotypic and genetic characteristics.

Material and Methods

Phenotypic and genetic characteristics

Goats are well adapted to the drier western region of South Africa and northern regions where bush encroachment is a problem (Figure 1). It is also in these areas where the Boer, Kalahari Red and Savanna goats are primarily farmed in commercial systems for meat production.

Of the three breeds the Boer goat has the longest official history with the formulation of breed standards in 1959 when the South African Boer Goat Association was founded (Campbell, 2003). The breed standards specify a red head and the Boer goat replaced many unimproved local strains of varying colours with the strict selection for a white body and red head depicted in figure 2. Boer goats are large, long-legged goats with short, soft hair and long ears. These goats have a sturdy head with a compressed nose and strong horns that have a gradual backward curve. They have fleshy,

Figure 1 . Distribution of the meat type goat breeds.

well-developed broad briskets, well-sprung ribs, broad backs and muscular legs (Sambraus, 1992) and well fleshed buttocks and thighs. The mature Boer goat buck weighs between 110 and 135 kg and does weigh between 90 and 100 kg (Malan, 2000). The Boer goat does are known for their good mothering ability (Figure 2) and can kid every seven to eight months. They have an exceptional ability to resist and survive diseases such as blue tongue, prussic acid poisoning and, to a lesser extent, enterotoxaemia (Malan, 2000; Erasmus, 2000).

The Kalahari Red (Figure 3) is believed to have originated from two lines, namely a line of red-headed Boer goat and another of the '*unimproved*' local goats in South Africa (Campbell, 2003). The Kalahari Red have a distinct red colour, shown in Figure 3, and are often used in crossbreeding to produce goats with a uniform, solid, red colour. They are fully pigmented and are able to endure heat and intense sunlight, as their dark coats and long ears provide good heat resistance (*http://studbook.co.za*). The breed has excellent walking ability and good mothering ability and they can kid three times in two years.

The white Savanna goat (Figure 4), also known as the white Boer goat, was developed from indigenous goats of Southern Africa during the past few decades (Campbell, 2003). The breed standards allow limited red, blue and black hairs (*http://ourfarmsite.com/web/goats/goatsavanna/breedstandards.html*). The Savanna goat has short kempy white hair with a black skin, horns, nose and udder, and during the winter the goats develop extra fluffy cashmere hair for protection. Their heads are fairly long and slightly curved with big, oval shaped ears. The forequarter is well muscled and of medium width, with a reasonably long neck for easy browsing. Does have excellent mothering traits and about 22% of their offspring are born as twins and triplets, under extensive conditions. The Savanna and Kalahari Red goats have been recognised in South Africa as official breeds since 1993 and 1990, respectively.

Morphometric traits

Morphometric data was collected from goats with an average age of 12 months in a recent study in 2007. The measurements taken and their full descriptions are reported in table 1. Goats were sampled from a number of stud herds in order to be representative of the different breeds (sample collection are indicated in figure 1) and linear traits were measured for a total of 42 Boer goats, 47 Kalahari Reds and 49 Savanna goats. The goats

Figure 2. Typic South African Boer goats with a white body and red head and neck.

Figure 3. Kalahari Red goats with a uniform red coat colour.

Figure 4. Typic flock of white Savanna goats.

Table 1. Description of morphometric measurements.

Measurement[1]	Description
Height (H)	Vertical distance to the ground, measured behind the whithers
Length (L)	From the anterior shoulder point to the posterior extremity of the pin bone
Loin width (LW)	Measured just in front of the haunches (os coxea)
Depth (D)	Between Corpus Sterni and the point between the shoulder blades
Heart girth (HG)	Measured just behind the shoulder
Hock length (HL)	From the front to back margin
Head width (HW)	Distance between eyes
Head length (HL)	Length of head
Neck circumference (N)	Circumference
Tail length (TL)	From the tail base to tip
Pelvic width (PW),	Between pelvis bones
Pelvic length (PL)	From pelvic bone to os coxea

[1] A tape measure and measuring-rod were used to obtain various body measurements (in cm).

were also classified according to qualitative characteristics including beardedness (absence or presence of beard), incidence of horns (horned or polled) and coat colour. A General Linear Model (GLM) procedure of SAS (1992) was applied for analyses of the different traits measured.

Genetic characterization

A genetic characterization of the local meat type breeds has been undertaken by the Department of Animal and Wildlife Sciences at the University of Pretoria. The blood samples were collected from the same areas as described for the phenotypic measurements. For the genetic characterization additional flocks were included to ensure that unrelated samples are collected as far as possible. The Boer goats (62) represented three areas, two different flocks from the Northern Cape (31), and two experimental populations of Boer goats (31 Eastern Cape and 17 Limpopo provinces) not subjected to selection. The 60 blood samples for the Kalahari Red were collected from six flocks and the 55 Savannah samples from two different flocks in the Northern Cape. Eighteen microsatellite markers were selected from a panel of markers recommended by the International Society for Animal Genetics (ISAG) for application in diversity studies. These markers were selected based on the degree of polymorphism and genome coverage (Table 2) and available on web at: *lprdad.fao.org/cgi-bin/getblob.cgi?sid=4d60c0a342d8413c49acc b8c1837ebf5,50005880* and background at *www.isag.org.uk/ISAG/all/ISAG2004_ISAGFAO_AGAGD.pdf ; ftp://ftp.fao.org/*

Table 2. Microsatellite marker information applied in this study.

Microsatellite marker	Chromosome number	Fluorescent label[1]	Product size range	Sequence
SRCRSP24	Unknown	Fam	162 – 174	F 5′– AGC AAG AAG TGT CCA CTG ACA G-3′
				R 5′ –TCT AGG TCC ATC TGT GTT ATT GC-3′
SRCRSP5	21	Tet	171 -183	F 5′ –GGA CTC TAC CAA CTG AGC TAC AAG- 3′
				R 5 –TGA AAT GAA GCT AAA GCA ATG C-3′
SRCRSP8	Unknown	Tet	210 – 260	F 5′ –TGC GGT CTG GTT CTG ATT TCA C-3′
				R 5′ –CCT GCA TGA GAA AGT CGA TGC TTA G- 3′
MCM527	5	Hex	155 – 173	F 5′ –GTC CAT TGC CTC AAA TCA ATT C- 3′
				R 5′ –AAA CCA CTT GAC TAC TCC CCA A- 3′
INRA 23	3	Tet	208 – 214	F 5′ –GAG TAG AGC TAC AAG ATAA AAC TTC- 3′
				R 5′ –TAA CTA CAG GGT GTT AGA TGA ACT CA- 3′
BM1329	6 (sheep)	Tet	168 – 182	F 5′ –TTG TTT AGG CAA GTC CAA AGT C- 3′
				R 5′ – AAC ACC GCA GCT TCA TCC- 3′
OARFCB20	2	Tet	99 – 125	F 5′ – AAA TGT GTT TAA GAT TCC ATA CAG TG- 3′
				R 5′ – GGA AAA CCC CCA TAT ATA CCT ATA C- 3′
CRSRD247	14	Fam	236 – 244	F 5′ – GGA CTT GCC AGA ACT CTA CAA T- 3′
				R 5′ –CAC TGT GGT TTG TAT TCA GG- 3′
ILST087	28	Fam	145 – 165	F 5′ – AGC AGA CAT GAT GAC TCA GC- 3′
				R 5′ –CTG CCT CTT TTC TTG AGA GC- 3′
SRCRSP23	Unknown	Fam	83 – 111	F 5′ – TGA ACG GGT AAA GAT GTG -3′
				R 5′ –TGT TTT TAA TGG CTG AGT AG- 3′
OARFCB11	2	Hex	142 – 150	F 5′ –GGC CTG AAC TCA CAA GTT GAT ATA TCT ATC AC- 3′
				R 5′ –GCA AGC AGG TTC TTT ACC ACT AGC ACC- 3′
ILST002	Unknown	Hex	118 – 127	F 5′ –TCT ATA CAC ATG TGC TGT GC- 3′
				R 5′ –CTT AGG GGT GAA GTG ACA CG- 3′
RM004	15	Tet	138 – 146	F 5′ –AG CAA AAT ATC AGC AAA CCT- 3′
				R 5′ –CCA CCT GGG AAG GCC TTT A- 3′
INRA63	18	Fam	174 – 190	F 5′ –ATT TGC ACA AGC TAA ATC TAA CC- 3′
				R 5′ –CCA CCT GGG AAG GCC TTT A- 3′
INRA006	3	Hex	109 – 123	F 5′ –AGG AAT ATC TGT ATC AAC CTC AGT C- 3′
				R 5′ –CTG AGC TGG GGT GGG AGC TAT AAA TA- 3′
MAF65	15	Tet	117 – 127	F 5′ – AAA GGC CAG AGT ATG CAA TTA GGA G- 3′
				R 5′ – CCA CTC CTC TGA GAA TAT AAC ATG- 3′
BM1258	23	Fam	102 – 106	F 5′ –GTA TGT ATT TTT CCC ACC CTG C- 3′
				R 5′ – GAG TCA GAC ATG ACT GAG CCT G(AT)- 3′

[1] Dye colour of fluorescent label Fam = Blue; Tet = Green and Hex = Yellow.

docrep/fao/010/a1250e/annexes/Reports%20from%20International%20Organizations/ISAG.pdf.

PCR reactions were carried out in a volume of 8.2 µl, containing 50 ng target DNA, 3.48 µM dNTP's, 10 mM TrisHCl (pH = 9.0), 1.5 mM $MgCl_2$, 1.74 unit Taq Polymerase enzyme (Goldstar) and 4.54pmol of each primer (microsatellite marker). Preparation of samples was followed by thermal cycling in a Thermal Controller (Perkin Elmer) using the following program: 12 minutes at 94°C followed by 33 cycles consisting of 45 sec at 94°C, 80 sec at 60 °C, 60 sec at 72°C and an extension step of 60 min at 72°C. GENESCAN-350 TAMRA was used as internal standard and samples were analyzed on an automated DNA-Sequencer (ABI 377). The Genescan version 2.0 and Genotyper for MacIntosch were used to determine the fragment sizes in base pairs. Hardy Weinberg Equilibrium, heterozygosity and effective number of alleles were calculated using POPGENE 3.2 (Yeh *et al*., 1999) and Microsattellite Toolkit (Park, 2001). A factorial correspondence analysis was performed to illustrate the relationship among the breeds using Genetix 4.03 (Belkhir *et al.*, 1996).

Results

Of the goats measured 13% of the Boer goats, 23% of the Kalahari Red and 25% of the Savanna goats were bearded. Seventy five percent of all the Boer goats had white bodies with red heads, while the remaining 25% had either speckled heads or a red spot on the body. The Kalahari Red goats were primarily red coated with a white or black spot appearing on the body of 15% of the population. Savanna goats were all white. Morphometric measurements analyzed were presented in table 3.

All the microsatellite markers tested were found to be in Hardy Weinberg Equilibrium, except for some markers in the Savanna goats.

The effective number of alleles showed little variation, from 2.9 in the Boer goat to 3.4 in the Kalahari Red goats. Preliminary heterozygosity

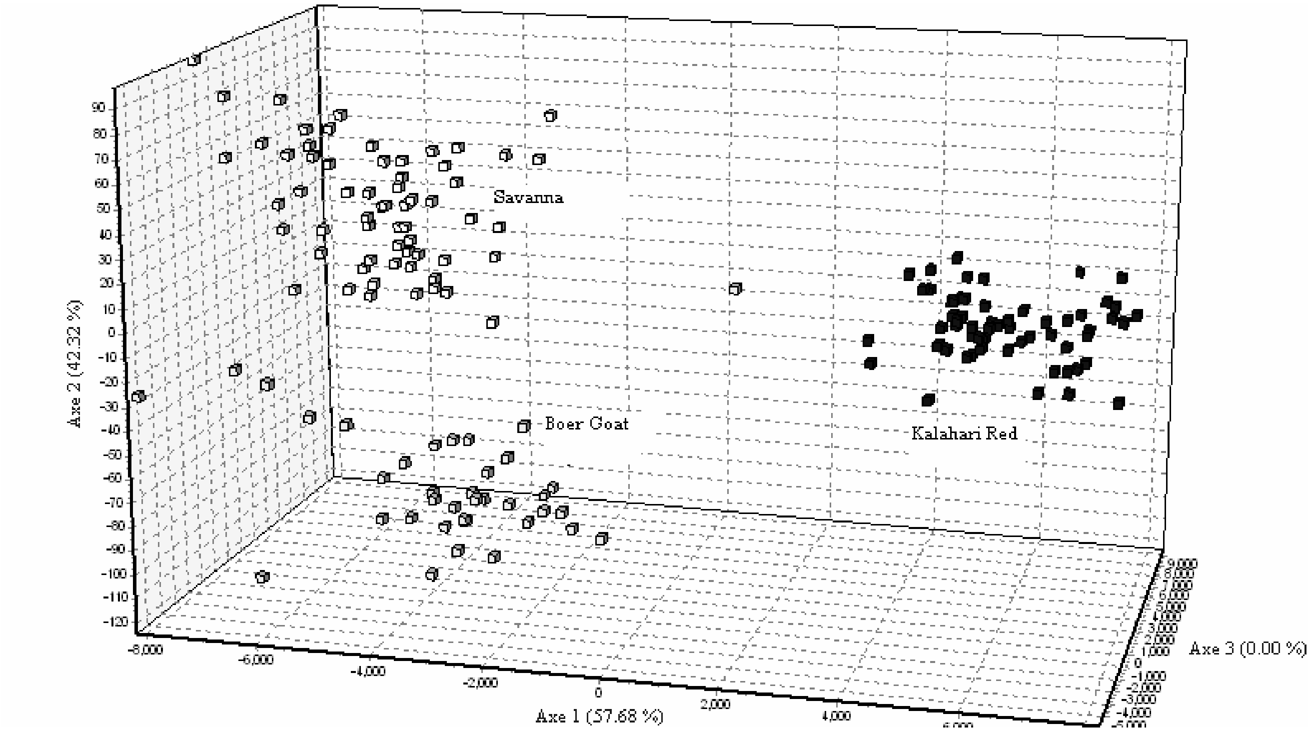

Figure 5 Assignment of individuals to the respective populations using a Factorial Correspondence Analyses.

Table 3. Statistical description of body measurements (cm) recorded for 42 Boer goats , 47 Kalahari Red and 49 Savanna goats.

Trait	Breed	Body measurements		Least square means[1]	Standard error (±)
		Min.	Max.		
Height (H)	Boer Goat	47.0	67.5	56.5^{a}	0.5
	Kalahari Red	49.3	60.2	54.1^{a}	0.5
	Savanna	47.8	61.9	55.7^{a}	0.5
Length (L)	Boer Goat	55.0	79.5	68.2^{ab}	0.8
	Kalahari Red	60.6	83.2	69.8^{a}	0.8
	Savanna	30.0	71.1	64.9^{b}	0.7
Depth (D)	Boer Goat	22.2	33.0	26.4^{ab}	0.3
	Kalahari Red	23.0	31.8	27.1^{a}	0.3
	Savanna	22.4	29.0	24.9^{b}	0.3
Heart Girth (HG)	Boer Goat	78.0	112.0	90.3^{ab}	1.0
	Kalahari Red	65.6	114.0	95.3^{a}	1.0
	Savanna	72.6	100.2	86.5^{b}	1.0
Hock Length (HL)	Boer Goat	16.5	34.0	28.3^{a}	0.5
	Kalahari Red	15.2	36.1	27.7^{a}	0.5
	Savanna	18.1	29.1	23.5^{b}	0.5
Head Width (HW)	Boer Goat	4.8	10.5	7.7^{a}	0.2
	Kalahari Red	4.8	8.9	6.6^{b}	0.3
	Savanna	4.2	7.3	5.6^{c}	0.2
Head Length (HL)	Boer Goat	13.0	21.0	17.2^{a}	0.3
	Kalahari Red	9.8	21.6	15.7^{b}	0.2
	Savanna	13.1	20.0	15.8^{ab}	0.2
Neck Circumference (N)	Boer Goat	33.2	57.0	48.3^{a}	4.0
	Kalahari Red	33.7	58.5	42.5^{ab}	3.8
	Savanna	30.4	65.4	37.7^{ab}	3.7
Tail Length (TL)	Boer Goat	6.0	17.0	12.2^{ab}	0.3
	Kalahari Red	10.4	19.2	13.2^{a}	0.3
	Savanna	9.6	19.0	13.3^{a}	0.3
Pelvic Width (PW)	Boer Goat	7.8	21.4	13.8^{a}	0.3
	Kalahari Red	9.0	13.5	11.1^{b}	0.3
	Savanna	8.4	17.7	11.4^{b}	0.3
Pelvic Length (PL)	Boer Goat	13.5	26.5	19.7^{a}	0.4
	Kalahari Red	16.0	24.8	20.5^{a}	0.3
	Savanna	16.7	27.4	19.1^{a}	0.3
Ear Length (EL)	Boer Goat	14.4	26.0	21.4^{a}	0.3
	Kalahari Red	14.0	18.5	19.2^{b}	0.2
	Savanna	16.3	22.7	19.5^{b}	0.2

[1] Superscripts differ significantly for $P < 0.001$.

Table 4. Number of samples, effective number of alleles and expected and observed heterozygosity for the three breeds.

Breeds	Mean n of samples	Ne[1]	Unbiased Hz (SD)	Observed H (SD)
S A Boer goat	31	2.9	0.57 (0.19)	0.54 (0.22)
Boer goats EC[2]	31	3.3	0.65 (0.15)	0.62 (0.20)
Boer goat[3]	17	3.1	0.62 (0.17)	0.66 (0.35)
Kalahari-Red	60	3.3	0.68 (0.10)	0.63 (0.13)
Savanna	55	3.4	0.69 (0.10)	0.61 (0.08)

[1]Ne = Effective number of alleles.
[2] = Experimental population of Boer goats Eastern cape province.
[3] = Experimental population of Boer goats Limpopo province.

values calculated for this study were all above 50% with the lowest value for the SA Boer goat (57%) and a slight difference between the Savanna (68%) and Kalahari Red (69%) (Table 4). Both the experimental flocks of SA Boer goat had higher heterozygosity values than the commercial flocks of the Northern Cape Province.

In figure 5 the results of a Factorial Correspondence Analysis are shown with the assignment of the individual goats analysed into three groups.

Discussion

Goats have been largely neglected as an animal genetic resource in South Africa when compared to cattle and sheep. Despite a number of research initiatives undertaken over the past 40 years on goat production, there are still aspects that require attention and a need for effective coordination of research programs to lead to the successful conservation and utilization of goats. The South African Boer goat, Savanna and Kalahari Red goats have only recently been classified as distinct breeds, while their phenotypic and genetic characterization are still not well defined.

Both the Boer goat and Savanna breeds have established breeders associations while a breeders club was founded for the Kalahari Red goats with set breed standards (*www.studbook.co.za/telers*). The breed standards consist of primarily phenotypic descriptions, colour and culling defects. Attention is also given to type traits related to functional efficiency. Except for the colour variation between the three breeds, the breed standards are quite similar and the aim is to select for a well adapted, functionally efficient meat type goat breed.

Morphometric measurements recorded for this study (reported in table 3) indicate a larger within breed variation (minimum and maximum) than between the breeds. Statistical differences were observed between the Savanna and the other two breeds for depth and length but not ($P < 0.001$) for height. The only trait where significant differences were observed among all three breeds was for head width, where the Boer goat had the broadest head and the Savanna the narrowest. The Boer goat had the largest pelvis with and the longest ears compared to the other two breeds ($P < 0.001$).

The differences in morphometric traits among the breeds are fairly insignificant and highlight the need for a genetic characterization to be able to distinguish the breeds accurately on a genotypic level and to ensure sufficient diversity within the breeds for long term conservation. The heterozygosity values estimated for the three breeds are relatively high and correspond with the observations for local South African breeds by Visser *et al.* (2004) and values reported in studies on goats by Martinez *et al*., 2006; Els *et al*., 2004; Li *et al*., 2002, but higher than those reported by Kumar *et al*, (2005) for Marwari goats. It is important to note that both the experimental populations of Boer goats not subjected to selection for improved performance had a higher genetic variation than the Boer goats sampled from the breeders (Table 4). The sample size of the goats sampled from the Limpopo flock was small and more samples need to be tested for further analyses. According to the Factorial Correspondence Analysis (Figure 5) the three breeds assign to three groups. The Kalahari Red goats can be distinguished as a group, while the SA Boer goat and Savanna tend to overlap. More samples of indigenous goat types and Angora mohair goats are currently being added for further analyses of genetic diversity and relatedness for a more detailed characterization of all South African goats.

The meat goat breeds are often noted in literature as having adaptive characteristics in terms of heat tolerance and feeding behavior (Erasmus, 2000; Malan, 2000). There is an urgent need to investigate these traits to ensure conservation of the unique genetic resource. Shrestha and Fahmy (2005) reported that nearly 800 farm animal genetic resources have already been lost and about 30 percent of the remaining species are associated with some degree of risk. The FAO predicts that 20 percent of livestock breeds are at risk of extinction and more than half of these breeds are likely to be found in developing countries (FAO, 2007).

Conclusion

Goat meat production in South Africa is relatively low compared to beef and mutton, but it plays an important role in African cultural activities and is the preferred meat in certain communities (Webb *et al.*, 2005). In addition to the local production, both SA Boer goat and Kalahari Red have been exported to Europe and the USA. It is important that breed standards for the locally developed breeds be revised and genetic analyses included to ensure that superior genetics will be conserved. Adaptive phenotypic characteristics of both the meat type breeds and indigenous types require further investigation for the long term conservation of goats as a unique animal genetic resource in South Africa.

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Genetic diversity and zebu genes introgression in cattle population along the coastal region of the Bight of Benin

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Summary

Genetic diversity and Zebu genetic introgression have been assessed in five subpopulations of cattle along the coastal region of Togo, Benin and Nigeria using 15 autosomal and one Y- specific microsatellite markers. Mean observed heterozygosity (Ho) ranges from 0.55 to 0.61 and the mean number of alleles (MNA) from 5.47 to 6.47. Genetic differentiation indexes (F_{st}), were significant between the five subpopulations ($P< 0.01$). Some possible population diagnostic alleles are identified with allele 254 at locus ILSTS033 and allele 182 at locus ILSTS005 found only in the population from Togo with frequencies of 5.41% and 12.82% respectively. Allele 226 of locus ILSTS103 is fixed in the Togolese population (100%) and almost fixed (98.75%) in the Benin-Valley population. Y chromosome analysis reveals male Zebu introgression in all five populations with a frequency of indicine Y chromosome ranging from 37.5% in Benin-Valley and Benin Plateau East to 100% for Benin Plateau West. Admixture analysis using the programme STRUCTURE (k = 2) confirms phenotypic observations suggesting different level of taurine background and therefore Zebu introgression amongst the populations. Within populations, variations in levels of Zebu admixture between herds were also detected. Whereas the valley population from Benin shows low level of Zebu introgression, it is the population from Benin Plateau East which is the purest.

Résumé

La diversité génétique et l'introgression de gènes de zébu dans la population de bovins le long de la côte du golfe de Guinée allant du Togo au Nigeria ont été évaluées à partir de 15 marqueurs microsatellites autosomes et un marqueur spécifique du chromosome Y. La moyenne des hétérozygotes Ho varie de 0,55 à 0,61 et le nombre moyen d'allèles (NMA) de 5,47 à 6,47. Les indices de différenciation génétique (F_{st}) sont différents entre les cinq sous populations ($P<0,01$). Des allèles spécifiques de population sont identifiés aux loci ILSTS033 (allèle 254) et ILSTS005 (allèle 182) dans la sous population du Togo avec des fréquences respectives de 5,41 et 12,82%. L'allèle 226 du locus ILSTS103 est totalement (100%) fixé dans la sous population togolaise et presque (98,75%) dans la sous population de la vallée au Bénin. L'évaluation du marqueur spécifique du chromosome Y révèle l'introgression de gènes de zébu dans les cinq sous populations allant de 37,5% dans la vallée du Bénin et sur le Plateau Est à 100% sur le Plateau Ouest. L'analyse de mélange utilisant le programme STRUCTURE (k = 2) confirme les observations phénotypiques concluant à l'introgression de gènes de zébu au sein des populations. Des variations de mélange sont observées entre troupeaux au sein d'une même sous population. Alors que les animaux dans la vallée au Bénin présentent un niveau faible d'introgression de gènes de zébu, c'est la sous population du Plateau Est qui paraît être la plus pure.

Resumen

La diversidad genética y la introgresión de genes de zebú en la población de bovinos a lo largo de la costa del golfo de Guinea que va desde Togo hasta Nigeria han sido evaluados a partir de 15 marcadores microsatelitares autosomos y un marcador específico del cromosoma Y. La media de heterocigosis Ho varía de 0,55 a 0,61 y el número medio de alelos (NMA) de 5,47 a 6,47. Los índices de diferenciación genética (F_{st}) son diferentes entre las cinco sub-poblaciones ($P<0,01$). Han sido identificados alelos específicos de poblaciones en los loci ILSTS033 (alelo 254) e ILSTS005 (alelo 182) en la sub-población del Togo con frecuencias respectivas de 5,41 y 12,82%. El alelo 226 del locus ILSTS103 está totalmente fijado (100%) en la sub-población togolesa y casi (98,75%) en la sub-población del valle del Benín. La evaluación del marcador específico del cromosoma Y revela la introgresión de genes de zebú en las cinco sub-poblaciones que van de 37,5% en el valle del Benín y en la Meseta Este, hasta 100% en la Meseta Oeste. El análisis de mezcla utilizando el programa STRUCTURE (k=2) confirma las observaciones fenotípicas que indican la introgresión de genes de zebú en el interior de las poblaciones. Variaciones de mezclas han sido observadas entre rebaños al interior de una misma población. Mientras que los animales del valle del Benín presentan un nivel de introgresión de genes de zebú bajo, la sub-población de la Meseta Este parece ser la más pura.

***Key words**: Cattle, Microsatellites, Genetic diversity, Zebu genes introgression.*

Introduction

West African taurine cattle (*B. taurus*) breeds are under threat of extinction due to uncontrolled breeding practices by farmers aiming to enhance the size and the productivity of their animals. However, it is recognised that animals of these breeds are well adapted to their local environments and remain productive in areas where Zebu or crossbreeds are often unable to survive (Agyemang *et al.* 1991; Uza, 1997). The phenotypic traits of these animals are the result of hundreds of years of natural selection in relation to the local environments under permanent tsetse, ticks and helminth challenge. It is clear that uncontrolled crossbreeding with exotic breeds poses a threat to the adaptive traits of this unique animal genetic resource. This uncontrolled crossbreeding is the result of poor agricultural policies with no long term breeding goals, each farmer developing his own objective with emphasis on short-term results.

In the early eighties, the Food and Agriculture Organisation of the United Nations started alerting public opinion on the subject of animal genetic resources conservation and management (FAO, 1981). At the Earth Summit in 1992 in Rio de Janeiro, 157 countries signed the United Nations convention on biological diversity and subsequently FAO (1992) launched a special program for the global management of farm animal genetic resources. The aim of this program is to maintain in each species a maximum genetic diversity of the gene pool to allow for future unforeseen needs in the development of sustainable animal production systems. In addition the program aims at prompt actions to preserve animal breeds at risk of extinction.

Studies in the last decade have shown that African cattle were most likely domesticated within the African continent, separately from the other centres of domestication in the Fertile Crescent and in the Indian sub-continent, from the wild African auroch *B. primigenius* (Bradley *et al.*, 1996). Their separate origin indicates that they represent a unique set of genetic characteristics. Today, the remaining pure African taurine cattle are only found within the West African taurine cattle living in tsetse-infected areas. These populations, given their origins and their adaptation to local environmental conditions (e.g. disease resistance), represent a unique genetic resource.

Introgression with Zebu cattle in West African taurine cattle populations, however, is common (MacHugh *et al*., 1997; Hanotte *et al*., 2000) and is diluting progressively the African taurine genetic background of these breeds. Ultimately, this introgression will result in the loss of the unique genetic adaptation of these breeds. Currently, the extent and pattern of Zebu introgression into the indigenous taurine populations is well described by Hanotte *et al*. (2002). This study, however, did not include the Lagune breed. The current paper is therefore a complementary study to that of Hanotte *et al*. (2002), targeting the Lagune breed in the Bight of Benin. Results of this study can be used to identify suitable pure West African taurine populations for their inclusion in breeding programs that aim at conserving and utilising these unique indigenous genetic resources. These results could also be the starting point for the implementation of a sustainable breeding programme for livestock production in that region.

Material and Methods

Sampling

Blood samples were collected from different cattle subpopulations in Benin, Nigeria and Togo. Forty animals, of which eight were males, were sampled for each identified subpopulation. Three subpopulations have been sampled in Benin, which are Benin Plateau West (BPW), Benin Valley (BV) and Benin Plateau East (BPE). Two neighbouring regions of the target area in Benin have been considered (Figure 1) in Nigeria (NG) and Togo (TG) resulting in a maximum of 200 sampled cattle.

Appropriate materials such as Wattman filter paper, evacuated blood collection tubes (5 ml) and Eppendorf tubes for stocking buffy coats were used for handling samples. Blood samples were collected from each animal in two evacuated blood collection tubes containing 3.2% EDTA and the buffy coat (white cells) was taken after spinning the tubes at 2400 rpm at ambient temperature. Collected buffy coats were added with 8M urea solution and kept at ambient temperature. To be on the safe side, blood samples were also collected on Wattman paper and dried at 40°C in oven, then stored at ambient temperature. Sampling included as many animals from different herds as possible to avoid direct relationship between sampled individuals. In other terms, one male and four females were sampled per herd and a total of eight herds were visited for each identified subpopulation. All samples were conveyed to the laboratory of genetics at ILRI campus in Nairobi (Kenya) for processing.

Laboratory procedures

DNA was extracted from the buffy coats with standard procedures as described by Sambrook *et al.* (1999). Sixteen markers, of which one was on the Y chromosome, were used for genotyping. They were *TGLA126*, *TGLA122*, *ILSTS033*, *ILSTS013*, *ILSTS008*, *ILSTS005*, *ILSTS006*, *ILSTS036*, *ILSTS028*, *ILSTS023*, *ILSTS103*, *ETH152*, *BM2113*, *BM1824*, *AGLA293* and *INRA124*. Polymerase Chain Reaction (PCR) for amplification of microsatellite loci were performed as described in Hirano *et al*. (1996) and Kemp *et al*. (1995).

Genotyping and gel analysis were performed using automatic DNA sequencer ABI 377 and associated analysis software Genescan^{TM} (version 3.1) and Genotyper^{TM} version 2.0).

Data analysis

Marker allele frequencies have been analysed using the Microsatellite toolkit program (Park, 2001). The genetic diversity of each population was evaluated by computing the mean number of alleles per locus (MNA), the observed heterozygosity (H_{obs}), and the expected heterozygosity (H_{exp}) using the microsatellite toolkit (Park, 2001) as well as GENEPOP, version 3.3 (Raymond and Rousset, 1995). Subpopulations have been checked for HWE using the exact probability test with GENEPOP. The level of genetic differentiation among populations was examined using *F*-statistics (Weir and Cockerham, 1984). Genetic distances between populations D_A (Nei *et al*., 1983) were calculated and used to construct a phylogenetic tree

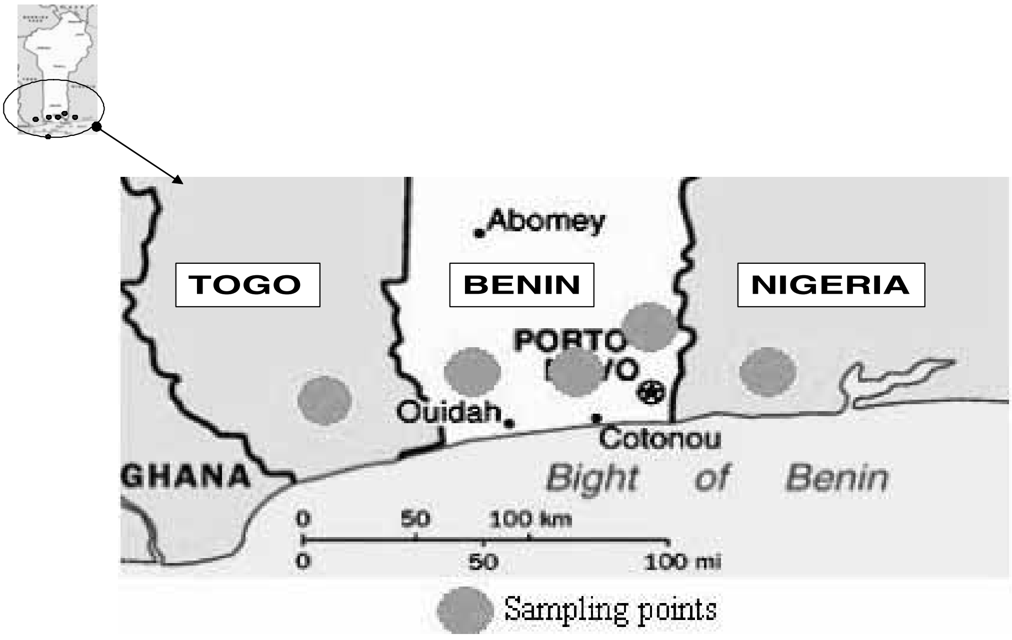

Figure 1.Benin map showing the sampled populations locations.

with the neighbour joining algorithm (Saitou and Nei, 1987). The level of Zebu introgression was estimated with the programme STRUCTURE using the ADMIX 1.0 software (Bertorelle and Excoffier, 1998). Correlations between phenotype and populations structure results were performed using Microsoft Excel.

Results

Genetic variation

From the five subpopulations under study here, 130 alleles were found for all 15 autosomal marker loci that have been genotyped over the 200 sampled animals (Table 1). The total number of alleles detected per locus ranged from 4 to 16 resulting in a mean number of alleles (MNA) per locus of 8.67. The number of alleles summed over the 15 loci per subpopulation ranged from 82 in BPE to 97 in TG (Table 1) giving a MNA per locus for each subpopulation varying from 5.47 to 6.47 (Table 2). These variations are not strong enough ($P>0.05$) to differentiate current subpopulations. However, allele 254 of the locus *ILSTS_033* and allele 182 of *ILSTS_005* are found solely in TG with a frequency of 5.41% and 12.82% respectively. Alleles 171 and 175 of *ILSTS_023* are equally distributed (50%) within TG and BV subpopulations. Further, allele 226 of locus *ILSTS_103* is fixed in TG (100%) whereas it is almost (98.75%) fixed in BV.

The expected heterozygosity computed over the 15 loci for each of the five subpopulations ranged from 0.593 (BV) to 0.673 (BPW) whereas the observed heterozygosity varied from 0.55 in BPE to 0.61 in BPW (Table 2).

None of the subpopulations deviated from HWE through all loci at 5 p. cent level. Out of the 15 loci under study, only loci *ILSTS006* ($P<0.006$), *ILSTS023* ($P<0.005$) and *ILSTS103* ($P<0.05$) deviated consistently from HWE for all five subpopulations (Table 3). Except those three loci, TG deviated ($P<0.05$) from equilibrium at two loci (*BM1824*, *BM2113*), BPW at four loci (*TGLA126*, *ILSTS033*, *ILSTS008*, *BM2113*), BV at two loci (*ILSTS008*, *ILSTS033*), BPE at three loci (*ILSTS033*, *ILSTS036*, *BM2113*), and NG at two loci (*ILSTS013*, *ILSTS036*).

Genetic distances and breed relationships

Table 4 summarizes genetic distances and gene differentiation indices between all pairs of subpopulations. The largest genetic distance (0.1183) was obtained between TG and BPE, whereas the smallest (0.0666) was obtained between

Table 1. Total number of alleles per locus and per subpopulation.

Locus	Togo	Benin			Nigeria	Total
		BPW	BV	BPE		
TGLA126	7	7	6	6	6	7
TGLA122	8	8	9	7	8	11
ILSTS033	7	5	4	7	6	9
ILSTS013	4	4	4	4	4	4
ILSTS008	4	5	4	3	3	5
ILSTS005	5	4	3	4	3	5
ILSTS006	8	5	8	5	5	9
ILSTS036	12	8	9	8	9	16
ILSTS028	6	8	6	6	7	10
ILSTS023	2	5	2	4	5	6
ILSTS103	1	5	2	4	5	7
ETH152	6	5	7	5	5	8
BM2113	12	10	7	6	9	12
BM1824	6	4	4	4	4	6
AGLA293	9	8	12	9	8	15
Total	97	91	87	82	87	130

Table 2. Comparison of genetic variability of five populations of cattle along the coastal region of Togo, Benin and Nigeria.

Populations	[1]MNA (±SE)	[2]H_{obs} (±SE)	3H_{exp} (±SE)
Togo	6.47 (±3.14)	0.5905 (±0.0202)	0.6410 (±0.0539)
Benin Plateau West	6.07 (±1.91)	0.6083 (±0.0200)	0.6725 (±0.0322)
Benin Valley	5.80 (±2.88)	0.5604 (±0.0204)	0.5930 (±0.0503)
Benin Plateau East	5.47 (±1.73)	0.5504 (±0.0204)	0.6194 (±0.0296)
Nigeria	5.80 (±2.01)	0.5603 (±0.0203)	0.6338 (±0.0383)

[1] Mean number of alleles per locus.
[2] Observed heterozygosity.
[3] Expected heterozygosity.

Table 3. Hardy-Weinberg exact probability test by population.

Locus	Togo	Benin			Nigeria
		BPW	BV	BPE	
TGLA126	0.1266 (0.0094)	0.0324 (0.0058)	0.9689 (0.0032)	0.3372 (0.0138)	0.1626 (0.0086)
TGLA122	0.0918 (0.0143)	0.1416 (0.0109)	0.5619 (0.0241)	0.3201 (0.0204)	0.2617 (0.0191)
ILSTS033	0.0122 (0.0035)	0.0000 (0.0000)	0.0302 (0.0026)	0.0018 (0.0009)	0.2594 (0.0157)
ILSTS013	0.3394 (0.0082)	0.2777 (0.0082)	0.9153 (0.0024)	0.5509 (0.0065)	0.0219 (0.0018)
ILSTS008	0.3769 (0.0107)	0.0052 (0.0014)	0.0024 (0.0007)	0.0842 (0.0049)	0.8024 (0.0036)
ILSTS005	0.1651 (0.0080)	0.0052 (0.0071)	0.3149 (0.0082)	0.7353 (0.0076)	0.6628 (0.0049)
ILSTS006	0.0000 (0.0000)	0.0000 (0.0000)	0.0000 (0.0000)	0.0057 (0.0018)	0.0000 (0.0000)
ILSTS036	0.0797 (0.0167)	0.1021 (0.0100)	0.1006 (0.0160)	0.0294 (0.0053)	0.0001 (0.0001)
ILSTS028	0.0805 (0.0088)	0.1186 (0.0129)	0.2908 (0.0173)	0.2782 (0.0152)	0.3055 (0.0202)
ILSTS023	0.0000 (0.0000)	0.0001 (0.0001)	0.0000 (0.0000)	0.0000 (0.0000)	0.0000 (0.0000)
ILSTS103	-	0.0003 (0.0003)	-	0.0000 (0.0000)	0.0183 (0.0035)
ETH152	0.0672 (0.0065)	0.4927 (0.0091)	0.3976 (0.0174)	0.9354 (0.0049)	0.3382 (0.0115)
BM2113	0.0396 (0.0076)	0.0110 (0.0028)	0.2903 (0.0158)	0.0089 (0.0016)	0.3507 (0.0163)
BM1824	0.0414 (0.0064)	0.9355 (0.0020)	1.0000 (0.0000)	0.8824 (0.0045)	0.0616 (0.0055)
AGLA293	0.5448 (0.0222)	0.6256 (0.0170)	0.2169 (0.0274)	0.0676 (0.0097)	0.0907 (0.0103)

NG and BPW. This result is in contrast to what would be expected given the geographic location of these subpopulations (Figure 1). The smallest coefficient of differentiation was obtained between TG and BPW, and the highest was between TG and BPE which is in agreement with the largest genetic distance obtained. The F-statistics results showed that the five populations were significantly different from each other (*P*=0.0001). Estimates of F_{ST} for each locus and for each population pair are summarized in Table 5.

The neighbour-joining tree based on genetic distance D_A is represented in figure 2. It shows the existing relationships among the five subpopulations according to studied loci. As it would be expected, BV and BPE are close subpopulations as shown in this figure.

Population structure (admixture)

Genetic admixture analysis shows that all five subpopulations are introgressed with Zebu genes but to different degrees (Figure 3), whereas subpopulations from TG and BPW harbour high levels of introgression at 0.753 and 0.651, respectively. BPE is the least introgressed with introgression coefficients equal to 0.188. BV and NG have intermediate coefficient, 0.309 and 0.390, respectively. On individual basis, the level of

Table 4. Genetic distance between five cattle subpopulations along the coastal region of Togo, Benin and Nigeria calculated using D_A (Nei et al., 1983) below diagonal and Weir and Cockerham (1984) F_{ST} above the diagonal.

	Togo	Benin Plateau West	Benin Valley	Benin Plateau East	Nigeria
Togo	-	0.0205	0.0341	0.0564	0.0493
Benin Plateau West	0.0795	-	0.0349	0.0310	0.0258
Benin Valley	0.0866	0.0917	-	0.0335	0.0463
Benin Plateau East	0.1183	0.0740	0.0809	-	0.0377
Nigeria	0.1103	0.0666	0.0914	0.0688	-

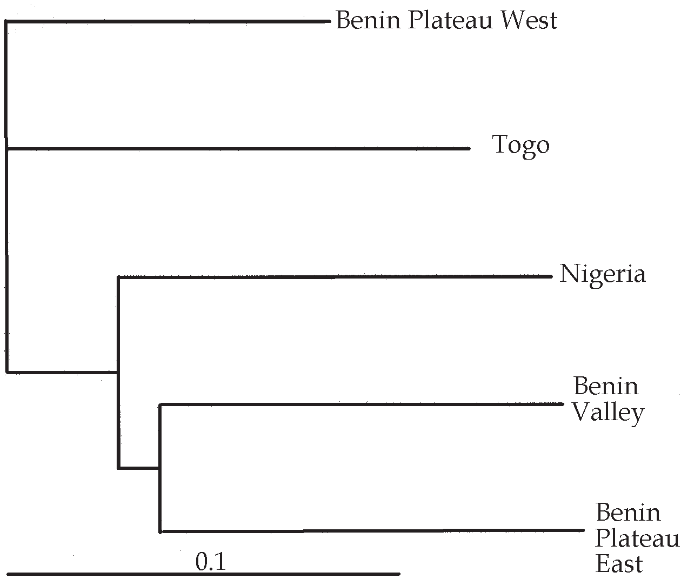

Figure 2. Neighbor joining dendogram showing the genetic relationship among the five sampled subpopulations along the coastal region from Togo to Nigeria.

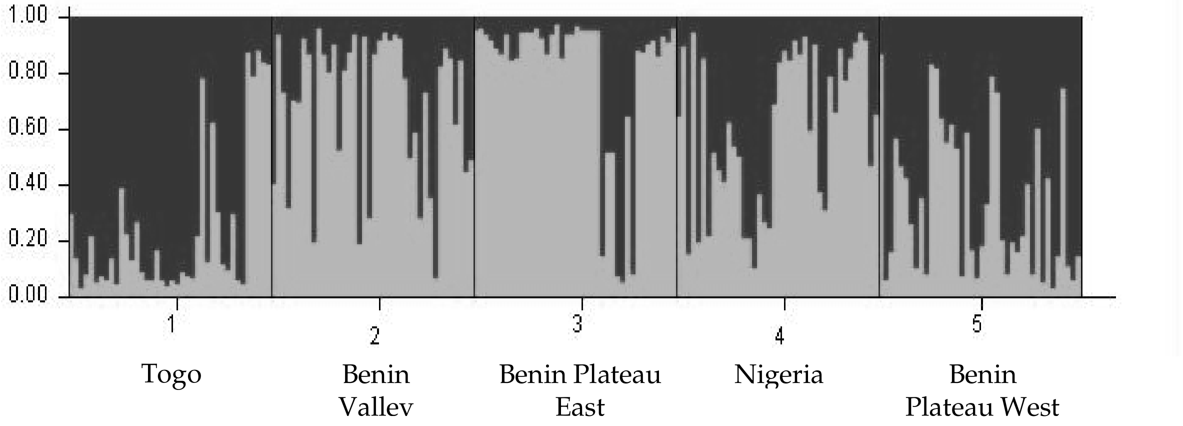

Figure 3. Admixture analysis showing zebu introgression in sampled subpopulations.

Table 5. Estimate of F_{ST} for each of the 15 loci and for each population pair.

Loci	TG/BV	TG/BPE	TG/NG	TG/BPW	BV/BPE	BV/NG	BV/BPW	BPE/NG	BPE/BPW	NG/BPW
TGLA126	0.0407	0.0369	0.0170	0.0060	0.0006	0.0006	0.0375	0.0538	0.0346	0.0118
TGLA122	0.0303	0.1558	0.0162	0.0340	0.0498	0.0256	0.0099	0.1476	0.0879	0.0096
ILSTS033	0.0302	0.0583	0.0703	0.0208	-0.0015	0.0268	0.0213	0.0659	0.0757	0.0190
ILSTS013	0.0049	0.0095	0.0432	-0.0055	-0.0007	0.0009	0.0316	0.0280	0.0346	0.0847
ILSTS008	0.0061	0.0561	0.0333	-0.0032	0.0053	-0.0101	0.0024	-0.0023	0.0607	0.0256
ILSTS005	0.0627	0.0315	0.0523	0.0442	-0.0043	-0.0120	0.0072	-0.0076	-0.0033	0.0080
ILSTS006	0.0007	0.0079	0.0923	-0.0032	0.0363	0.0924	0.0056	0.1066	-0.0056	0.1163
ILSTS036	-0.0052	0.0009	0.0036	0.0006	-0.0047	0.0050	0.0053	-0.0004	-0.0012	-0.0041
ILSTS028	0.0363	0.0478	0.0132	0.0149	-0.0120	-0.0032	0.0065	0.0086	0.0062	0.0146
ILSTS023	0.0000	0.1077	0.1950	0.1281	0.1081	0.1955	0.1285	0.0183	-0.0050	0.0041
ILSTS103	0.0000	0.2046	0.1727	0.1606	0.1813	0.1465	0.1391	-0.0009	-0.0101	0.0020
ETH152	0.0193	0.0695	0.0320	-0.0119	0.0339	0.0156	0.0125	-0.0012	0.0617	0.0248
BM2113	0.0713	0.0317	0.0107	0.0032	0.0419	0.0609	0.0383	0.0234	0.0333	0.0106
BM1824	0.0846	0.0485	0.0714	-0.0037	0.0309	-0.0113	0.0562	0.0181	0.0478	0.0494
AGLA293	0.0765	0.0618	0.0026	0.0022	0.0777	0.0644	0.0688	0.0523	0.0397	0.0162
All loci	0.0341	0.0564	0.0493	0.0205	0.0335	0.0463	0.0349	0.0377	0.0310	0.0258

TG=Togo; BPW=Benin Plateau West; BV=Benin Valley; BPE=Benin Plateau East; NG=Nigeria.

Figure 4. Typical Lagune cattle from Benin Plateau East (height is 81 cm; girth circumference is 112 cm).

Zebu introgression varies from 0.028 in TG to 0.967 in BPE.

Analysis of the *Y* chromosome reveals male Zebu introgression in males of all five subpopulations with a frequency of indicine *Y* chromosome ranging from 37.5% in BV and BPE to 100% for BPW. TG and NG have respectively 87.5 and 62.5%. The correlation coefficient between the admixture results and those of the *Y* chromosome analysis is 0.93.

Discussion

With the upgrade breeding performed by livestock producers along the coastal regions of the three countries involved in this study, the observed variation between populations was expected. Indeed, looking for taller animals, mainly for market purposes, Borgou breed and Zebu have been introduced in diverse herds (Figure 5) resulting in the higher MNA for these populations. This is the case in TG and BPW (Table 2). This result is supported by the admixture analysis which gives the higher proportion of Zebu genes to subpopulations TG and BPW. In contrast, the subpopulation BPE has the least genetic variation in terms of MNA associated with a low heterozygosity. The low genetic variation in this subpopulation could be explained by the higher level of inbreeding in this subpopulation. This explanation is supported by the management system of these animals. Farmers used to keep their animals under their own habitat during night, then they are tethered to trees and moved from time to time to access forage. Bulls are owned by few people that hire them to non-owners for breeding. This means that breeding is under control, so as to ensure these animals are kept as pure as possible for their use in certain ritual ceremonies and as a dowry. Subpopulations TG and BV, however, have in common some alleles, that is allele 171 and 175 from *ILSTS023* at 50%, allele 226 of locus *ILSTS103* at the rate of 100% for the former and 98.75% for the latter. This result is surprising given that they are separated by subpopulation BPW which has lower frequency for these alleles (results not shown).

Genetic distances between pairs of subpopulations, coefficients of differentiation and

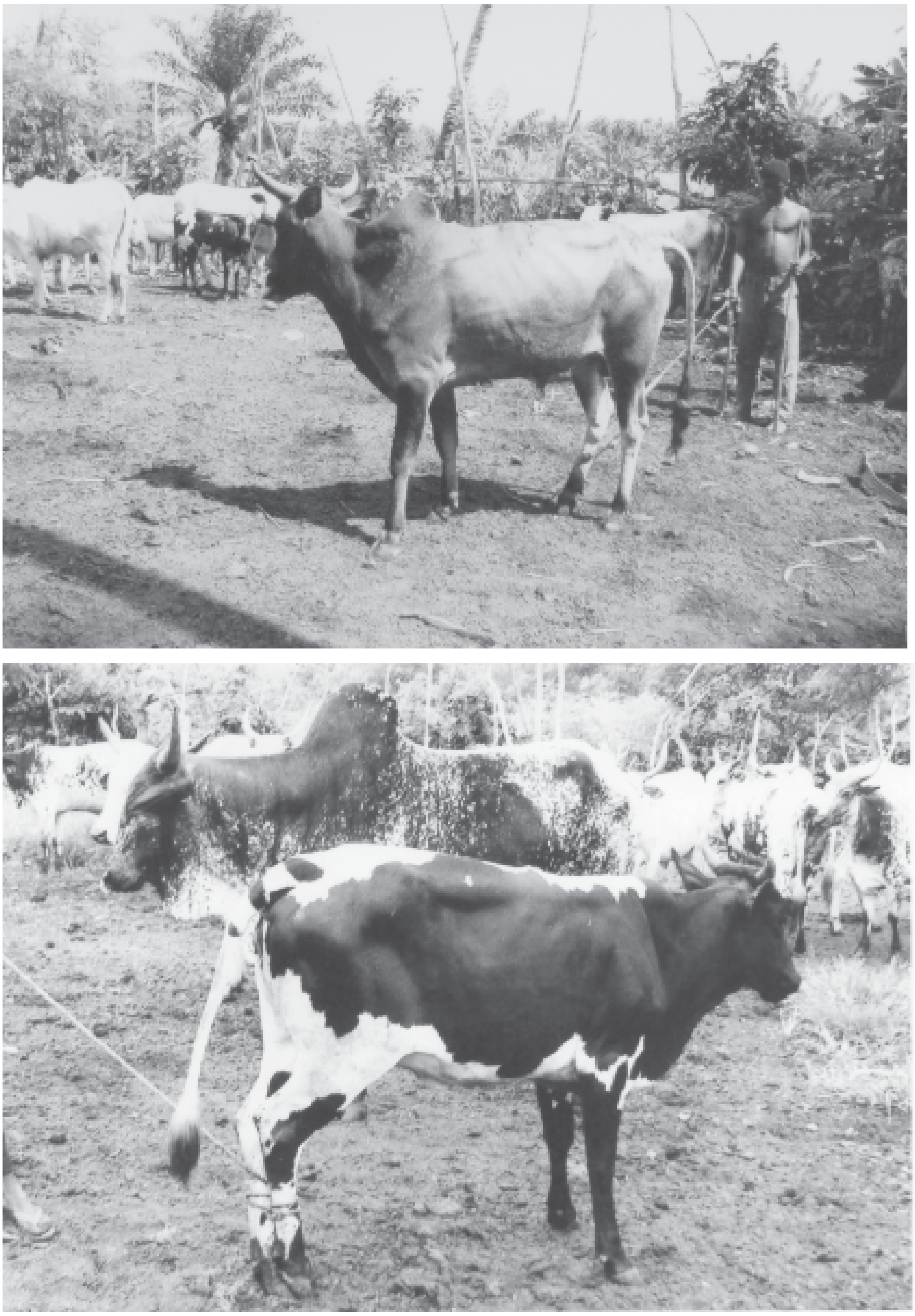

Figure 5. Zebu breeds that have been introduced in herds in the coastal regions.

F_{ST} confirm that the five subpopulations are different, although some results showed patterns that were not expected. We would expect the largest genetic distance to be between TG and BPE on one side and between NG and BPW on the other. The latter showed the least distance which is in contrast to what would be expected given the geographic location of these subpopulations (Figure 1). According to the admixture analysis, TG and NG showing the highest introgression of Zebu genes would be closer - that is not the case in current results. This could be explained by different sources of gene pools that have been used to perform the introgression. The existing relationships among subpopulations through the neighbour-joining tree clearly show that BV and BPE are close subpopulations as one could predict from figure 1.

Concurrently to blood sampling, height at wither and girth circumference were measured to relate the phenotype with genotype. There is quite an agreement between the results of the admixture model analysis and the phenotype of animals (correlation coefficient equals to 0.59), that is the higher the percent of Zebu genes, the higher is the height at wither. The availability of data on control animals (pure Zebu and pure Lagune) would have better strengthened current results.

The hypothesis that animals in the valley would be less introgressed by Zebu is true, but the population of Benin Plateau East is even purer than the one targeted in our study.

Conservation futures

The major objective of this study was to determine the level of Zebu introgression within cattle populations along the coastal regions of the Bight of Benin. This region is known to originally be the cradle of the Lagune cattle breed (Figure 4), animals of small size with a wither height varying from 90 to 100 cm and a heart girth from 130 to 137 cm. As this study has demonstrated, there is a high tendency for Zebu or other breeds to be introgressed in this breed. Some herds and to some extent at least two populations, have been shown to be less polluted with Zebu blood. Throughout this study we placed an emphasis on naming cattle populations instead of breeds given the extent of crossbreeding, and current results support this point of view.

The hypothesis of the current study was to encounter cattle with low level of Zebu introgression that could be used for genetic resources conservation and it was expected to meet those animals in BV. Results of this study have shown that the purest taurine cattle were instead located in BPE. If such a conservation programme was to be undertaken, we would advise on the use of animals from BPE.

The status of BPE animals is the result of the breeding system in force in this area and for which objectives are clearly defined at the farmers' level. Therefore a sustainable way of handling the market for these animals remains to be identified. Indeed, there should be a strong marketing study that could identify market problems and define likely solutions. There should also be a sensitisation programme to make stakeholders be aware of different changes that might intervene. A contest and show program with good prizes could be a way of attracting farmers in that region to recognise the effort they are deploying on this breed. Any breeding programme, whatever is its goal, should integrate the indigenous knowledge and use of these animals. Throughout these actions, studies of the biochemical as well as the culinary quality of meat and milk produced from these animals should be undertaken to support the promotion of this breed.

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Evaluación de la variabilidad y potencial genético de poblaciones de bovinos criollos colombianos

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Resumen

El presente trabajo presenta un análisis de la variabilidad y el potencial genético de las poblaciones de bovinos criollos utilizados en un Programa Nacional de Fomento, desarrollado por organimos gubernamentales (Ministerio de Agricultura y Desarrollo Rural, Instituto Colombiano Agropecuario y Corpoica). Se hizo el análisis de la información productiva de poblaciones de las razas Romosinuano, Costeño con Cuernos, Sanmartinero y Blanco Orejinegro, mediante el uso de la metodología BLUP, se calcularon los valores genéticos directos para peso al nacimiento, destete, 16 meses y ganancia de peso al destete y se realizó el análisis de la distribución de los animales por sus valores genéticos. Se encontró que en cada una de las razas existe una alta proporción de animales con valores genéticos positivos, siempre superior al 50%, lo cual indica una amplia variabilidad genética y posibilidad de selección de individuos mejoradores, que asegurarán el progreso genético en el programa de fomento que será desarrollado.

Summary

This work is an analysis of the variability and genetic potential of Colombian Creole cattle populations used in a national promotion program developed by the governmental organisations of the Ministry of Agricultural and Rural Development, the Colombian Agricultural Institute and the Colombian Corporation for Agricultural Research (CORPOICA). The analysis of productive information was made for populations of Romosinuano, Costeño con Cuernos, Sanmartinero and Blanco Orejinegro breeds, through use of BLUP methodologies, and was calculated using the direct additive genetic values for birth, weaning and 16 month weight and daily weight gain to weaning. This resulted in an analysis of animal distributions by their genetic values. It was found that each breed had a high proportion of animals with positive genetic values, always greater than 50%, which indicates a high genetic variability and genetic selection potential for improved animals. These factors assure the potential for genetic improvement in the promotion program that will be developed.

Résumé

Ce travail présente une analyse de la variabilité y du potentiel génétique des populations de bovins créoles utilisés dans un Programme National de Vulgarisation mis en place par des organismes gouvernementaux (Ministère de l'Agriculture et Développement Rural, Institut Agronomique Colombien et Corpoica). On a réalisé une analyse de l'information productive des populations des races Romosinuano, Costeño con Cuernos, Sanmartinero et Blanco Orejinegro, à l'aide de la méthodologie BLUP. On a calculé les valeurs génétiques directes pour le poids à la naissance, au sevrage, à 16 mois, et pour le gain de poids au sevrage. Une analyse de la distribution des animaux selon leurs valeurs génétiques a été réalisée. On a trouvé que dans chacune des races il existe une proportion élevée d'animaux avec des valeurs génétiques positives, toujours supérieur à 50%, ce qui indique une large variabilité génétique et la possibilité de sélection des individus améliorateurs, qui garantiront le progres génétique dans le programme de vulgarisation qui sera mené à terme

Key words*: Creole cattle, Genetic evaluation, Genetic variability.*

Introducción

Uno de los factores que influye sobre la baja eficiencia que presentan los sistemas tradicionales de producción bovina, en el trópico bajo colombiano es el uso inadecuado del recurso genético animal, ya que se ha utilizado razas foráneas y sus cruzamientos de manera indiscriminada sin ninguna evaluación y se ha dejado de utilizar el ganado criollo sin que existan razones técnicas y económicas que indiquen que los animales foráneos sean superiores.

Los trabajos que se conocen de cruces Criollo-Cebú han reportado niveles de heterosis del 6 al 12% para peso al destete y del 13 al 25% para peso a los 18 meses (Martinez y González, 2000; Martínez y Chavez, 2001; Martinez, 1999; Martinez *et al*., 1994; Hernandez, 1998). Es de anotar que todos los cruzamientos se hicieron sin un criterio estricto de selección en los paternales (ni en la raza Criolla, ni en el Cebú). Hoy disponemos de herramientas que nos permiten mejorar la fiabilidad de los resultados esperados como son las evaluaciones genéticas; con base en ellas podemos seleccionar machos y hembras Criollos y (en lo posible) machos y hembras Cebú para un uso intensivo en cruzamiento industrial o comercial.

La conservación de los recursos genéticos animales carece de sentido si no se hace una utilización comercial de ellos en los diversos agroecosistemas nacionales. La palabra conservación implica preservación y utilización racional y hasta ahora los recursos de Bancos de Germoplasma Animal sólo soportan la preservación propiamente dicha.

La responsabilidad confiada a CORPOICA por parte del Ministerio de Agricultura en Convenio con el Instituto Colombiano Agropecuario, ha permitido el mantenimiento de los Bancos de Germoplasma *in situ* con estrategias de apareamiento circular cíclico, fortaleciendo de manera simultánea un sistema de Bancos de Germoplasma *in vitro* (Martinez *et al*., 2005). Las condiciones actuales de los Bancos de acuerdo con su tamaño, las circunstancias financieras que implican el manejo de ellos y la necesidad de hacer la promoción de estas razas, hacen imperativo aumentar el tamaño de las poblaciones y procurar el mejoramiento genético de las mismas. Por esto se está desarrollando el Programa Nacional de Fomento de Bovinos Criollos, como un esfuerzo de El Ministerio de Agricultura y Desarrollo Rural, el Instituto Colombiano Agropecuario (ICA) y Corpoica, que se han planteado como objetivo, promover la utilización de bovinos de las razas criollas adaptadas al ambiente colombiano, que permita promover por parte de los ganaderos la cria de estas razas, y tener una información útil para implementar un plan de mejoramiento ganadero.

Para conseguir un mejoramiento genético sostenido, es necesario implementar estrategias de selección de las poblaciones, que consiste en la identificación de los individuos (machos y/o hembras) que mejor comportamiento productivo presentan, de acuerdo a los objetivos del productor y de esta forma se aumenta la frecuencia de genes favorables en la expresión de determinado carácter. Pero normalmente no tenemos información específica sobre los genes que los candidatos a selección poseen, sino que tenemos información fenotípica del individuo o de sus parientes (Telo L., 2002; 2004).

Este trabajo, tuvo como objetivo la utilización de metodologías de modelos mixtos para realizar la evaluación genética de cada una de las poblaciones de bovinos criollos de las razas Romosinuano (ROMO), Costeño con cuernos (CCC), Ubicadas en el C.I. Turipaná (Cereté Cordoba), la raza Sanmartinero (SM), ubicada en el C.I. La Libertad (Villavicencio, Meta), y la raza Blanco Orejinegro (BON), ubicada en la Estación Experimental El Nus (San Roque, Antioquia), que fueron seleccionadas para un programa de fomento y multiplicación de bovinos criollos en Colombia.

Materiales y Métodos

La información productiva fue obtenida de los núcleos de animales de las razas Criollas que se mantiene como Banco de Germoplasma. Cada una de las bases de datos comprende la información generada desde el año 1980 hasta el año 2004. Se analizaron los registros para características de peso de nacimiento (PNac), peso ajustado a los 270 días (Pdtte), peso a los 480 días (P16m) y ganancia de peso desde el nacimiento hasta el destete (GP).

Se empleo el Procedimiento de Modelos Generales Lineales (GLM) del paquete estadístico SAS (Statistical Analysis System), para el calculo de las medidas de tendencia central y variación de datos fenotípicos, el modelo incluyó efectos de año

(1980-2004), sexo y número de parto (1-10). El modelo utilizado se describe así:

$$Y_{ijk} = \mu + \alpha_i + \beta_j + \lambda_k + e_{ijk}$$

Donde:
μ = promedio general de la variable;
α_i = Efecto de año de nacimiento del animal;
β_j = Efecto de sexo del animal;
λ_k = Efecto de número de parto en que nace el animal;
e_{ijk} = error experimental.

Para el análisis genético se utilizó el modelo, que se describe a continuación:

$$Y=X\beta+Za+Zm+Zp+e$$

Utilizando las ecuaciones del modelo mixto (EMM) (Henderson, 1975; 1988), donde Y es un vector de observaciones, β es un vector de soluciones para efectos fijos (año de nacimiento, sexo, número de parto) y X es la matriz de incidencia de los efectos fijos y Z es la matriz de incidencia de los efectos aleatorios; a es el vector de soluciones para valores genéticos, m es el vector de soluciones para efecto materno y p es el vector de soluciones para efectos de ambiente permanente, e corresponde a los valores residuales.

La estructura de (co)varianza de los efectos aleatorios para las características evaluadas fue:

$$V\begin{bmatrix}\mathbf{a}\\ \mathbf{m}\\ \mathbf{pe}\\ \mathbf{e}\end{bmatrix}=\begin{bmatrix}\mathbf{A}\sigma_a^2 & \mathbf{A}\sigma_{am} & 0 & 0\\ \mathbf{A}\sigma_{am} & \mathbf{A}\sigma_m^2 & 0 & 0\\ 0 & 0 & \mathbf{I}_{pe}\sigma_{pe}^2 & 0\\ 0 & 0 & 0 & \mathbf{I}_n\sigma_e^2\end{bmatrix}$$

En este caso A es el numerador de la matriz de parentesco, σ_a^2 es la varianza aditiva genética directa, σ_m^2 es la varianza aditiva genética materna, σ_{am} es la covarianza genética aditiva directa-materna, σ_{pe}^2 es la varianza de ambiente materno permanente, σ_e^2 es la varianza residual, e I_{pe} e I_n son las matrices identidad con orden igual al numero de madres y registros respectivamente. Los cálculos de heredabilidad aditiva directa, fueron hallados mediante componentes de varianza a partir del modelo animal por medio de la siguiente fórmula:

$$h_d^2 = \sigma_a^2 / \sigma_f^2$$

donde:
h_d^2 = Heredabilidad aditiva directa,
σ_a^2 = Varianza genética aditiva directa,
σ_f^2 = Varianza fenotípica total.

Para el caso de los componentes genéticos de tipo materno la heredabilidad se estimó mediante la siguiente fórmula:

$$h_m^2 = \sigma_m^2 / \sigma_f^2$$

donde
h_m^2 =Heredabilidad de los componentes genéticos maternos,
σ_m^2 =Varianza genética materna,
σ_f^2 = Varianza fenotípica total.

También se calculó el valor de exactitud de cada estimación como

$$r_{AP}^2 = 1 - C^{ii}\lambda$$

donde: $\lambda = \sigma_e^2 / \sigma_a^2$ y C^{ii} representa un mismo elemento en la matriz C^{-1}, como ha sido descrito por Misztal y Wiggans (1988) y Meyer (1989). Se presenta la media de los valores de exactitud para toda la población.

Mediante el Programa *Derivative Free Restricted Maximum Likelihood* (DFREML) (Smith y Grazer, 1986) se estimaron componentes de varianza de cada una de las características y a partir de estos se calcularon los parámetros genéticos. Los componentes de varianza genéticos aditivos directos y maternos para los diferentes pesos evaluados fueron también analizados mediante el paquete sistematizado *Multi Trait Derivative Free Restricted Maximun Likelihood* (MTDFREML) (Boldman *et al*.,1991; 1993), usando como valores de inicio los obtenidos en DFREML, esto permitió estimar valores genéticos (VG) directos y maternos (no presentados). Con los valores genéticos individuales se calcularon los valores promedio anuales y se hizo un grafico de la distribución de los valores individuales para peso al nacimiento, destete, ganancia al destete y peso a los 16 meses y se determinó la proporción de individuos con valores genéticos mayores de cero y menores de cero, como un indicativo de la tendencias, para lo cual se utilizaron procedimientos de regresión lineal.

Tabla 1. Comportamiento productivo de hembras de cada una de las razas criollas utilizadas en programas de fomento.

Razas criollas	PNac		Pdtte		GP		P16m	
utilizadas	Hembras	Machos	Hembras	Machos	Hembras	Machos	Hembras	Machos
BON	25,5±3,7	28,13±3,43	164,70±61,8	202,78±25,60	517,98±218,7	542,32±240,8	204,54±87,60	240,17±27,86
SM	27,0±2,9	26,74±3,32	165,32±60,2	166,92±50,90	550,23±305,2	520,84±250,6		
ROMO	28,7±6,1	31,55±3,84	175,95±74,9	187,11±63,83	563,78±231,8	581,23±214,1	226,20±80,60	236,47± 95,10
CCC	28,352±4,6	30,40±3,56	164,13±36,2	200,80±56,60	548,25±110,6	650,25±188,5	205,52±27,12	239,00±108,3

Tabla 2. Parámetros genéticos en la raza BON (Gallego et al., 2006), ROMO (Martinez y Pérez, 2006), y CCC (Martínez y Herazo, 2006).

Parámetros genéticos	Peso al nacimiento	Peso al destete ajustado a 240 días	Peso ajustado a los 480 días
Raza BON			
h_d^2	0,38±0,017	0,18±0,022	0,095±0,025
h_m^2	0,03±0,015	0,05±0,025	0,032±0,022
h_t^2	0,41±0,050	0,24±0,056	0,128±0,050
P^2	0,06±0,031	0,04±0,02	0,062±0,045
e^2	0,51±0,022	0,70±0,08	0,080±0,032
Raza ROMO			
h_d^2	0,25±0,001	0,34±0,063	0,330±0,066
h_m^2	0,06±0,003	0,19±0,054	0,100±0,046
ram	-0,37±0,002	-0,34±0,133	-0,050±0,021
h_t^2	0,28	0,435	0,380
P^2	0,03±0,002	0,09±0,031	0,069±0,028
e^2	0,71±0,003	0,47±0,045	0,570±0,05
Raza CCC			
h_d^2	0,17±0,001	0,21±0,074	0,172±0,001
h_m^2	0,01±0,003	0,05±0,038	0,040±0,001
h_t^2	0,17	0,235	0,192
ram	-0,89±0,003	-0,13±0,037	-0,380±0,0001
P^2	0,04±0,0001	0,04±0,029	0,001±0,0001
e^2	0,81±0,0003	0,72±0,059	0,818±0,0001

Resultados y Discusión

Mediante el uso de la metodología del modelo snimal empleando el procedimiento BLUP, se realizó la predicción de los valores genéticos individuales en cada población y con esta información se graficó la distribución de estos valores para los animales de cada una de las razas y que fueron en parte utilizados para ser entregados en el Programa Nacional de Fomento de los Bovinos criollos; esta información da una idea de la variabilidad genética de las características y del potencial genético de la población dada la proporción de individuos con valores genéticos positivos.

En la tabla 1 se muestra el comportamiento productivo de las hembras y machos que fueron seleccionados para ser entregados en el programa de fomento. Las razas Romosinuano y Costeño con cuernos (CCC) presentan los mayores pesos al nacimiento; en cuanto al peso al destete, los valores de los machos Sanmartinero son inferiores a los de las demás razas y muy similares a los pesos registrados para las hembras, igual comportamiento se nota para peso al destete. En general estos valores son similares a los reportados para estas

Figura 1. Población de hembras de la raza Blanco Orejinegro perteneciente al Banco de Germoplasma situado en la E.E. El Nus de CORPOICA ubicada en el municipio de San Roque, Antioquia.

razas (Martínez, 2001; Treviño, 2001; Pérez y Moreno, 1999).

En cuanto a los parámetros genéticos, varios autores han reportado valores de heredabilidad directa, materna, total y efecto de ambiente permanente y efecto residual. Gallego *et al.*, (2006) reportaron en la raza BON, para la característica peso al nacimiento, un valor para la heredabilidad directa de 0,38±0,017 y la materna 0,03±0,015, este último considerado bajo, posiblemente debido al bajo efecto del genotipo de la vaca sobre el peso del ternero. Se obtuvo un valor medio alto de para la heredabilidad total (0,41±0,050). La heredabilidad total para el peso al destete fue de 0,24±0,056. Se estimó un valor de 0,18±0,022 para la heredabilidad directa y 0,0599±0,025 para la materna, lo que indica que el 24% de varianza fenotípica o total, se atribuye al efecto de genes de acción aditiva, 5% a los efectos genéticos maternos y el 70% restante a las variaciones genéticas no aditivas y al ambiente. Para la característica peso ajustado a los 480 días se estimaron valores bajos con heredabilidad total de 0,128±0,05, directa de 0,095±0,0250 y materna de 0,0329±0,022.

Para la característica peso al nacimiento se encontró en la población Romosinuano, Martínez y Pérez (2006) han reportado valores de heredabilidad directa de 0,25±0,001, heredabilidad materna de 0,06±0,03 y heredabilidad total de 0,28, valores considerados bajos, excepto para la heredabilidad total para la cual se reporta una heredabilidad media. Para la característica PD en terneros Romosinuano se obtuvo un valor de heredabilidad directa de 0,34±0,06, heredabilidad materna de 0,19±0,054 y heredabilidad total de 0,43. Para la heredabilidad materna el valor reportado es considerado bajo, lo que demuestra el poco efecto que ejercen los genes maternos sobre el PD en terneros Romosinuano, contrario a esto la heredabilidad directa y total para esta característica de crecimiento son medias mostrándonos el efecto moderado ejercido por los genes del propio animal sobre la característica en mención, La heredabilidad total estimada para el P16m en terneros Romosinuano fue de 0,38, se encontró una heredabilidad directa de 0,33±0,06 y una heredabilidad materna de 0,10±0,04, inferior a la registrada para PD, esto refleja las variaciones en el potencial de producción de leche de las vacas (Plasse *et al.*, 2002). La mayoría de trabajos donde registran caracteres posdestete se realizan solamente hasta el año de edad y por esto son difíciles las comparaciones, a causa de que en el trópico, el periodo de estrés posdestete se extiende

Figura 2. Vaca de la raza Sanmartinero perteneciente al Banco de Germoplasma situado en el C.I. La Libertad de CORPOICA ubicado en el municipio de Villavicencio, Meta.

hasta el año de edad. Por eso generalmente se considera que el pesaje a 18 meses es mas apropiado para el estudio de diferencias genéticas y como criterio de selección. (Plasse *et al*., 2002)

La raza CCC presentó el menor valor de heredabilidad para peso al nacimiento (h_t^2=0,17), consistente con los resultados de las demás razas, con valores de correlación negativa entre efectos directos y maternos. Para el peso al destete, tambien presentó menores valores, comparado con las demás razas (h_t^2=0,23) y con un valor de heredabilidad materna baja y similar a la encontrada en la raza BON. Similarmente, en el carácter de peso a los 16 meses, tambien presentó valores intermedios (h_t^2=0,19), superior a lo encontrado en la raza BON, pero inferior a lo encontrado en la raza ROMO, con un bajo efecto materno, similar a lo encontrado para las otras razas.

En cuanto al efecto de ambiente permanente en cada una de las razas y en general para todas las caracteristicas, fue bajo y varió entre 0,0012 y 0,069, ambos en el carácter peso a los 16 meses y en las razas CCC y ROMO respectivamente. Esto indica que puede ser eliminado este efecto del modelo de análisis sin afectar de manera importante la estructura y resultados de análisis de la información.

En la tabla 3 se muestran los valores genéticos directos promedio para cada una de las poblaciones de las razas criollas que se utilizaron en el programa de fomento. Es de resaltar que en este caso sólo se computa el promedio con los valores de los animales que se utilizaron para el programa de fomento. Se puede apreciar que solamente se encuentran valores negativos para peso al nacimiento en BON y SM, y para peso al destete, solamente se registra promedios de valores genéticos negativos para hembras y machos de la raza Sanmartinero y hembras de la raza Romosinuano. Para las demás características, se tienen promedios de valores genéticos positivos en todas las razas. Esto indica una buena calidad genética de las poblaciones, para las características de peso al destete, ganancia de peso del nacimiento al destete y para el peso a los 16 meses.

En las siguientes figuras se muestra la distribución de los valores genéticos individuales en la población, organizados por sexo, por debajo

Tabla 3. Valores genéticos promedio (V.G.P.) y exactitud promedio (r_{AP}^2) para caracteres de crecimiento en hembras de cada una de las razas criollas utilizadas en programas de Fomento.

	PNac.			Pdtte.			GP			P16m		
Raza	Hembras	Machos	r_{AP}^2	Hembras	Machos	r_{AP}^2	Hembras	Machos	r_{AP}^2	Hembras	Machos	r_{AP}^2
BON	-0,270	0,110	0,67	4,000	6,878	0,56	15,030	23,894	0,52	1,580	4,716	0,49
SM	-0,324	-0,251	0,52	-8,000	-4,540	0,50	17,000	12,063	0,49			
ROMO	0,152	0,354	0,55	-1,202	1,962	0,52	3,737	6,779	0,51	0,076	0,084	0,49
CCC	0,014	0,019	0,48	0,996	2,911	0,57	4,951	12,122	0,57	1,510	2,544	0,49

del cero (0,0) se encuentran una superficie que indica la proporción (número de animales con respecto al total de animales) que presentan valores negativos y por encima de cero, la superficie indica la proporción de animales con valores genéticos positivos.

Raza Blanco Orejinegro

Como se puede apreciar para la raza Blanco Orejinegro (Figura 1) el 51% de las hembras tienen valores genéticos negativos para peso al Nacimiento, (Hembras 72/141), mientras que el restante 49% (69/141) presentan valores genéticos positivos, similar a lo encontado para los machos [49% negativos (51/104) y 51% de animales positivos (53/104)]

Para el peso al destete en la raza BON, ya se tiene una mayor proporción de individuos con valores genéticos positivos tanto en hembras [21% negativos (30/141) y 79% positivos 111/141] como en machos [21% negativos (22/104) y 79% positivos (82/104)] indicando que en general los animales presentan buenas posibilidades de selección para esta variable. Similar comportamiento puede ser observado para el carácter ganancia de peso, donde en las hembras se presentan 79% de individuos con

Figura 3. Toro de la raza Romosinuano perteneciente al Banco de Germoplasma situado en el C.I. Turipaná de CORPOICA ubicado en el municipio de Cereté Cordoba.

Figura 4. Toro de la raza Costeño con Cuernos perteneciente al Banco de Germoplasma situado en el C.I. Turipaná de CORPOICA ubicado en el municipio de Cereté Cordoba.

valores genéticos positivos (111/141) [21% de individuos negativos (30/141)] y 83% de los machos con valores genéticos positivos (86/104) [17% de individuos machos, con valores negativos (18/104)]

Para el peso a los 16 meses de edad se encontró que el 69% de las hembras entregadas con fines de fomento tuvieron valores genéticos positivos (97/141) y tan sólo un 31% presentaron valores negativos (44/141), similar a lo encontrado en los machos donde el 79% (82/104) de los machos seleccionados para fomento tuvieron valores genéticos superiores al promedio de la población y sólo un 21% presentaron valores inferiores (22/104). Para esta raza es muy evidente la alta proporción de individuos mejorantes tanto en machos como en hembras, lo que indica que la población seleccionada para el plan de fomento tiene una buena base genética para selección, que permitirá asegurar el progreso genético al aplicar estrategias de mejoramiento genético.

Raza Sanmartinero

En el caso de la raza Sanmartinero (Figura 2), por el peso al nacimiento, se encontró - para las hembras - un 71% de animales con valor genético negativo (150/209) y solamente un 29% de individuos positivos (59/209) y para los machos, 72% de individuos con valores negativos (114/158) y 28%) positivos (44 /158). Similar comportamiento se pudo apreciar para el carácter peso al destete, donde para el 74% de las hembras (155/209) se estimaron valores genéticos negativos y sólo el 26% (54/209) positivos y en los machos, el 65% de individuos con valores genéticos negativos (104/158) y un 35% positivos (54 /158)

Por el contrario, la característica peso al destete, en esta población presentó un predominio de animales con valores genéticos positivos tanto en machos como en hembras (56% positivos (115/209) y 44% negativos (94/209) y en machos 59% de animales positivos (92 /158) y sólo 41% de animales negativos (66/158). Esto indica para esta raza, que este carácter puede constituirse en objetivo de selección, dado que muestra amplia variabilidad fenotípica y genética y que la población presenta valores genéticos promedio superiores a cero, garantizando el progreso genético que se puede obtener seleccionando por este carácter.

Raza Romosinuano

En la raza Romosinuano (Figura 3), se encontró proporciones levemente superiores de animales con valores genéticos superiores para peso al nacimiento, ya que el 55% de las hembras (73/135) presentaron valores genéticos positivos, mientras que el 45% presentaron valores negativos (62/135), y en los machos el 58% (44 /76) presentaron valores positivos y sólo el 42% (32/76) negativos. Similar comportamiento se apreció para el peso al destete, donde el 55% de las hembras (73/135) y el 60% de los machos (45 /76) presentaron valores genéticos positivos y para el carácter ganancia de peso al destete, donde el 57% de las hembras (76/135) y el 58% de los machos (44/76) presentaron valores genéticos positivos.

Para el Peso a los 16 meses, también se presentaron proporciones levemente superiores de animales con valores genéticos positivos, pues el 59% de las hembras (79/135) y el 57% de los machos (43 /76) presentaron valores genéticos positivos. Para esta raza, se encuentra una amplia variabilidad genética y valores genéticos en promedio positivos, lo que indica la mayor posibilidad de seleccionar individuos mejorantes en la población.

Raza Costeño con cuernos

En la raza Costeño (Figura 4) solamente el carácter peso al nacimiento presentó similares proporciones de animales con valores genéticos positivos y negativos en Hembras [47% (67/140) negativos y 53%(73/140) positivos] y machos [51% (36/70) negativos y 49%(34/70) positivos], para el peso al destete, se encontró una mayor proporción de individuos con valores genéticos positivos en hembras [45%(63/140) negativos y 55%(77/140) positivos], pero superior proporción en machos con valores genéticos positivos [38% (27/70) negativos y 62%(43/70) positivos], similar a lo encontrado para la ganancia de peso al destete, donde el 58% de las hembras (80/140) presentaron valores genéticos positivos (42% (60/140) con valores genéticos negativos) y en los machos el 62 % de los individuos (43/70) presentaron valores genéticos positivos. Pero el carácter peso a los 16 meses presentó una diferencia considerable, con una alta proporción de individuos con valores genéticos positivos, en este caso el 70% de las hembras (97/140) y 73% de los machos (51/70), presentaron valores genéticos positivos y complementariamente el 30% (43/140) de las hembras y el 27% (19/70) de los machos presentaron valores genéticos negativos.

En esta población, se puede decir que al realizarse una selección de parentales, para las características de crecimiento, hay una alta proporción de individuos que pueden ser utilizados como animales mejorantes, dada la mayor proporción de individuos con valores genéticos positivos para la mayoría de caracteres. Esto también es un indicio de la amplia variabilidad genética que presenta esta raza para las variables de crecimiento, al igual que en el resto de las razas criollas analizadas. Con estas poblaciones fue iniciado un Programa Nacional de Fomento de Bovinos criollos (Anzola *et al*., 2005) en diferentes regiones del territorio Colombiano, el cual tiene como objetivo promover la utilización de bovinos de las razas criollas, que actualmente se encuentran en amenaza de extinción y además se busca obtener información útil para implementar un plan de mejoramiento genético con miras a incementar su capacidad productiva, y para esto se tiene como punto de partida poblaciones con suficiente variabilidad genética para los procesos de selección.

Conclusiones

De acuerdo a los resultados obtenidos, se puede concluir que cada una de las razas evaluadas presenta proporciones variables de animales con valores genéticos positivos y negativos variando entre razas. La mayor proporción de individuos con valores genéticos positivos para las características de crecimiento fue la raza BON y CCC, lo que indicaría mayor potencial para selección. Además se encontraron similares proporciones de individuos con valores positivos y negativos entre machos y hembras, indicando una alta variabilidad genética sin diferencias entre sexos. Por otra parte, el carácter peso a los 16 meses presentó en general en todas las razas una alta proporción de animales con valores genéticos positivos, indicando que este puede ser el carácter con mayor potencial para tener en cuenta al iniciar un programa de mejoramiento genético. El uso de este tipo de metodologías para la evaluación de las poblaciones locales puede ser de gran utilidad para el desarrollo y la gestión genética tanto en términos de conservación como para mejoramiento, pues en el primer caso da un indicio del estado de conservación al evaluar las tendencias en los valores de consanguinidad y parámetros genéticos, que deben mantenerse estables en el tiempo. En el caso de mejoramiento, la determinación de los valores genéticos permite aplicar procesos de selección más precisos y con resultados más predecibles. Este trabajo es un ejemplo de su aplicación en poblaciones experimentales y en programas de fomento y multiplicación de cuatro razas locales en Colombia.

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Molecular characterization of two common Chadian cattle breeds

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Summary

In previous studies, significant differences in *Mycobacterium bovis* infection prevalence was reported between two Chadian cattle breeds. Those findings and the established differentiation due to phenotypic characteristics suggest that the two breeds (Arab and Mbororo) are genetically different. To evaluate the genetic structure and the differences between these breeds, the genetic diversity within and between breeds was evaluated based on a total of 205 multilocus genotypes (21 microsatellite loci).

All of the loci under investigation were polymorphic and the number of alleles ranged from 4 to14 within the two populations. The analysis of population fixation resulted in a F_{ST} value of 0.006. Further the population assignment of the individual genotypes and the exact test of population differentiation did not support the hypothesis that the samples drawn from the two populations are genetically different. Population admixture and sample collection are discussed as possible reasons for the rejection of the hypothesis. Finally, recommendations for sample collection in extensive systems are given.

Resumé

Dans des études précédentes on avait observé des différences significatives dans les infections par *Mycobacterium bovis* chez les races bovines de Chadian. Ces observations et la différence due aux caractéristiques phénotipiques suggèrent que les deux races (Arabe et Mbororo) sont génétiquement différentes. Pour évaluer la structure génétique et les différences entre ces races on a évalué la diversité génétique dans et entre races sur un total de 205 génotypes multiloci (21 loci microsatélites). Tous les loci étudiés étaient polymorphiques et le nombre d'allèles allaient de 4 à 14 dans les populations. L'analyse de la fixation de la population a donné un F_{st} de valeur 0,006. Après l'asségnation des génotypes individuels à la population et le test exact de différence de la population, l'hypothèse des échantillons sortis de deux populations génétiquement différentes n'était pas correcte. Le mélange des populations et la saisie des échantillons sont étudiés comme possible cause du rejet de l'hypothèse. Pour finir, on présente une série de recomandations pour la saisie des échantillons dans des systèmes extensifs.

Resumen

En estudios anteriores se observaron diferencias significativas en infecciones prevalentemente por *Mycobacterium bovis* en dos razas bovinas de Chadian. Estos hallazgos y la diferenciación establecida debida a las características fenotípicas sugieren que las dos razas (Arabe y Mbororo) son genéticamente distintas. Para evaluar la estructura genética y las diferencias entre estas razas, se evaluaron la diversidad genética dentro y entre razas en un total de 205 genotipos multiloci (21 loci microsatélites). Todos los loci estudiados eran polimórficos y el número de alelos iba de 4 a 14 dentro de las dos poblaciones. El análisis de fijación de la población resultó en F_{st} con valor 0,006. Tras la asignación de genotipos individuales a la población y el test exacto de diferenciación de la población quedó eliminada la hipótesis de que las muestras sacadas de las dos poblaciones eran genéticamente diferentes. La mezcla de poblaciones y la recogida de muestras se discuten como posibles motivos que hicieron rechazar la hipótesis. Por fin, se presentan una serie de recomendaciones para la recogida de muestras en sistemas extensivos.

***Key words**: Cattle breeds, Africa, Molecular characterization, Genetic diversity, Genotyping, Cluster analysis, Populations.*

Introduction

Mycobacterium bovis (*M. bovis*) is the causative agent of bovine tuberculosis (BTB). Bovine tuberculosis is a zoonotic disease and one question of interest is its importance in the human tuberculosis epidemic, fostered by HIV/AIDS in different parts of Africa (Ayele *et al*., 2004; Cosivi *et al*., 1998). Such investigations are extensive, as the tuberculosis epidemic and spread depend on a variety of factors such as complex interactions between different *Mycobacterium tuberculosis* complex strains, non-tuberculus Mycobacteria, susceptibility of host cattle breeds, the public health status and other environmental factors. To further investigate those complexities a large project is currently running in cooperation with Laboratoire de Recherches Vétérinaires et Zootechniques de Farcha, N'Djaména, Chad; Sokoine University of Agriculture, Morogoro, Tanzania; Laboratoire Central Vétérinaire, Bamako, Mali; Ecole Inter-Etats des Sciences et de Médecine Vétérinaires, Dakar, Senegal; the Swiss Tropical Institute (STI), Basel, Switzerland and the Swiss Federal Institute of Technology (ETH), Zürich, Switzerland.

In a previous study, differences between host cattle breeds regarding the prevalence of infections with *M. bovis* were reported (Hilty, 2006). In Chad as well as in Cameroon (Hilty, 2006), a higher prevalence in the Mbororo breed was found in comparison with the Arab breed, and the hypothesis was that the distinct prevalence might be due to a differential susceptibility in the two breeds. Further research on the susceptibility of different host breeds and the genetic diversity between these breeds are goals of the overall project. So far, the genetic characterizations of the samples collected at the slaughterhouses in Chad have been completed and are the subject of the presented study.

As compared to Europe, characterisation of animal genetic resources (AnGR) in Africa receives less attention. In the country report of Chad (FAO, 2007b), no molecular characterization of Chadian cattle breeds was reported. However, adequate characterization of AnGR is a prerequisite for successful management programmes and for informed decision making in national livestock development (FAO, 2007a). Even if the two breeds Mbororo and Arab are not at risk of extinction (derived from FAO, 2007c) the data collected at the slaughterhouses in Chad is expected to be worthy of detailed analysis of the molecular aspects of each. The aim of this study was the molecular characterization of the two breeds including the assessment of genetic diversity within and between populations. Such a characterization is not only of interest regarding the differences in BTB prevalence in the two breeds but also in respect to the description of indigenous African cattle breeds and African cattle husbandry systems.

Material and Methods

Breeds

The genotyped animals belong to the two breeds Mbororo and Arab. All of them were kept in a long distance transhumant system by pastoralists, thereby passing the border between Chad and the Central African Republic and spending the dry season in the Central African Republic. The transhumant system is the main cattle production system in Chad. Seventy five percent of the national herds are kept by pastoralists and almost 50% of Chadian export revenues are generated within this system (FAO, 2007b).

The Mbororo cattle, also known as Red Fulani, belong to the subgroup Fulani of the West African Zebu cattle. In Chad a population size of 300 000 heads was reported in year 1992 (FAO, 2007c). This breed has long, lyre-shaped horns and a thoracic, sometimes intermediate hump (FAO, 2007c) (Figure 1). The lactation yield is poor with 2 kg of milk per day at the peak of lactation (FAO, 2007b). The carcass dressing out is low (40% - 42%), but FAO (2007b) reported the good quality of the breed's hides for leather production. The breed is robust and adapted to different climates, i.e. the breed is kept in dry as well as humid regions of Chad (FAO, 2007b).

The Arab Zebu (or Shewa) has a well developed dewlap and short horns (Zibrowski, 1997). Coat colour is red – maroon in the sahel-zone and predominantly white in the south-east and west (FAO, 2007b). Figure 2 shows some Arab animals from Chad before slaughter. Milk yield per lactation varies from a minimum of 454 kg to a maximum of 1 814 kg in a lactation length varying from 240 to 396 days (DAGRIS, 2007). Other than the entirely

Figure 1. Mbororo cattle at the slaughterhouse in Chad (photo Ngandolo B.N.R.).

Figure 2. Arab cattle at the slaughterhouse in Chad (photo Ngandolo B.N.R.).

Table 1. Age structure and average age of the sampled individuals (grouped by sex and breed).

Sampled individuals	Sex	No.	Age (mean)	Number of animals per age class (years)										
				1	2	3	4	5	6	7	8	9	10	11
Arab	Male	34	4.206	6	4	6	2	6	3	3	2	2	0	0
	Female	97	6.701	2	1	3	6	6	20	26	21	9	1	2
Mbororo	Male	38	3.079	2	18	7	4	4	0	2	1	0	0	0
	Female	36	5.611	1	5	3	2	2	6	9	7	1	0	0

desert regions, the breed is kept in all other regions of Chad. It is estimated, that 75% to 90% of Chadian cattle belong to this breed (FAO, 2007b). A population size of 4 902 000 heads was reported in year 1992 (FAO, 2007c).

Genotyping

Blood samples were taken from animals before slaughter at three different abattoirs in Southern Chad. Additionally, information about the breed, age, sex, transhumance system, borders crossed, residence during the dry season and the location of the slaughter house of each animal was recorded. The age structure and gender of the sampled animals are shown in table 1.

Blood was allowed to clot, transported on ice to the Laboratoire de Recherches Vétérinaires et Zootechniques in Farcha and stored at -80°C until further processing. DNA was extracted using the QIAamp® DNA Blood Mini Kit (QIAGEN, Cat. No. 51106) from clotted blood corresponding to 238 individual animals. Handling was carried out according to the Blood and Body Fluid Spin Protocol (derived from Qiagen, 2007). DNA was transported to Europe where genotyping was conducted by Van Haeringen Laboratories, Wageningen, Netherlands. All microsatellites were chosen from the FAO-list (FAO, 2004).

A remarkable degradation of the DNA was observed over time. This problem caused a high fraction of missing genotypes, especially for the most recent genotyped multiplexes. Markers for individuals with missing information for seven and more markers were omitted from further analysis. Finally, 205 genotypes (131 Arab and 74 Mbororo) for 21 microsatellites were included for statistical analysis.

Statistical analysis

For the statistical investigations the packages ARLEQUIN 3.01 (Excoffier *et al*., 2005), STRUCTURE 2.1 (Pritchard *et al*., 2000) and FSTAT 2.9.3.2 (Goudet, 1995) were applied. Deviation from Hardy-Weinberg- Equilibrium (HWE) was tested for each locus in each population using ARLEQUIN (number of steps in MCMC =100 000). The significance level was set to *P*-value <0.001.

FAO- markers are assumed to be polymorphic, selectively neutral and to segregate independently from other loci (FAO, 2004). In ARLEQUIN a likelihood ratio test of linkage disequilibrium is implemented for genotypic data with unknown gametic phase. This test was conducted on the data setting the number of permutations to 10 000 and the significance level to 0.05.

The number of alleles per locus, the average number of alleles per breed, the observed and expected heterozygosity per locus and breed were calculated as indicators for the genetic variability within the two breeds. The relevant results were part of the testing on HWE with ARLEQUIN. Further breed specific alleles (i.e. private alleles) were counted.

FSTAT (Goudet, 1995) was used for the assessment of Wrights fixation indices and the respective standard errors. Further, the computations given in ARLEQUIN to conduct population comparisons and population differentiation were conducted. Additionally genotype assignment was derived with this package.

Clustering analysis was conducted with STRUCTURE 2.1 (Pritchard *et al*., 2000). The length of burning period for the MCMC was set to 10 000 with 10 0000 replications after burning. The number of clusters was varied from 2 to 5.

Table 2. Number of genotypes (N), number of alleles, fraction of missing genotypes observed heterozygosity, expected heterozygosity and P-value for HWE-testing for the Arab sample and the Mbororo sample, respectively.

	Arab (131)						Mbororo (74)					
Marker	No.	Alleles	Missing (%)	Obs_het	Exp_het	*P*-value	No.	Alleles	Missing (%)	Obs_het	Exp_het	*P*-value
BM1818	129	9	1.5	0.814	0.813	0.894	69	9	6.8	0.783	0.844	0.238
BM1824	131	7	0.0	0.672	0.746	0.003	74	4	0.0	0.703	0.743	0.910
BM2113	131	8	0.0	0.771	0.827	0.809	74	9	0.0	0.824	0.822	0.734
CSRM60	131	10	0.0	0.595	0.568	0.677	74	8	0.0	0.541	0.610	0.202
CSSM66	131	11	0.0	0.771	0.832	0.322	74	9	0.0	0.757	0.838	0.006
ETH10	129	8	1.5	0.798	0.769	0.382	74	8	0.0	0.797	0.803	0.237
ETH225	129	9	1.5	0.605	0.635	0.725	74	8	0.0	0.689	0.714	0.341
ETH3	131	8	0.0	0.618	0.600	0.504	74	7	0.0	0.514	0.553	0.842
HAUT27	113	7	13.7	0.664	0.744	0.374	66	7	10.8	0.727	0.746	0.797
ILSTS006	126	10	3.8	0.651	0.687	0.631	70	10	5.4	0.786	0.750	0.654
INRA23	130	12	0.8	0.708	0.745	0.526	74	10	0.0	0.595	0.665	0.281
SPS115	131	7	0.0	0.496	0.497	0.810	74	7	0.0	0.338	0.348	0.766
TGLA122	126	14	3.8	0.683	0.716	0.154	72	11	2.7	0.722	0.704	0.686
TGLA126	131	8	0.0	0.786	0.755	0.756	74	8	0.0	0.716	0.756	0.055
TGLA227	131	10	0.0	0.618	0.621	0.287	74	11	0.0	0.500	0.572	0.223
TGLA53[1]	93	16	29.0	0.763	0.787	0.747	60	15	18.9	0.567	0.768	0.002
ETH152	131	6	0.0	0.511	0.525	0.827	73	5	1.4	0.507	0.527	0.815
ETH185	129	14	1.5	0.806	0.823	0.478	74	11	0.0	0.662	0.757	0.282
HEL5[1]	96	7	26.7	0.573	0.770	0.000	52	6	29.7	0.500	0.751	0.000
ILSTS005	121	6	7.6	0.760	0.792	0.386	71	5	4.1	0.732	0.752	0.895
INRA32	126	10	3.8	0.714	0.826	0.033	72	10	2.7	0.806	0.815	0.949
INRA35	128	8	2.3	0.500	0.534	0.091	71	7	4.1	0.577	0.671	0.004
MM12	131	14	0.0	0.832	0.839	0.962	74	11	0.0	0.838	0.859	0.489
Mean[2]		9.3		0.684	0.709			8.3		0.672	0.707	
SD[2]		2.5		0.106	0.113			2.1		0.133	0.127	

[1] Excluded.

[2] After exlcusion of markers TGLA53 and HEL5.

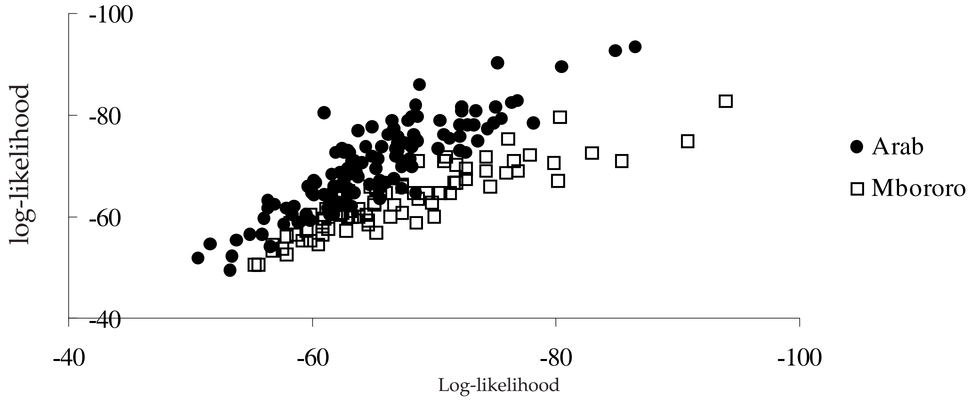

Figure 3. Log-likelihood of each individual's multilocus genotype in the population sample Arab and Mbororo, respectively, assuming that it comes from this population.

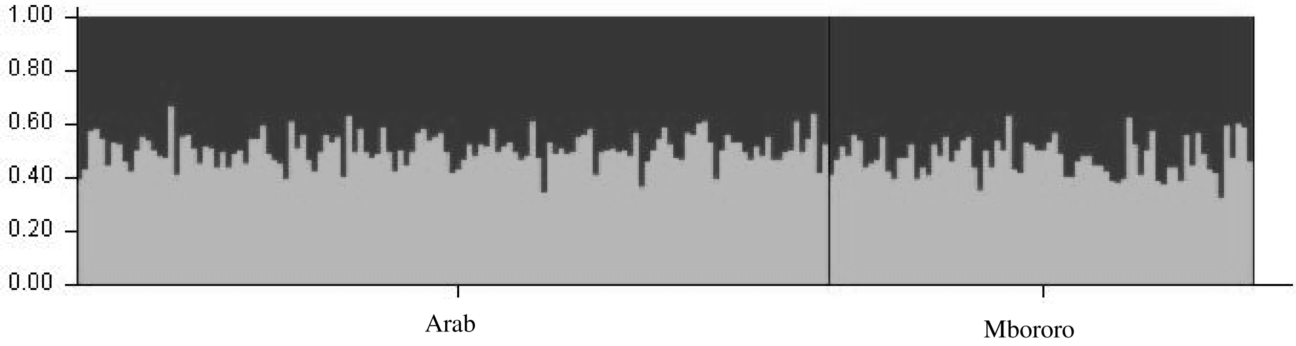

Figure 4. STRUCTURE clustering result for k=2 clusters.

Results

Information content of markers and genetic variability within populations

Table 2 gives an overview of the genotyped markers, the number of individuals with a genotype (N), the number of observed alleles, the fraction of animals with missing genotypes, the observed heterozygosity and the expected heterozygosity and the respective *P*-value for HWE-testing for the two populations, Arab and Mbororo, separately.

Genetic diversity between populations and cluster analysis

The total degree of population subdivision according to Weir and Cockerham (1984) was found to be:
F_{IT}= 0.042 (± 0.008)
F_{ST}= 0.006 (± 0.002)
F_{IS}= 0.037 (± 0.008).

Figure 3 shows the results for the genotype assignment implemented in ARLEQUIN. The program calculates the log-likelihood of each genotype under the assumption that it belongs to the respective population.

The results of the clustering analysis assuming two clusters, are given in figure 4. The number of clusters (k) investigated is user defined. The k resulting in the highest logarithmic probability is seen as the most probable number of subpopulations. For our data the highest log-likelihood was found for k = 2 .

Discussion

Information content of markers and genetic variability within populations

Marker HEL5 significantly deviates from HWE and was therefore excluded from further analysis. Further, TGLA53 was omitted as its fraction of missing genotypes was above 20%. After exclusion of the above mentioned markers, 205 individual genotypes for a total of 21 microsatellites remained for further analysis (Table 2).

Testing linkage disequilibrium revealed that for each population three pairs of loci do not segregate independently ($P<0.001$) (results not shown). However, as all of the markers in linkage disequilibrium are mapped to different chromosomes, the markers are informative regarding diversity studies and are not excluded from further analysis (Peter, 2005).

The number of alleles per locus ranged from 4 up to 14. The minimum was found in the Mbororo sample at the loci BM1824, the maximum at the three loci TGLA122, ETH185 and MM12 of the Arab sample (table 2). These findings show that the two populations are polymorphic for all of the 21 loci under investigation. The chosen loci all fulfil the rule of thumb given by FAO, that markers for diversity studies should segregate with at least 4 alleles per population (FAO, 2004). The mean number of alleles was 9.3 (± 2.5) for the genotypes belonging to the breed Arab and 8.3 (± 2.1) for the genotypes belonging to the Mbororo breed, averaging 8.8 (± 2.3) (Table 2) for the total sample.

28 alleles at 13 loci out of the 203 alleles were found to be so called private alleles (results not shown). A private allele is defined as an allele found in one population but in no other (Woolliams and Toro, 2007). In our study the highest frequency of a private allele was 2.8% only. Thus, their influence on differences in the allelic frequencies between populations is expected to be low.

The average observed heterozygosity was found to be 0.684 (± 0.106) in the Arab and 0.672 (± 0.133) in the Mbororo populations, respectively. The average expected heterozygosity was 0.709 (± 0.113) for the Arab population, and 0.707 (± 0.127) for the Mbororo population (Table 2). The mean number of alleles per locus and the expected heterozygosity are seen as informative measures for the assessment of genetic diversity within populations (Hanotte and Jianlin, 2005; Toro and Caballero, 2004). The mean number of alleles per locus found in the present study is lower than the 11.5 alleles per microsatellite locus observed by Ibeagha-Awemu *et al*. (2004) in West/Central African cattle breeds. The expected heterozygosity for the nine *Bos indicus* breeds investigated by Ibeagha-Awemu *et al*. (2004) ranged from 0.703 – 0.744. Our estimates correspond with the lower end of this range.

Generally, it has to be questioned if the samples drawn for our study represent random samples from the Mbororo and Arab breed . The number of animals sampled is adequate, however, the animals were all kept in one region of southern Chad and the size of the two samples was not equal. A balanced affiliation of both sexes is not given for the Arab sample (table 1). Further, the animals from a pastoralist system arriving at abattoir do not necessarily cover all age classes of a population (Table 1). For both breeds the average age of the sampled cows was about 2.5 years higher than the average age of the sampled bulls (Table 1). Considering bulls, animals from the older age classes (> 6 years) are under represented in both breeds, indicating that the majority of bulls are slaughtered at a younger age (Table 1). Older animals might have undergone selection as they had to survive the dry season, long treks, disease pressures and other forces arising within this system. Due to these various factors, the assumption of two random samples cannot be warranted.

Genetic diversity between populations and cluster analysis

The F_{ST} indicates that the genetic diversity between the two samples is very low. A high proportion of the F_{IT} is accounted for by the within-heterozygote deficiency (F_{IS}). The low F_{ST} is seen as a first incidence, and might be hard to elaborate genetic differences between the samples of Mbororo and Arab cattle.

The distributions of the log-likelihoods for the genotype assignment shown in figure 3 overlap to a certain amount. Again it is not possible to clearly distinguish between the two populations. This result was further confirmed with the exact test of population differentiation implemented in ARLEQUIN (results not shown). The differentiation test between all samples revealed in P-value > 0.05, i.e. based on the genotypic information - the two populations do not significantly differ.

The algorithm implemented in STRUCTURE (Pritchard *et al*., 2000) constructs genetic clusters from a collection of individual multi-locus genotypes. Therefore the fraction of each individual's genotype that belongs to each cluster is estimated (Rosenberg *et al*., 2001). It identifies sub-populations which differ in their allele frequencies.

The bars in figure 4 show, that for none of the 205 individuals can the genome be clearly assigned to the Arab cluster or the Mbororo cluster. Furthermore, no relation between the participation of an individual's genome fraction and its initially assigned population (x-axis in figure 4) was found.

Rosenberg *et al*. (2001) showed that the power of clustering depends on the variability of markers, the number of markers and the number of individuals genotyped. For less diverged populations they propose to genotype more than 12-15 markers for 15-20 individuals of the hypothetical populations to get accurate clustering results. For our data those recommendations are fulfilled. Therefore the clustering results further support the notion that that the samples under investigation do not reflect genetically different populations.

Before slaughtering the sampled individuals were phenotypically assigned to the two breeds Mbororo and Arab. Even if relying on different individuals sampled, the reported differences in BTB prevalence between the two breeds (Hilty, 2006) leads to the hypothesis that genetic differences exist and might become obvious in investigating the molecular diversity. However, the analysis of the samples investigated here and the chosen microsatellites do not support this hypothesis. Those findings are somewhat unexpected. They might be explained with effects regarding the sampling of animals kept in transhumance systems. Unfortunately, no data about the herd affiliation was available. As already mentioned above, different age structures were observed between sexes. There is a certain chance that 'old' female individuals (5 to 8 years) are the ones that survived for example BTB infection and are therefore overrepresented in both samples. Such sampling effects can result in diminished differences between breeds.

Mbororo and Arab animals are kept by nomadic pastoralists of two different ethnic groups, where cattle breeds are named after them. This connection appears to be rather loose and both groups often keep Arab and Mbororo cattle inter-mixed in their herds (Dr. C. Diguimbaye-Djaibe and B.N.R. Ngandolo, personal communications). Another possibility is that migration of animals between herds and breeds occur. These aspects support the rejection of the hypothesis due to population admixture. Admixture between populations homogenizes allele frequencies between populations. Therefore, the exploration of differences in allele frequencies between admixed populations does not lead to significant testing results. This conclusion is further supported by the Country Report of Chad (FAO, 2007b) which records that important admixture between Arab and Mbororo exists.

Based on our study, we fully support the statement that sample collection is the most important step in any diversity study (FAO, 2007a). In extensive production system the lack of pedigree information (Eding and Meuwissen, 2001; Ruane, 1999) may hamper the collection of representative samples. To overcome this difficulty well planned data collection and the collection of additional information like herd affiliation, records of geographical coordinates and photo documentation of sampling sites, animals and flocks. are highly recommended (FAO, 2007a). Otherwise, the interpretation of genotyping results and statistical analysis become hard and loose their explanatory power.

Conclusions

Considering phenotypes solely, one would have presumed the samples represented two different breeds. However, our study does not confirm genetic differences between the two samples. Here, the potential of genetic characterisation studies in extensive systems becomes obvious. The presented results increase information about cattle breeds kept in pastoralist systems and supports the notion that regular admixture between the two breeds occurs.

Collecting samples at slaughterhouses for semi-feral populations seems promising in comparison with the complex collection of field samples. Nevertheless, careful sample collection procedures remain the most important step. In this context the need for supplementary information (description of the breeds, herd information, information about herd management etc.) is underlined. For this purpose, the pastoralists arriving at slaughterhouse might be asked to fill in a questionnaire. Future research also requires investigations on cattle husbandry and herding practices of African pastoral communities where very little information is available. No detailed information about the influence of non-genetic factors on differences in disease prevalence (i.e. BTB) between breeds is available.

Increased information about the genetic composition of breeds as well as their production system allows for better understanding of pastoralist systems in general and of specific threats - such as zoonotic diseases – arising within such systems.

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Characterization of Banni buffalo of Western India

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Summary

The Banni buffaloes distributed in the Kachchh region of Gujarat state in western India are medium to large in body size with a compact body and typical coiled horns. Mean body length, heart girth and height at withers estimated during the survey were 153.7±0.4 cm, 205.5±0.6 cm and 136.7±0.2 cm, respectively. Data on 397 adult milking buffaloes from Banni area based on interviews with farmers, revealed the mean age at first calving to be 39.7±0.4 months, a mean service period of 66.4±1.3 days, a mean lactation length of 293.3±1.5 days and a mean peak yield of 15.7±0.1 litres. Genetic diversity analysis of Banni buffaloes using a set of 15 heterologus bovine microsatellite markers revealed a high degree of allelic polymorphism with a total of 81 alleles and a mean of 5.4. The observed heterozygosity was found to be moderate with a mean of 0.506 and ranged from 0.125 (ILSTS 045) to 0.795 (ILSTS 008). The mean F_{IS} value (0.181) across 15 microsatellite loci was significantly positive indicating heterozygote deficiency in the population. The test for Hardy-Weinberg equilibrium revealed seven of the 15 microsatellite loci analyzed showing significant deviations.

Résumé

Les buffles de Banni ont distribué dans la région de Kachchh d'état de Gujarat dans Inde de l'ouest sont moyen à grand dans la taille de corps avec le corps compact et les cornes embobinées typiques. La longueur de corps, la circonférence de coeur et la hauteur moyens à se rabougrit estimé pendant l'étude étaient 153,7±0,4 cm, 205,5±0,6 cm et 136,7±0,2 cm respectivement. Les données sur 397 buffles de milking adultes du secteur de Banni ont basé l'entretien de fermiers, révélés signifier que l'âge vêlant au début pour être 39,7±0,4 mois, signifier la période de service de 66.4±1,3 jours, la longueur de lactation moyenne de 293,3±1,5 jours et signifie le rendement de sommet de 15,7±0.1litres. L'analyse génétique de diversité de buffles de Banni utilisant une série de 15 heterologus les bornes de microsatellite bovines ont révélé un haut degré de polymorphisme d'allelic avec un total de 81 alleles et un moyens de 5,4. Le heterozygosity observé a été trouvé pour être modéré avec un moyens de 0,506 et étendant de 0,125 (ILSTS 045) à 0,795 (ILSTS 008). La valeur moyenne de FIS (0,181) à travers 15 lieux de microsatellite était indiquer le manque de heterozygote significativement positif dans la population. Le test pour l'équilibre de Hardy-Weinberg a révélé sept des 15 lieux de microsatellite ont analysé montrant des déviations significatives.

Resumen

Los búfalos de Banni se distribuyen en la región de Kachchh, en el Estado de Gujarat en el oeste de la India. Son de tamaño medio-grande, cuerpo compacto y cuernos típico enroscados. La largura del cuerpo, la circunferencia del torax y la altura media durante el estudio fueron de 153,7±0,4 cm; 205,5±0,6 cm y 136,7±0,2 cm, respectivamente. Los datos sobre 397 búfalos de leche de la zona de Banni se basan sobre encuestas a los ganaderos y muestran una media de edad al primo parto de 39,7±0,4 meses, un periodo medio de monta de 66,4±1,3 días, una media de lactación de 293,3±1,5 días y una producción media de 15,7±0,1 litros. Los análisis sobre diversidad genética de los búfalos de Banni con la utilización de 15 marcadores microsatelitares heterologus bovinos han mostrado un grado elevado de polimorfismo alelico con un total de 81 alelos y una media de 5,4. La heterocigosis observada ha sido moderada con una media de 0,506 y un rango de 0,125 (ILSTS045) a 0,795 (ILSTS008). La media del valor F_{is} (0,181) entre los 15 loci microsatelitares fue positiva de forma significativa, lo que indica un déficit de heterocigosis en la población. El test Hardy-Weinberg de equilibrio muestra siete de los 15 loci microsatelitares analizados con desviaciones significativas.

Key words: *Banni buffaloes, Phenotypic characterization, Production performance, Genetic diversity, Microsatellites markers.*

Introduction

Water buffalo (*Bubalus bubalis*) is the mainstay of the Indian dairy industry with a contribution of about 54% of the total milk production in the country. Buffaloes are valuable not only as milk producers, but have multiple roles in rural livelihood system, where it forms a part of the cultural structure of the society apart from employment generation and nutritional security. In some areas, buffalo keeping is a way of life for certain social groups, particularly amongst tribal people (the Todas of Nilgiris in Tamil Nadu) and pastoralists/semi pastoralists (the Maldharis of Banni area in Gujarat). India possesses a wide variety of buffalo genetic resources comprising 10 well recognized breeds and many lesser known populations which are equally important to buffalo husbandry in India. Characterization and documentation of these lesser known buffalo populations in different parts of the country is of prime significance.

The Banni area of Kachchh district in Gujarat state is one of the finest pasture lands in Asia with about 30 varieties of grasses and is well known for its livestock wealth. The Banni buffalo, which was evolved by the Maldhari community in this region, has good adaptability to harsh climatic conditions, drought resistance and survival on scanty fodder and shrubs. They have good genetic potential for milk production and form a main source of livelihood for Maldharis. Also, Banni buffaloes are gaining popularity among the farmers and private dairy owners in North Gujarat and Mumbai (Maharashtra) due to their high milk production potential, fairly good lactation length, hardy nature and regular breeding. However, information

Figure 1. Breeding tract of Banni buffaloes in Kachchh district of Gujarat state in Western India.

regarding this buffalo population is very scanty in the literature. The present study was undertaken with the following objectives:

1. To evaluate the Banni buffalo for its morphological characteristics and production performance in its natural habitat.
2. To assess the genetic diversity of Banni buffalo using heterologus microsatellite markers.

Material and Methods

Information on Banni buffalo regarding their habitat, distribution and management practices was collected using preset questionnaires. Data regarding various morphometric traits were recorded on 397 adult buffaloes from the Banni area. Data on production and reproduction traits were collected based on interviews with farmers in different parts of the breeding tract. Blood samples were collected from unrelated animals from various villages in the breeding tract (Figure 1). As pedigree records are not available under field conditions, care was taken by way of interviewing the farmers in order to ascertain that the animals tested during sample collection were not related. Genomic DNA was extracted from whole blood following the standard Phenol-Chloroform extraction method (Sambrook and Russell, 2001). A total of 15 heterologus bovine specific microsatellite markers evaluated in buffaloes for genetic diversity studies (Navani *et al.*, 2002) were utilized to generate microsatellite genotypic data on 47 animals. The PCR conditions were standardized for all the 15 primer pairs and PCR was carried out in the PTC-200 Thermal Cycler (MJ Research, Inc, MA, USA) using cycling conditions: 2 min at 94°C, followed by 30 cycles of 1 min at 94°C, 1 min at precise annealing temperature, 1 min at 72°C and final extension at 72°C for 10 min. PCR products were resolved on 6% denaturing PAGE (Sequi GT System, Bio-Rad, USA) and allele size estimated using a 10bp ladder (Invitrogen, Life Technologies, CA, USA) run in parallel to the samples. Gels were stained by the silver staining method of Bassam *et al.*(1991) and genotypes were scored manually for each microsatellite locus.

Different measures of genetic variation such as observed number of alleles (n_a), effective number of alleles (n_e), observed (H_o) and expected heterozygosity (H_e) estimates were computed after Nei (1973) using POPGENE software (Yeh *et al.,1999*). Polymorphism Information Content was calculated in accordance to Botstein *et al.* (1980). Tests for departure from Hardy-Weinberg equilibrium and Ewens Watterson's test for neutrality of markers (Manly, 1985) were performed using POPGENE software.

Results and Discussion

Habitat, distribution and population status

Banni buffaloes are distributed throughout the Kachchh district of Gujarat and in some parts of the Banaskantha and Patan districts of North Gujarat. These buffaloes are centered between the Hajipir and Khavada areas of Kachchh district. Typical Banni animals are seen in Bhirandara, Hodka, Luna, Mithadi, Udama, Dhorda, Goravali, Kaduli, Rabviry and Kakar villages of Banni region (Bhuj circle) and in Anjar, Bhachua, Nakhatrana and Lakhpat circles of Kachchh district. The Banni area is about 840 square miles of flat land comprised of about 45 villages, which are bounded by a desert area (Rann of Kachchh) in the North. The Banni region is one of the finest pasture lands supporting a traditional livestock system. The name '*Banni*' buffalo originated from the name of this region and the Maldharis (traditional livestock keepers) evolved this population through conventional breeding.

Rainfall in this area is generally very erratic (250-500 mm) with average maximum and minimum temperatures of 42°C and 12°C respectively. The soil of the Banni area is highly calcareous, saline and loam sandy with poor water holding capacity, low permeability and is prone to erosion. The nature of the soil has limited agricultural farming to a great extent in this area and grasses grow naturally in the rainy season. Moreover, Banni area has been preserved for the grazing of livestock by the Maldharis under the regulations of the district revenue department.

The total cattle and buffalo population in the Kachchh district of Gujarat is 3 190 000 and 1 780 000, respectively (17th Livestock Census, 2003, Government of India). Most of the buffalo population in the district except in eastern Kachchh region is of Banni type, reared especially for milk production. Among the cattle population, only a negligible 0.013% are estimated to be crossbreds with the farmers rearing Zebu cattle, mostly for draught purposes. Thus it is clear that farmers in this region prefer buffaloes as their main milk animals. However, according to the Maldharis of this region, there has been a decline in Banni buffaloes in the last two decades. This declining trend is mainly because of a significant reduction in pasture land due to drought in consecutive years and extensive vegetation by *Prosopis julioflora* (Israeli Babool), an undesirable weed for livestock grazing. Also, selling of buffaloes by Maldharis to farmers in North Gujarat and in cities like Mumbai, Ahmedabad, Surat and Pune for milk production has substantially affected the population status.

Management practices

Banni buffaloes are mostly maintained by Maldharis whose livelihood is totally dependent on buffalo rearing for the sale of milk, milk products and animals. In each village, herds of buffaloes are maintained by a group of villagers under an exclusive traditional production system. The animals are taken to the forests in the evening, stay for grazing overnight and come back to the owner's door early in the morning. Most of the time, the owners do not accompany the animals, and the buffaloes follow the routine on their own. The animals stay loose in the village near the owner's house and no special housing and supplementary feeding is provided.

Two types of production systems were found to exist in the Banni area. One is an extensive management system as described above which is prevalent in the Nakhatrana and Hajipir areas (Lower Banni region), where only one time milking is practiced as transport facilities for marketing milk are very limited. The Maldharis produce *khoa,* an indigenous milk product from buffalo milk made by concentration, which is later sold for sweet preparation. However, in areas like Anjar, Mundara, Bhachua, Hodka and Khavada (Greater Banni region), where comparatively better transport and marketing facilities are available, twice daily milking is practiced. Also, animals are relatively better fed with concentrate feeding during the time of milking and a semi-intensive type of production system with some housing is practiced in this region. Banni buffaloes are very docile in nature and are often milked by women villagers.

The Maldharis in Banni area breed their animals through their own buffalo bull adopting natural mating only. Artificial insemination is not practiced in this area. The survey of the Banni tract also revealed that the Maldharis are well aware of the importance of their breeding bull and they are very careful in selecting a bull calf from their high yielding buffaloes with good morphological

Figure 2. The head of a Banni buffalo.

Figure 3. A breeding bull of Banni buffalo.

features. Another important tradition prevalent in the Maldharis of Banni area is that they never allow mating between the bull and his daughters. Also, they use a breeding bull only for three years in a herd after which they exchange it with other villages thus avoiding possible inbreeding within Banni buffalo population. Thus the practice of breeding and replacement of bulls by Maldhari herdsmen, plays a very important role in the genetic improvement of production performance, fertility and maintenance of body conformation and morphological features in Banni buffaloes.

Physical characteristics

The Banni buffalo is medium to large in body size with a compact body and typical coiled horns, often with double coiling. The head of a Banni buffalo (Figure 2) is wide with slight depression in the middle and no slope towards base of the horns. The face is comparatively elongated and straight with wide muzzle. Eyes are prominent, black and bright. The body is generally covered with hair. The neck of Banni buffaloes is medium and thin without skin folds over the region. The dewlap is almost absent in both the sexes. The chest is slightly deep and the barrel is long with well sprung ribs. The hind quarter is wide, heavy and well developed. The back is wide at the hip joint and overall the body is wedge shaped. The legs are medium in length with broad bones and hooves are black, small in size and firmly attached, which might be the effect of adaptation to grazing under extensive production systems.

The skin is soft, thin and generally black in colour but a few animals are also observed possessing copper colour. In some animals white patches are also observed on forehead, lower legs and tail. The udder of Banni buffaloes is well developed, round in shape and squarely placed. The hind and fore quarters are uniformly well developed. Typically, the whole udder of a Banni buffalo looks like four equal divisions with teats well attached to each quarter. The majority of animals have conical teats with round and pointed tips. The breeding bull, a she-buffalo and a herd of Banni buffalo are presented in figures 3, 4 and 5 respectively.

Morphological traits

The overall least squares means along with their standard error for various morphological traits are presented in table 1. The mean values for most of the morphological traits in Banni buffalo were found to be higher than that of Mehsana buffaloes (Pundir *et*

Table 1. Mean ± S.E and range of different morphological traits in Banni buffalo.

Trait	Mean±S.E (cm)	Range (cm) Min	Range (cm) Max
Body length	153.7±0.4	147	157
Heart girth	205.5±0.6	195	211
Height at withers	136.7±0.2	132	139
Face length	53.7±0.2	52	54
Ear length	29.3±0.1	28	30
Height at hip bone	127.8±0.3	125	129
Height at pin bone	120.3±0.3	117	121
Height at elbow joint	70.9±0.2	68	72
Distance between hip bone	55.4±0.3	53	57
Distance between pin bone	27.9±0.1	27	28
Tail length	88.4±0.5	87	91
Tail switch length	64.2±0.4	62	66
Width of forehead	26.6±0.1	26	29

Table 2. Mean ± S.E and range of different performance traits in Banni buffalo.

Trait	No.	Mean ± S.E	Range Min.	Range Max.
Age at first calving (months)	337	39.7±0.4	38.1	41.5
Service Period (days)	350	66.4±1.3	60.0	71.0
Calving interval (months)	349	12.2±0.7	11.9	12.4
Services per conception	375	1.0±0.1		
Lactation length (days)	348	293.3±1.5	282.0	298.0
Dry period (days)	347	71.8±1.4	69.0	74.0
Peak milk yield (litres)	397	15.7±0.1	12.0	17.0

Figure 4. A she-buffalo of Banni.

al., 2000) whereas they are fairly similar to that of reported for Murrah buffaloes (Nivsarkar *et al.,* 2000).

Performance

The overall least squares means ± S.E for various production and reproduction traits of Banni buffaloes as recorded based on interviews with farmers are presented in table 2. The mean age at first calving observed for Banni buffaloes (39.7±0.4 months) was found to be less than that reported for Murrah [43.9+0.2 months (Dhara, 1994) to 53.9+0.7 months (Kumar, 2000)] and Mehsana buffaloes [42.8+0.4 months (Pundir *et al.*, (2000)]. Similarly reproductive traits like service period and calving interval were found to be less than that of Murrah (Sadana *et al.,* 2006) and Mehsana buffaloes (Pundir *et al.,* 2000). The mean peak milk yield in Banni buffalo was estimated to be 15.7±0.1 litres However, it should be mentioned that the values obtained in the present study are based on the reports of the farmers gathered through structured questionnaires. Hence data recording needs to be initiated in farmers herds of Banni buffaloes regarding various performance characteristics to delineate the breed descriptor.

Genetic characterization of Banni Buffaloes

Genetic diversity measures

Different measures of genetic variation like observed number of alleles, effective number of alleles, observed and expected heterozygosity and polymorphism information content (PIC) with respect to Banni buffaloes are presented in table 3. A high degree of allelic polymorphism was found to exist in the Banni buffalo population with 12 of the 15 microsatellite loci analyzed exhibiting 4 or more alleles. A total of 81 alleles was observed across 15 microsatellite loci ranging from 2 (ILSTS 045 and ILSTS 073) to 10 (ILSTS 058). The observed heterozygosity was found to be moderate with a mean of 0.506 and a range of 0.125 (ILSTS 045) to 0.795 (ILSTS 008) across different microsatellite loci. The overall mean polymorphism information content was found to be 0.578 with 11 of the 15 microsatellite loci having values of more than 0.5, 3 having values between 0.25 and 0.50 and only one microsatellite locus (ILSTS 019) having a PIC value of less than 0.25. According to Botstein *et al.,* (1980), those polymorphic markers which were classified as highly informative had a PIC value

Table 3. Measures of genetic variation across 15 microsatellite loci in Banni buffalo.

Locus	No.	n_a	n_e	Ho	He	Nei's He	PIC
CSRM 060	40	5	2.42	0.625	0.594	0.587	0.547
ILSTS 026	43	4	2.04	0.488	0.515	0.509	0.463
HEL 013	45	7	4.88	0.644	0.804	0.795	0.765
ILSTS 030	39	5	2.86	0.564	0.659	0.651	0.607
ILSTS 033	43	6	3.18	0.256	0.694	0.686	0.638
ILSTS 017	41	4	3.05	0.610	0.681	0.673	0.618
ILSTS 019	46	3	1.22	0.196	0.183	0.181	0.172
ILSTS 045	32	2	1.93	0.125	0.490	0.482	0.366
ILSTS 058	41	10	5.68	0.610	0.834	0.824	0.803
ILSTS036	46	6	4.11	0.717	0.765	0.757	0.715
ILSTS095	40	8	2.38	0.200	0.587	0.580	0.556
ILSTS052	41	7	4.32	0.634	0.778	0.768	0.737
ILSTS073	44	2	1.88	0.523	0.474	0.469	0.359
ILSTS061	38	7	2.94	0.605	0.669	0.660	0.630
ILSTS008	39	5	3.94	0.795	0.756	0.746	0.700
Mean	41	5.4	3.12	0.506	0.632	0.624	0.578

No.=No. of observations.
n_a=observed no. of alleles.
n_e=effective no. of alleles.
Ho=Observed heterozygosity.
He=Expected heterozygosity.
PIC=Polymorphism Information Content.

Table 4. Locus wise heterozygote deficit (F_{IS}) and Hardy Weinberg equilibrium at 15 different microsatellite loci in Banni buffalo.

Locus	F_{IS}	H-W Equilibrium DF	Chi-Square	P-Value
CSRM 060	-0.065	10	8.72	0.559
ILSTS 026	0.041	6	13.51	0.036
HEL 013	0.189	21	43.14	0.003
ILSTS 030	0.133	10	25.41	0.005
ILSTS 033	0.627	15	82.16	0.000
ILSTS 017	0.093	6	7.58	0.270
ILSTS 019	-0.082	3	0.48	0.924
ILSTS 045	0.741	1	18.37	0.000
ILSTS 058	0.260	45	59.07	0.078
ILSTS 036	0.052	15	52.86	0.000
ILSTS 095	0.655	28	110.21	0.000
ILSTS 052	0.174	21	31.12	0.072
ILSTS 073	-0.115	1	0.47	0.411
ILSTS 061	0.083	21	18.70	0.604
ILSTS 008	-0.066	10	9.76	0.462
Overall	0.181	-	-	-

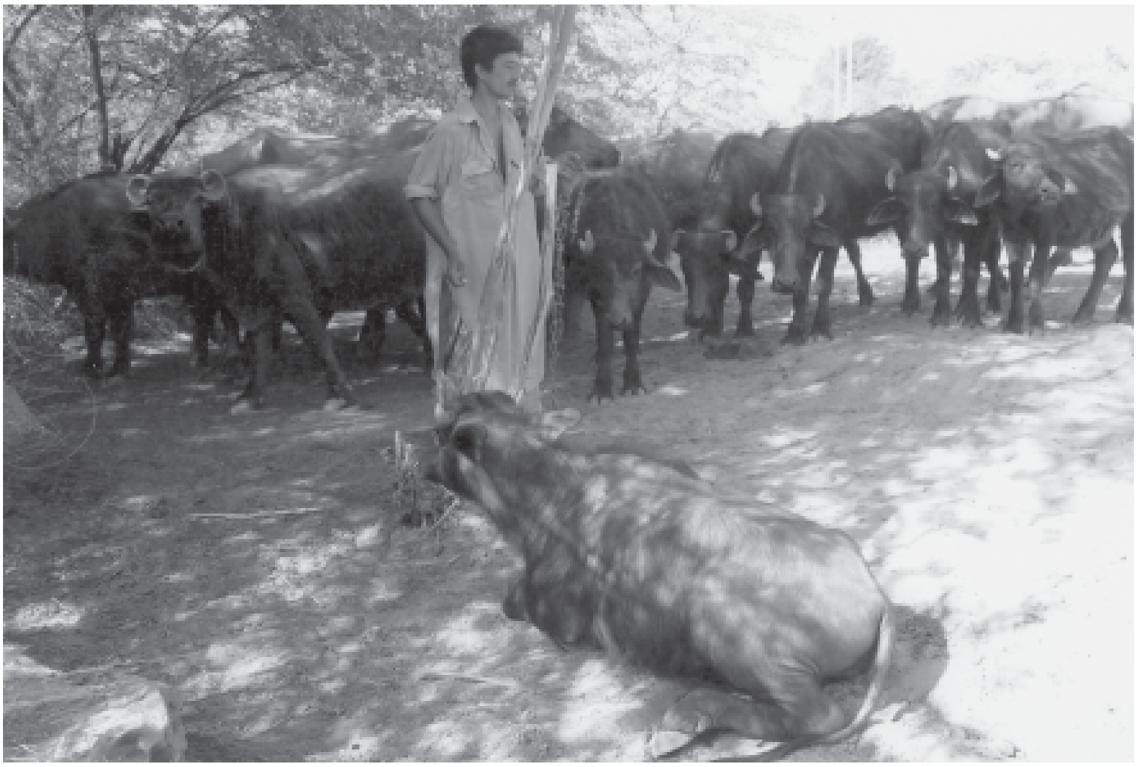

Figure 5. A herd of Banni buffalo.

greater than 0.5, reasonably informative a PIC value ranging between 0.25 and 0.50 and relatively less informative if the PIC value was below 0.25. The allelic diversity and observed heterozygosity values are comparable to those reported for Bhadawari and Tarai buffaloes (Arora *et al.,* 2004), while they were relatively lower compared to that reported for other buffalo breeds by Kumar *et al.,* (2006) with a different set of microsatellite markers.

Heterozygosity deficit and Hardy-Weinberg equilibrium

The mean F_{IS} (0.181) across 15 microsatellite loci was significantly positive indicating considerable heterozygosity deficit within the population. Seven of the 15 microsatellite loci analyzed showed significant deviations from Hardy-Weinberg equilibrium (Table 4). These results showed the possible existence of subdivisions within the population. Possible reasons could include selective breeding with fewer available bulls and relatedness of a few samples analyzed as proper pedigree records are not available under field conditions. However, the major role of selective breeding in the heterozygosity deficit was not supported by the results of Ewens-Watterson neutrality test as all the microsatellite markers under the present study except ILSTS 008 were found to be neutral. The observed F-value for ILSTS 008 did not fall within the range of 95% confidence interval when the test was performed using 1000 simulated samples. Thus, the genetic analysis showed that Banni buffaloes have a reasonably moderate level of diversity as reflected by average heterozygosity estimates.

Conclusion

Banni buffalo, reared in the Kachchh region of western India by the traditional Maldhari community are found to have a better production potential under an extensive management system. They are found to have moderate genetic variation as revealed by microsatellite markers. Their genetic diversity combined with their superior production potential and demand make a strong case for the necessity of initiating genetic improvement programs. Further studies need to be carried out in order to establish their genetic superiority by means of performance recording under field conditions. Also, analysis with a greater number of microsatellite markers and comparisons with other buffalo breeds of the region will delineate the genetic structure of this germplasm of western India.

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Establishing a conservation flock for "Vorwerkhuhn" chicken breed – a case study of *in-situ* conservation of local chicken breeds in Germany

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Background

There is an increasing concern about losing genetic diversity in farm animals, and poultry genetic resources are considered to be one of the most endangered (Crawford, 1990). A large number of local dual-purpose breeds used at the beginning of the last century have been replaced with highly specialised lines. Market orientated intensive livestock breeding programs tend to concentrate on just a limited number of breeds, and the proportion of low-input, low-output breeds used in agricultural production in developed countries has been decreased almost to zero. Decreasing numbers of breeds results in reduced genetic variability, and limits the flexibility of future breeding programs. On the other hand, an increase in income in these countries leads to a rise in demands for specialised food, diversification in the product supply, and changes in preferences of production conditions.

In developed countries, a wide spectrum of poultry breeds comprising, to some degree, the genetic diversity of local middle-level food producers no longer used, are nowadays maintained by fancy breeders. Clearly, without their efforts many of these poultry breeds would have disappeared. However, in most cases fanciers aim at achieving a certain phenotype. This may lead to inbreeding, and as a consequence of inbreeding depressions, crossbreeding between populations follows, in most cases unrecorded. Pedigree records and performance information are missing. Consequently, a classification and labeling of individuals given by an investigator might not accurately describe the true genetic structure of the gene pool, and limit the success of conservation and utilisation of genetic resources.

Objective

Success in animal breeding is dependent on the genetic composition of populations. Efficient in-situ conservation and utilisation of genetic resources require a population management system that allows the maintenance of genetic variability within a given population. Thus, the goal of the Vorwerkhuhn project is to establish a conservation flock of chickens according to a well defined concept recommended by FAO (FAO, 1998).

Principle

The conservation flock of the Vorwerkhuhn chicken was established in 1999 by collecting individuals from fancy breeders. At that time, the breed was at risk of extinction. The project started with nine breeders, and currently 14 breeders are involved. The genetic management of the population is based on sire rotation, i.e. each sire is replaced by one of his sons in every generation. This principle of rotating sires (via hatching eggs) across families avoids mating of closely related birds, and hence reduces the inbreeding rate. Each breeder keeps one breeding sire which he got from direct neighbour within the breeding chain, and four breeding females. All birds have pedigree information from the father's side. Sire families are usually established in January of each year, and hatching eggs are collected for three hatches. The first hatching eggs rotate, i.e. they are given to the next breeder in the chain. From these, males hatched are the potential sires for the next generation. The second and third hatches within the breeding season are used to obtain the potential breeding hens. The generation interval is one year.

Record keeping

All pedigree information and phenotypic records (including body weight) are recorded electronically. Information is available to the founder population. All potential breeding cocks and dams are phenotypically evaluated (in the fall) according to the breed standard. The weight of hatching eggs (which should be above 54g) is recorded as well as body weight at weeks 2, 8, 16, and 20 weeks of age. A few breeders record laying performance during the whole year – this is optional.

Veterinary control

Blood samples from two males and two females in each flock are taken and checked for *salmonella pullorum* and *mycoplasma gallisepticum* infection. Excrements (one sample per flock collected from four different sites in each chicken house) are analysed for endoparasites, bacteria in general, and salmonella. In some cases (depending on the region) blood samples are tested for H5- and H7-antibodies.

Cross breeding and niche market

Population management and flock book recording require additional effort. Financial support is hardly forthcoming from public sources, and hence breeders need to find other ways. Since the laying performance of the Vorwerkhuhn is rather low (about 180 eggs) and eggs are small (50-55g), it is difficult to place the breed into a niche market. To improve the economic situation for breeders we started a crossing experiment to obtain hybrids for egg (and partly meat) production. Thereby, the conservation flock is being maintained through pure breeding only. We used hens from a commercial line from Lohmann Tierzucht GmbH (Lohmann Tierzucht is supporting the project) to be mated with Vorwerkhuhn cocks. Chicks can be colour sexed. This hybrid is called the 'Kollbecksmoor Huhn'. Our first results show that this hybrid has acceptable laying performance (250 eggs, 60g) and the bird can be sold at a reasonable price at small producers.

Perspectives

Under current conditions, it difficult to define the genetic features of a given poultry breed and to establish it in niche markets. Overall, the Vorwerhuhn project has contributed to identifying ways in which to establish conservation flocks in practice, and the difficulties facing breeders. Their continued existence will depend on the motivation of breeders to continue this activity, public acceptance and support, and the success of the crossbred Kollbecksmoor Huhn in niche markets.

Additional information

More information of the Vorwerhuhn conservation flock can be found at: *http://www.erhaltungszucht-vorwerkhuhn.de/index.html.* To learn more about the "Kollbecksmoor Huhn" look at: *http://www.kollbecksmoorhuhn.de/.*

In chickens, a similar conservation flock as for the Vorwerkhuhn has been established for the breed "Ostfriesische Möwen" (*http://www.ostfriesische-moewen.de*, contact: Michael Ruhnau, E-Mail: *M-Ruhnau@t-online.de*).

The Society for the Conservation of Old and Endangered Livestock Breeds (GEH) has initiated a wide range of activities to conserve endangered breeds of farm animal genetic resources in Germany (Address: Am Eschenbornrasen 11, D-37213 Witzenhausen, Tel. 05542/1864, Fax: 05542/72560; E-Mail: *info@g-e-h.de* - Internet: *http://www.g-e-h.de*).

List of References

Crawford, R.D. 1990. Origin and history of poultry species. In: Poultry Breeding and Genetics (Crawford, R.D., Ed.), Elsevier, Amsterdam, The Netherlands, pp. 1-42.

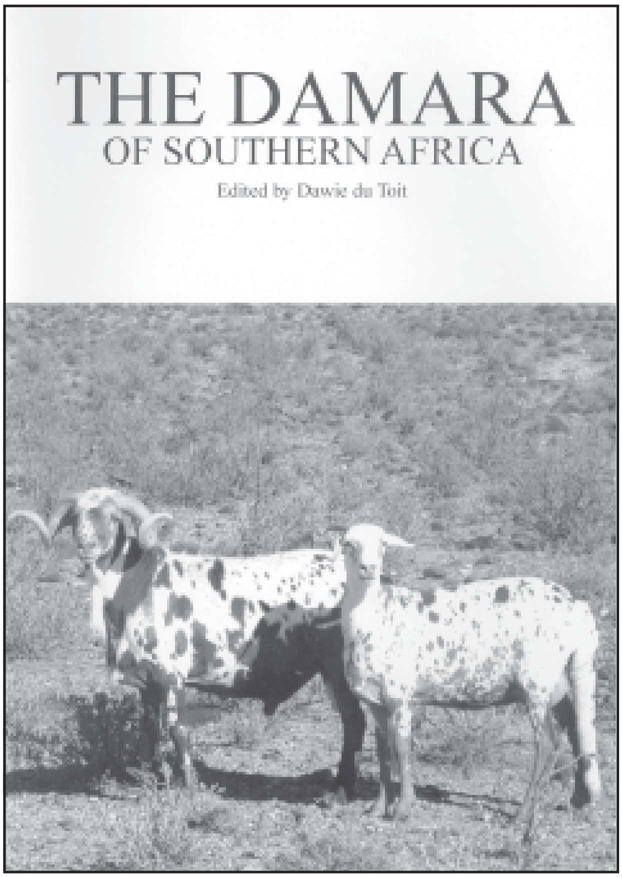
FAO. 1998. Secondary Guidelines: Management of Small Populations at Risk, 1998 <*http://dad.fao.org/en/home.htm*>

The Damara of Southern Africa,

D. du Toit (Ed.)

Published in 2007, pp. 128
ISBN 978-0-620-38877-1

The core of this new book on the Damara sheep breed of Southern Africa consists of two papers on the colour genetics of the Damara, one by Professor Phillip Sponenberg and one by Roger Lundie. The former presents and overview of coat colours and patterns in the Damara. The latter, and longer, paper provides an introduction to sheep coat colour genetics and then seeks to relate the colour patterns of the Damara to what is known in woolled breeds. The discussion of colour genetics is put into context by a number of shorter chapters. The book starts with a brief history of the breed. A chapter on conservation describes some of the management principles that need to be borne in mind to ensure that the status of the Damara as an adapted landrace is maintained for the future. A chapter on commercial farming with the Damara focuses on the value of the fitness traits that make it ideally suited for production under harsh African conditions; a short discussion of carcass and meat quality characteristics is also included. The book is beautifully illustrated with many colour photographs.

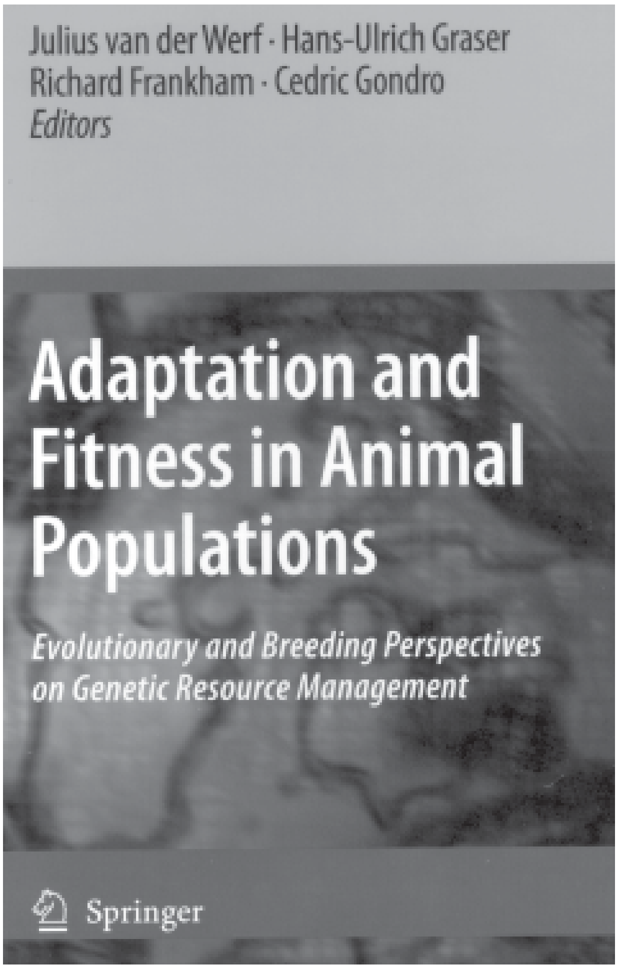


Adaption and fitness in animal populations. Evolutionary and breeding perspectives on genetic resources management.

J. van der Werf, H.-U. Graser, R. Frankham & C. Gondro (Eds)

Published by Springer Science
Published in 2009, pp. 258
ISBN: 978-1-4020-9004-2

This book, the outcome of a symposium held in Armidale Australia in 2007, brings together a series of papers by some of the world's leading scientists in animal breeding and evolutionary genetics. As the title indicates, the objective was to explore the concepts of adaptation and fitness and their relevance to the management of (particularly animal) genetic resources for food and agriculture. The book comprises four sections: modelling fitness; maintaining fitness, the genetic basis of adaptation; and strategies for managing diversity – each made up of three papers and a summary of the discussion that followed the respective session of the symposium. The target audience is quantitative geneticists, animal and plant breeders, evolution and population geneticists, ecologists, researchers and graduate students.



Julius van der Werf · Hans-Ulrich Graser
Richard Frankham · Cedric Gondro
Editors

Adaptation and Fitness in Animal Populations

Evolutionary and Breeding Perspectives on Genetic Resource Management

Springer

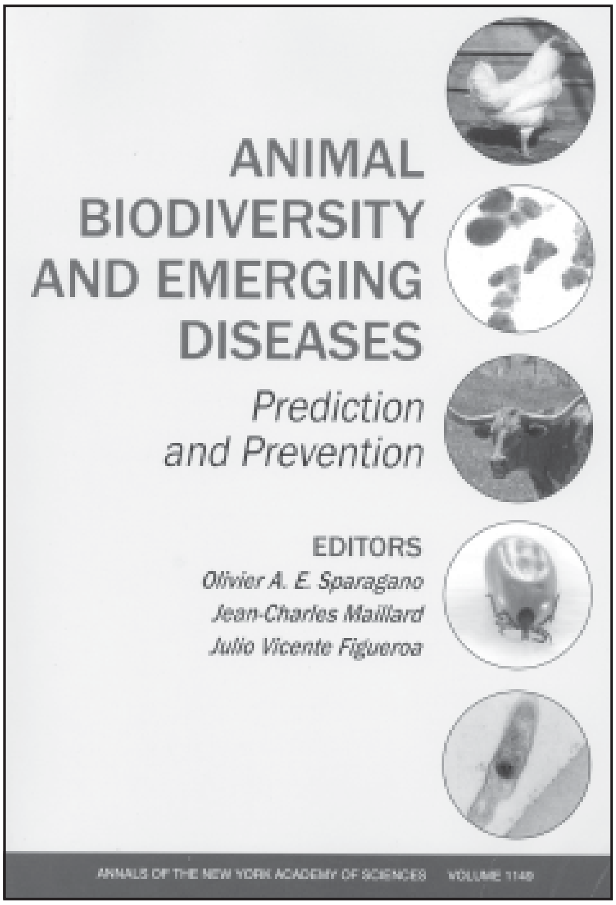
Animal diversity and emerging diseases. Prediction and prevention

O.A.E. Sparagano, J-C Maillard and JV. Figueroa (Eds)

Annals of the New York Academy of Sciences, Volume 1149
Published by Blackwell Publishing on behalf of the New York Academy of Sciences, Boston Massachusetts, United States of America
Published in 2008, pp. 404.
ISBN: 978-1-57331-714-6

This publication is a compilation of communications and posters presented during the Ninth Biennial Conference of the International Society for Tropical Veterinary Medicine (STVM), held in Merida, Mexico, in June 2007. The approximately 100 articles are grouped into 13 sections: globalization; anti-arthropod vaccines; genetics; viruses; *Anaplasma; Babesia*; helminths; ticks and tick-borne diseases; farm animal diseases; microbiology; wildlife; *Trypanosoma/Leishmania*; and general tropical veterinary medicine. The coverage ranges from cellular pathogenesis to the driving forces of global pandemics. Its target audience includes researchers, academics, governmental and NGOs representatives, technicians, veterinarians and other professionals from the industry sector interested in tropical veterinary medicine.

The introduction, written by Jean-Charles Maillard and Olivier A.E. Sparagano, respectively president and president-elect of the STVM, notes the potential role of genetic diversity in reducing the risk of disastrous economic consequences in the event of epidemics, and concludes that "*All players involved in the farming production pipeline, whether political, economical or professional, should be aware of the importance of valorizing biodiversity through the diversification other animal strains used for breeding. Strains with different potential and qualities would, in turn, diversify economic markets and offer a wider choice of products to the consumer*."



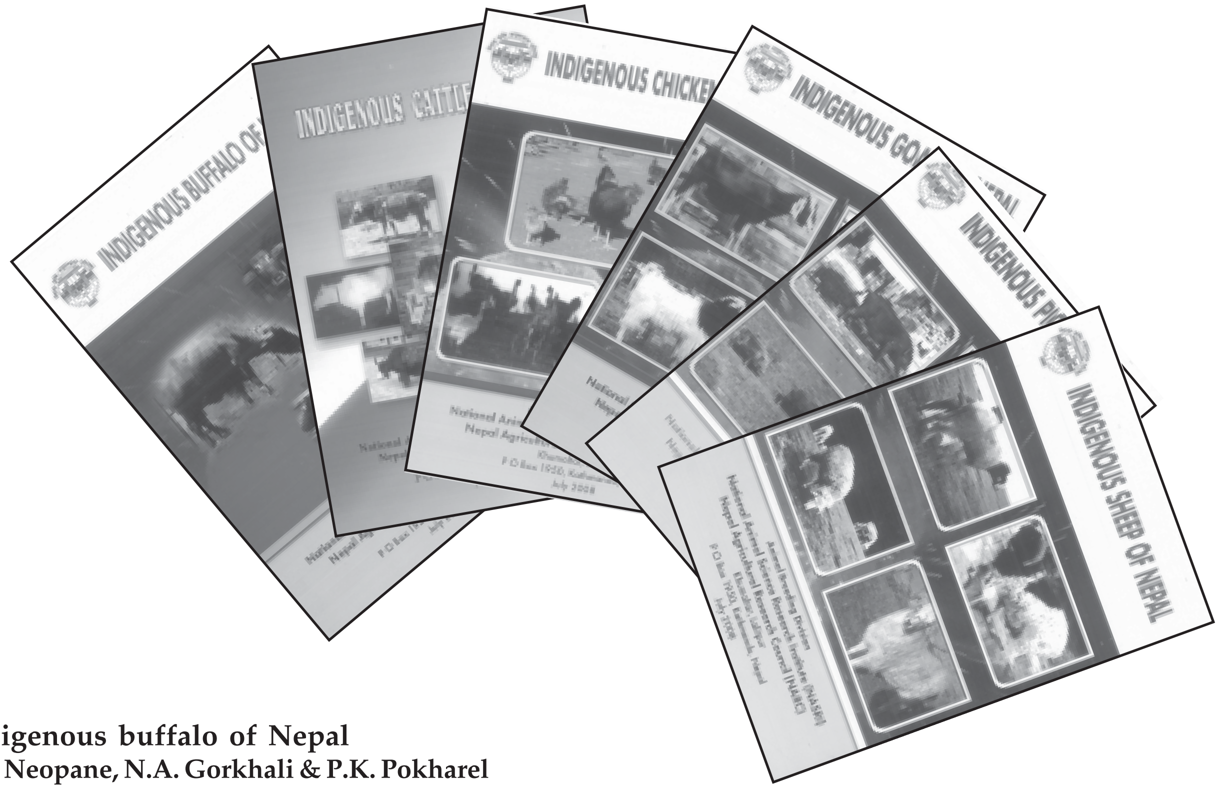
ANIMAL BIODIVERSITY AND EMERGING DISEASES

Prediction and Prevention

EDITORS

Olivier A. E. Sparagano
Jean-Charles Maillard
Julio Vicente Figueroa

ANNALS OF THE NEW YORK ACADEMY OF SCIENCES VOLUME 1149



Indigenous buffalo of Nepal

S.P. Neopane, N.A. Gorkhali & P.K. Pokharel
Nepal Agricultural Research Council, Kathmandu.
Published in 2007, pp. 14.

Indigenous cattle of Nepal

S.P. Neopane & P.K. Pokharel
Nepal Agricultural Research Council, Kathmandu.
Published in 2005, pp. 18.

Indigenous chicken of Nepal

S.P. Neopane & N.A. Gorkhali
Nepal Agricultural Research Council, Kathmandu
Published in 2008, pp. 10.

Indigenous goats of Nepal

S.P. Neopane & P.K. Pokharel
Nepal Agricultural Research Council, Kathmandu
Published in 2008, pp. 14.

Indigenous pigs of Nepal

S.P. Neopane & R. Kadel
Nepal Agricultural Research Council, Kathmandu
Published in 2008, pp. 10.

Indigenous sheep of Nepal

S.P. Neopane, N.A. Gorkhali & P.K. Pokharel
Nepal Agricultural Research Council, Kathmandu
Published in 2008, pp. 14.

Chickens, goats, pigs and sheep are the latest species to be added to the series of pamphlets on indigenous livestock from the Nepal Agricultural Research Council. Pamphlets on cattle and buffalo were published in 2005 and 2007, respectively. Each publication provides information on the distribution of the breeds within the country, their phenotypic and in some cases molecular characteristics, their performance levels and an estimate of their risk status and population trends. A further section is devoted to the specific positive attributes of the indigenous animals - multiple uses, marketable products and adaptation to local topography, feed resources, climate, etc. In several of the pamphlets it is suggested that these positive attributes are not duly recognized. The final section of each pamphlet outlines future prospects for the indigenous breeds and their production systems, including descriptions of initiatives taken or planned in the fields of, characterization, genetic improvement, marketing and conservation. All pamphlets contain a number of photographs (colour in the case of cattle, black and white for the other species).

Editorial policies and procedures

The mission of the Animal Genetic Resources Information Bulletin (AGRI) is the promotion of information on the better use of animal genetic resources of interest to food and agriculture production. All aspects of the characterization, conservation and utilization of these resources are included, in accordance with the Convention on Biological Diversity.

AGRI will highlight information on the genetic, phenotypic and economic surveying and comparative description, use, development and maintenance of animal genetic resources; and on the development of operational strategies and procedures which enable their more cost-effective management. In doing this AGRI will give special attention to contributions dealing with breeds and procedures capable of contributing to the sustainable intensification of the world's medium to low input production environments (agro-ecosystems), which account for the substantial majority of the land area involved in livestock production; the total production of food and agriculture from livestock; and of our remaining farm animal genetic resources.

Views expressed in the paper published in AGRI represent the opinions of the author(s) and do not necessarily reflect those of the institutions which the authors are affiliated, FAO or the Editors.

The suitability of manuscripts for publication in AGRI is judged by the Editors and reviewers.

Electronic publication

AGRI is available in full electronically on the Internet, in addition to being published in hard copy, at: *www.fao.org/dad-is*

Types of articles

The following types of articles are published in AGRI.

Research articles

Findings of work on characterization, conservation and utilization of farm animal genetic resources (AnGR) in well described production environments, will be considered for publication in AGRI. Quality photographs of these genetic resources viewed in the primary production environment to which they are adapted, accompanying the manuscripts are encouraged.

Review articles

Unsolicited articles reviewing agro-ecosystems, country-level, regional or global developments on one or more aspects of the management of animal genetic resources, including state-of-the-art review articles on specific fields in AnGR, will be considered for publication in AGRI.

Position papers

Solicited papers on topical issues will also be published as deemed required.

Other published material

This includes book reviews, news and notes covering relevant meetings, training courses and major national, regional and international events and conclusions and recommendations associated with the outcomes of these major events. Readers are encouraged to send such items to the editors.

Guidelines for authors

Manuscript submission

Manuscripts prepared in English, French or Spanish with an English summary and another summary in either French or Spanish, should be submitted to AGRI Editor, AGAP, FAO, Viale delle Terme di Caracalla, 00153 Rome, Italy. Additionally the manuscript must be sent as a WinWord Electronic Mail attachment to *agri-bulletin@fao.org*.

Photographs, coloured or black and white, and figures must be always sent by mail.

Manuscripts should be typed double-spaced and with lines numbered in the left margin. All pages, including those of references, tables etc., must be consecutively numbered. The corresponding author is notified of the receipt of a manuscript.

For manuscripts that are accepted after revision, authors are encouraged to submit a last version (3½" disc format) in Word 6.0 for Windows of their revised manuscript along with the printed copy.

Preparation of the manuscript

The first page of the manuscript must include the running head (abbreviated title), title, names of authors, institutions, full addresses including postal codes and telephone number and other communication details (fax, e-mail, etc.) of the corresponding author. The running head not exceeding 45 characters plus spaces, should appear at the top of page 1 of the manuscript entirely in capital letters. The title of the manuscript is typed in upper and lower case letters. The title should be as brief as possible not exceeding 150 characters (including spaces) with species names when applicable. Authors, institutions and addresses are in upper and lower case italics. There is one blank line between the title and the authors. Addresses are typed as footnotes to the authors after leaving one blank line. Footnotes are designated numerically. Two lines are left below the footnotes.

Headings

Headings of sections, for example Summary, Introduction, etc., are left-justified. Leave two blank lines between addresses footnotes and Summary and between the heading Summary and its text. Summary should not exceed 200 words . It should be an objective summary briefly describing the procedures and findings and not simply stating that the study was carried on such and such and results are presented, etc. Leave one line between the summary text and Keywords which is written in italics as well as the keywords themselves. All headings of sections (14 regular) and sub-sections (12 regular) are typed bold and preceded and succeeded by one blank line and their text begins with no indention. The heading of a sub-subsection is written in italics, and ends with a dot after which the text follows on the same line. Keywords come immediately after the summaries. They should be no more than six, with no "and" or "&".

Tables and figures

Tables and figures must be enclosed with the paper and attached at the end of the text according their citation in the document. Photos will not be returned

Tables

Tables, including footnotes, should be preceded and succeeded by 2 blank lines. Table number and caption are written, above the table, in italics (12) followed by a dot, then one blank line. For each column or line title or sub-title, only the 1st letter of the 1st word is capitalized. Tables should be numbered consecutively in Arabic numerals. Tables and captions should be left justified as is the text. Use horizontal or vertical lines only when necessary. Do not use tabs or space-bar to create a table but only the appropriate commands.

Figures

Figures including titles and legends should be preceded and succeeded by two blank lines. Figure number and title are written, below the figure, in italics (12) and end with a dot. The term figures includes photos, line drawings, maps, diagrams etc.

All the submitted diagrams, must be accompanied with the original matrix of the data used to create them. It is strongly advised to submit diagrams in Word 6.0 or Excel 5.0. Figures should be numbered consecutively in Arabic numerals.

References

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

- Example for reference in a periodical is:
  Köhler-Rollefson, I. 1992. The camel breeds of India in social and historical perspective. Animal Genetic Resources Information 10, 53-64.
- When there are more than one author:
  Matos, C.A.P., D.L. Thomas, D. Gianola, R.J. Tempelman & L.D. Young. 1997. Genetic analysis of discrete reproductive traits in sheep using linear and nonnlinear models: 1. Estimation of genetic parameters 75, 76-87.
- For a book or an ad hoc publication, e.g., reports, theses, etc.:
  Cockrill, W.R. (Ed.). 1994. The Husbandry and Health of the Domestic Buffalo. FAO, Rome, Italy, pp. 993.
- For an article in the proceedings of a meeting:
  Hammond, K. 1996. FAO's programme for the management of farm animal genetic resources. In C. Devendra (Ed.), Proceedings of IGA/FAO Round Table on the Global Management of Small Ruminant Genetic Resources, Beijing, May 1996, FAO, Bangkok, Thailand, 4-13.
- Where information included in the article has been obtained or derived from a World Wide Web site, then quote in the text, e.g. "derived from FAO. 1996" and in the References quote the URL standard form:
  FAO. 1996. Domestic Animal Diversity Information System, *http://www.fao.org/dad-is/*, FAO, Rome, Italy.

For all future manuscript dispatch and correspondence regarding AGRI, please use the following mailbox:

agri-bulletin@fao.org

Thanks for the collaboration

Normes et règles éditoriales

L'objectif du Bulletin d'information sur les ressources génétiques animales (AGRI) est la vulgarisation de l'information disponible sur la meilleure gestion des ressources génétiques animales d'intérêt pour la production alimentaire et agricole. Tous les aspects relatifs à la caractérisation, la conservation et l'utilisation de ces ressources seront pris en considération, suivant les normes de la Convention pour la Biodiversité.

AGRI désire diffuser de l'information sur la génétique, les enquêtes phénotypiques et économiques et les desciptions comparatives, l'utilisation et la conservation des ressources génétiques animales, ainsi que toute information sur le développement de stratégies opérationnelles et de normes qui puissent permettre une meilleure gestion de la relation coût/efficacité. C'est pour cela que AGRI prendra spécialement en considération toutes les contributions référées aux races et aux normes capables de permettre une intensification durable des milieux (agroécosystèmes) à revenus moyens et bas dans le monde; qui comprennent la majeur partie des terres consacrées à l'élevage, à la production totale des aliments et l'agriculture provenants de l'élevage; et tout ce qui reste comme ressources génétiques des animaux domestiques.

Les opinions exprimées dans les articles publiés dans AGRI appartiennent seulement aux auteurs et donc ne représentent pas nécessairement l'opinion des instituts pour lesquels ils travaillent, la FAO ou les éditeurs.

L'opportunité ou non de publier un article dans AGRI sera jugée par les éditeurs et les réviseurs.

Publication électronique

En plus de sa version imprimée, la version totale de AGRI se trouve disponible sur Internet, sur le site: *http://www.fao.org/dad-is/*

Types d'articles

Les articles suivants pourront être publiés sur AGRI.

Articles de recherche

Seront prises en considération pour leur publication sur AGRI les études sur la caractérisation, la conservation et l'utilisation des ressources génétiques des animaux domestiques (AnGR) accompagnées d'une bonne description du milieu. On encourage les auteurs à envoyer des photographies de bonne qualité qui montrent les races en question dans leur milieu naturel de production.

Révisions

Occasionnellement, des articles contenant une révision des agroécosystèmes, au niveau national, régional ou mondial, avec un ou plusieurs aspects se rapportant à la gestion des ressources génétiques animales, y compriss les mises à jour des différentes zones de AnGR, seront pris en considération.

Articles spécifiques

Ponctuellement, des articles sur des thèmes spécifiques pourront être demandés pour la publication d'éditions spéciales.

Autre matériel pour publication

Ceci comprend la révision de livres, nouvelles et notes de réunions importantes, cours de formation et principaux évènements nationaux, régionaux et internationaux; ainsi que les conclusions et recommandation par rapport aux objectifs des ces principaux évènements. Les auteurs sont priés d'envoyer ce genre de matériel aux éditeurs.

Guide pour les auteurs

Présentation du manuscript

Les articles se présenteront en anglais, français ou espagnol, avec un résumé en anglais et sa traduction en français ou en espagnol; ils seront envoyés à l'éditeur de AGRI, AGAP, FAO, Viale delle Terme di Caracalla, 00153 Rome, Italie. En outre, l'article devra être envoyé par courrier électronique comme document attaché en version WinWord à *agri-bulletin@fao.org*. Les photographies, en couleur ou en blanc et noir, seront toujours envoyées par courrier normal.

Les manuscripts se présenteront à double interligne et avec le numéro correspondant à chaque ligne sur la marge gauche. Toutes les pages seront numérotées, y compriss celles avec les références bibliographiques, les tableaux, etc. L'auteur recevra une lettre lui donnant bonne réception de son document.

Lorsqu'un article, après sa révision, sera accepté, on demandera à l'auteur d'envoyer la version finale révisée sur disquette (format 31/2") en Word 6.0 x Windows, ainsi qu'une copie sur papier.

Préparation du manuscript

Sur la première page du manuscript on indiquera le titre de l'article en abrégé, le titre et noms des auteurs, des institutions, les adresses complètes (y compris code postal et numéro de téléphone); ainsi que tout autre moyen de contact tel que télécopie, courriel, etc. avec l'auteur principal. Le titre abrégé ne devra pas dépasser 45 caractères, plus les espaces nécessaires, et s'écrira sur la partie supérieure de la page 1 du manuscript en majuscules. Le titre en entier du manuscript sera écrit en majuscules et minuscules; il devra être aussi bref que possible, sans dépasser 150 caractères (y compris les espaces nécessaires), et avec l'indication des noms des espèces. Les noms des auteurs, des institutions et les adresses seront en italique et en lettres majuscules et minuscules. On laissera un espace en blanc entre le titre et les noms des auteurs. Les adresses seront indiquées comme de bas à pied de page pour chacun des auteurs après avoir laissé un espace en blanc après les noms. Chaque note de bas de page sera numérotée. On laissera deux espaces en blanc après les adresses.

Titres

Les titres de chaque chapitre, par exemple Résumé, Introduction, etc. seront alignés à gauche. Laisser deux espaces en blanc entre les notes de bas de page avec les adresses et le Résumé, et entre le titre Résumé et le texte qui suit. Le résumé ne devra pas dépasser les 200 mots. Il s'agira d'un résumé objectif faisant une brève description des processus utilisés et des résultats obtenus, et non pas une simple présentation du travail réalisé avec une description générale des résultats. Laisser un espace en blanc entre la fin du texte du résumé et les mots clés, qui seront écrits en italique ainsi que le titre Mots clés. Les mots clés seront au maximum six et il ne devra pas y avoir de et ou &. Tous les titres principaux de chapitre (14 regular) et sous-chapitre (12 regular) seront en gras avec un espace en blanc avant et après. Le texte commencera sans retrait. Un titre à l'intérieur d'un sous-chapitre s'écrira en italique, suivi d'un point, avec le texte à continuation.

Tableaux et figures

Les tableaux et les figures iront à la fin du texte en suivant l'ordre d'apparition dans le texte. Les photographies ne seront pas dévolues aux auteurs.

Tableaux

Les tableaux, y compris les notes de bas de page, devront avoir un espace en blanc avant et après. Le numéro du tableau et le titre s'écriront sur la partie supérieure en italique (12) avec un point à la fin et un espace en blanc en dessous. Sur chaque colonne, titre d'en-tête ou sous-titre, seulement la première lettre du premier mot sera en majuscule. Les tableaux et leur titre seront alignés à gauche, ainsi que le texte. Les lignes verticales et horizontales seront utilisées seulement si nécessaire. Ne pas utiliser les "tabs" ou la barre d'espacement pour créer un tableau.

Figures

Les figures, y compris les titres et les légendes, seront précédés et suivis de deux espaces en blanc. Le numéro de la figure et le titre s'écriront sur la partie supérieure en italique (12) avec un point à la fin. Sous la rubrique figure on trouvera les photographies, les graphiques, les cartes, les diagrammes, etc. Dans le cas des diagrammes, la matrice originale avec les données utilisées pour son élaboration devra être envoyée. On recommande l'utilisation de Word 6.0 ou Excel 5.0 pour la présentation des diagrammes.

Références

Toute référence présente dans le texte devra apparaître sur la liste des références, et chaque référence 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.

- Exemple dans le cas d'une 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.
- Lorsqu'il s'agit de plus d'un auteur:
  Matos, C.A.P., D.L. Thomas, D. Gianola, R.J. Tempelman & L.D. Young. 1997. Genetic analysis of discrete reproductive traits in sheep using linear and nonnlinear models: 1. Estimation of genetic parameters 75, 76-87.
- Dans le cas d'un livre ou d'une publication ad hoc, par example un rapport, une thèse, etc.:
  Cockrill, W.R. (Ed.). 1994. The Husbandry and Health of the Domestic Buffalo. FAO, Rome, Italy, pp. 993.
- S'il s'agit d'un acte d'une réunion:
  Hammond, K. 1996. FAO's programme for the management of farm animal genetic resources. In C. Devendra (Ed.), Proceedings of IGA/FAO Round Table on the Global Management of Small Ruminant Genetic Resources, Beijing, May 1996, FAO, Bangkok, Thailand, 4-13.
- Lorsque l'information contenue dans l'article ait été obtenue ou dérive d'un site World Wide Web, il faudra mettre le texte entre guillemets; par example "tiré de la FAO. 1996" et indiquer dans les Références la forme standard URL:
  FAO. 1996. Domestic Animal Diversity Information System, *http://www.fao.org/dad-is/*, FAO, Rome, Italy.

Pour tout envoi de manuscripts ou correspondence au sujet d'AGRI, vous êtes prié d'utiliser l'adresse suivante:

agri-bulletin@fao.org

Merci pour votre collaboration

Reglas y normas editoriales

El objetivo del Boletín de Información sobre Recursos Genéticos Animales (AGRI) es la divulgación de la información sobre una mejor gestión de los recursos genéticos animales de interés para la producción alimentaria y agrícola. Todos los aspectos referidos a la caracterización, la conservación y el uso de estos recursos serán tomados en consideración, de acuerdo con el Convenio sobre la diversidad biológica.

AGRI publicará información sobre genética, encuestas fenotípicas y económicas y descripciones comparativas, uso, desarrollo y conservación de los recursos genéticos animales, así como sobre el desarrollo de estrategias operacionales y normas que permitan una gestión más eficaz de la relación costo/eficacia. Por ello, AGRI prestará especial atención a las contribuciones referidas a razas y normas capaces de contribuir a la intensificación sostenible de los medios (agroecosistemas) con ingresos medios y bajos en el mundo, que comprenden casi la mayor parte de las tierras dedicadas a la producción ganadera; la producción total de alimentos y agricultura provenientes de la ganadería; y el resto de los recursos genéticos de animales domésticos.

Los puntos de vista expresados en los artículos publicados en AGRI son solamente las opiniones de los autores y, por tanto, no reflejan necesariamente la opinión de las instituciones para las cuales trabajan dichos autores, de la FAO o de los editores.

La oportunidad o no de publicar un artículo en AGRI será juzgada por los editores y revisores.

Publicación electrónica

Además de su publicación impresa, la versión íntegra de AGRI se encuentra disponible electrónicamente en Internet, en el sitio: *www.fao.org/dad-is/*

Tipos de artículos

Serán publicados en AGRI los siguientes tipos de artículos:

Artículos sobre investigación

Se tomarán en consideración para su publicación en AGRI los estudios sobre la caracterización, conservación y uso de los recursos genéticos de los animales domésticos (AnGR) con una buena descripción del entorno. Se agradecerá el envío de fotografías de calidad que presenten a las razas en cuestión en su ambiente natural de producción.

Artículos de revisión

Se podrán tomar en consideración ocasionalmente aquellos artículos que presenten una revisión de los agroecosistemas, a nivel nacional, regional o mundial, con el desarrollo de uno o más aspectos referidos a la gestión de los recursos genéticos animales, incluidas las revisiones sobre el estado actual de las distintas áreas de AnGR.

Artículos específicos

Se solicitarán puntualmente artículos sobre temas específicos para ediciones especiales.

Otro material para publicación

Incluye la revisión de libros, noticias y notas referidas a reuniones importantes, cursos de formación y principales eventos nacionales, regionales e internacionales, así como conclusiones y recomendaciones relacionadas con los objetivos de estos principales eventos. Se invita a los lectores a enviar este tipo de material a los editores.

Guía para los autores

Presentación del manuscrito

Los artículos se presentarán en inglés, francés o español, junto con un resumen en inglés y su traducción en francés o español, y se enviarán al editor de AGRI, AGAP, FAO, Viale delle Terme di Caracalla, 00153 Roma, Italia. El artículo deberá ser enviado en versión WinWord en fichero adjunto por correo electrónico a *agri-bulletin@fao.org*. Las fotografías, color o en blanco y negro, se enviarán siempre por correo normal.

Los manuscritos se presentarán con doble espacio y con el número correspondiente a cada línea en el margen izquierdo. Todas las páginas serán numeradas, incluidas las de las referencias bibliográficas, cuadros, etc. El autor recibirá una notificación sobre la recepción de su documento.

En el caso de aceptación de un artículo después de su revisión, se solicitará al autor una versión final de su artículo revisado en disquete (formato 31/2") en Word 6.0 x Windows, así como una copia impresa del mismo.

Preparación del manuscrito

En la primera página del manuscrito se indicará el título abreviado del artículo, títulos y nombres de los autores, instituciones, direcciones completas (incluido código postal y número de teléfono); así como otros medios de contacto tales como fax, correo electrónico, etc. del autor principal. El título abreviado no deberá sobrepasar los 45 caracteres más los espacios correspondientes, y aparecerá en la parte superior de la página 1 del manuscrito en mayúsculas. El título entero del manuscrito se escibirá en mayúsculas y minúsculas. Dicho título debe ser lo más breve posible y no sobrepasar los 150 caracteres (incluidos los espacios necesarios), con los nombres de las especies, si necesario. Los nombres de los autores, instituciones y direcciones se escribirán en cursiva y en letras mayúsculas y minúsculas. Se dejará una línea en blanco entre el título y los nombres de los autores. Las direcciones se escribirán como notas de pie de página de cada autor después de dejar una línea en blanco entre los nombres y éstas. Cada nota de pie de página con la dirección será indicada numéricamente. Se dejarán dos líneas en blanco después de las direcciones.

Títulos

Los títulos de cada sección, por ejemplo Resumen, Introducción, etc., serán alineados a la izquierda. Dejar dos líneas en blanco entre las notas de pie de página con las direcciones y el Resumen y entre el título Resumen y el texto que sigue. El resumen no deberá exceder de 200 palabras. Deberá ser un resumen objetivo que describa brevemente los procesos y logros obtenidos, y no una presentación de cómo se ha llevado a cabo el estudio y una descripción genérica de los resultados. Dejar una línea en blanco entre el final del texto del resumen y las palabras clave, que se escribirán en cursiva así como el titulo Palabras clave. No deberán ser más de seis y no deberán contener "y" o "&". Todos los títulos principales de capítulo (14 regular) y subcapítulo (12 regular) serán en negrita e irán precedidos y seguidos de una línea en blanco. El texto correspondiente empezará sin sangrado. Un título dentro de un subcapítulo se escribirá en cursiva e irá seguido de un punto con a continuación el texto correspondiente.

Cuadros y figuras

Los cuadros y las figuras se incluirán al final del texto siguiendo el orden de cita dentro del mismo. Las fotografías no serán devueltas a sus autores.

Cuadros

Los cuadros, incluidas las notas de pie de página, deberán ir precedidos y seguidos por dos líneas en blanco. El número del cuadro y su título se escribirán en la parte superior en cursiva (12) con un punto al final y seguido de una línea en blanco. En cada columna o título de encabezamiento o subtítulo, sólo la primera letra de la primera palabra irá en mayúscula. Los cuadros irán numerados de forma consecutiva con números árabes. Los cuadros y sus títulos se alinearán a la izquierda, así como el texto. Se utilizarán líneas horizontales o verticales sólo cuando sea necesario. No utilizar tabuladores o la barra espaciadora para crear un cuadro.

Figuras

Las figuras, incluidos los títulos y leyendas, irán precedidas y seguidas de dos líneas en blanco. El número de la figura y el título se escribirán en la parte superior en cursiva (12) con un punto al final. La palabra figura incluye las fotografías, los gráficos, los mapas, los diagramas, etc. En el caso del diagrama se enviará la matriz original con los datos utilizados para crearlo. Se recomienda encarecidamente la utilización de Word 6.0 o Excel 5.0 para la presentación de los diagramas.

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.

- 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.
- Cuando se trate de más de un autor:
  Matos, C.A.P., D.L. Thomas, D. Gianola, R.J. Tempelman & L.D. Young. 1997. Genetic analysis of discrete reproductive traits in sheep using linear and nonnlinear models: 1. Estimation of genetic parameters 75, 76-87.
- En el caso de un libro o de una publicación ad hoc, por ejemplo informes, tesis, etc.:
  Cockrill, W.R. (Ed.). 1994. The Husbandry and Health of the Domestic Buffalo. FAO, Rome, Italy, pp. 993.
- Cuando se trate de un artículo dentro de las actas de una reunión:
  Hammond, K. 1996. FAO's programme for the management of farm animal genetic resources. In C. Devendra (Ed.), Proceedings of IGA/FAO Round Table on the Global Management of Small Ruminant Genetic Resources, Beijing, May 1996, FAO, Bangkok, Thailand, 4-13.
- Cuando la información contenida en el artículo haya sido obtenida o derive de un sitio World Wide Web, poner el texto entre comillas; por ejemplo "sacado de la FAO. 1996" e indicar en las Referencias la forma estándar URL:
  FAO. 1996. Domestic Animal Diversity Information System, *http://www.fao.org/dad-is/*, FAO, Rome, Italy.

Se ruega enviar los manuscritos o la correspondencia relativa a AGRI a la dirección siguiente:

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Gracias por su colaboración

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