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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 - Measuring diversity

In the early 1990s, FAO formulated and proposed the MoDAD (Measurement of Domestic Animal Diversity) initiative to use DNA markers to genetically characterize and quantify the diversity of breeds from the world's major livestock species, to contribute to the design of cost-effective management programmes for animal genetic resources (AnGR). The proposal helped prompt individual countries to begin to apply the ideas of MoDAD. Since that time, continual efforts have been made to improve the global coordination of molecular characterization studies. FAO collaborated with the International Society of Animal Genetics (ISAG) to create the ISAG-FAO Advisory Group on Animal Genetic Diversity to establish standards. The Advisory Group produced guidelines, including recommended microsatelllite markers for the major livestock species (*http://lprdad.fao.org/cgi-bin/getblob.cgi?sid=-1,50006252).* Also, international organizations, such as the European Union, funded characterization studies in multiple countries (see *www.econogene.eu* as an example). The International Livestock Research Institute, in cooperation with partners such as the FAO-IAEA Joint Division, has evaluated breed diversity across Africa and Asia. Individual countries have supported studies, both of their own breeds and in developing countries.

Molecular characterization has been completed for more than 1 000 breeds. Nevertheless, the original goals of MoDAD are far from realized. Several thousand breeds remain to be characterized and no global analysis of independent studies has been done. For these reasons, characterization is among the strategic priorities of the *Global Plan of Action for AnGR*.

Several activities are underway to increase the number of breeds characterized and to use the existing data more effectively. The European Union is supporting the project GLOBALDIV, which aims to provide a "*global view of livestock biodiversity and conservation*". GLOBALDIV is a network of approximately 30 experts, including FAO staff. Its objectives include reviewing methods for characterization, integrating data and disseminating experience from past studies, identifying future research priorities, and training personnel in AnGR characterization, conservation and utilization.

Scientists who plan future studies should ensure that their data can be standardized and included in global analysis in the most efficient and informative manner. Future work planned in GLOBALDIV includes the meta-analysis of existing data from independent studies. Scientists interested to participate in meta-analyses are encouraged to contact the AnGR group at FAO (via e-mail: *DAD-IS@fao.org*) whose members can also provide guidance on the collection of critical complementary information on phenotypes and farming system.

High-throughput genotyping methods based on single nucleotide polymorphisms (SNP) are rapidly replacing microsatellites for many applications. The ISAG-FAO Advisory Group is keeping abreast of these developments. The possible switch from microsatellites to SNP will, however, require research to allow the integration of data across platforms, as well as the design of SNP panels that correctly capture AnGR diversity. In the meantime, the current ISAG-FAO guidelines (with the newest marker lists) on molecular characterization remain valid. As always, molecular studies must be complemented with concurrent collection and analysis of phenotypic, farming system, and geographical data, as molecular studies cannot provide a proper picture of a breed's value if done in isolation.

The Editors

Éditorial - Mesurant la diversité

Au début des années 90 la FAO a proposé et formulé le MoDAD (Mesure de la diversité des animaux domestiques), une initiative qui utilise les marqueurs du DNA pour caractériser de du point de vue génétique et quantifier la diversité des races principalement présentes entre les espèces au niveau mondial, afin de contribuer au schéma des programmes de gestion des ressources génétiques animales (AnGR) avec des coûts effectifs. Cette proposition a aidé d´une manière efficace certains pays dans la mise en œuvre immédiate des idées du MoDAD. Depuis, des efforts ont été conçus pour améliorer la coordination globale des études de caractérisation moléculaire. La FAO a collaboré avec la Société Internationale de Génétique Animale (ISAG) dans la création d´un Groupe Consultatif pour la Diversité Génétique Animale ISAG-FAO, pour établir les standards nécessaires. Ce groupe a élaboré des directrices qui comprennent les marqueurs micro satellitaires pour la majorité des espèces domestiques (*http://lprdad.fao.org/cgi-bin/getblob.cgi?sid=-1,50006252*). Parallèlement, des organisations internationales telles que l´Union Européenne, ont réalisé des études de caractérisation dans différents pays (voir comme exemple *www.econogene.eu*). L´Institut International de Recherche sur l´Elevage en collaboration avec des partenaires comme la Division Conjointe FAO-IAEA, ont réalisé une évaluation sur la diversité en Afrique et en Asie. Certains pays ont contribués à ces études à titre individuel, aussi bien avec leurs propres races comme avec celles des pays en développement.

La caractérisation moléculaire a été complétée sur plus de 1 000 races. Cependant, les objectifs initiaux du MoDAD sont encore loin d´être atteints. Il reste encore des milliers de races à caractériser, et une analyse global des études indépendantes n'a pas été réalisée. En conséquence, la caractérisation se trouve parmi les priorités stratégiques du *Plan d'Action Mondial pour les Ressources Zoogénétiques*. Plusieurs activités sont en voie de développement pour améliorer le nombre de races caractérisées et pour utiliser les données existantes de façon efficace. L´Union Européenne soutient le projet GLOBALDIV qui a comme objectif fournir "*une vision globale de la biodiversité et conservation des races*". GLOBALDIV est un réseau d'environ 30 experts, parmi lesquels certains appartenant à la FAO. Ses objectifs comprennent, entre autres, la révision des méthodes de caractérisation à travers l'intégration des données et des expériences de vulgarisation existantes en provenance des études précédentes et en identifiant les priorités de recherches futures, ainsi comme la formation du personnel de AnGR dans les domaines de la caractérisation, conservation et utilisation.

Les chercheurs qui planifient les études futures devront s´assurer que leurs données puissent être standardisées et inclues dans les analyses globales d´une manière plus efficace et informative. Les futurs travaux de GLOBALDIV comprennent le méta analyse des données existantes en provenance d´études indépendantes. On encourage les chercheurs intéressés à participer à ces métas-analyses a contacter avec le groupe AnGR de la FAO (par email: *DAD-IS@fao.org*) dont les membres peuvent également fournir des renseignements sur la saisie d'information critique complémentaire sur les phénotypes et sur les systèmes d´élevage.

Les investissements importants sur les méthodes de classification de génotypes basés sur les polymorphismes nucléotides individuels (SNP), vont rapidement remplacés les microsatellites dans différentes applications. Le groupe consultatif ISAG-FAO suit de près tous ces développements. Le passage probable de microsatellites à SNP exigera cependant une recherche qui permettra l´intégration des données d´une plate-forme à l´autre, ainsi que le dessin de bases SNP qui incluront correctement la diversité AnGR.

Entre temps, les directrices actuelles du groupe ISAG-FAO en matière de caractérisation moléculaire (qui comprennent la liste des nouveaux marqueurs), sont encore valable. Il est donc nécessaire que les études moléculaire soient complémentées avec les saisies actuelles et avec les analyses phénotypiques, de système d´élevage, et de données géographiques, étant donné que les études moléculaires ne peuvent fournir une bonne vision des valeurs des races si celles-ci sont faites d´une manière isolée.

Les Editeurs

Editorial - Midiendo la diversidad

A principios de los años 90 la FAO formuló y propuso el MoDAD (Medición de la diversidad en los animales domésticos), iniciativa que utiliza los marcadores de ADN para caracterizar genéticamente y cuantificar la diversidad de las razas mayormente presentes a nivel mundial entre las especies, con el objetivo de contribuir al diseño de programas de gestión de los recursos zoogenéticos (AnGR) con costos efectivos. La propuesta ayudó al establecimiento inmediato en algunos países de la aplicación de las ideas del MoDAD. Desde entonces se han llevado a cabo esfuerzos continuos para mejorar la coordinación global de los estudios de caracterización molecular. La FAO colaboró con la Sociedad Internacional de Genética Animal (ISAG) en la creación del Grupo Consultor sobre Diversidad Zoogenética ISAG-FAO, para establecer los estándares necesarios. Este grupo ha elaborado unas líneas directrices que comprenden los marcadores microsatelitales para la mayor parte de las especies ganaderas (*http://lprdad.fao.org/cgi-bin/getblob.cgi?sid=-1,50006252).* Al mismo tiempo, organizaciones internacionales, tales como la Unión Europea, han realizado estudios de caracterización en distintos países (ver *www.econogene.eu* como ejemplo). El Instituto Internacional de Investigación Ganadera en colaboración con socios, tales como la División Conjunta FAO-IAEA, ha realizado una evaluación sobre la diversidad en toda África y Asia. Algunos países han contribuido en estos estudios a título individual, tanto de sus propias razas como aquéllas de países en desarrollo.

La caracterización molecular ha sido completada en más de 1 000 razas. Sin embargo, los objetivos iniciales del MoDAD están lejos de ser alcanzados. Quedan todavía varios miles de razas por caracterizar y no se ha realizado un análisis global sobre los estudios independientes. Por estas razones, la caracterización está entre las prioridades estratégicas del *Plan de Acción Mundial para los Recursos Zoogenéticos*.

Varias actividades están siendo desarrolladas para mejorar el número de razas caracterizadas y para utilizar los datos existentes de forma más efectiva. La Unión Europea apoya el proyecto GLOBALDIV, que tiene como objetivo proporcionar una "*visión global de la biodiversidad y conservación de las razas*". GLOBALDIV es una red que cuenta aproximadamente con 30 expertos, incluidos algunos de la FAO. Sus objetivos comprenden, entre otros, la revisión de los métodos de caracterización a través de la integración de datos y divulgación de experiencias obtenidas de estudios llevados a cabo en el pasado, la identificación prioridades de investigación para el futuro, así como la formación de personal en la caracterización, conservación y utilización de los AnGR.

Los investigadores que planifican los futuros estudios deben asegurarse de que sus datos puedan ser estandarizados e incluidos en los análisis globales de la forma más eficaz e informativa posibles. Los futuros trabajos en GLOBALDIV incluyen el meta-análisis de datos existentes provenientes de estudios independientes. Se anima a los investigadores interesados en participar en estos meta-análisis a que contacten con el grupo AnGR de la FAO (por email: *DAD-IS@fao.org*) cuyos miembros pueden también proporcionar asesoramiento sobre la recogida de información crítica complementaria sobre fenotipos y sistemas de cría.

Las altas inversiones en métodos para la clasificación de genotipos basados en los polimorfismos de nucleótidos simples (SNP) están rápidamente sustituyendo los microsatélites en varias aplicaciones. El Grupo Consultor ISAG-FAO sigue muy de cerca estos desarrollos. Sin embargo, el paso probable de microsatélites a SNP requerirá,una investigación que permita integrar los datos de una plataforma a otra, así como el diseño de bases SNP que incluyan correctamente la diversidad AnGR.

Mientras tanto, las actuales líneas directrices de ISAG-FAO sobre caracterización molecular (que comprenden la lista de nuevos marcadores), siguen siendo válidas. Como siempre, los estudios moleculares deben ser complementados con la recopilación simultánea y el análisis de datos referidos al fenotipo, sistemas de cría, y distribución geográfica, ya que los estudios moleculares no pueden proporcionar una visión adecuada del valor de una raza si éstos se realizan de forma aislada.

Los Editores

Characterisation and conservation programme of the Alberes cattle breed in Catalonia (Spain)

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Summary

The Alberes cattle breed is a Catalonian autochthonous bovine population located in the Alberes Massif (north east of Spain), in the eastern extreme of the Pyrenees Mountains, and is well adapted to this zone in which it mainly makes use of forest resources. Cows are small sized and rustic, living under a semi-feral management system with minimal human contact. Traditionally, two coat colour varieties, Black and Fawn, have been described. Nevertheless, in both coat colour types the wild-type allele (E^+) of the extension locus predominates. The Alberes breed clusters within the Cantabrian trunk, although some other breeds may also have influenced the population during its history. All of the females are used for replacement and the surplus males are destined for fattening despite their low meat potential. Age at first calving ranges between 3 and 4 years. The 2007 census estimated the number of adult animals at 138 females and 9 males. The Alberes breed is considered as an *Endangered Breed* according to the FAO classification and intends to start an *in situ* minimum kinship conservation programme and also a cryoconservation scheme with embryos and semen.

Résumé

La race Alberes est une population bovine autochtone qui se trouve dans le Massif de Alberes (Nord-Est de l'Espagne), dans la zone de l'extrême Est des Pyrénées. Cette race est bien adaptée à la zone et elle est capable de bien valoriser ses ressources alimentaires, aussi bien herbacées que forestales. Il s'agit d'animaux de petite taille et rustiques qui vivent en liberté toute l'année avec un minimum de contact humain. Traditionnellement on décrit deux variétés de couleur du manteau : la variété noire et la Fagina, bien que dans les deux cas il existe une prédominance de l'allèle E+ brun dans le locus d'extension. La race Alberes fait partie du bloc Cantabrique, bien que d'autres races aient eu une influence sur cette population tout au long de l'histoire. Toutes les femelles sont tenues pour le replacement. Les veaux mâles son mis à l'engraissement malgré le faible potentiel de viande de cette race. L'âge à la première mise bas se situe entre 3 et 4 ans. Le dernier recensement des animaux adultes avec morphotype Alberes (2007) a montré un total de 138 femelles et 9 mâles, ce qui place la population dans la catégorie de race en danger de disparition d'après la classification de la FAO. Pour cette raison un programme formel de conservation a été mis en route qui comprend la conservation in situ à travers un programme de parentage minimum et in vitro à travers la cryoconservation d'embryons et de semence.

Resumen

La raza Alberes es una población bovina autóctona localizada en el Macizo de las Alberes (Noreste de España), en el extremo oriental de los Pirineos, y está bien adaptada a la zona siendo capaz de aprovechar los recursos alimenticios de la zona,

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tanto herbáceos como forestales. Son animales de pequeño formato y rústicos, que viven en libertad todo el año, con mínimos contactos con las personas. Tradicionalmente se han descrito dos variedades de color de capa, la variedad Negra y la *Fagina*, aunque en los dos tipos predomina el alelo castaño E^+ del locus de extensión. La raza Alberes se encuadra en el tronco Cantábrico, aunque otras razas han influido en esta población a lo largo de su historia. Todas las hembras se guardan para reposición. Los terneros machos son cebados a pesar del limitado potencial carnicero de esta raza. La edad al primer parto se sitúa entre los 3 y 4 años. El último censo (2007) de animales adultos con morfotipo Alberes ha arrojado un total de 138 hembras y 9 machos, lo cual sitúa a la población en la categoría de raza en peligro de extinción de acuerdo con la clasificación de la FAO. Por ello se ha iniciado recientemente un programa formal de conservación que incluye la conservación *in situ* mediante un programa de parentesco mínimo e *in vitro* a través de la crioconservación de embriones y semen.

***Key words**: Endangered population, Conservation programme, Production system, Physical characteristics, Genetic diversity.*

Introduction

The Alberes cattle are a semi-feral bovine Catalonian breed, located in the Natural Park of the Alberes Massif (200-1 100 m a.s.l.), in the eastern extreme of the Pyrenees (Figure 1). It is distributed between the *Alt Empordà* region (Spain) and the *Vallespir* region (France).

The first description of the Alberes cattle breed was carried out by Mascort (1957), who classified the Alberes population as having three main types:

1. Type A: the most abundant, being of small size with a black coat colour and degradations in the abdomen.
2. Type B: with two varieties, one with a toasted straw colour coat (it was assumed to have been genetically improved), and the other with a coat colour varying from white to light brown or fawn (called *"Fagina"*). It was also a cow with a small frame.
3. Type C: Brown Swiss crossbred animals.

Almost three decades later, Sánchez Belda (1984) wrote about an endangered small breed located in that region, with a chestnut brown coat that was darker in winter, and almost black in males. The calves were born with a light brown coat.

Figure 1. The Alberes cattle is located in the Natural Park of the Alberes Massif (200-1 100 m a.s.l.), in the eastern extreme of the Pyrenees (latitude: 42º 26' 07''N; longitude: 6º 39' 30'' W).

Nevertheless, he described a large variability of coat colour tonalities. A similar description was given by García-Dory *et al*. (1990), who suggested the inclusion of the Alberes breed within the Cantabrian trunk, which contains the *Asturianas*, *Monchina* and *Tudanca* breeds, among others. Subsequently, Martell (1991) and Jordana *et al*. (1999) took the terminology of the local caretakers and described two varieties: the Black Alberes, perhaps the oldest variety, and the *Fagina* or Fawn Alberes, this last name coming from the fruit of the beech tree (*Fagus sylvatica*), abundant in the Alberes region. According to these authors, the Black variety is the most numerous in the *Empordà* region (Catalonia, Spain), while the Fawn variety, also called *Massanessa*, a name derived form the *Massana* river, is predominant in the *Roussillon* region (France).

Since these preliminary descriptions were offered, no formal studies to characterise the current status of the breed have been done in order to start a conservation or improvement programme. For this reason, the *Departament d'Agricultura, Ramaderia i Pesca de la Generalitat de Catalunya* has promoted and funded several studies whose results are summarised in this paper.

Production System

This breed, characterised by small-sized animals with a straight cranial profile and short horns, lives free all year round in the *Baussitges* rangeland. This has a total area of 2 181 ha, consisting of 1 482 ha of forest and shrubland and 699 ha of grassland. Mediterranean oak woodlands, mainly holm oak (*Quercus ilex* L.), but also cork oak (*Quercus suber* L.) and pubescent oak (*Quercus humilis* Mill.) dominate the landscape on the slopes. Acidic grasslands, dominated by *Festuca ovina* and *Carex cariophyllea*, with dwarf shrubs of heather (*Calluna vulgaris* L.), are the common vegetation on the crests, above 900 m a.s.l. The animals are grouped in three herds, each of them grazing near an old farmhouse (called *Freixe*, *Castanyers* and *Roig*, respectively), where animals receive supplementary feed, such as alfalfa pellets, in adverse periods, mainly in winter. In general, individuals remain in the herd where they are born. Each herd consists of a group of cows with their calves, usually led by a female or a few dominant females. The males live more independently although they are also linked to a particular herd. When the environmental temperature increases, in spring and summer, the animals graze on grasslands of the crests and neighbouring forests (Figure 2).

Selection of the diet

With the aim of determining the natural diet composition of the Alberes cows, Bartolomé *et al*. (2004) collected faecal samples in two environments (woodlands and grasslands) of the *Baussitges* rangeland during two periods: spring and autumn. Using the methodology of microhistological analyses of faeces, two hundred fragments of leaf epidermis were identified from each sample. The results showed that ligneous components occur with most frequency (75% of the diet) in the samples collected in the forest throughout the year, whereas forbs and grasses represented the highest fraction of the diet (60%) only in the spring samples collected from grasslands.

These data suggest that the Alberes cow is a versatile animal in terms of diet selection, which varies depending on the vegetation available in each period. The large proportion of woody components allows us to consider the Alberes cattle population as a browser throughout the year and a grazer only in spring and summer, when the animals can graze on herbaceous pastures. The pressure that this bovine breed exerts in the Mediterranean forest mass suggests that it is a very interesting element in the management of the natural resources associated with the contingency of forest fire (Bartolomé *et al.*, 2004).

Reproductive and productive aspects

The age at first calving ranges from 3 to 4 years. Natural service is the only reproduction system used. Replacement is carried out with all of the heifers, because the percentage of mortality throughout the year is high, although difficult to assess. Despite this practice, the population has not increased in the last few years. The bulls are chosen according to their conformation, leg soundness, rusticity and their conformation to the breed profile.

Once a year, all of the animals are brought together in a ceremony called '*esquellada*' (*esquella* is '*bell*' in the Catalan language). The animals are restrained within small fences in order to worm them and to extract blood samples for the obligatory veterinarian control. On this day young animals are identified with a plastic numbered earring and with an electronic ruminal bolus, and the cowbells of the

Figure 2. Alberes cattle in a woodland area.

Figure 3. A typical Alberes Black bull.

Figure 4. A typical Alberes Black cow.

Figure 5. An Alberes cow with two daughters.

adult cows are checked and repaired, or changed if needed, in order to locate them across the range. Male calves not chosen for breeding are sent for fattening, whereas females go for herd replacement. The day ends with a lunch based on typical products of the region with the farmer, caretakers, family and friends.

Physical Characteristics of the Breed

The Alberes cattle are a small sized breed, with an average weight of 350 kg for the mature bulls and 275 kg for the mature cows (Mascort, 1957). The general aspect is of rustic animals without a defined productive aptitude (Figures 3 and 4).

The current animals have an elongated head of compact aspect, with an inter-horn diameter narrower than the inter eye-socket diameter. The forehead has a straight profile with a medium fringe, more pronounced in calves. The eyes are prominent and the facial area is elongated, with a light coloured muzzle-band. The horns are short and hook-shaped, with a circular section and are of medium size. The neck is long and flat with a dewlap of broken profile, larger in males than in females. The trunk is flat, deep and narrow, with a prominent and divided wither. The shoulders present low muscular development and are well attached to the trunk. The back and loin have poor muscular development. The abdomen is voluminous and the rump usually has a horizontal profile, with an elevated sacred crest and reduced muscular development of the rear region, which causes the consequent projection of the bones and an advanced tail-head. The mammary system is rudimentary and is covered by fine, long and generally lighter hair. The legs are of medium length, strong and with well defined joints, the rear ones usually not being correctly formed. The rump is straight or concave, with poor development. Pasterns are short, with small but strong and always pigmented toes.

The skin is abundant, with pigmented mucous membranes. The coat tonality can vary during the year: it is long and decoloured in winter, but a moult can give thin and brilliant hair if the spring has been favourable. It is possible to observe a wide variety of colours from almost matt black to fawn. There are also lighter colourings to a different extent in the lumbar line and at the bottom of the trunk (armpit, sternal region, mammary system, testicles, etc.).

Zoometric study

In order to characterise the size of the animals in the current population and to compare it with published data, 18 zoometric measurements were studied (Tables 1, 2 and 3) taken with a zoometric stick and a tape (Alderson, 1999; Aparicio, 1984; Sañudo, 1986). Body condition was evaluated according to Lowman *et al.* (1976). The score range is from 1 to 5. A score of 1 indicates a very poor body condition and 5 means an excellent body condition. These measurements allow us to calculate some morphologic, ethnologic and functional indexes (Tables 4 and 5). Only animals aged four years and older, with black, chestnut brown or fawn coat were included in the study, since other coat colours could indicate a crossbred origin.

Average measurements by sex, herd and coat colour are presented in tables 1, 2 and 3. The results indicate that, according to the classification of Felius (1995), the Alberes breed has a small size (115-125 cm height at withers). Males are around 6 cm taller (height at withers), longer (10.7 cm of length from shoulder to tuber ischii) and their chest is larger (the chest girth is 11.8 cm larger) than females. Body condition was also better in males than in females (3 vs 2.3). Alberes cattle have 10.4 cm less height at withers and 12.2 cm less at chest girth than the *Bruna dels Pirineus* breed, considered a medium sized breed. The results described in table 4 are related to the herd of origin. A clear grading of the size of animals appears. Animals from the *Freixe* herd are larger than the animals from the *Castanyers* herd (124.0 cm of height at withers in *Freixe* vs 117.2 cm in *Castanyers*), *Roig* animals being situated between these two herds. Nevertheless, some of the measurements presented a great variability and the differences did not always achieve statistical significance. The body condition score registered is poor, consistent with irregular oestrous. The consequences would be longer reproduction cycles and a low numeric productivity. Results shown in table 3 indicate no differences in size between the initial two coat colour varieties described which suggest that the differences in size among cows would have an environmental origin rather than a genetic basis.

The morphologic, ethnologic and functional indexes presented in tables 4 and 5 are calculated in order to determine the breed purpose or potential. The height slope shows that the Alberes cattle is 1.68 cm taller in the foreleg than in rear legs, similar to White Park animals. The length index (1) (Table 4) confirms that the Alberes cattle are taller

Table 1. Number of animals recorded (No), least squares means (LSM), standard error (S.E.), minimum (Min.) and maximum (Max.) of the morphological measures (cm) and body condition (according to Lowman et al., 1976) by sex.

	Males					Females				
	No	LSM	S.E.	Min.	Max.	No	LSM	S.E.	Min.	Max.
Height at withers	5	126.4[a]	2.6	118	133	84	120.6[b]	0.7	106	134
Height at medium back	5	123.1[a]	2.6	113	128	84	119.7[a]	0.7	102	134
Height at rump	5	127.2[a]	2.8	122	137	83	122.2[a]	0.7	108	136
Height at the tuber ischii	5	116.2[a]	2.5	114	119	84	113.4[a]	0.7	96	133
Depth of chest (thorax)	4	62.2[a]	2.1	58	68	76	59.9[a]	0.5	49	70
Chest circumference	4	187.6[a]	7.0	168	190	71	175.8[b]	3.1	138	200
Cannon perimeter	5	19.5[a]	0.5	19	20	71	17.8[b]	0.2	16	21
Length from shoulder to pins (tuber ischii)	5	157.2[a]	4.7	145	174	84	146.5[b]	1.2	124	176
Length from withers to pins (tuber ischii)	5	133.2[a]	3.5	125	140	85	124.9[b]	0.9	106	147
Rump length from hips (tuber coxae) to pins (tuber ischii)	5	51.9[a]	1.5	49	54	86	47.8[b]	0.4	41	58
Width of chest	4	38.2[a]	1.9	30	44	77	31.1[b]	0.5	23	40
Pelvic width	5	44.5[a]	1.4	39	51	84	43.8[b]	0.4	37	51
Intercoxae width	5	43.8[a]	1.5	39	48	84	40.7[b]	0.4	34	52
External interischii width	5	23.9[a]	1.1	22	27	84	23.3[a]	0.3	19	30
Internal interischii width	5	9.4[a]	0.5	8	11	83	11.8[b]	0.1	9	14
Head length	4	51.2[a]	1.8	51	53	78	48.1[a]	0.5	23	56
Head width	4	26.9[a]	1.7	23	31	78	23.4[b]	0.4	20	50
Body condition	3	3.0[a]	0.3	3	3	81	2.3[b]	0.1	1	3

Within a row, least squares means with the same superscript did not differ significantly ($P<0.05$).

Table 2. Number of animals recorded (No), least squares means (LSM), standard error (S.E.), minimum (Min.) and maximum (Max.) of the morphological measures, cm, and body condition (according to Lowman et al., 1976) by herds.

	Castanyers					Roig					Freixe				
	No	LSM	S.E.	Min.	Max.	No	LSM	S.E.	Min.	Max.	No	LSM	S.E.	Min.	Max.
Height at withers	30	117.2^{a}	1.1	106	134	15	120.5^{a}	1.5	108	129	39	124.0^{b}	0.9	113	134
Height at medium back	30	118.3^{a}	1.1	102	134	15	118.6$^{a.b}$	1.5	105	129	39	122.0^{b}	0.9	109	131
Height at rump	29	120.1^{a}	1.2	108	135	15	121.3^{a}	1.7	111	130	39	125.3^{b}	1.0	110	136
Height at the tuber ischii	30	110.1^{a}	1.0	96	123	15	113.6$^{a.b}$	1.5	106	121	39	116.0^{b}	1.0	102	133
Depth of chest (thorax)	28	59.5^{a}	0.8	50	70	12	59.3^{a}	1.2	49	65	36	60.9^{a}	0.7	53	68
Chest circumference	30	160.9^{a}	2.3	138	200	2	192.0^{b}	9.1	190	194	39	174.6^{b}	2.1	148	200
Cannon perimeter	30	17.5^{a}	0.2	16	21	5	18.0^{a}	0.5	17	19	36	17.8^{a}	0.2	16	20
Length from shoulder to pins (tuber ischii)	30	143.8^{a}	1.9	124	176	15	146.3$^{a.b}$	2.7	125	165	39	149.2^{b}	1.7	131	163
Length from withers to pins (tuber ischii)	29	123.6^{a}	1.5	110	147	17	124.8^{a}	1.9	106	136	39	126.3^{a}	1.3	108	144
Rump length from hips (tuber coxae) to pins (tuber ischii)	30	46.7^{a}	0.6	42	58	16	46.3^{a}	0.8	41	52	40	50.2^{b}	0.5	44	56
Width of chest	28	29.7^{a}	0.7	23	38	13	31.4$^{a.b}$	1.0	27	39	36	32.2^{b}	0.6	24	40
Pelvic width	30	41.7^{a}	0.6	37	51	15	45.0^{b}	0.8	38	51	39	44.8^{b}	0.5	38	50
Intercoxae width	30	39.2^{a}	0.6	34	52	15	41.4^{b}	0.9	34	47	39	41.5^{b}	0.5	35	48
External interischii width	30	22.9^{a}	0.5	19	30	15	22.7^{a}	0.7	20	27	39	24.3^{b}	0.4	20	29
Internal interischii width	29	11.6^{a}	0.2	8	13	15	11.5^{a}	0.3	10	13	39	12.2^{b}	0.2	11	14
Head length	28	48.0^{a}	0.5	40	56	13	48.6$^{a.b}$	0.4	44	51	37	49.9^{b}	0.4	46	54
Head width	28	22.1^{a}	0.3	20	27	13	22.6$^{a.b}$	0.4	20	24	37	23.4^{b}	0.2	21	28
Body condition	28	2.4^{a}	0.1	2	3	15	2.3^{a}	0.1	2	3	38	2.2^{a}	0.1	1	3

Within a row, least squares means with the same superscript did not differ significantly ($P<0.05$).

Table 3. Number of animals recorded (No), least squares means (LSM), standard error (S.E.), minimum (Min.) and maximum (Max.) of the morphological measures, cm, and body condition (according to Lowman et al., 1976) by coat colour.

	Black					Fawn				
	No	LSM	S.E.	Min.	Max.	No	LSM	S.E.	Min.	Max.
Height at withers	54	121.1[a]	0.9	107	134	20	121.1[a]	1.5	107	134
Height at medium back	54	119.7[a]	0.8	102	134	20	121.1[a]	1.4	109	134
Height at rump	54	123.2[a]	0.9	108	135	20	122.0[a]	1.5	110	134
Height at the tuber ischii	54	113.8[a]	0.9	96	133	20	113.3[a]	1.4	100	125
Depth of chest (thorax)	47	60.5[a]	0.6	49	70	20	60.0[a]	0.9	53	66
Chest circumference	46	170.8[a]	2.2	145	200	17	167.0[a]	3.6	138	200
Cannon perimeter	46	17.7[a]	0.2	16	21	17	17.5[a]	0.3	16	20
Length from shoulder to pins (tuber ischii)	54	146.3[a]	1.4	124	176	20	146.6[a]	2.4	131	167
Length from withers to pins (tuber ischii)	55	124.8[a]	1.1	106	147	21	125.1[a]	1.7	112	144
Rump length from hips (tuber coxae) to pins (tuber ischii)	56	48.4[a]	0.5	41	58	20	47.9[a]	0.9	41	56
Width of chest	48	31.8[a]	0.5	26	40	20	30.2[a]	0.8	23	39
Pelvic width	54	43.8[a]	0.5	37	51	20	43.3[a]	0.8	37	50
Intercoxae width	54	40.6[a]	0.5	34	52	20	41.1[a]	0.8	37	48
External interischii width	54	23.4[a]	0.4	20	30	20	23.7[a]	0.6	21	27
Internal interischii width	54	11.7[a]	0.1	9	14	20	12.2[a]	0.2	10	14
Head length	49	49.3[a]	0.4	44	56	20	48.4[a]	0.6	40	51
Head width	49	22.8[a]	0.2	20	28	20	23.0[a]	0.3	22	25
Body condition	52	2.4[a]	0.1	1	3	19	2.0[b]	0.1	1	3

Within a row, least squares means with the same superscript did not differ significantly ($P<0.05$).

Table 4. Average of eight morphological indexes of the Alberes cattle compared to Pirenaica and White Park breeds (according to Alderson, 1999).

	Alberes	Pirenaica	White Park
Height slope (cm)	1.68	7.00	2.07
Length index[1]	2.08	1.90	1.97
Length index ([2])	1.04	1.26	1.11
Rump length index	0.38	0.32	0.59
Balance	1.04	0.62	0.86
Width slope (cm)	9.61	-	-
Depth index	0.50	0.67	0.56
Foreleg length (cm)	60.65	44.00	56.31

Results of the calculations for individual animals indexed. Height slope: rump height - withers height; Length index

[1]Body length/chest (thorax) depth; Length index.

[2]Body length/withers height; Rump length index: rump length/withers to hip length; Balance: (hip width x rump length)/(chest depth x chest width); Width slope: hip width - chest width; Depth index: chest depth/withers height; Foreleg length: withers height - chest depth.

Table 5. Average of functional and ethnologic indexes of the Alberes cattle compared to the Pirenaica breed.

	Reference[1]	Alberes	Pirenaica[2]
Relative thorax depth index	More than 50	49.70	66.67
Transversal pelvic index	More than 33	33.76	41.67
Longitudinal pelvic index	No more than 37	39.57	40.15
Body index	83-90 medium	83.28	-

Note: All estimates are expressed in %.

[1]For beef cattle, by Sañudo (1986).

[2] Mendizábal *et al*. (1998).

than they are wide. The balance parameter indicates the slight development of the posterior third compared with the anterior part. The ethnologic and functional indexes (Table 5) show that the Alberes animals are low to medium sized animals with limited meat characteristics.

Genetic Diversity of the Alberes Cattle

The most important goal in the conservation of animal genetic resources is to maintain the variability of the population, assuming a correlation between genetic variation and the viability of the population. In recent years, FAO has proposed molecular methodologies based on the analysis of microsatellites loci as one of the most powerful tools for genetic-population studies (Goldstein and Schlotterer, 1999).

As a first step to establish a conservation programme it is advisable to determine if the Alberes cattle breed is composed of two clearly differentiated subpopulations or if it is of a unique genetic identity with a great chromatic diversity that we would have to maintain, as the zoometric study suggested. In this context, Casellas *et al.* (2004) have considered the genetic diversity of the Alberes cattle with the study of the relations between the Black and *Fagina* varieties, and classified this population in relation to other European cattle breeds. Casellas *et al.* (2004) studied 16 microsatellite loci, which are included in the AIRE2066 European Concerted Action list (FAO list). All microsatellites analysed were polymorphic in the Alberes population, as well as within-herd or within-colour variety. The number of alleles detected per locus fluctuated between 3 and 10, and average values were higher in the Black variety than in *Fagina* animals (5.9±0.4 vs 4.9±0.3), and similarly higher in the *Castanyers* herd (5.3±0.5) than in the *Roig* (5.0±0.4) or *Freixe* herds (4.7±0.3). The relative values of heterozygosity, both the observed heterozygosity (H_o) and the expected heterozygosity (H_e) values, were similar for each colour type variety, and fluctuated between 0.662 and 0.649 for total

Table 6. Growth, meat and carcass quality of the Alberes calves (Black and Fawn).

	No	Mean	Score
Growth, kg/d	91	1.11	
Carcass weight, kg	35	251.31	
Area of *longissimus thoracis* muscle, cm^2	8	39.76	
Conformation score	28	7.61	R- / R
Fatness score	28	4.93	2 / 2+
Intramuscular fat	22	1.41	Scarce
Meat colour	17	2.83	Light red
Fat colour	12	0.00	Light

animals. These results are comparable with those obtained in other European breeds (Kantanen *et al.*, 2000). The F-statistics showed a lack of genetic differentiation based on the coat colour (Black or Fawn) of the individuals. The non-significant F-statistics estimates in the Alberes breed indicate that there is no inbreeding in the population. These values could also be explained by the existence of gene flow with other populations (e.g., *Bruna dels Pirineus*, *Gasconne*, *Charolaise* …) as suggested by Mascort (1957), among others. The Alberes breed clusters within the Cantabrian trunk, which also suggests that although the Alberes population has felt the influence of some other breeds, the animals within the Cantabrian trunk may have contributed the most to the gene pool of the current population, coinciding with results previously reported by García-Dory *et al*. (1990) and Jordana *et al*. (1991).

Coat Colour

According to Klungland (1995), coat colour is governed by two main genes: the extension and agouti loci. The extension locus, identified as the Melanocyte Stimulating Hormone Receptor Gene (MC1R), and located at the 18th chromosome (Werth *et al.*, 1996), has three common alleles: E^D (dominant black), E^+ (chestnut, also called "wild type") and *e* (recessive red or brown). A fourth allele, E^1, was also described (Rouzaud *et al.*, 2000), which is the allele responsible for the brown phenotype coat colour of the *Gasconne* breed, also described in the Brown Swiss breed. Phenotypically, the Alberes population has been divided into two coat colour varieties, Black and Fawn, with intermediate tonalities. This observation suggested the presence of the E^+ allele with a probable intervention of the agouti allele (Figure 5). Allele frequencies were calculated to determine the distribution of the extension alleles in the Alberes population. The results confirm the predominance of the E^+ allele in the two varieties (Table 7). This allele is also observed predominantly in other Spanish breeds from the Cantabrian Trunk like the *Asturiana de los Valles* and *Asturiana de la Montaña* (Royo *et al.*, 2004). In summary, from a genetic point of view, Black and Fawn varieties are predominantly chestnut brown and the preservation of this identity must be a future objective. We propose selecting for breeding animals with the E^+ allele in homozygosis whenever possible.

Evaluation of Growth and Carcass Quality

To establish the quantitative and qualitative meat production potential of the Alberes calves, a fattening trial was carried out. The age of calves at the beginning of the study fluctuated between six and nine months although we did not know the precise age of each animal because the birth date is not usually recorded in the management system of the Alberes breed. Individuals were housed in barns in reduced groups (an average of 10 young bulls per group) where they were fed *ad libitum* with a specific diet based on standard concentrate meal (crude protein around 14% or slightly higher; energy of 1 UFC kg^{-1}; and balanced for Ca and P) and straw for the maintenance of ruminant ability. No special management or treatment was given to the animals. At the end of the fattening period, calves were slaughtered. Twenty four hours after slaughter, standard quality carcass measurements were taken on the left half-carcass, according to the methodology described by De Boer *et al.* (1974) and Piedrafita *et al.* (2003). Meat quality evaluation was done subjectively to appreciate the intramuscular fat content (Australian system, scale 1-6), as well as

fat and meat colour (this last factor is an indicative measurement of the pH which allows for the identification of possible dark meat). The reduced daily gain meant a reduced slaughter weight (Table 6). Carcass muscular development was also limited, as is indicated by a small rib eye area and a small conformation score. On the whole, the results indicate a low meat production potential of Alberes calves.

Temperament Evolution of Semi-feral Alberes Calves

A study on the temperament evolution of beef calves coming from extensive management systems was carried out on 84 entire male Alberes calves (Fina *et al.*, 2006). After weaning, male calves from two consecutive years were reared in feedlot barns during the fattening period, weighed and graded for a temperament score once a month (Grandin *et al.*, 1993). Behavioural records were analysed under a repeated measures model, testing the influence of several systematic sources of variation.

Three systematic effects reached statistical significance:

1. weight of the calf at the beginning of the fattening period;
2. initial temperament score, and
3. restraint session within the initial temperament score.

Calves with moderate and high temperament scores at the beginning of the fattening period tended to moderate their temperament, whereas calm calves did not show a significant trend. These results suggest that behavioural agitation decreases over time in excitable calves, reaching an acceptable level of tameness for these animals. The effect of the initial weight could be related to calf age, suggesting that older calves were less adaptable to intensive fattening systems (Fina *et al.*, 2006)

Census

The census was updated every year during the *'esquellada'*. In the year 2007, a total of 425 animals were counted, comprising 273 Freixe animals, 97 *Castanyers* animals and 55 Roig animals. This census includes animals of all ages and types (Black, Fawn and crossbred animals). Given the absence of birth records, the estimation of the age of the animals has been inferred both from the observation of the teeth and the horn rings. Both methods can have limited reliability because the erosion degree used to determine the age can follow a different pattern in other reference populations. In turn, a ring usually appears every year on the horn, but a horn ring can also appear in cases of suboptimal nutrition. Despite these limitations, these procedures allowed us to distribute the animals among the categories presented in table 8.

Table 7. Allele frequencies by coat colour for the MC1R.

	Allele			
Variety	E^D	E^+	E^1	*e*
Black	0.02	0.72	0.12	0.14
Fawn	--	0.55	0.06	0.39

Table 8. Census of the Alberes population registered at the last count (2006). An adult individual is 3 or more years old.

	Males		Females	
	Young	Adults	Young	Adults
Black	15	9	30	106
Fawn	2	0	14	32
Crossbred origin	40	1	57	119
Total	57	10	101	257
Total	67		358	

It is also interesting to report that from the last three restraints, all of the animals older than 6 months were identified with a ruminal transponder according to the methodology of the "Report from the Commission to the Council and the European for Parliament on the possibility of introduction of electronic identification bovine animals", dated 25 January 2005.

Conservation Programme

As stated previously, the last count gave a population size of 425 animals, but only 138 adult females and 9 adult males had the Black or Fawn coat colour and were considered as having the Alberes morphotype. The current population size fits the category of Endangered Breed proposed by the FAO (Scherf, 2000) and the Critically Endangered category (less than 100 breeding cows) according to the EAAP classification (*www.tiho-hannover.de/einricht/zucht/eaap/factors.htm*).

The low effective population size has created a dramatic situation, and starting a conservation programme has become vital. The combination of live and cryoconservation can result in very potent conservation strategies because it can achieve all of the objectives for conservation, can reduce the genetic drift substantially and the population can still evolve and adapt to its environmental circumstances (Meuwissen *et al.*, 1994). The effectiveness of live conservation schemes depends on the effective population size and the management of genetic variance through effective selection and mating of the animals.

For these reasons, a Minimum Kinship Conservation Programme has recently started. To carry out this programme it is necessary to register the individual pedigrees of the potential replacement males and females in order to be able to maintain maximum genetic variability. This effort would be completed by microsatellite analyses to fully assign the parents of the calves. Furthermore, an in vitro conservation programme of semen and embryos representing the genetic variability of this population has recently been started.

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Genetic diversity among four short stature cattle populations of India

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Summary

The genetic diversity, genetic differentiation and relationship between four short stature cattle populations of south India - Punganur, Iduki, Kasargod and Vatakara - was studied, using 24 microsatellite loci. A total of 164 alleles were observed. The mean number of alleles per locus was 6.58 with mean observed and expected heterozygosity values of 0.70 and 0.75 respectively. The relative magnitude of gene differentiation (F_{ST}) was 6% and was significant except between the Iduki and Kasargod populations. The negative F_{IS} values obtained for the majority of loci indicated a lack of population structure in the four populations. Both phylogenetic and correspondence analysis exhibited a closeness between Iduki and Kasargod animals. The results indicated that all four populations were outbred and Kasargod and Iduki animals should be considered as one even though these are reared for different purposes.

Résumé

La diversité génétique, la différence génétique et les relations entre 4 populations bovines de petite taille du Sud des Indes, Punganur, Iduki, Kasargod et Vatakara, ont été étudiés en utilisant 24 loci microsatellites. Un total de 164 allèles ont été observés. Le nombre moyen d'allèles par locus était de 6,58 avec une valeur d'hétérozigosité moyenne observée et espérée de 0,70 et 0,75, respectivement. La grandeur relative du gène de différentiation (FST) était de 6% et était significative sauf entre la population Iduki et la Kasargod. Les valeurs négatives de FIS obtenues pour la majorité des loci indiquent un manque de structure dans les 4 populations. Les analyses de correspondances et phylogénétiques montrent un lien plus étroit entre les animaux Iduki et Kasargod. Les résultats indiquent que les 4 populations étaient hors croisement et les animaux Kasargod et Iduki devraient être considérés comme une seule population, même s'ils sont élevés pour des buts différents.

Resumen

La diversidad genética, la diferencia genética y las relaciones entre 4 poblaciones bovinas de pequeño tamaño des sur de la India, Punganur, Iduki, Kasargod y Vatakara, han sido estudiadas utilizando 24 loci de microsatélites. Un total de 164 alelos han sido observados. El número medio de alelos por locus era de 6,58 con un valor de heterocigosidad media observada y esperada de 0,70 y 0,75, respectivamente. El tamaño relativo del gen de diferenciación (FST) era de 6% y resultaba significativo salvo entre la población Iduki y Kasargod. Los valores negativos de FIS obtenidos para la mayoría de los loci indican una falta de relación estrecha entre los animales Iduki y Kasargod. Los resultados indican que las 4 poblaciones estaban fuera de cruce y que los animales Kasargod y Iduki deberían considerarse como una sola población, a pesar de ser criados con objetivos distintos.

Key words: *Microsatellite genotyping, Statistical analysis, Genetic diversity, Populations, Dendrogram.*

Introduction

India has a large population of humped cattle (*Bos indicus*) estimated to be 186 million (Livestock Census, 2003). Most of the animals are best described as 'local cattle' and are poor yielders of milk. These animals have been mostly kept for draught purposes and have not been subjected to any kind of selection for a specific trait. Of late, cross breeding of indigenous cattle with exotics (*Bos taurus*) has become common especially in the states of India which have natural resources to feed

the cattle. The local cattle of Kerala and Andhra Pradesh have been described as small animals with the height of the animals varying from 90 to 105 cm. There are four populations of these small sized cattle (*Bos indicus*) which inhabit the hilly terrain with an altitude of 1500 meters above mean sea level (Figure 1). These are locally named as Punganur, Iduki, Kasargod and Vatakara. The high range small cattle called Iduki have been reported to number less than 2 000 (AnilKumar and Raghunandanan, 2003). These animals have been bred for meat as sacrificial animals during festival seasons. Kasargod cattle have their utility only as producers of organic manure for areca nut plantations and are very poor yielders of milk. Vatakara and Punganur cattle produce 3-5 kg of milk per day and 500-550 kg per lactation (Rao *et al.*, 2000). All the populations are facing extinction primarily due to economic considerations and are being replaced with crossbreds. The head counts of these cattle have been reduced to a few hundreds (AnilKumar and Raghunandanan, 2003; Rao *et al.*, 2000).

Figure 1. Distribution of four cattle populations.

To date no information is available on the status of these animals at a molecular level. The present study was therefore undertaken to study the genetic diversity, gene flow, genetic structure and relationship among these breeds using 24 microsatellite loci in order to have some genetic basis for conservation or undertaking other management decisions regarding these genetic resources.

Materials and Methods

Microsatellite genotyping

Blood samples were collected from 102 genetically unrelated animals. The DNA was isolated using the standard protocol of Phenol Chloroform extraction (Sambrook *et al*., 1999). Twenty four microsatellite loci were selected for the study, including 13 markers (INRA063, ETH225, ILSTS005, INRA035, ETH152, ETH10, CSSM66, BM1818, ILSTS006, MM12, CSRM60, HAUT24 and HAUT27) that appear in the new FAO MoDAD marker set (Hoffmann *et al*., 2004).

The PCR conditions were standardized for all of the 24 primer pairs selected for the study. The variables, which required standardization, included annealing temperature, $MgCl_2$ concentration, quantity of primers, Taq polymerase and dNTPs. The PCR products were loaded on 6% denatured polyacrylamide gel electrophoresis (PAGE) using urea as denaturing agent. The standard DNA markers were simultaneously run in the gel for sizing of the alleles. The PAGE was run for a sufficiently long period for proper resolution of alleles. The polyacrylamide gel was fixed in acetic acid (10%) and stained with silver nitrate following standard protocol (Bassam *et al.*, 1991). To avoid any mistyping, the various alleles of the different breeds were simultaneously run on the same gel.

Statistical analysis

The deviations from the Hardy-Weinberg Equilibrium (HWE) for all locus-population combinations were determined using GENEPOP ver. 3.3 (Raymond and Rousset, 1995). Hardy-Weinberg proportions were assessed by exact test (Guo and Thompson, 1992), using Markov chain randomization to estimate unbiased p-values for each locus in each population. The allele frequency, mean numbers of alleles per locus,

observed heterozygosity and expected heterozygosity were estimated using POPGENE software (Yeh *et al*., 1999). The PIC value was calculated as per Botstein (1983). The F statistics for each locus (Weir and Cockerham, 1984) between populations (F_{ST}) and the estimate of average inbreeding coefficient (F_{IS}) for each population were calculated and tested using FSTAT version 2.9.3 (Goudet, 2001). The recent bottleneck was inferred for all populations studied using a Wilcoxon signed rank test (Cornuet and Luikart, 1996). The calculations implemented in the program BOTTLENECK version 1.2.02 (Cornuet and Luikart, 1996) were based on 10 000 simulation replicates.

An unweighted pair group method using an arithmetic average (UPGMA) dendrogram was constructed from Nei's standard Genetic Distances (DS, Nei 1972) with DISPAN (Ota, 1993). The robustness of the dendogram topology was evaluated with a bootstrap of 1 000 re-samplings of loci with replacement. The inter-individual distances were estimated using allele sharing distance and neighbor joining algorithms (Saitou and Nei, 1987).

Since the phylogenetic reconstruction may not readily take into account the effects of admixture between the populations, we performed correspondence analysis as an alternative approach to understand the genetic relationship among the populations. The correspondence analysis and number of migrants per generation (Wright, 1969) were calculated using the GENETIX software version 4.05 (Belkhir *et al*., 2004). The analysis of molecular variance (AMOVA) was carried out as implemented in ARLEQUIN Software (Excoffier *et al*., 2005).

Results

Genetic Diversity

A total of 164 microsatellite alleles were amplified in 24 loci and 102 animals belonging to the four breeds . The numbers of alleles observed in the four populations were 113, 131, 134 and 134 in Kasargod, Punganur, Vatakara and Iduki animals, respectively. The number of alleles varied from 4 (ILSTS 97 and ILSTS 101) to 12 (CSSM 66). A total of 21 alleles were found to be private alleles unique to one population (eight in Vatakara, seven in Punganur, five in Iduki and one in Kasargod). The frequencies of 17 private alleles were more than 2.5% in their respective population while four alleles were at low frequency. The maximum frequency of private alleles was 34.21% in Punganur animals (CSSM 66 size 164). The mean numbers of alleles were 4.71±0.32 (Kasargod), 5.58±0.32 (Vatakara), 5.58±0.29 (Iduki) and 5.46±0.34 (Punganur). The mean numbers of alleles were not significantly different among the four cattle populations (Table 1). The effective numbers of alleles were 3.62, 3.53, 2.99 and 3.36 for the four populations respectively as a large proportion of alleles in the populations were at low frequency. The observed heterozygosity ranged from 0.72±0.04 (Kasargod) to 0.78±0.03 (Punganur), while the expected heterozygosity ranged from 0.66±0.02 (Kasargod) to 0.70±0.02 (Iduki). These values were not significantly different among the four cattle populations.

All the loci showed no significant deviation ($P<0.01$) from HWE in the Vatakara, Kasargod, Iduki and Punganur breeds when alternative hypothesis H_1 was heterozygosity deficiency except locus ILSTS 006 in the Iduki and locus MM I2 in the Punganur. When the alternative hypothesis H_1 was heterozygotic excess five loci in Vatakara, three in Iduki and seven in Punganur deviated from HWE. The only locus that was common in the three populations for deviation from HWE was ETH 10. The results of Weir and Cockerham's F-Statistics for each locus across all the populations are given in table 2. The F_{IS} values for most of the loci are negative which shows no inbreeding, rather it indicates the mating of individuals which are less related than the average relationship of the population (outbreeding). The mean F_{IS} value was found to be -0.14 which is significantly different from zero. The relative magnitude of the gene differentiation (F_{ST} estimator) was 6%. The highest numbers of migrants (Nm) were estimated between the Kasargod and Iduki and least between Punganur and Kasargod cattle.

Genetic differentiation among populations

Significant ($P<0.001$) genetic differentiation was detected among all the populations although the differentiation values ranged from 0.032 between the Kasargod and Iduki to 0.70 between the Kasargod and Punganur (Table 3). The genetic relationship between the four populations was determined using Nei's standard genetic distance (D_S). The largest genetic distance was estimated between Punganur and Kasargod cattle, 0.21, while the least distance was between Iduki and Kasargod cattle. The un-rooted UPGMA

Table 1. Number of alleles Observed (No) and Effective (Ne) and Heterozygosities Observed (Ho) and Expected (He).

	Vatakara				Iduki				Kasargod				Punganur			
Locus	No	Ne	Ho	He	No	Ne	Ho	He	No	Ne	Ho	He	No	Ne	Ho	He
ILSTS11	6	3.29	0.89	0.71	4	2.20	0.59	0.56	4	1.96	0.67	0.51	3	2.05	0.85	0.52
ILSTS97	3	2.71	0.59	0.64	4	3.02	0.74	0.68	2	1.86	0.55	0.48	3	2.86	0.92	0.66
HAUT27	7	3.49	0.86	0.73	6	4.52	0.96	0.80	5	3.13	0.80	0.72	3	2.10	0.97	0.53
ILSTS6	3	2.62	0.62	0.63	4	2.22	0.26	0.56	4	3.14	0.36	0.71	5	3.82	0.88	0.75
ILSTS5	5	4.28	0.68	0.78	5	4.19	0.86	0.78	4	3.03	0.83	0.70	5	3.01	0.97	0.68
ILSTS30	5	3.04	0.93	0.68	5	3.05	0.83	0.69	3	2.07	0.83	0.54	4	1.96	0.47	0.50
ILSTS31	3	1.76	0.55	0.44	5	2.65	0.83	0.64	5	2.72	0.83	0.66	4	1.97	0.65	0.50
ILSTS95	6	5.74	0.96	0.84	7	5.90	0.95	0.85	6	4.17	0.80	0.80	7	4.38	0.84	0.78
CSSM66	7	4.23	0.93	0.78	5	3.32	0.74	0.71	6	3.16	0.58	0.71	7	4.11	0.82	0.77
ILSTS26	4	2.00	0.52	0.51	5	2.63	0.73	0.63	3	2.18	0.64	0.57	4	2.15	0.61	0.54
ILSTS101	4	1.52	0.32	0.35	4	2.39	0.78	0.60	4	1.87	0.58	0.49	4	2.58	0.77	0.62
ILSTS92	6	4.50	1.00	0.79	6	3.96	0.83	0.76	4	3.79	1.00	0.77	6	4.63	0.78	0.80
ILSTS36	4	2.98	0.83	0.68	4	3.13	0.62	0.70	5	3.27	0.58	0.72	5	3.25	0.79	0.70
CSRM60	8	6.16	0.97	0.85	9	6.87	0.91	0.87	10	5.88	1.00	0.87	9	5.97	0.97	0.84
ETH225	7	3.40	0.71	0.72	7	3.46	0.78	0.73	3	1.88	0.58	0.49	6	2.76	0.75	0.65
ETH10	7	5.26	1.00	0.82	7	4.34	1.00	0.79	6	3.97	0.91	0.78	5	3.32	0.97	0.71
ILSTS89	6	4.79	0.97	0.81	7	4.18	1.00	0.78	7	4.30	1.00	0.80	8	5.60	0.95	0.83
BM1818	8	4.15	0.72	0.77	7	4.88	0.83	0.81	5	3.32	0.73	0.73	7	4.42	0.87	0.78
ILSTS33	8	3.21	0.86	0.70	7	3.42	0.95	0.72	4	2.59	0.83	0.64	7	2.43	0.61	0.60
HAUT24	6	3.55	0.90	0.73	5	3.69	0.86	0.75	4	2.51	0.43	0.65	4	2.26	0.80	0.57
INRA35	6	4.92	0.72	0.81	7	4.12	0.65	0.77	5	3.10	0.58	0.71	5	2.66	0.63	0.63
INRA63	5	3.96	0.79	0.76	4	1.84	0.35	0.47	4	2.36	0.67	0.60	7	6.13	0.87	0.85
ETH152	4	1.50	0.35	0.34	4	1.78	0.50	0.45	5	2.07	0.58	0.54	6	2.01	0.53	0.51
MM12	6	4.06	0.79	0.77	6	3.08	0.57	0.69	5	3.60	0.92	0.75	7	4.33	0.53	0.78
Mean	5.58	3.63	0.77	0.69	5.58	3.53	0.75	0.70	4.71	3.00	0.72	0.66	5.46	3.36	0.78	0.67
	±0.32	±0.16	±0.03	±0.02	±0.29	±0.18	±0.03	±0.02	±0.32	±0.19	±0.04	±0.02	±0.34	±0.15	±0.03	±0.02

dendrogram reveals that the populations of Kasargod and Iduki are closely related and join first followed by the Vatakara and then the Punganur. The bootstrap values were 61% based on 1 000 replications (Figure 2). The Punganur individuals cluster together (Figure 3) while the rest were admixed in the tree. Figure 4 represents the first three axes which explain 48.67, 34.19 and 17.14% of the total variation respectively. The plot reveals a similar pattern as genetic relationship from phylogenetic analysis. The two populations of Iduki and Kasargod are very similar and form a single cluster and the Punganur formed a distinct cluster. The self assignment gave an accuracy of 95% in the four populations. All the individuals in the Vatakara and Punganur groups were correctly assigned to their respective populations while three individuals of the Iduki and two individuals of the Kasargod were miss-assigned among the two populations owing to low genetic differentiation between the two populations. The Wilcoxon test revealed no evidence for recent genetic bottleneck in any of the four populations. The analysis of Molecular variance revealed significant differentiation among the populations. 12% of the total variation was among populations while 88% variation was among individuals.

Discussion

In this study we investigated the genetic diversity in four south Indian breeds of cattle which are of short stature measuring around one meter in height which have not undergone any selection for milk or draft purposes (AnilKumar and Raghunandanan, 2003). The mean numbers of alleles were not significantly different in the four populations. The results were similar to other *Bos indicus* reports of 5.86 and 5.82 in Red Kandhari and Deoni cattle, respectively (Sodhi *et al.*, 2005). The heterozygosity values are higher than reported in African cattle including *Bos taurus* and *Bos indicus* breeds of cattle, ranging from 0.432 to 0.658 (MacHugh *et al.*, 1997)

Table 2. F statistics and number of migrants (Nm).

Locus	F_{IS}	F_{IT}	F_{ST}	Nm
ILSTS11	-0.34	-0.23	0.08	2.94
ILSTS97	-0.16	-0.07	0.08	2.94
HAUT27	-0.33	-0.23	0.07	3.09
ILSTS6	0.18	0.23	0.07	3.50
ILSTS5	-0.17	-0.13	0.04	6.55
ILSTS30	-0.30	-0.25	0.04	5.46
ILSTS31	-0.31	-0.23	0.06	3.74
ILSTS95	-0.12	-0.06	0.05	5.12
CSSM66	-0.06	0.10	0.15	1.44
ILSTS26	-0.13	-0.07	0.05	4.36
ILSTS101	-0.23	-0.18	0.04	6.40
ILSTS92	-0.18	-0.14	0.03	7.33
ILSTS36	-0.03	-0.01	0.03	9.38
CSRM60	-0.15	-0.12	0.02	9.77
ETH225	-0.12	-0.06	0.05	4.71
ETH10	-0.28	-0.24	0.03	7.33
ILSTS89	-0.25	-0.20	0.04	6.57
BM1818	-0.04	-0.01	0.03	8.98
ILSTS33	-0.25	-0.20	0.04	5.78
HAUT24	-0.15	-0.03	0.10	2.31
INRA35	0.09	0.15	0.06	3.74
INRA63	-0.02	0.10	0.12	1.92
ETH152	-0.09	-0.05	0.04	6.34
MM12	0.04	0.09	0.06	4.24
Mean	-0.14	-0.07	0.06	4.08

Table 3. Between population F_{ST} (Upper triangle) and Nei's standard genetic distance (Lower triangle).

Populations	Vatakara	Iduki	Kasargod	Punganur
Vatakara	-	0.045	0.050	0.066
Iduki	0.151	-	0.032	0.066
Kasargod	0.171	0.134	-	0.070
Punganur	0.188	0.194	0.206	-

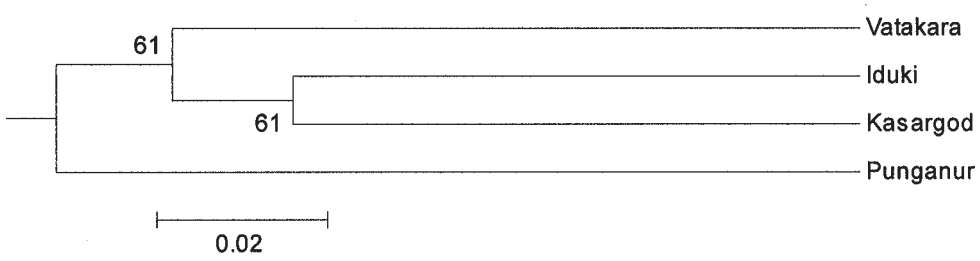

Figure 2. Dendrogram of four cattle populations with bootstrap values.

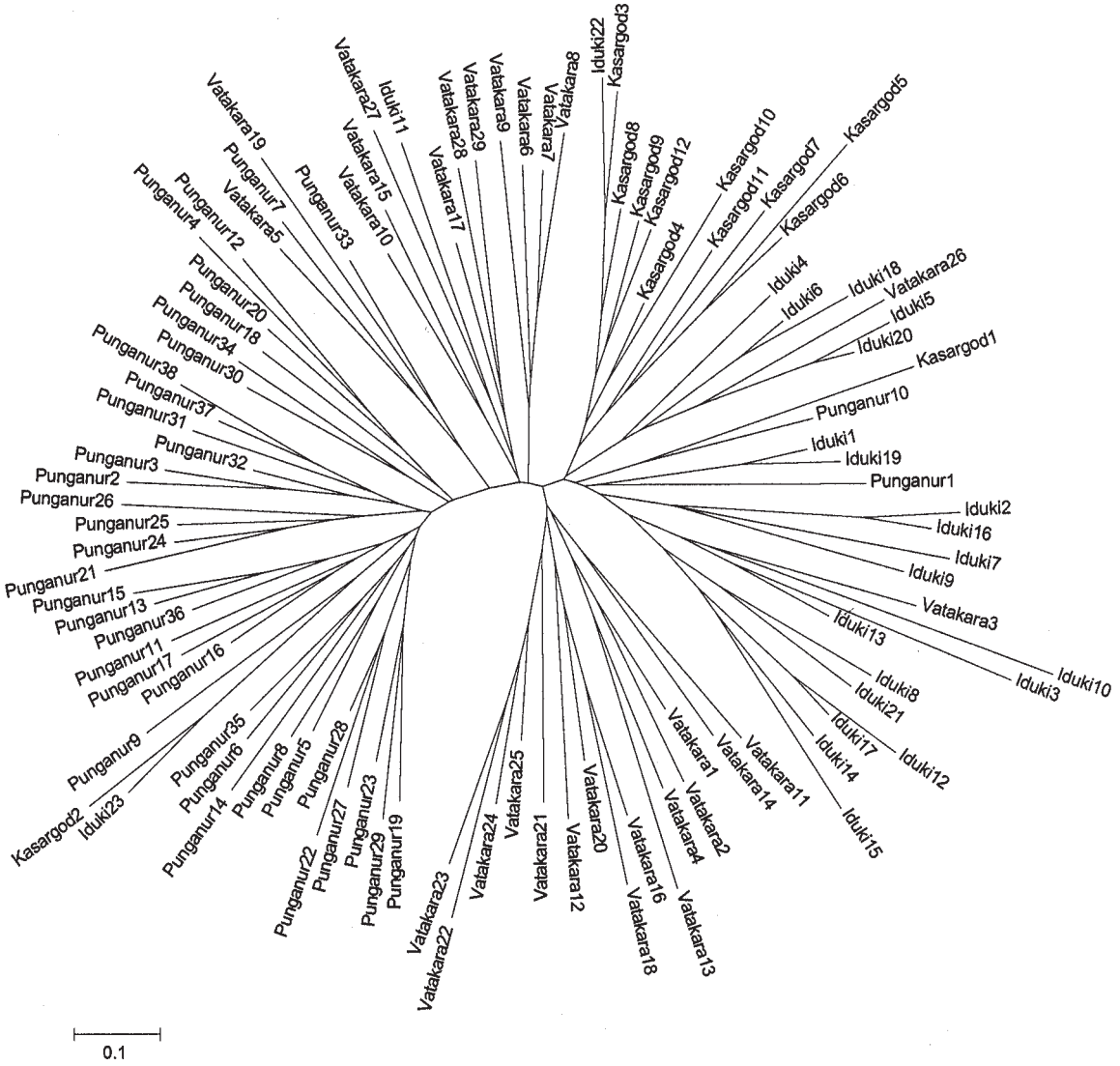

Figure 3. Radiation tree using NJ algorithm and genetic distance by allele sharing.

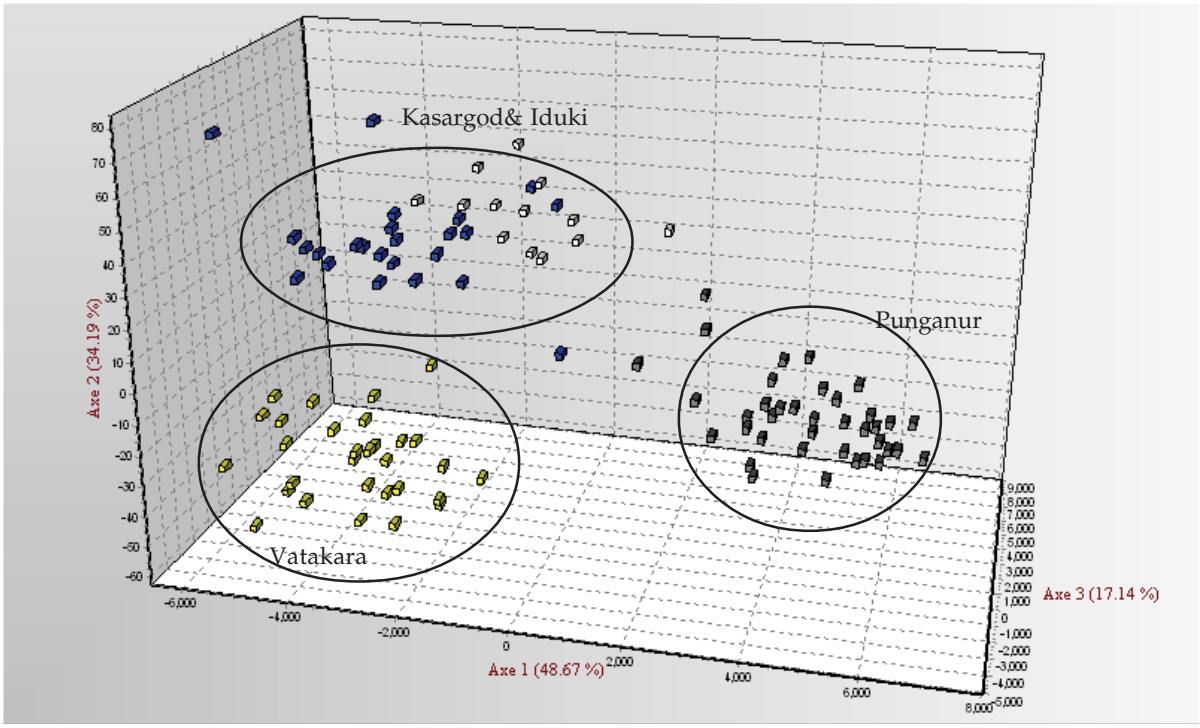

Figure 4. Correspondence analysis of four cattle populations.

or than the one obtained in north European cattle, ranging from 0.45 to 0.67 (Kantanen *et al.*, 2000). This indicates lack of population structure.

The mean F_{IS} values across all the populations was -0.137 which was significantly different from zero and may be due to outbreeding taking place for increase in milk yield. The history reveals large breeds like the Sahiwal and Gir (*Bos indicus*) cattle of India having been used for improving the milk yield of these cattle in the pre-independence era before the introduction of crossbreeding with exotics (*Bos taurus)*. The F_{ST} estimates were significantly different from zero for all the loci with a mean value of 0.058 indicating that the populations are moderately differentiated. The differentiation among the population is low (10.7 - 19.35%) compared to other breeds of cattle (MacHugh *et al.*, 1997; Kantanen *et al.*, 2000) and 11% in *Bos indicus* cattle breeds (Sodhi *et al.*, 2005). This low differentiation may be due to the result of out crossing with other milk breeds for improvement in milk yield. This seems especially the case in Punganur and Vatakara cattle where the size of animals is comparatively larger (more than one meter) and milk yield was also higher. Similarly the genetic distance (0.134) was least between Iduki and Kasargod animals and highest between the Punganur and Kasargod (0.206). The bootstrap values were 61%. The Nm values present an indirect measure of the gene flow and gave values of 7.47 migrants between Kasargod and Iduki animals and least values of 3.31 between Kasargod and Punganur cattle. This represents the effective number of migrants among the populations.

Little or no differentiation between Kasargod and Iduki breeds of cattle is supported by the assignment test. The self assignment gave an accuracy of 95% in the four populations. Similar results of 80-100% correct assignment amongst different breeds have been reported by several authors (MacHugh *et al.*, 1998; Bjørustad and Røed, 2001; Moudet *et al.*, 2002; Achmann *et al.*, 2004). The two populations of Iduki and Kasargod are very similar and have a high gene flow between them and form a single genetic cluster and thus can be considered as one. The stepwise mutation model (SMM) being most conservative did not reveal any evidence for recent genetic bottleneck in any of the four populations. The status report on Punganur cattle (Country Report, 2004) described it as threatened on the basis of phenotypic characteristics and count of heads but that it has been found to be an out-bred population.

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Indigenous sheep resources of Ethiopia: types, production systems and farmers preferences

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Summary

Ethiopia has a diverse sheep population, numbering 23.6 million, in parallel with its diverse ecology, production systems and communities. A comprehensive phenotypic and genetic characterization of Ethiopian sheep populations was initiated in 2005 to provide a nationwide framework for the management of sheep genetic resources. In this paper, we describe the indigenous sheep types in terms of physical characteristics, eco-regional distribution and community affinity. We also present relationships of sheep types with agricultural production systems, and farmers'/pastoralists' assessment of their sheep types. Fourteen traditionally recognized sheep types were identified and physically described.

The sheep types could be categorized into four groups (sub-alpine short-fat-tailed, highland long-fat-tailed, lowland fat-rumped and lowland thin-tailed) based on their ecological distribution, tail types (fat-tail versus thin-tail), tail form/shape, and fiber type. There is high morphological and ecological diversity among the major sheep groups as well as among the sheep types. There is also a strong relationship between sheep types, ethnic groups and production systems. Assessment of the genetic distinctiveness of the traditional sheep types is important for developing rational conservation-based improvement programs. Molecular genetic assessment of the population structure is a follow up activity.

Résumé

L'Ethiopie possède différentes populations ovines, 23,6 millions, selon les différentes écologies, systèmes de production et communautés. En 2005 a été mis en place un programme de caractérisation phénotipique et génétique des populations ovines en Ethiopie dans le but de créer un cadre national pour la gestion des ressources génétiques ovines. Dans cet article nous décrivons les types d'ovins indigènes du point de vue des caractéristiques physiques, de distribution eco-régionale, et affinités entre communautés. Nous présentons également les relations des types d'ovins avec les systèmes de production agricole et une enquête menée parmi les éleveurs/pastoralistes. Nous avons identifié 14 types traditionnels d'ovins qui sont décrits du point de vue physique.

Les différents types se divisent en 4 groupes: sous-alpine à queue grasse courte; haute montagne à longue queue grasse; plaine gras postérieur; et plaine queue fine, et selon leur distribution écologique, types de queues (queue grasse versus queue fine), forme de la queue, et type de fibre. Il existe une grande diversité morphologique et écologique entre la plupart des groupes principaux ovins ainsi qu'entre les types d'ovins même. Il existe aussi une forte relation entre les types d'ovins, les groupes ethniques et les systèmes de production. L'évaluation des différences génétiques des types d'ovins traditionnels est importante pour le développement des programmes de conservation basés sur l'amélioration. L'évaluation génétique moléculaire de la structure de la population sera l'activité de suivi.

Resumen

Etiopía posee diversas poblaciones de ovinos, 23,6 millones, que varían según la ecología, los sistemas de producción y las comunidades. En el 2005 se inició un programa de caracterización fenotípica y genética des las poblaciones ovinas en Etiopía con el fin de crear un marco nacional para

la gestión de los recursos genéticos ovinos. En este artículo se describen los tipo de razas indígenas desde el punto de vista de las características físicas, de la distribución eco-regional, y de las afinidades entre comunidades. Presentamos también las relaciones de los tipos de ovinos con los sistemas de producción agrícola y una encuesta realizada entre los ganaderos y pastores.

Se han identificado 14 tipos tradicionales de ovinos que se describen desde el punto de vista físico. Los diferentes tipos se dividen en 4 grupos: sub-alpinos con cola gorda corta; alta montaña con cola gorda larga; llanura con cuarto posterior graso; y llanura con cola delgada, y según su distribución ecológica, tipos de cola (cola grasa versus cola delgada), forma de la cola y tipos de fibra. Existe una gran diversidad morfológica y ecológica entre la mayor parte de los grupos principales de ovinos así como entre los tipos de ovinos mismos. También hay une relación importante entre los tipos de ovinos, los grupos étnicos y los sistemas de producción. La evaluación de las diferencias genéticas de los tipos de ovinos tradicionales es importante para el desarrollo de los programas de conservación basados en la mejora. La evaluación genética molecular de la estructura de la población será una de las actividades de seguimiento..

Key words: *Ethiopia, Sheep resources, Characterization, Physical characteristics.*

Introduction

Ethiopia has a diverse indigenous sheep population, numbering 23.6 million head (CSA, 2006), in parallel with its diverse ecology, production systems and ethnic communities. At the national level, sheep and goats account for about 90% of live animals/meat (FAO, 2004) and 92% of skin and hide (FAO, 1994) export trade value. At the farm level, sheep contribute as much as 22-63% to the net cash income derived from livestock production in the crop-livestock production system (Gryseels, 1988; Zelalem and Fletcher, 1993). In the lowlands sheep, with other livestock, are a mainstay of pastoral livelihoods.

Characterization of sheep resources is a prerequisite for their rational utilization. In developing regions, there exist types of farm animal species which owe their distinct identity to a combination of traditional 'breeding objectives' and geographical and/or cultural separation by communities which own them (Rege 2002). African (Epstein, 1971) and Ethiopian sheep (MOA, 1975) have been traditionally classified based on tail type and fiber type because of the evolutionary significance of these characters. Galal (1983) and Sisay (2002) described the physical characteristics and eco-regional distribution of some of the sheep types in Ethiopia. However, earlier classifications and descriptions were incomplete at a national level. A comprehensive nationwide phenotypic and genetic characterization of Ethiopian sheep was therefore initiated in 2005. In this paper, we describe and synthesize the indigenous sheep types in terms of physical characteristics, eco-regional distribution and ethnic affinity. We also present relationships of sheep types with agricultural production systems, and farmers'/pastoralists' assessment of their sheep types.

Materials and Methods

An Ethiopian sheep breed survey was conducted in 2005. Fourteen traditionally recognized, phenotypically distinct, and/or geographically/ecologically isolated populations were surveyed. Depending on the trait, 18 to 40 full-mouth adult ewes from each population were sampled. The FAO (1986) qualitative and quantitative sheep breed descriptor list was used to characterize the populations phenotypically. Qualitative variables observed included coat color, fiber type, face profile, ear form, presence of horn, tail type and tail shape. Quantitative characters measured were body weight, withers height, body length, heart girth, substernal height, ear length, tail length, tail width and hair length. Information regarding flock size and composition was collected through a questionnaire. Data on ewe litter size was collected using farmer recall method. Farmers were asked to recall the reproductive history of each full-mouth breeding female. Using the Rapid Rural Appraisal technique, informal group and key informant discussions with farmers and livestock experts were conducted to gather information on breed distribution, farmers' assessments of their sheep types and farming practices. In addition, we made extensive field observations, reviews of grey and published literature and personal communications. Population estimates of sheep types were extracted, based on their geographic distribution, from regional and zonal sheep population estimates (CSA, 2005).

Results and Discussion

Sheep types

The fourteen sheep types were categorized into four groups (sub-alpine short-fat-tailed, highland long-fat-tailed, lowland fat-rumped, lowland thin-tailed) based on their ecological distribution, geographic proximity, tail types and tail form/shape (short vs long). Earlier studies used tail type (MOA, 1975) and eco-regional distribution (Sisay, 2002) to describe some of the sheep types. Inclusion of tail form/shape in the current study enabled identification of two groups of fat-tailed sheep which differ in other important characteristics.

Sub-alpine short-fat-tailed

Sub-alpine short-fat-tailed sheep inhabit a contiguous central-northern highland area (2 000 - 3 600 m) between 9.11 and 14.59° N and 36.31 and 39.81° E (Figure 1). The group includes seven sheep types (Figures 4 and 5) which are characterized by their short fat tail well above the hocks (Table 1). They are also characterized by small size (Table 2), coarse wool and low ewe reproduction. Litter size ranges from 1.0±0.01 in Menz (Figure 4) to 1.09±0.05 in Farta. The short-fat-tailed Washera sheep are an exception. It is short-haired, large-sized and prolific (litter size = 1.8). Hair coat is found in several East African fat-tailed sheep that have interbred with hairy thin-tailed sheep (Epstein, 1971).

Highland long-fat-tailed

The group is distributed over the southern and south-western mid-highlands (1 500 to 2 500 m) between 10.40 – 5.85° N and 34.50 – 40.29° E (Figure 1). The tail is fat and long reaching the hocks, broad at the base and upper third with a

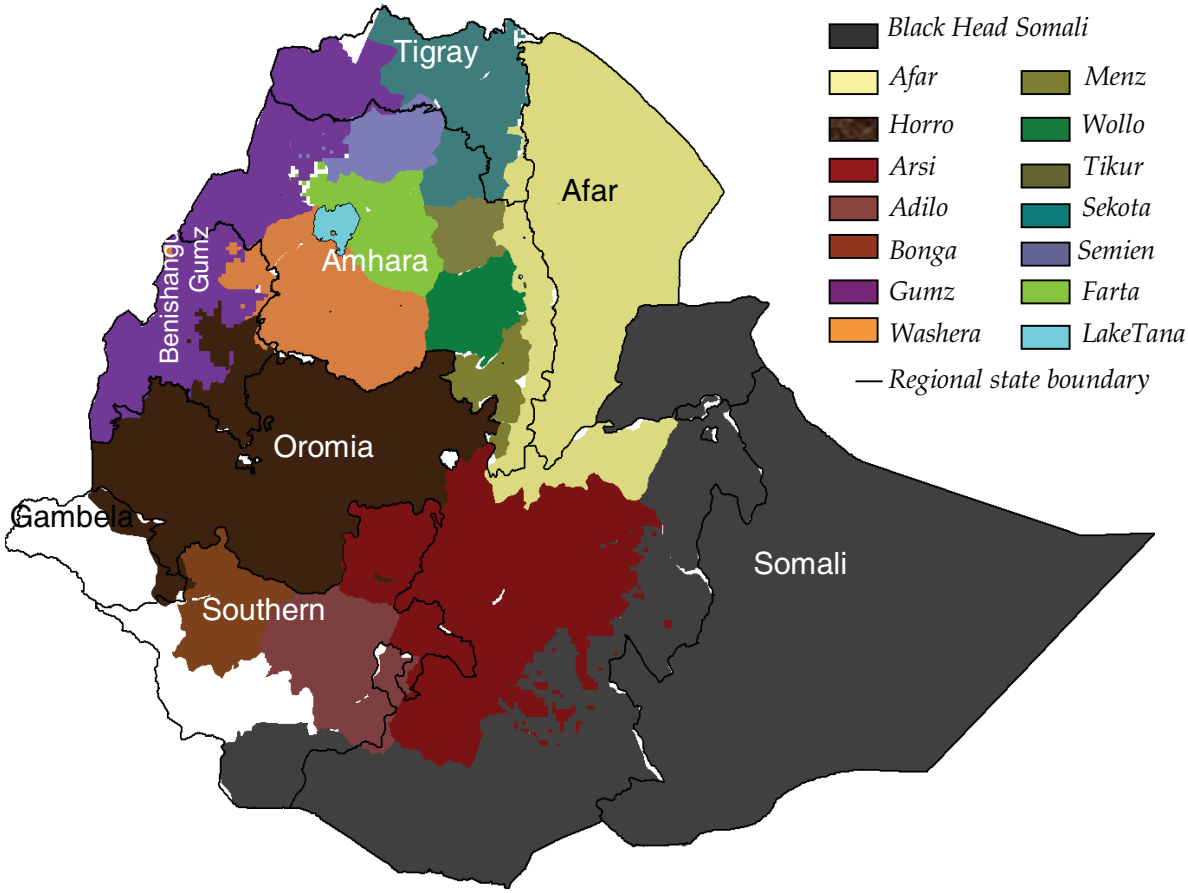

Figure 1. Geographic distribution of sheep types

Table 1. Sheep types and their ecology, geographic distribution, distinguishing physical features and population sizes.

Sheep types	Other names	Ecology	Geographic distribution	Important physical features[1]	Population (000)
Sub-alpine short-fat-tailed group					
Menz	Legegora, Shoa, Abyssinian, Ethiopian highland sheep	Sub-moist/dry, sub-alpine highlands (2 500 and 3 200 m);	North Shoa zone of Amhara State	Short fat tail turned-up at end; small body size; short-legged; long fleece with coarse wool; commonly black with white patches, white, brown, white with brown patches; straight-faced; horned males; short semi-pendulous ears with 12% rudimentary ears in the population. Kept by Amhara community	971.4
Sekota	Tigray highland, Abergelle	Cool, dry/sub-moist highlands (2 000 m); semi-arid river valley	Wag Himra zone of Amhara State and Tigray State	Short fat tail turned-up at end and fused with main part; medium-sized; Predominantly brown or white coat, few blacks with brown belly; white animals have finer hair or wooly udder-coat; semi-pendulous or rudimentary ears in Wag Himra and Tigray, predominantly rudimentary in Tekeze valley. Reared by Agew, Tigray and Amhara communities	732.3
Semien		Alpine mountains (3 000-4 000 m) including Semien Wildlife park;	North Gondar zone of Amhara State (Debark, Dabat, Janamora, Wegera)	Short fat tail; well developed wooly undercoat; plain brown, plain white, brown/white with white/brown patches, plain black and black with brown belly; unique long laterally spiral horn in males and short horns in most females; largest of the highland wooled sheep. Reared by Amhara community	347.6
Tikur		Sub-alpine highlands (3 000 m)	North Wollo zone of Amhara State	Short fat tail; wooly undercoat; Predominantly black (60%) coat; small body size; majority short semipendulous ears, 24% rudimentary ears. Reared by Amhara communities	525.3
Wollo		Cood highland (2 000-3 200 m)	South Wollo zone of Amhara State	Short-fat-tail with short twisted/coiled end, occasionally turned up at end; Small size; well developed wooly undercoat; Predominantly black, white or brown, either plain or with patches of white, black or brown; long hair with wooly undercoat; horned males. Reared by Amhara communities	1 395.9
Farta		Sub-moist highland (2 000-2 500 m)	South Gondar zone; Gondar zuria, Belesa, Dembia districts	Short fat tail; medium size; wooly under coat; Commonly white (37.5%), brown (27.5%) and black with brown belly (15%), white/brown with brown/white patches; males are horned. Reared by Amhara communities	555.6
Washera	Agew, dangilla	Wet, warmer mid-highlands (1 600-2000 m)	West and East Gojam and Agew Awi zones of Amhara state; Dangur, Madura and Alefa Takusa districts	Short fat tail; large body size; short-haired; predominantly brown; both males and females are polled; reared by Amhara and Agew communities	1 227.7

[1]*Coat colors are in order of frequency in the population.*

(... continued)

Sheep types	Other names	Ecology	Geographic distribution	Important physical features[1]	Population (000)
Highland long-fat-tailed group					
Adilo		Wet, warmer mid-highland (1 800-2 000 m)	North Omo, Derashie, Gedio and Amaro zones of Southern state; some northern Borena districts (1 300 – 2 400 m)	Long fat tail; Large size; short-haired; males are short-horned and 18.4% of ewes are horned; predominantly brown (943%), brown with white patches (32%), black (16%), black (19%) and black with brown patch (9%). Reared by southern nationalities	407.7
Arsi-Bale		Mainly wet, cool and warmer highlands (2 000-3 300); sub-moist lowlands	Arsi, Bale, E. Shoa, W. Harerghie zones, some districts in Borena zones of Oromia; Hadya, Gurage, Kembata & Sidama zones	Long fat tail with twisted end in some animals; medium size; hairy fiber, especially in adult ewes, males have minor wool growth in some parts of body; Males and most females (52%) are horned; Large size; coat colors are brown (35.1%), brown with white patches (24.3%), black, white, and combinations of above colors. Reared by Oromo communities	6345.1
Horro		Cool, wet highlands (2 991 m) to humid mid-highlands (1 600 m).	East Welega, West Welega, Illubabor, Jimma and West Shoa zones of Oromia, and some bordering Gambella and Benishangul districts	Long fat tail extending below hock, either straight (51.4%) or coiled/twisted (48.6%) at the tapering end; prominent fat tail in males; Large, leggy and prolific; dominant colors are brown and fawn, belly is lighter especially in adult ewes, less frequent are black, white, brown with white patches; both sexes are polled. Reared by Oromo, Benishangul and Gambella communities	3409.3
Bonga	Gesha, Menit	Humid mid-highland zone (1 200 – 2 500)	Keffa, Sheka and Bench zones of Southern State	Long fat tail with straight tapering end (98.4%); hair sheep; Large size; predominantly plain brown (57.9%) or with black (.9%) or white (5.3%) shade, plain white (10.5%) or with brown patches (10.5%), and black (2.6%); both sexes are polled. Reared by Keffa, Sheka and Bench communities	517.5

[1]*Coat colors are in order of frequency in the population.*

(... continued)

Sheep types	Other names	Ecology	Geographic distribution	Important physical features[1]	Population (000)
Lowland fat-rumped group					
Afar	Adal, Danakil	Mainly arid lowland(<1 000 m); mid-highland (1 200–1 900 m)	Afar state; boardering Tigray, Amhara; E. & W. Harerghe and E. Shoa of Oromia	Wide fat tail, in some large fat tail reaching below the hock; hair fiber; medium size; characteristically uniform creamy white/ beige coat; rudimentary ear; polled; dewlap. Reared by Afar, Amhara, tigray communities	681.9
BHS	Wanke, Ogaden, Berbera black head	Mainly arid lowlands (215-900 m); highlands (up to 2 000 m)	Somali state; lowlands of Bale, Borena and south Omo zones; part of east Harerghe	Short fat rump with a stumpy appendage; uniform white body and black head and neck; polled; convex face, especially in males; short, outward forward drooping ear; well developed dewlap. Reared by Somal, Oromo, Konso and South Omo communities	906.2
Lowland thin-tailed group					
Gumz		Moist lowlands (< 1 000 m)	Benishangul-Gumz state; lowlands of North Gondar	Long thin tail; some what dwarf; convex face profile; long pendulous ear; commonly plain brown or with patch (39.4%), white with brown or black patch (21%), black (15.8%), white, black with white patch, brown with black patch; polled. Reared by Gumz and Amhara communities	50.9

[1]*Coat colors are in order of frequency in the population.*

Table 2. Body weight (kg) and linear body measurements (cm) of full-mouth adult ewes (± Standard Deviation).

Sheep type	No.	Body weight	Withers height	Body length	Heart girth	Substernal height	Ear length	Tail length	Tail width	Hair length
Adilo	36	28.1±.5	65.5±.4	62.1±.5	71.8±6	35.8±.5	11.7±.5	28.1±1	6.7±.3	4.4±.2
ArsiBale	34	28.6±.6	64.1±.6	62.3±.8	73.3±.6	35.3±.4	11.0±.1	28.4±.6	6.2±.3	4.2±.1
Bonga	38	34.2±.8	66.7±.6	69.4±.5	73.5±.7	36.4±.4	9.8±.2	25.9±.9	8.1±.3	2.9±.1
Farta	39	28.3±.7	67.9±.5	65.7±.7	72.0±.7	37.3±.4	9.9±.3	22.9±.8	9.6±.2	7.5±.3
Gumz	38	31.0±.8	62.9±.7	65.8±.7	72.1±.7	32.9±.5	11.2±.2	31.6±.5	7.2±.2	3.6±.3
Horro	37	35.4±.8	70.0±.6	71.6±.6	76.9±.8	38.1±.4	10.8±.2	35.6±.6	9.9±.3	2.6±.1
Menz	40	20.1±.3	57.5±.5	58.5±.4	65.7±.4	30.9±.3	6.8±.4	17.0±.6	7.9±.2	7.9±.3
Sekota	40	26.6±.7	62.3±.6	62.2±.6	69.9±.5	33.5±.4	4.4±.5	19.9±.8	9.5.3	6.5±.5
Semien	33	26.9±.4	66.6±.6	64.7±.6	73.2±.6	35.9±.5	8.3±.5	12.8±.6	9.6±.2	8.2±.3
Afar	18	31.0±1	63.6±.8	58.3±.8	70.6±.6	35.6±.6	3.8±.4	19.1±.7	16±.9	3.2±.3
Tikur	34	25.4±.6	64.1±.6	63.6±.6	69.7±.6	35.9±.5	6.8±.5	17.3±.6	8.9±.3	7.4±.3
Washera	44	32.8±.9	69.4±.3	66.7±.5	74.1±.6	38.6±.3	10.6±.1	n.a	n.a	6.3±.3
BHS	22	27.9±.8	63.3±.6	59.9±.9	71.5±.6	35.1±.6	9.6±.4	14.7±.6	14±.9	4.0±.3
Wollo	37	21.7±.5	62.7±.6	61.2±.5	67.6±.5	34.3±.4	8.7±.3	20.4±.6	7.2±.2	7.9±.4

n.a.: data not available.

Figure 2. Highland long-fat-tailed ewe (e.g. here is Horro sheep).

Figure 3. Highland long-fat-tailed rams (e.g. here is Horro sheep).

Figure 4. Sub-alpine short-fat-tailed ewe (e.g. here is Menz sheep).

Figure 5. Sub-alpine short-fat-tailed ram (e.g. here is Simien sheep).

Figure 6. Lowland thin-tailed ewes (e.g. here is Gumz sheep).

Figure 7. Lowland thin-tailed ram (e.g. here is Gumz sheep).

Figure 8. Lowland fat-rumped ewe (e.g. here is BHS sheep).

long tapering end. The group is large-sized (Table 2), short-haired, predominantly brown and prolific (litter size = 1.29±0.06 - 1.55±0.12).

The group includes Horro (Figure 2 and 3), Arsi-Bale, Bonga and Adilo. An earlier study (MOA, 1975) described Horro as thin-tailed and Arsi-Bala as fat-tailed, while Galal (1983) and Epstein (1971) described Horro and Arsi-Bale as fat-tailed. Such inconsistencies could be due to the unique tail shape in this group which could be the result of influence from a thin-tailed ancestor.

Lowland fat-rumped

Afar and Black-Head-Somali (BHS) sheep constitute the lowland fat-rumped group (Figures 8 and 9). BHS has been classed with the fat-tailed (Hilzheimer cited by Epstein, 1971) and fat-rumped group (Epstein, 1971), while Galal (1983) described the tail as short and fat, with the rump being also fatty. Adal (Adal and Afar are synonymous) sheep are also traditionally described as fat-tailed, but categorized as fat-rumped (Epstein 1971). Our observation is that BHS be classified as fat-rumped and Afar as fat-tailed sheep. Here, BHS and Afar are classified under the same group as, from a systematic point of view, fat-rumped and fat-tailed sheep are more closely related than other sheep types (Epstein, 1971). Physical characteristics and distribution are given in table 1.

Lowland thin-tailed

This group is represented by a single population (Table 1) and is found adjacent to the thin-tailed sheep region of the Sudanese desert (Figures 6 and 7). They are moderately prolific (litter size = 1.28±0.06).

Sheep types and production systems

For this study, the classification of livestock production systems by Alemayehu (*www.fao.org*) was adapted. There appears to be a strong relationship between the sheep types and production systems (Table 3). Breeds with high growth rate and prolificacy, like Adilo and Bonga sheep, are associated with tethering systems where few breeding ewes and/or fattening males are kept. Good milking and long-legged Black Head Somali sheep are suited to the nutrition and nomadic habit of the pastoral community. Flock size and composition by sheep types and production system is presented in table 4.

Table 3. Sheep types and major sheep production systems in Ethiopia.

	Characteristic features of production systems			
Production systems	Environment	Main products	Scale of production and management	Sheep breeds
Sub-alpine sheep-barley system	Sub-alpine (> 3000 m)	Meat, fiber, manure, skin; unreliable, long-season barley	Medium scale sheep production; Semi-intensive, low-input[1]	Simien[2], Tikur[2], Menz[2], Wollo[2], Farta[3], Arsi-Bale[4], Horro[4]
Highland cereal-livestock system	Highlands (1 500-3 000 m)	Mainly cereal cropping; meat, manure, skin	Small scale sheep production; semi-intensive, low-input	Washera[2], Sekota[2], Horro[3], Arsi-Bale[3], Wollo[4], Farta[2], BHS[4]
Highland perennial crop system	Highlands (1 500-2 000 m)	Mainly perennial cash crops (coffee, inset, khat); meat, skin	Minor sheep production; semi-intensive, low-input; some practice tethering	Bonga[2], Adilo[2], Horro[3], Arsi-Bale[3]
Lowland crop-livestock system	Wet lowland (Up to 1 000 m)	Cereals, sesame, cotton; meat, skin	High level of livestock keeping; semi-intensive, low-input	Gumz[2], Afar[4], Arsi-Bale[4], BHS[4]
Pastoral/agro-pastoral system	Semi-arid/arid (up to 1 000 m)	Meat, milk, skin; minimal or no cropping	Rangeland-based large-scale sheep production; extensive, low-input	Afar[2], BHS[2]

[1]Based on feeding, veterinary care, housing.
[2]Major portion of or the whole sheep population is managed under the system.
[3]Significant portion of the sheep population is managed under the system.
[4]Minor portion of the sheep population is managed under the system.
Source: based on Alemayehu (*www.fao.org*).

Farmers' assessment of sheep types

The farmers'/pastoralists' assessment of their sheep is presented in table 5. Farmers owning large-sized sheep with uniform coat color, particularly brown, valued their breed as good or excellent. There is a tendency to select against black sheep among the heterogeneous sub-alpine wool breeds. This is due to a decreased market demand for black sheep and black wool. The sub-alpine sheep types were evaluated as highly adapted to the harsh natural environment and low input production systems. The socio-economic roles of most of the breeds were ranked as high. This is because of their high market value, including the export market for BHS and Afar, and their role as a source of family food like milk among pastoralists. The importance of these roles for a given breed, however, varies according to the production system. Under highland perennial/cash crop systems, for instance, sheep contribute less to the farm livelihood.

Conclusion

This study provided an overview of the characteristics of Ethiopian sheep. Four morphologically distinct categories of Ethiopian sheep were recognized: sub-alpine short-fat-tailed, highland long-fat-tailed, lowland fat-rumped/tailed and lowland thin-tailed. Morphological diversity in Ethiopian sheep is related to ecological zones, ethnic communities and production systems. Assessment of the genetic distinctness of the traditional sheep types is

Table 4. Average flock size and flock structure.

Sheep type/production system	No. of flocks	Average flock size	Average no. of ewes	Average no. of rams	Average no. of lambs
Alpine sheep-barley	50	23.32	13.95	1.22	5.91
Menz	19	25.89	16.94	1.45	4.71
Tikur	10	16.11	10.45	1.00	3.50
Wollo	12	16.40	10.40	1.20	6.00
Simien	10	9.21	5.80	0.25	2.50
Highland crop-livestock	53	10.37	5.90	0.47	3.01
Horro	29	9.43	5.31	0.34	2.10
Sekota	12	11.18	6.64	1.00	3.00
Farta	12	10.45	6.73	0.27	3.80
Washera					
Arsi-Bale	15	27.14	13.64	1.07	9.15
Highland perennial crop	53	3.45	1.77	0.02	1.64
Adilo	22	3.24	1.71	0.09	2.14
Bonga	31	3.60	1.80	0.07	1.44
Lowland crop-livestock	11	11.80	7.50	0.70	5.14
Gumz	11	11.80	7.50	0.70	5.14
Pastoral system	99	54.37	27.37	8.47	18.54
BHS	99	54.37	27.37	8.47	18.54
Afar	n.a.				

n.a.: data not available.

Figure 9. Lowland fat-rumped ram (e.g. here is BHS sheep).

Table 5. Farmers' assessment of sheep types on physical, production and adaptation traits and socio-economic importance.

Traits/types	Horro	Menz	Sekota	Simien	Farta	Tikur	Gumz	Washer	Wollo	Adilo	Arsi	Bonga	BHS	Afar
Color	4	2	3	4	4[1]	1	4	4	2	4	2	4	4	4
Appearance/size	3	1	4	4	4	2	3	4	1	4[2]	4	4	4	3
Growth rate	3	1	3	4	4	2	3	4	1	4	4	4	3	3
Fertility	4	4	4	3	3	4	2	4	4	3	4	4	3	4
Prolificacy	4	1	2	2	2	1	2	4	1	4	3	4	2	3
Meat quality	3	4	3	4	4	3	4	4	4	3	4	4	4	3
Skin quality	4	4	4	4	4	2	2	4	3	3	2	3	3	3
Wool	n.a.	2		2	2	1	n.a.	n.a.	1	n.a.	1	n.a.	n.a.	n.a.
Temperament	4	3	4	3	4	4	4	4	4	2	1	4	4	4
Mothering ability	4	3	2	3	4	2	2	4	4	4	4	4	4	4
Disease tolerance	2	3	3	4	4	3	2	3	3	2	4	2	4	4
Hardiness	2	4	4	4	4	4	3	2	4	2	4	2	4	4
Market value	4	4	3	3	4	1	2	4	2	4	4	4	2	3
Socioeconomic importance	H	H	H	H	H	I	N	H	H	N	H	N	H	H

1 = Poor, 2 = Average, 3 = Good, 4 = Excellent.
H = Highly important, I = Important, N = Not much important.
n.a. = data not applicable.
[1]All coat colors except black were preferred.
[2]Farmers prefer to have fattening males with long horns, which most Adilo rams lack.

important for developing rational conservation-based improvement programs. Molecular genetic assessment of the population structure is a follow up activity.

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Inventaire des différents écotypes de la race Barbarine en Tunisie

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Résumé

Cette étude s'est intéressée à l'identification des différents écotypes de la race Barbarine, principale race ovine à queue grasse en Tunisie. Un inventaire national a été conduit dans les différents étages bioclimatiques du pays allant du Nord subhumide jusqu'au Sud Saharien, en passant par le Centre semi-aride. Les principaux résultats ont permis de mettre en évidence au sein de cette race 10 écotypes différents:

1. Quatre écotypes au Nord, de grand format à tête rousse, de grand format à tête noire, à robe noire, et de type "*Sardi*" à museau, "*lunettes*" et membres noirs.
2. Quatre écotypes au Centre, de format moyen avec dominance de la tête rousse, à tête rousse avec une liste frontale blanche, à tête claire tirant vers le blanc et à tête rousse et à queue arquée.
3. Deux écotypes au Sud, de petit format à tête rousse, et de type "*Sagâa*" avec une tête blanche, un museau et des "*lunettes*" de couleur brune.

Cette diversité d'écotypes au sein de la race Barbarine constitue un apport nouveau aux connaissances des races ovines autochtones. Jusqu'à maintenant, seuls deux écotypes, à tête rousse et tête noire, étaient répertoriés au sein de la race Barbarine.

Summary

The objective of this study was to identify potential ecotypes within the Barbarine sheep breed, the major fat tail breed in Tunisia. A national survey was carried out within the country where the main flocks in different agro-ecological regions were visited. As part of this inventory, a variety of ecotypes were photographed and described. The main results showed that the Barbarine breed has a reservoir of 10 different ecotypes. In the northern region, four ecotypes were found: large size black face, large size brown face, all black and "*Sardi*". In the centre, four ecotypes were found: medium size brown face, brown face with a white line in the middle, yellow face, and brown face with a curved tail. In the southern region, two ecotypes were encountered: small size brown face and "*Sagaa*". All these ecotypes were well represented in their agro-ecological regions and constitute a genetic pool for the Barbarine breed which has, until this date, had only two known ecotypes (brown and black face).

Resumen

El objetivo de este estudio era identificar el potencial de ecotipos dentro de la raza ovina Barbarine, la raza de cola grasa más importante en Túnez. Se ha llevado a cabo una encuesta nacional y se visitaron las diversas regiones agroecológicas donde se encuentran la mayoría de estos rebaños. Como parte de este inventario, también se han fotografiado y descrito toda una variedad de ecotipos. Los principales resultados muestran que la raza Barbarine se encuentra en 10 ecotipos distintos. En el norte de la región se encontraron cuatro ecotipos : gran tamaño con cara negra; gran tamaño con cara marrón; toda negra; y "*Sardi*". En el centro, se encontraron otros cuatro ecotipos: tamaño medio con cara marrón; cara marrón con línea blanca en medio; cara amarilla; y cara marrón con cola curvada. En la zona sud se encontraron dos ecotipos: tamaño pequeño con cara marrón y "*Sagaa*". Todos estos ecotipos están bien representados en sus regiones agroecológicas y constituyen un grupo genético para la raza Barbarine que había tenido hasta ahora solo dos ecotipos conocidos: cara marrón y cara negra.

Key words*: Sheep, Barbarine, Ecotypes, Production, System, Inventory.*

Photo 1a. Ecotypes Barbarine à tête noire.

Photo 1b. Ecotypes Barbarine à tête rousse.

Introduction

La Tunisie est un pays connu par son élevage de moutons et le consommateur tunisien a tendance à préférer plus la viande ovine que bovine. L'élevage ovin a toujours compté parmi les productions essentielles de l'agriculture et comme l'activité la plus importante de la production animale tunisienne. Les ressources ovines autochtones se distinguent par leur adaptation aux conditions climatiques et de milieu. Depuis des siècles, les ovins et en particulier la race Barbarine ont pu valoriser les parcours maigres des régions semi-arides et arides. L'aptitude des animaux à pâturer dans des conditions d'extrême chaleur estivale et à supporter la soif a très tôt été remarquée par les éleveurs de ces régions. Deux périodes ont caractérisé l'évolution des effectifs ovins (Ben Dhia, 1995): la période allant de 1931 à 1951 et celle après 1952. Pour la première période, les effectifs ovins ont fluctué, marquant l'incidence profonde de la pluviométrie et les aléas climatiques sur le cheptel. Pendant la deuxième période, malgré la diminution des aires pastorales et l'effet des aléas climatiques, les effectifs des petits ruminants ont augmenté. Cette augmentation trouve sa justification dans les efforts nationaux investis pour soutenir les éleveurs dans les années de sécheresse par la mise en œuvre de divers mécanismes de sauvegarde du cheptel, par un apport alimentaire d'orge et de foins et des campagnes sanitaires.

Quatre principales races ovines, représentant un effectif de quatre millions de femelles, sont rencontrées dans le pays: la Barbarine (60% des effectifs), la Queue Fine de l'Ouest (35%), la Noire de Thibar (2%), et la Sicilo-Sarde (2%). Les trois premières races sont à vocation bouchère et la dernière est l'unique race ovine laitière d'Afrique du Nord. Les étages arides et désertiques comptent environ 50% d'ovins, l'étage semi-aride en compte 40% et uniquement 10% d'ovins sont rencontrés dans les zones humides et sub-humides.

Les exploitations de petite taille (<10 ha) détiennent environ 40% des effectifs ovins dans le pays. Celles comprises entre 10 et 100 ha hébergent 48% du cheptel national ovin alors que 12% seulement des effectifs se trouvent dans les exploitations supérieures à 100 ha (Bedhiaf, 2006).

La Barbarine est l'unique race ovine à queue grasse qui soit répartie sur tout le territoire tunisien, allant des côtes Nord (Humide et subhumide) jusqu'au Sahara (aride et désertique), en passant par l'étage semi-aride (Djemali *et al*., 1995). Cette race semble avoir été introduite en Tunisie par les Phéniciens dans le millénaire avant J.C. et aurait comme origine les steppes de l'Asie Centrale. Mason (1967) situe cette date vers le IV^{ème} siècle avant J.C. Jusqu'au III^{ème} siècle après J.C., la Barbarine a cohabité avec une autre race ovine à queue très longue et fine, mais uniquement le mouton Barbarin de l'époque était considéré comme le prototype "noble" de l'espèce, présent dans les représentations des scènes de sacrifice et des cérémonies religieuses. La Barbarine ne s'est définitivement installée en Tunisie qu'à partir de l'an 1050 (Khaldi, 2004).

Tchamitchian *et al*., (1966) (cité par Sarson, 1972), Khaldi (1989) et Djemali *et al*., (1994) ont décrit deux écotypes différents chez la race Barbarine: l'un à tête rousse, l'autre à tête noire, ces derniers étant le plus souvent moins

Photo 2. Ecotype Barbarine à robe noire.

Photo 3. Ecotype Barbarine " Sardi".

Photo 4. Ecotype Barbarine à liste frontale blanche.

photosensibles. De même, ces auteurs ont évoqué à la même époque l'existence de types divers au sein de ces deux variétés selon les zones climatiques où ils se sont peu à peu différenciés dans leur conformation et leur forme générale. C'est dans ce cadre que l'objectif de cette étude était de faire un inventaire sur tout le territoire tunisien dans le but d'identifier les différents écotypes au sein de cette race.

Matériel et Méthodes

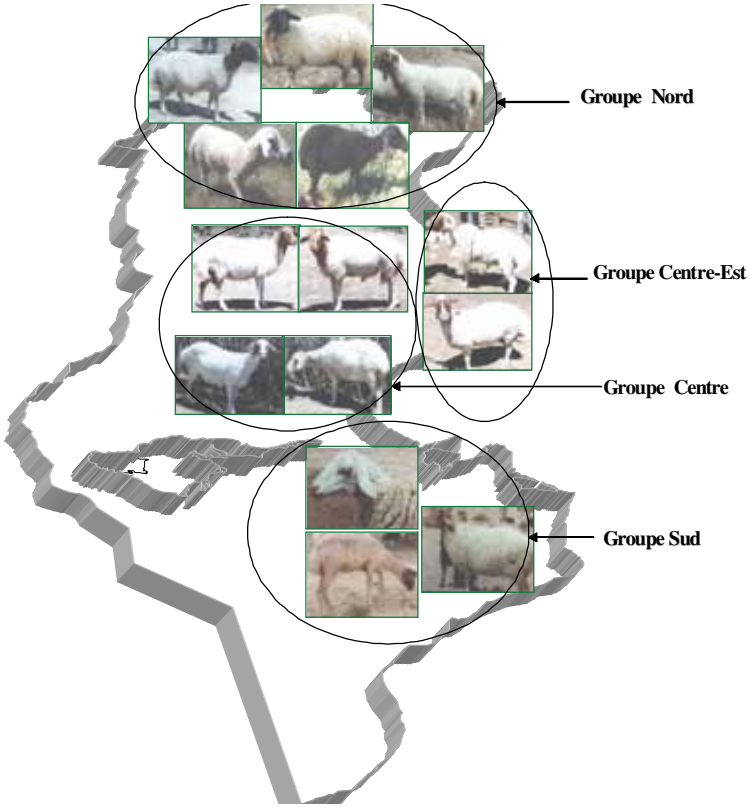
Un inventaire des différents écotypes de la race Barbarine a été réalisé pendant une période de 4 mois où des visites d'une équipe de spécialistes en ovins ont été réalisées auprès des principaux troupeaux ovins existant sur le territoire tunisien qui englobe plusieurs étages bioclimatiques.

La Tunisie occupe une place de transition entre le climat méditerranéen et le Sahara. Son site géographique au milieu du Bassin Méditerranéen et sa forme étirée sur 7° de latitude procure une gamme de climats. D'une façon générale, la pluviométrie décroît régulièrement du nord au sud, passant de plus de 1 000 mm jusqu'à moins de 50 mm dans l'extrême sud; Néanmoins, l'obstacle formé par la grande Dorsale Tellienne constitue une limite naturelle divisant le pays en deux zones bien distinctes.

- Le nord de la Dorsale où la pluviométrie est supérieure ou égale à 400 mm. Dans cette zone, relativement favorable, l'élevage bovin prédomine largement.
- Le sud de la dorsale, zone à moins de 400 mm, réservée essentiellement à l'élevage des petits ruminants et du dromadaire.

Dans cette étude, la race Barbarine est définie par son standard se distinguant par une tête de taille moyenne, un chanfrein droit voire légèrement convexe, des oreilles longues et pendantes et une queue grasse. La toison est de couleur blanche. L'écotype est le groupe d'animaux appartenant au standard de la race Barbarine mais qui se distingue par, au moins, un caractère morphologique différent (couleur de la tête, de la toison et/ou format de l'animal) qui se transmet d'une génération à une autre. Deux écotypes de la race Barbarine sont traditionnellement connus et décrits (voir par exemple, Sarson, 1972): l'écotype à tête rousse et celui à tête noire.

Des troupeaux appartenant aux secteurs privés et étatiques ont fait l'objet de cet inventaire où les principaux écotypes rencontrés ont été photographiés et décrits. Les écotypes retenus dans



Carte 1. Répartition géographique des écotypes identifiés au sein de la race Barbarine

Tableau 1. Caractéristique phénotypique des écotypes Barbarine à tête noire et à tête rousse.

	Mâle	Femelle
Poids moyen	75 kg	50 kg
Tête	Fort à chanfrein saillant	Fin, allongé et couvert de poil fin noir ou
Couleur	Rousse et noire	roux Rousse et noire
Oreilles	Légèrement plus courtes et plus larges	Longues et légèrement pendantes
Cornes	Présentes ou non (larges et soudées)	Absentes
Cou	Plus court et fort	Long
Poitrine	Large et profonde	
Dos	Long, bassin large	
Toison	Dense et tassée à mèches longues, bien répandue sur le corps. Laine de finesse moyenne (présence de jarre)	
Queue	Grosse, grasse et bilobée	
Membres	Assez forts, moyennement longs pour la femelle et courts chez le mâle. Les extrémités sont noires ou rousses selon la variété. Les cuisses sont bien développées chez le mâle	

cette étude sont ceux répondant au standard de la race Barbarine avec au moins une spécificité morphologique qui les distingue et ils étaient rencontrés d'une manière fréquente dans les troupeaux des régions visitées.

Répartition Géographique des Différents Écotypes de la Race Barbarine

Plusieurs écotypes, répondant au standard de la Barbarine et connus par les éleveurs comme étant

des animaux de race Barbarine, ont été identifiés, dont les plus représentatifs sont décrits selon les régions où ils sont le plus rencontrés (Carte 1). Trois groupes d'écotypes de la Barbarine sont distingués dans cet inventaire.

Ecotypes de race Barbarine de grands formats dans le Nord du pays

Ces écotypes sont rencontrés essentiellement dans le Nord du pays, à pluviométrie abondante et où les conditions herbagères sont bonnes. Ils sont caractérisés, en général, par un grand format avec une hauteur au garrot de 75 cm. Les animaux de ces écotypes ont, en moyenne, un poids vif de 75 kg pour les mâles et de 50 kg pour les femelles (Tableau 1). Quatre écotypes différents ont été identifiés. En plus des deux écotypes traditionnellement connus de la Barbarine, à tête rousse et à tête noire (Figure 1a et 1b), deux autres écotypes ont été inventoriés: La Barbarine à robe toute noire (Figure 2) et la Barabrine caractérisée par la couleur noire du museau, des "*lunettes*" et de l'extrémité de ses membres (Figure 3). Cet écotype est connu sous le nom de "*Sardi*" par les éleveurs.

Les écotypes du Nord sont rencontrés dans des systèmes de production où les fourrages sont cultivés dans l'exploitation, en irrigué ou en sec, pour nourrir le cheptel. Les concentrés sont auto-produits ou achetés de l'extérieur.

Ecotypes de formats moyens dans le Centre du pays

Ces écotypes sont de format moyen avec une hauteur au garrot comprise entre 65 et 70 cm. Le poids moyen est de 70 kg chez les mâles et de 45 kg chez les femelles. Ce type est caractérisé par sa forme générale ramassée. En plus de l'écotype à tête rousse, mais de format moyen, trois nouveaux écotypes ont été inventoriés: un écotype qui se distingue par sa tête rousse présentant une liste frontale blanche (Figure 4), un deuxième écotype à tête de couleur rousse claire tirant vers le blanc (Figure 5) et un troisième écotype à tête rousse et avec une queue archée se trouvant, en particulier dans la zone littorale du Centre-Est du pays (Figure 6). Il est connu sous le nom "*Hazgui*" par les éleveurs de la région.

Ecotypes de petits formats dans le Sud du pays

Peuplant les régions arides du pays (Gabès et Tataouine), ces écotypes sont de petit format, avec une hauteur moyenne au garrot de 55 cm et un poids moyen de 55 kg chez les mâles et de 40 kg chez les femelles. En plus de la Barbarine à tête rousse mais de petit format, il a été identifié un nouvel écotype ayant une tête blanche avec un

Photo 5. Ecotype Barbarine à tête blanchâtre.

Photo 6. Ecotype Barbarine du Sahel à queue arquée "Hazgui".

Photo 7. Ecotype Barbarine à tête rousse.

Photo 8. Ecotype barbarine " Sagaa".

museau et des "*lunettes*" de couleur brune. Cet écotype est connu par les éleveurs de la région par le nom "*Sagaa*".

Tous les écotypes du Centre et du Sud sont rencontrés dans des systèmes d'élevage basés essentiellement sur l'utilisation de la végétation naturelle provenant des zones montagneuses, des parcours et des terres marginales pour nourrir les animaux. La complémentation alimentaire du cheptel est exceptionnelle ou absente. Ces systèmes concernent, le plus souvent, les troupeaux de taille réduite. Ils se caractérisent par l'utilisation d'une main d'œuvre familiale et d'une couverture sanitaire presque inexistante.

Suite à cet inventaire, il apparaît que la race Barbarine est très riche en écotypes répondant au standard de la race avec des différences phénotypiques apparentes selon les zones climatiques du pays. Le gradient Nord-Sud sur le format des animaux, allant d'une taille plus grande au Nord et qui diminue en allant vers le Sud, fait penser qu'il est lié à la disponibilité des ressources alimentaires plus riche au Nord et rares au Sud. Cependant une étude récente du polymorphisme moléculaire a montré une variabilité génétique entre écotypes (Ben Sassi, 2007). Cette biodiversité constitue un réservoir génétique bien adapté aux conditions climatiques souvent difficiles et mériterait d'être caractérisée et évaluée (Hodges 1986; FAO, 1998). En effet, la sécurité alimentaire dépend, entre autre, de la gestion et de la conservation de toutes les ressources génétiques dans leur milieu naturel. Delgado *et al*., (1999) ont rapporté que l'augmentation de consommation des produits d'origine animale va être plus importante dans les pays en voie de développement que dans les pays développés.

Conclusion

La Tunisie, caractérisée par des conditions climatiques très fluctuantes, renferme des races ovines autochtones très anciennes et adaptées, dont la plus importante en nombre et en écotypes est la race Barbarine. Elle est rencontrée dans toutes les régions de la Tunisie allant des côtes Nord (Humide et subhumide) jusqu'au Sahara (aride et désertique) en passant par l'étage semi-aride caractérisant la région du centre. Cette race s'est révélée riche en biodiversité. Un total de dix écotypes a été identifié dans ces étages bioclimatiques différents. S'agit-il de différences phénotypiques où génétiues ? Une étude de la diversité moléculaire de ces différents écotypes de la Barbarine est actuellement en cours.

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On-farm investigation of local chicken biodiversity and performance potentials in rural areas of Jordan

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Summary

On-farm surveys were conducted to investigate the biodiversity of local chickens and their performance potential. The study was carried out in rural areas of northern Jordan. A sample of 846 adult local chickens was phenotypically characterized based on morphology, feather colors, comb shape and performance. Body measurements for cluster analyses were recorded on 460 adult females. The most predominant chicken type was the Jordan Baladi (67.3%) followed by the Pakistani (27.7%) and the Brahma (5%). Cluster analyses showed that the three populations are distinct. The Jordan Baladi and the Pakistani were closer to each other than the Brahma. Plumage colors were observed either as single color or mottled (a mix of many colors). The latter was the most predominant (23.1 %) followed by black (19.5%) and light brownish (19.1%). The single comb type was the most predominant (80.3%). Hens of the local chicken reached sexual maturity at about 22-30 weeks of age. The average clutch number was 1-5 per year, with 18-30 eggs per clutch. Each hen laid on average 68.9±3.3 eggs per year. The body size of adult females and males was about 1 240±10g and 1 890±30g, respectively. Indiscriminate crossbreeding was taking place frequently. Genetic characterization would complement the phenotypic characterization and should be conducted. This would help to initiate a program for the preservation of genetic diversity in local chickens in Jordan.

Résumé

Une enquête a été menée au nord de la Jordanie pour caractériser la diversité des poules locales ainsi que leur potentiel de production. Les informations recueillies sur un échantillon de 846 poules adultes portaient entre autres sur les caractéristiques morphologiques, la couleur du plumage et la forme de la crête. Il existe trois principales variétés de poules locales: le Baladi (67,3%), le Pakistani (27,7%) et le Brahma (5%). La couleur du plumage est soit uniforme soit composite. Les plumages bigarrées (23,1%), uniformément noires (19,5%) et uniformément brun clair (19,1%) sont prédominantes. La majorité (80,3%) des poules ont une seule crête. Les poules locales atteignent leur maturité sexuelle entre 22 et 30 mois d'âge. Le nombre moyen de couvée par an varie entre 1 et 5 et le nombre d'oeufs par couvée entre 18 et 30. Chaque poule couve en moyenne 68,9±3,3 oeufs par an. Le poids moyen de la femelle adulte est de 1 240±10 g et celui du male adulte de 1 890±30 g. Des métissages incontrôlés sont fréquents. Une caractérisation génétique est indispensable pour confirmer les résultats de la présente étude et pour l'initiation d'un programme de préservation de la diversité génétique existante entre et dans les races locales de poules en Jordanie.

Resumen

Se ha llevado a cabo una encuesta en el norte de Jordania para caracterizar la diversidad de las razas de gallinas locales así como su potencial de producción . Las informaciones recogidas sobre una muestra de 846 gallinas adultas comprendían, entre otras, las características morfológicas, el color de las plumas y la forma de la cresta. Existen tres principales razas de gallinas locales: la Baladi (67,3%), la Pakistani (27,7%) y la Brahma (5%). El color de la pluma es o bien uniforme o bien compuesto. Predominan los plumajes compuestos con el 23,1%, los negros con el 19,5% y los marrones

Figure 1a. Black Baladi female.

Figure 1b. Baladi male with single comb type.

Figure 2. Pakistani male.

claros con el 19,1%. La mayoría de las gallinas tienen una sola cresta (80,3%). Las gallinas de raza local alcanzan la madurez sexual entre los 22 y 30 meses. La media de nidadas por año varía entre 1 y 5 y el número de huevos por nidada entre 18 y 30. Cada gallina incuba una media de 68,9±3,3 huevos por año. El peso medio de la hembra adulta es de 1,240±10 gr y el del macho adulto de 1,890±30 gr. Son frecuentes los cruces incontrolados. Es indispensable iniciar una caracterización genética para confirmar los resultados del presente estudio y para poder iniciar un programa de conservación de la diversidad genética existente entre y dentro de la razas locales de gallinas en Jordania.

***Keywords**: Genetic resources, Jordan, Local chicken, Performance, Phenotype diversity.*

Introduction

'Local chicken' is the general term given to those chickens kept in an extensive system, scavenging free-range, having no identified description, and being dual-purpose and unimproved (Horst, 1989; Pedersen, 2002). Indigenous breeds of chickens are supposed to be more adapted to local environmental conditions and diseases. Horst (1989) considered the indigenous fowl populations a gene reservoir, particularly in respect of those genes that have adaptive values in tropical conditions. One of the important reasons to conserve local chicken genetic resources is to keep genetic variation within and between local breeds. The future improvement and sustainability of local chicken production systems is dependent upon the availability of this genetic variation (Benítez, 2002).

The total chicken population in Jordan was estimated to be 24 million birds of exotic commercial breeds (FAO, 2004b) and one million of local breeds (Abdelqader and Wollny, 2004). The annual per capita consumption of chicken meat and eggs is 22 kg and 175 eggs, respectively (Jordan Ministry of Agriculture, 2005). The local chicken breeds in Jordan are composed of different non-descript types. The production system is small-scale scavenging in a free-range environment. Local chickens constitute a significant portion of human livelihood and contribute significantly to food security (Gondwe, 2004). Local chickens are strictly linked to rural households in Jordan. There is no information available on the diversity among different phenotypes and their approximate performance potential. At present, Jordan has an action plan for the conservation of livestock genetic resources, but this plan is more directed towards small ruminants and imported dairy cattle than toward local poultry breeds (FAO, 2004a). Local chicken populations have been neglected in conservation and development programs. Instead,

high-input/high-output exotic genotypes were introduced and supported. No studies have been carried out to date to characterize local chickens in Jordan. The objectives of this study were to provide basic information about the diversity of different phenotypes of local chicken and to investigate their productive and reproductive potentials under scavenging conditions.

Materials and Methods

Study area

The study was carried out in rural areas of the northern districts of Jordan (Irbid, Ajlun, Jarash, Almfraq). The center of the geographical coordinates is latitudes 32º 33' N and longitudes 35º 50' E. The area is of Mediterranean climate, characterized by dry, hot summers (June-August) and cold, wet winters (December-February). The rainy season is from November to April. The annual precipitation is approximately 200 - 350 mm. The average monthly temperature ranges from 5 ºC in January to 32 ºC in August (Jordan Meteorological Department, 2007).

Scope of the study

The study was conducted to investigate the diversity of different local chicken phenotypes and performance potentials. On-farm studies and surveys were run from October 2004 to February 2005 and from May to July 2005. A total of 120 households selected from 18 villages were included in the study. Data were collected through personal interviews with the head of the family or the caretaker of the chickens.

Figure 3. Brahma female with feathered legs.

Data collection

A sample of 846 adult local chickens was described. General body morphology, feather colors and comb shape were recorded. Farmers were asked about the local names of the different phenotypes, and the criteria they used to distinguish between them. Morphological measurements were recorded on 460 hens of one year old and older for clustering analysis. Ten morphological traits were measured on each hen: body length (BL), neck length (NL), height at thorax (HT), height at hipbone (HB), hip width (HW), withers width (WW), body weight (BW), heart girth (HG), tail slope (TS) and comb shape (CS). Body traits were measured using a measuring tape while the hen was standing upright. The prevalence of other poultry species was also recorded. Performance data were collected through direct observation, measurements and farmer interviews. The annual egg production was estimated by counting the number of clutches per hen per year and the number of laid eggs per clutch. Data relating to body weight and egg weight were taken by direct measurement. Adult males and females were weighed using a hanging type scale, Salter Model 12.

Statistical analysis

SAS-program version 8 (SAS, 1999) was used for all statistical analysis. PROC FREQ procedure was used to calculate the frequency of different phenotypes within local chickens. PROC MEANS procedure was used for the descriptive statistics of performance data. Before clustering analysis, data were standardized to zero mean and a unit standard deviation because of different units of measurements. Stepwise discriminant procedure was applied to determine which morphological traits would be used in the final clustering analysis; this procedure determines the variables that have more discriminant power than the others. The CANDISC procedure was used to perform uni- and multivariate analyses to derive canonical functions, and to show the clustering among these three types. PROC CLUSTER procedure was used to find out the degree of morphological variations between the clusters. Mahalanobis distances were generated during the canonical discriminate analysis to perform cluster analysis. These distances were used to construct a dendrogram using the unweighted pairs group method analysis.

Results

Phenotype diversity and morphological description

Besides chickens, other poultry species were kept by households. Chickens prevailed over all other poultry species (92% of the poultry population). Pigeons were the second most prevalent species after chickens (5%), followed by guinea fowl (2%) and other poultry species (1%). Farmers get their stocks of chicken either by buying birds from the market, or by hatching eggs by natural brooding or in small artificial hatcheries.

The results showed that the local chicken populations in Jordan are composed of different non-descript types such as the Jordan Baladi (Figures 1a and 1b) which was the most predominant type (Table 1), followed by the Pakistani (Figure 2) and Brahma (Figure 3). These three types were kept in the same system under the same conditions; therefore they were classified generally under one common name as local. Jordan Baladi is the indigenous type which has cohabited with people since time immemorial. They have horizontal body position and large vertical tail. They are characterized by a smaller body size when compared to he Pakistani and Brahma. Pakistani chickens are supposed to have been introduced to Jordan by the Pakistani communities. This type has larger body size than the Jordan Baladi and an upright stance. Their tail slope tends to be horizontal rather than vertical. They have soft and long feathers, prominent shoulders, a narrow stern and long neck (Figure 2). The Brahma is very similar to the Asiatic breed known as the 'Brahma' and is supposed to have been introduced either by traders or hobbyists. This type has a very large body size and heavy bone and muscles. Birds are highly feathered with feathered legs and toes (Figure 3). Cluster analysis showed that the three types were characterized as three distinct clusters. The Jordan Baladi and the Pakistani were closer to each other than to the Brahma. Measurements that were best able to separate the populations, as judged from stepwise discriminant analysis were: BW, TS, BL, HG and HB. Mahalanobis distances estimated between the three types are presented in table 2. The distances between all pair-wise were significant ($P<0.0001$). The largest distance was between the the Jordan Baladi and Brahma while Pakistani was the closest to the Jordan Baladi. The dendrogram (Figure 4) shows two closer clusters; Jordan Baladi and Pakistani, joined by the Brahma which was significantly separated from the others.

Table 1. Distribution of different phenotypes among 846 adult local chickens in the study area.

Item	Phenotype	Number	Per cent
Morphology	Normal	741	(87.6)
	Naked neck	8	(0.9)
	Feathered leg	64	(7.6)
	Frizzled	5	(0.6)
	Dwarf	17	(2.0)
	Tail less	11	(1.3)
Feather color	Mottled (many colors)	195	(23.1)
	Black	165	(19.5)
	Light brownish	162	(19.1)
	Brown and black	144	(17.0)
	White	69	(8.2)
	Spotted with black and white	60	(7.1)
	Grey	33	(3.9)
	Black and white	18	(2.1)
Origin	Baladi	570	(67.3)
	Pakistani	234	(27.7)
	Brahma	42	(5.0)
Comb type	Single	679	(80.3)
	Buttercup	73	(8.6)
	Double	42	(5.0)
	Pea	32	(3.8)
	V-shaped with feathered cap	20	(2.3)

Table 2. Mahalanobis distance between local chicken types in Jordan based on morpho-structural variables.

Type	Jordan Baladi	Brahma	Pakistan
Baladi	0.00		-
Brahma	76.88	0.00	-
Pakistan	9.91	48.75	0

Table 3. Means (±SD) of productive and reproductive parameters of local chicken in Jordan.

Performance parameter	Mean	SD	Minimum	Maximum
Number of clutches per year	2.64	0.13	1	5
Egg production per hen per year	68.90	3.31	18	130
Ag at first lay (week)	25.80	0.17	22	30
Female body weight (g)	1 240	10.00	900	1 700
Male body weight (g)	1 890	30.00	1 100	2 600
Egg weight (g)	47.90	0.66	32.0	60.0

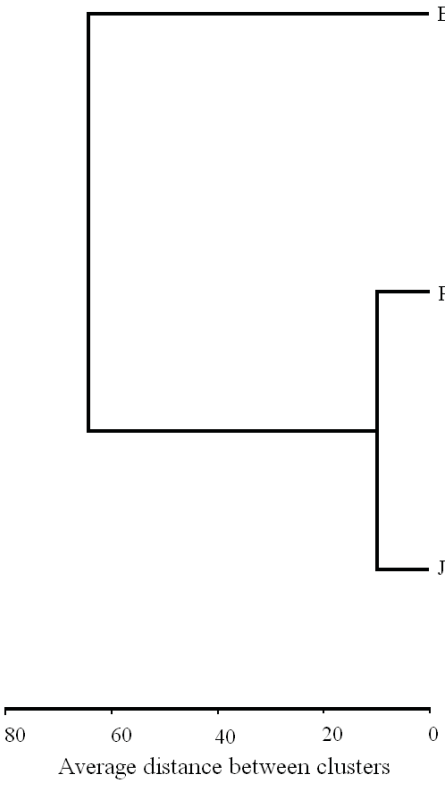

Figure 4. Dendrogram showing relationship among local chicken populations in Jordan.

Other distinctive phenotypes like Naked Neck (Figure 5), Frizzled (Figure 6) and Tailless (Figure 7) were found in small numbers. Table 1 shows the phenotypic characterization of the local chicken in Jordan. Local chickens were highly heterogeneous in feather color (Figure 8). The most predominant plumage was the mottled feather (mixed colors of plumage, including black, white, brown, red, spangled green, yellow, etc.) followed by black and light brownish. Many comb variants were found, the most frequent comb shape was the single type (Figure 1b) other types like Buttercup (Figure 9) and V-shape with feathered cap (Figure 10) were recognized in different proportions (Table 1).

Productive and reproductive performance

Means of productive and reproductive parameters of local chicken in Jordan are summarized in table 3. All farmers kept their chickens under free-range conditions where inputs are limited. However, there were wide variations in productive and reproductive potential. Numbers of clutches ranged between 1-5 per year with 18-30 eggs per clutch. However, not all hens become broody and a small number of hens were observed to have continuous egg laying throughout the year. There was a wide range of variability in body size of the birds. Adult females ranged in live body weight from 900 to 1 700 g and similarly males ranged from 1 100 to 2 600 g.

Figure 5. Naked neck male.

Figure 6. Frizzled male for marketing.

Figure 7. Tail less bird.

Discussion

In the current study, the Baladi chicken was the predominant type, which was easily recognized by farmers. Multivariate discriminant analysis of morphological traits has been successfully used to estimate the genetic variation within and between local breeds (Zaitoun *et al*., 2005; Herrera *et al*., 1996; Jordana *et al*., 1993).

The use of cluster analysis in this study was successful in differentiating the local chicken populations based on morphological traits. The present study showed a considerable genetic variability between the three main types of local chickens in Jordan. Great phenotypic variations seem to be the main characteristic of local chickens throughout the world (Wimmers *et al*., 2000; Pedersen, 2002). Local chickens in Jordan were highly heterogeneous in appearance and plumage colors. Naked Neck gene and Frizzled phenotypes were occasionally observed. The Naked Neck gene is highly prevalent in Ethiopia and about 50% of chickens are found to be of this type (Tadelle *et al*., 2003a) while only 2% of chickens were found to be Naked Neck in Senegal. There were also wide variations in the productive and reproductive performance of local chicken phenotypes. Wide variations in performance were also reported in the literature (Missohou *et al*., 1998; Pedersen, 2002; Gondwe, 2004). Considerable variations in egg weight and body size were reported by Minga *et al*. (1989). Similarly, the high variations in clutch number and size observed in this study were in general agreement with previous findings of Mwalusanya *et al*. (2002) in Tanzania and Tadelle *et al*. (2003a) in Ethiopia.

Another report from Ethiopia demonstrated that local chickens had 3-4 clutches per year, with 15-20 eggs per clutch (Dessie and Ogle, 2001). Benabdeljelil and Arfaoui (2001) investigated the performance of native chickens in Morocco. They found that hens produced 2-3 clutches per year with annual an production of about 78 eggs. Age at first lay (age at sexual maturity) in the current study was similar to the range proposed by Gueye (1998), from 24 to 32 weeks; Dessie and Ogle (2001), about 28 weeks; and Gondwe (2004), about 25.5 weeks. Other authors reported a greater maturity age of up to 42 weeks (Mwalusanya *et al*., 2002; Tadelle *et al*., 2003b). Male and female body sizes were similar to those found elsewhere (Benabdeljelil and Arfaoui, 2001; Dessie and Ogle, 2001).

The wide variations in local chicken performance are ascribed in this study to many factors, mainly the variations in management practices between households, the effects of crossbreeding with exotic lines, the availability of scavenging feed resources and feed supplements. Some farmers kept chickens of exotic strains free-roaming together with local chickens. Consequently, indiscriminate crossbreeding occurred. Furthermore, none of the farmers in the study area implement planned crossbreeding in the flock. This will ambiguously affect the frequencies of phenotypes in the population.

Therefore, based on phenotypic assessment, quantitative estimates of the substitution of local genetic material due to uncontrolled crossbreeding were difficult. To assess the impact of crossbreeding and to what extent it was taking place is a very important goal. However, due to the high phenotypic heterogeneity in the local chickens and unplanned crossbreeding, such an approach seems

Figure 8. Local chicken with different colored variants.

Figure 9. Duplex Buttercup comb shape.

Figure 10. V-shaped comb type with Feather cap.

to be fruitless. The remaining local genetic resources are threatened by improper management, particularly crossbreeding. There is a need to plan a conservation program for local chicken breeds. To conceive an objective plan to conserve the local chicken we need to find out the genetic composition of the local breeds and compare it with other populations.

Conclusion

The Jordan Baladi, Pakistani and Brahma are characterized as distinct types of local chickens in Jordan. Significant morphological variations between the three types were detected. Body weight, tail slope, body length, heart girth and height at hipbone showed the largest discriminatory power. The high diversity in local chicken phenotypes is major evidence of high genetic variability. Further research should investigate the on-farm performance of each type. Genetic characterization based on molecular assessment should be run to evaluate the genetic diversity between and within local chicken types.

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Phenotypic characterization of the Guajolote (*Meleagris gallopavo gallopavo*) in Mexico

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Summary

The study was conducted to investigate the phenotypic diversity of Guajolote present in small backyard poultry operations. From September 2004 to July 2006, in 54 municipalities in the coastal region of Oaxaca, Mexico 768 "*guajalotes*" growers were visited. Eleven different phenotypes of Guajolote, previously described as turkey varieties, have been identified. The phenotypes identified and their frequency are: Bronze (30.1%), Black (29.0%), Royal Palm (13.4%), Auburn (5.3%), Bourbon Red (5.2%), Narragancet (2.6%), Spotted (2.4%), Brown (2.2%), Slate (1.7%), White (1.5%) and Imperfect Albino (0.2%). The remainder (6.4%) were not identified as a phenotype previously described. This is the first report about the phenotypic differentiation of Guajolote in Mexico.

Résumé

Une étude a été mise en place pour connaître la diversité phénotypique des "*guajalotes*" (une espèce de dinde) dans les petites exploitations avicoles de basse cour. De septembre 2004 à juillet 2006 on a visité 768 producteurs dans 54 municipalités de la côte de la région de Oaxaca (Mexique). On a identifié 11 phénotypes différents de "*guajalotes*" qui avaient été décrits précédemment comme étant des variétés de dinde. Les phénotypes identifiés avec leur présences respectives sont: Bronze (30,1%); Black (29%); Royal Plan (13,4%); Auburn (5,3%); Bourbon Red (5,2%); Narragancet (2,6%); Spotting (2,4%); Brown (2,2%); Slate (1,7%); White (1,5%); et Albinisme imparfait (0,2%), le reste de l'échantillon n'a pas été identifié parmi les phénotypes indiqués ci-dessus. Il s'agit du premier rapport sur la différence phénotypique des "*guajalotes*" au Mexique.

Resumen

Se elaboró un estudio para conocer la diversidad genética de los Guajolotes presentes en las pequeñas explotaciones avícolas de traspatio. De Septiembre de 2004 a Julio de 2006 en 54 municipios de la región costa de Oaxaca, México; se visitaron 768 productores. Hasta el momento se han identificado 11 fenotipos diferentes de Guajolotes descritos anteriormente. Los fenotipos identificados y su frecuencia son: Bronze (30.10%), Black (29.01%), Royal Palm (13.36%), Auburn (5.27%), Bourbon Red (5.24%), Narragancet (2.62%), Spotting (2.41%), Brown (2.19%), Slate (1.74%), White (1.53%) y Albinismo imperfecto (0.21%), el resto de la muestra no fue identificado como algún fenotipo descrito anteriormente. Este es el primer reporte sobre diferenciación fenotípica de Guajolotes para México.

***Key words:** Backyard poultry, Color of feather, Genetics, Turkey, Variety.*

Introduction

Mexico has brought to the world one of the three most important species of domestic birds in current poultry farming: the turkey, (*Meleagris gallopavo*). There is a general agreement that domestication of this bird by one of the Central American cultures took place on actual Mexican territory (Hale *et al.*, 1962; Schorger, 1966; Crawford, 1990; Henson, 1992).

Nowadays, what people know as Guajolote (*M. g. gallopavo*) are domesticated, nondescript native birds whose productive characteristics are unknown. Turkeys, which had been derived from the Mexican subspecies (*M. g. gallopavo*), were brought to northeastern America from Europe from the 16th century, where they interbred with the

eastern subspecies (*M. g. silvestris*) forming the bronze bird that became the foundation for nearly all domestic lines specialized for meat production (Crawford, 1990).

In Mexico, Guajolote breeding is practiced mainly in backyard conditions along with native birds that have not been genetically selected. Such birds exhibit great variability in regard to their size, weight and phenotype (Jerez *et al.*, 1994). In rural communities, they have an important economic, social and cultural value (Diaz, 1976).

Guajolote breeding in backyards is common in rural communities (Saucedo, 1984), peri-urban areas and deprived areas in big cities (Aquino *et al.*, 2003). In rural communities, Guajolotes are mainly kept for domestic use or gifts, a tradition that has lasted through the centuries.

In Mexico, it is recognized that the study of the native Guajolote is an urgent necessity and, as a consequence of the poor production conditions of the backyard system (Aquino *et al.*, 2003), the possibility of extinction in the short term cannot be ruled out (SAGARPA, 2003). Paradoxically, even though the actual turkey descended from the Guajolote, which was domesticated in Mexico, at the present time a native breed has not been reported or characterized in this country (FAO, 2006).

It is important to study the Guajolote and its production potential, because while it is possible to cross it with the turkey, with fertile offspring, there is a resulting loss of very important characteristics like adaptation to different environmental, sanitary and nutritional conditions. The turkey and the Guajolote are not the same; the Guajolote has more genetic variation than the turkey due to genetic isolation and a longer period of genetic adaptation to local environmental conditions, but is less studied than the turkey. In the USA the turkey is characterized in 31 varieties (Sponenberg *et al.*, 2000, 2005). Some of these varieties have phenotypic similarities to the Guajolote. Therefore, this study was conducted for the purpose of evaluating the phenotypic diversity of the Guajolote in backyard poultry farming setings in Mexico, using varieties of turkey as a reference.

Materials and Methods

From September 2004 to July 2006, 768 backyard turkey growers located in different communities distributed in the 54 coastal municipalities of Oaxaca, Mexico were visited.

They lie between coordinates 16° 45′ latitude north and 96° 20′ longitude east, with an altitude range of 0 – 3 000 meters. The prevailing vegetation is diverse: oak trees, pine trees, thorny bushes, dense or medium sub-deciduous jungle, seasonal evergreen forest, low deciduous jungle, medium jungle or low evergreen, mangrove swamps, sterns, palm trees, savanna and pastureland (Torres-Colin, 2004). The predominant climates are: temperate sub-humid C (w1), warm semi-dry Bs1hw, warm sub-humid Aw1, semi-warm sub-humid (A)C(w1) and warm humid Am(f) (Trejo, 2004).

In each backyard operation, photographs were taken to determine the color pattern of each bird. When there was no access to the birds because they were grazing out in the countryside, the information was obtained directly from the producers. The results obtained were analyzed with descriptive statistics (Steel *et al.*, 1997). The comparison of the color pattern of the birds observed with the standard breeds was executed by a direct comparison of the pictures taken, and compared with different photographs and breed descriptions (Platt, 1925; Robertson, 1929; Hutt and Mueller, 1942; Robertson at al., 1943; Marsden and Martin, 1945; Asmundson, 1945, 1950,1955; Nestor and Renner, 1979; Savage, 1990; Savage and Attamangkune,1990; ALBC, 2006; Savage and Zakrzewska, 2006).

Results and Discussion

The most frequent distribution (Table 1) was that of the Guajolote with plumage of the phenotype identified as 'Bronze' (Marsden and Martin, 1945; Savage, 1990; ALBC, 2006; Savage and Zakrzewska, 2006). They were found with a frequency of 30.1%,and were recognizable by their iridescent green feathers on the neck, breast, wings and back; the primary and secondary feathers of the tail and wings are alternatively black and white stripes (Figure 1).

The completely black feathers (Figure 2), belong to the second most common type of coloration (29.0%) and corresponds to the 'Black' phenotype (Platt, 1925; Asmundson, 1945; Savage, 1990; ALBC, 2006; Savage and Zakrzewska, 2006); followed by the pattern of white feathers over all the body with areas of black feathers on the neck, back and wings (Figure 3) that belongs to the 'Royal Palm' or 'Palm' phenotype (Asmundson, 1945; ALBC, 2006; Savage and Zakrzewska, 2006). This phenotype was found with a frequency of 13.4%.

Figure 1. Guajolote of Bronze phenotype.

Figure 2. Guajolote of Black phenotype.

Figure 3. Guajolote of Royal Palm phenotype.

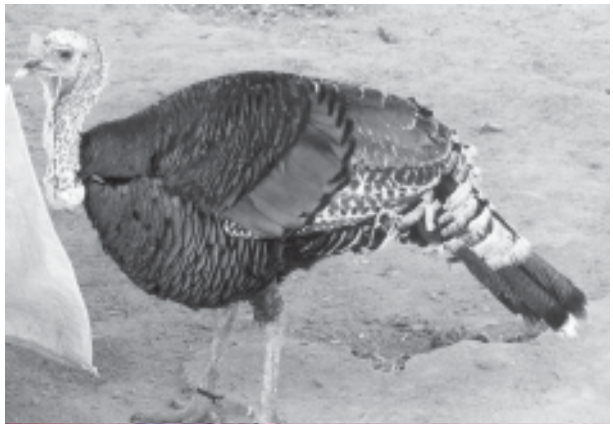

Figure 4. Guajolote of Auburn phenotype.

Figure 5. Guajolote of Bourbon Red phenotype.

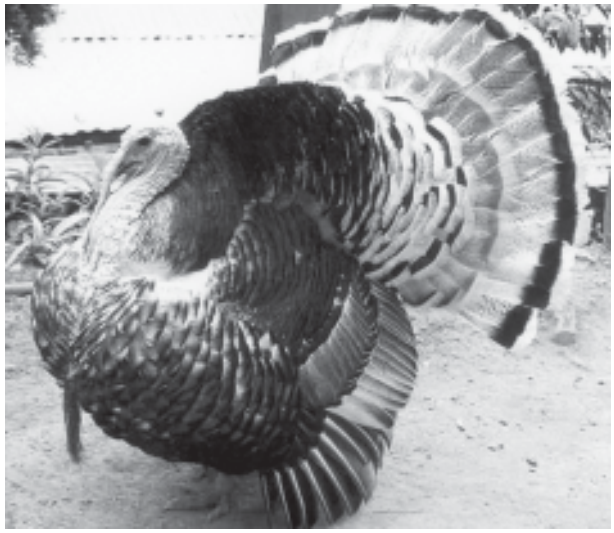

Figure 6. Guajolote of Narragancet phenotype.

Table 1. Frequency of color phenotypes observed in guajolotes of the coast of Oaxaca, Mexico.

Color	%
Bronze	30.1
Black	29.0
Royal Palm / Palm	13.4
Auburn	5.3
Bourbon, Bourbon Red, Red	5.2
Narragancet	2.6
Spotting	2.4
Brown	2.2
Slate	1.7
White	1.5
Imperfect Albino	0.2
Not characterized[1]	6.3

[1]Phenotype do not meet the previously described characteristics.

Figure 7. Guajolote of Spotting phenotype.

Figure 8. Guajolote of Brown phenotype.

In black Guajolotes where the characteristic bronze pattern is substituted by a reddish brown color, the feathers of the tail are reddish brown with black and white stripes (Figure 4) and occurred with a frequency of 5.4%. They were identified as the 'Auburn' phenotype (Asmundson, 1950; Savage and Zakrzewska, 2006); and birds with a reddish brown color with white feathers on the wings (Figure 5) were recognized as the 'Bourbon', 'Bourbon Red' or 'Red' phenotype (Robertson, 1929; Savage, 1990; ALBC, 2006) and occurred with a frequency of 5.2%.

The color pattern of the feathers characteristic of the 'Narragansett' phenotype (Robertson, 1929; Savage, 1990; ALBC, 2006; Savage and Zakrzewska, 2006) was identified by their white color with dark gray feathers on the neck, wings and breast; the feathers on the tail of a bronze color also have black and white stripes (Figure 6). This phenotype had a frequency of 2.6%.

Figure 7 shows a Guajolote type with a frequency of 2.4%, with adult white plumage and a black pigmentation on all the feathers, mainly on the neck, sides and wings, without stripes on the

Figure 9. Guajolote of White phenotype.

Figure 11. Guajolote of Imperfect Albino phenotype.

feathers. These were identified as the 'Spotted' phenotype (Asmundson, 1955; Savage, 1990). Birds with brown plumage (Figure 8) occurred with a frequency of 2.2% and were identified as the 'Brown' phenotype (Savage, 1990; Savage and Attamangkune, 1990; Savage and Zakrzewska, 2006).

Guajolotes of the 'White' phenotype were identified (Figure 9), with completely white plumage (Robertson *et al.*, 1943; Nestor and Renner,

Figure 10. Guajolote of Slate phenotype.

1979; Savage, 1990; Savage and Zakrzewska, 2006) and Guajolotes with ash grey coloring belonging to the 'Slate' phenotype, occurred with a frequency of 1.7% (Figure 10) (Platt, 1925; Savage, 1990; ALBC, 2006). Finally, birds with white feathers but with some kind of pigmentation were identified as the '*Imperfect Albino*' phenotype, which had an observation frequency of 0.2% and are shown on Figure 11 (Hutt and Mueller, 1942; Asmundson, 1945; Savage, 1990).

The rest of the sample (6.3%) are birds whose phenotypes do not meet the previously described characteristics. Figures 12, 13 and 14 show examples of them.

This great diversity of genotypes could be the result of the genetic variation accumulated through centuries of domestication of the species (Crawford, 1990).There is a possibility that in rural communities a hybridization took place between wild turkeys (*M. g. mexicana* and *M. g. intermedia*), that still exist in Mexico, (Hale, *et al.*, 1962; Starker, 1985) and the feral Guajolote or domestic bird (*M. g. gallopavo*). It is important to recognize the Guajolote genetic diversity that still exists in Mexico in order to design and develop rescue and recovery programs for this species, which is used by the agricultural and indigenous communities.

Figure 12. Guajolote without a described phenotype.

Figure 13. Guajolote without a described phenotype.

Figure 14. Guajolote without a described phenotype.

Nevertheless, it is necessary to conduct a detailed investigation in order to determine if there are phenotypes that have not been previously described, and establish a Guajolote classification by genotypes, breeds or varieties using molecular genetics.

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Survey and characterization of South Kanara buffaloes in India

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Summary

Kanarese buffaloes are medium built animals distributed in the South Kanara region on the west coast of South India. These buffaloes are dual purpose animals used mainly for agricultural operations in wet fields and for some milk production. They are famous for racing in water-bound fields. South Kanara buffaloes are moderate milk yielders producing about two to seven litres daily for a lactation period that ranged between 210 to 360 days. Genetic diversity analysis was performed using 10 microsatellite markers in a panel of 48 unrelated animals. The average number of alleles was estimated to be 6.30 with an average heterozygosity of 0.62 per locus. The population showed departure from the Hardy-Weinberg equilibrium at all of the 10 loci tested. The heterozygote deficiency was estimated as 9.2% suggesting the presence of considerable inbreeding in the population. The allele frequency distribution followed the normal L-shaped form suggesting that the breed had not encountered a genetic bottleneck in the recent past.

Résumé

Les buffles Kanarese sont des animaux de taille moyenne qui se trouvent dans le Sud Kanara, région de la côte Ouest du Sud des Indes. Ces buffles sont des animaux à doubles propos utilisés surtout dans les travaux agricoles des régions humides et pour quelque production de lait. Ils sont connus pour les courses dans les champs inondés. Les buffles du Sud de Kanara ont une production de lait limitée, environ deux à sept litres par jour pendant la période de lactation, qui va de 210 à 360 jours. L'analyse de la diversité génétique a été réalisé en utilisant 10 marqueurs microsatéllites sur un échantillon de 48 animaux sans relations. Le nombre moyen d'allèles a été estimé à 6,30 avec une moyenne d'hétérocygosité de 6,20 par locus. La population montrait une déviation de l'équilibre de Hardy-Weinberg dans tous les 10 loci testé. Le manque d'hétérocygosité a été estimé à 9,2%, ce qui indique la présence importante de consanguinité dans la population. La fréquence de distribution des allèles suit la forme normale de L, ce qui indique que la race n'a pas rencontré une limite génétique récemment.

Resumen

Los búfalos Kanarese son animales de tamaño medio que se encuentran en el sur de Kanara, en la región de la costa oeste des sur de la India. Estos búfalos son animales de doble propósito utilizados sobre todo en los trabajos agrícolas en zonas húmedas y para algo de producción de leche. Se conocen también por las carreras en campos inundados. Los búfalos des sur de Kanara tienen una producción de leche limitada, alrededor de dos a siete litros por día durante el periodo de lactación, que va de 210 a 360 días. El análisis de la diversidad genética se ha realizado utilizando 10 marcadores microsatelitares sobre una muestra de 48 animales sin relación entre sí. La media de alelos se ha estimado en 6,30 con una media de heterocigosis de 6,20 por locus. La población muestra una desviación del equilibrio de Hardy-Weinberg en todos los 10 loci analizados. La falta de heterocigosis se ha estimado en 9,2%, lo que indica la presencia de consanguinidad en la población. La frecuencia de distribución de los alelos sigue la forma normal de L, lo que indica que la raza no ha encontrado recientemente ningún límite genético.

***Keywords**: Status, Characteristics, Genetic diversity, Microsatellites, Bottleneck.*

Introduction

India is a virtual repository of buffalo genetic resources and is the major buffalo rearing country

in the world. Around 57% of the world buffalo population is found in India and buffaloes contribute 54% of the total milk produced in the country. Furthermore, they play an important role in the rural economy through other means as well, including draught power, dung, urine and other minor products. The genetic diversity of Indian buffaloes is represented by ten recognized breeds and 16 lesser known populations. Many of these are known for their adaptability to harsh climatic conditions, tolerance to tropical diseases and survival under meager feeding and poor management practices.

South Kanara buffaloes are one such lesser-known populations, but are famous for their speed in '*Kambla*' racing and wet-field agricultural operations. Also known as '*Kanarese*' and '*Malabar*' buffaloes, these animals were originally found in the coastal regions of the former South Kanara district in Karnataka state, which included the Mangalore and Udupi regions. There was a sect of Hindus known as '*Jain Bants*' who owned and developed this hardy breed of buffaloes. Buffalo racing has traditionally been one of the great sources of amusements of these people and every rich Bant kept his own '*Kambla*' field for buffalo racing.

South Kanara buffaloes were first mentioned by Gunn (1909) and subsequently by Littlewood (1936) and Cockrill (1974), who described the famous '*Kambla racing*' involving these animals in this region. However, information on characteristics, performance levels and management practices are scant in the literature. In the present study an attempt has been made to characterize this breed through a systematic survey in the breeding tract and genetic diversity analysis using microsatellite markers.

Material and Methods

A survey was conducted in 13 villages selected randomly from different parts of the breeding tract, to collect information on various aspects of buffalo husbandry in the region. Data collection on various management practices followed in the breeding tract and different performance traits were generated by interviewing the farmers using a structured questionnaire. A total of 47 farmers were interviewed to record the habitat, housing system, feeding management and breeding practices followed in the tract. Performance traits like daily milk yield, lactation length, age at first calving and calving interval were recorded on 48 animals based on the reports of the farmers. Physical characteristics regarding colour, appearance, horn pattern, head, face and barrel were recorded in adult buffaloes of both sexes (N=63) and udder characteristics were recorded in adult females (N=51) during the survey. Eight different body measurements were recorded on 107 animals of different age and sex, and were analyzed accordingly. The body measurements recorded included body length, height at withers, heart girth, paunch girth, face length, ear length, horn length and tail length.

A total of 48 blood samples were collected randomly from unrelated animals in different regions of the breeding tract following the MoDaD guidelines (Measurement of Domestic Animal Diversity, FAO, Rome). DNA was extracted from whole blood using standard protocol (Sambrook *et al.*, 1989). The DNA isolation procedure involved lysis of red blood cells, digestion of proteins using Proteinase-K and precipitation of proteins using phenol:chloroform:isoamyl alcohol. A set of 10 microsatellite markers originally identified in cattle and evaluated in buffaloes (Navani *et al.*, 2002) were utilized for the present study. PCR was performed with 100 ng of genomic DNA in a 25 µl reaction volume with an initial denaturation of 95°C for 2 minutes, 30 cycles of 92°C for 45 s, 55°C for 45 s, 72°C for 45 s and finally extension at 72°C for 10 minutes. The amplified products were resolved on 6% denaturing Urea-Polyacrylamide gels (Sequi GT system, Bio-Rad, USA) and alleles were detected by silver staining (Bassam *et al.*, 1991).

The fragment sizes were calculated by comparing the electrophoretic mobility of the alleles with standard size DNA marker ladder which was run along the PCR product. The allele frequencies, observed and expected heterozygosities and departure from Hardy-Weinberg equilibrium were calculated using POPGENE software (Yeh, *et al.*, 1999). Polymorphism Information Content was calculated using the formula given by Botstein *et al*. (1980). The population was tested for the occurrence of any recent reduction in the effective population size using the BOTTLENECK program (Piry *et al.*, 1999).

Results and Discussion

Breeding tract

South Kanara buffaloes are medium built animals distributed originally in the former South Kanara

region around Mangalore and Udupi on the west coast of India. This region is bounded by coast line on the west while a range of mountains called the Western Ghats separates it from the east. The Western Ghat region is characterized by natural shoal forests which are rich in highly diversified fauna and flora. Towards the east, the Western Ghats gradually fade into semi-mountainous regions and the plain lands of the Shimoga district. However, the presence of buffaloes in their original habitat has decreased substantially while more such animals are found in the adjoining Shimoga district (Figure 1).

Ecological settings

Geographically, the breeding tract is situated between 12°57′ to 14°39′ N latitude and 74° to 75°52′ E longitude. The altitude is about 600 metres above mean sea level. The total geographical area of the breeding tract is 14 849 square kilometres. The entire breeding tract is classified into three agro-climatic zones based on rainfall pattern, soil and climate namely the coastal zone, hilly zone and southern transitional zone. The coastal zone includes the strip of land along the west coast in the Dakshin Kannad and Udupi districts. The hilly zone includes the region around the Western Ghats in the Dakshin Kannad and Shimoga districts. The southern transitional zone includes the eastern plains of the Shimoga district.

The general climate of the district is classified as humid with medium to heavy rainfall in the Kharif season (June – September) followed by a mild winter (October – January). The summer months are moderately hot with scanty rainfall. The average annual rainfall is around 180 cm. Rice is the major crop of the region with maize, cotton, sugarcane and groundnut also being cultivated.

Status of buffaloes in the breeding tract

According to the 17th Livestock census (2003), the cattle and buffalo population of Karnataka state is 9.54 and 3.99 millions, respectively. The State has 5.2% and 4.1% of the total cattle and buffalo population of the country respectively. The trend of the buffalo population from 1972 to 1997 in the

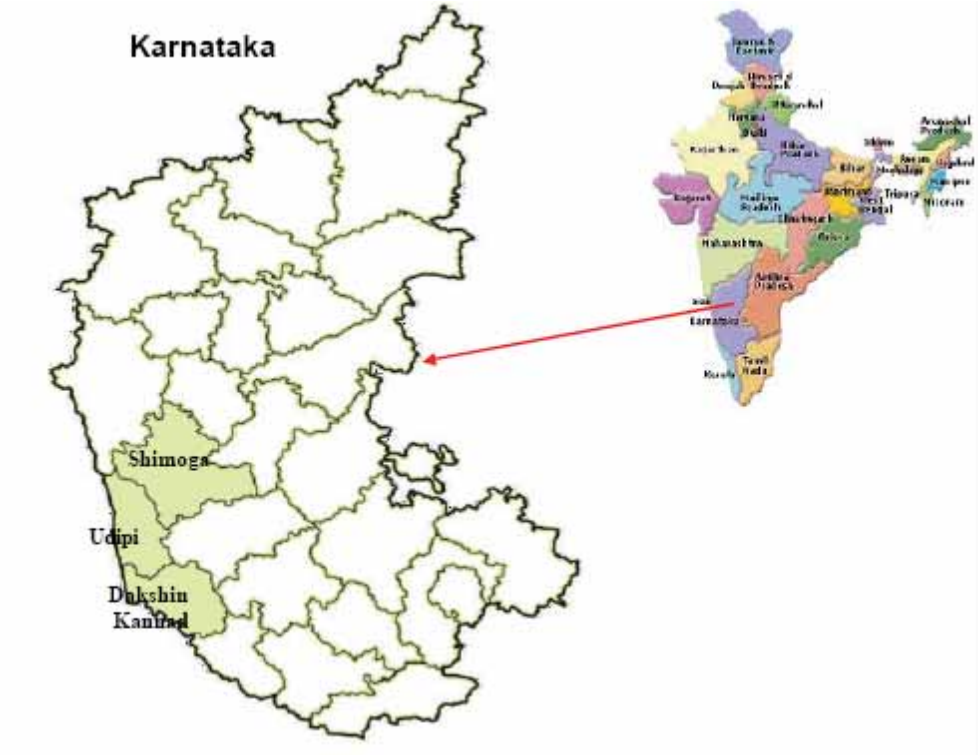

Figure 1. Breeding tract of South Kanara buffaloes.

State showed an increase of 33.6% while it declined by 8.7% from 1997 to 2003. There was also a decline in the total cattle population of 11.9% in the corresponding period (1997 to 2003) with higher reductions in indigenous animals (16.8%). The crossbred cattle population increased by 23.9% during this period. This shows a trend of shifting preference towards crossbred cattle as preferred milk animals in the region.

In the districts of Dakshin Kannad, Udupi and Shimoga which comprise the breeding tract of South Kanara buffaloes, the total buffalo population is 269 200 (Table 1). This consists of animals of the South Kanara type, graded Murrah and Surti and non-descript animals. Murrah/Surti graded buffaloes constitute 3.5% of the total buffalo population in the breeding tract. Although the buffaloes of the South Kanara type are found to be more common in all three districts, the population of non-descript animals is relatively higher in urban areas than in the countryside. Among the three districts, the population of buffaloes in Dakshin Kannad and Udupi are considerably lower, where crossbred cattle have replaced them as dairy animals. However, in Shimoga district, the population of buffaloes is four times higher than that of crossbred cattle suggesting a preference for these animals. The possible reason for this scenario is a difference in the agricultural pattern between these areas. Dakshin Kannad and Udupi districts are in the coastal zone and are comparatively more fertile than the interior Shimoga region, a large area of which is covered by forests. Most of the remaining area of this district is rain-fed with irrigation facilities restricted to only two circles (*Taluks*). These South Kanara buffaloes are thus able to thrive better than crossbreds in the comparatively low input system of the Shimoga region.

Buffalo husbandry practices

Housing

Animals are housed close to the human dwellings. In most cases, closed housing is provided (81.8%). In most instances (62.5%), the animals and humans are housed in different parts of the same building, with separate structures in the remaining cases. Most of the constructions are permanent (63.6%) with thatched roofs covered with paddy straw or tiled roofs. Floors are generally uneven without proper drainage facilities (Figure 2). In peri-urban areas, the animals are overcrowded with less than the minimum required floor space of 3.5 square meters (ICAR, 2002) being provided. In rural areas, the practice of allowing the animals to wallow in the nearby water sources is prevalent (66.7%). Mostly the animals wallow around noon after grazing in the fields under a hot sun (Figure 3).

Table 1. Population status of cattle and buffaloes in the breeding tract.

Species	Dhakshin Kannad	Shimoga	Udupi
Buffalo male			
< 1 year	833	14 911	898
1-3 years	1 431	11 289	887
Breedable males	375	1 606	208
Work animals	14 949	11 350	37 731
Breeding and work	584	576	328
Others	123	670	129
Buffalo female			
< 1 year	1 373	26 814	1 865
1-3 years	1 532	25 616	1 378
In milk	2 875	55 993	3 824
Dry females	1 564	37 508	1 473
Heifers	345	6 408	374
Others	78	1 263	92
Total	26 062	194 004	49 187
Cattle			
Crossbred	109 193	59 012	91 053
Indigenous	222 349	465 939	235 004
Total	331 542	524 951	326 057

Feeding

Paddy straw, dry mixed grasses and green grasses are the main sources of roughage. Wheat bran, cotton seed cake, groundnut cake and rice bran are given as concentrates. About half (45.5%) of the farmers provide concentrates to the milking animals; 0.5 to 2 kg of concentrate is usually given to the lactating animals at the time of milking. Some farmers even feed the animals with kitchen wastes and hotel wastes; this practice is more prevalent in the urban areas.

Figure 2. Typical animal house in the breeding tract.

Figure 3. South Kanara buffaloes wallowing in a pond.

Breeding

Breeding of buffaloes is highly disorganized in the breeding tract. Natural service is commonly practiced with only 9.9% of the farmers in the urban and peri-urban areas using artificial insemination. In the rural areas A.I. is completely absent and even the availability of breeding bulls is inadequate with usually no more than two to three animals per village. Although A.I. services are available in some urban areas, semen of South Kanara buffaloes is not available and the farmers have to opt for either Murrah or Surti semen. As a result, the proportion of graded South Kanara buffaloes and non-descript animals are more common in the urban areas.

Physical characteristics

South Kanara buffaloes are well-built medium-sized animals. The coat colour varies from brown to silver grey and black. Their skin is black. Below the knees, the hair colour is generally brownish white. The head is fairly long with a broad forehead. Ears are moderately long and erect. The neck is long with a moderately thick dewlap. Horns are flat, corrugated and curved, projecting backward, sideward and downward at the neck. Shoulders are long and slope smoothly with the body. The barrel is well built and medium in size with a straight and wide back. Legs are strong with hard hooves. The udder is moderately developed with teats of medium size and squarely placed behind the hind legs. The tail is fairly long, thin and flexible ending in a black switch. Figures 4 and 5 show typical male and female South Kanara buffaloes, respectively.

Body measurements

The mean and standard error of eight different body measurements in different age groups are presented in table 2. The body length, height at withers, heart girth and paunch girth ranged from 84 to 188 cm, 93 to 189 cm, 117 to 181 cm and 131 to 196 cm. respectively. Face length and ear length ranged from 37 to 55 cm and 15 to 28 cm respectively. The length of horns varied from 23 to 87 cm in the adult animals.

Table 2. Body measurements of South Kanara buffaloes in different age groups.

Parameters	Young Calves (< 2 weeks) (17)	Calves (6 – 12 months) (13)	Young Stock (> 1 to < 3years) (14)	Adults	
				Male (12)	Female (51)
Body length (cm)	49.4±2.3	60.3±1.6	68.8±2.5	124.5±2.5	112.8±3.3
Height at withers (cm)	61.4±1.4	73.3±1.2	85.5±1.6	119.0±1.0	113.1±2.9
Heart girth (cm)	59.7±1.6	80.2±1.8	97.8±5.0	169.5±0.5	154.2±2.9
Paunch girth (cm)	57.1±1.7	88.0±2.6	104.5±4.6	170.0±2.0	165.2±3.2
Face length (cm)	21.3±0.4	27.9±0.6	31.8±1.3	44.5±1.5	42.5±0.7
Horn length (cm)	-	-	11.5±3.3	51.0±5.0	42.1±2.2
Ear length (cm)	12.7±0.5	16.4±0.3	6.8±0.3	20.5±1.5	20.9±0.6
Tail length (cm)	31.6±1.3	42.3±1.0	51.8±3.8	92.0±2.0	72.5±1.8

Figures in parentheses indicate number of observations.

Table 3. Measures of genetic variation at 10 microsatellite loci in South Kanara buffaloes.

Locus	Allele size range	n_o	n_e	Heterozygosity			PIC	F_{IS}
				Observed	Expected	Nei's		
ILSTS 017	113-125	7	6.15	0.896	0.846	0.838	0.817	-0.069
ILSTS 073	143-149	3	2.32	0.000	0.575	0.569	0.477	1.000
ILSTS 052	139-185	10	6.98	0.750	0.866	0.857	0.841	0.125
HEL 013	168-188	6	3.25	0.563	0.700	0.693	0.651	0.188
ILSTS 061	137-163	8	5.73	0.521	0.834	0.826	0.803	0.369
ILSTS 058	123-153	10	6.81	1.000	0.862	0.853	0.837	-0.172
ILSTS 026	140-150	4	2.67	0.800	0.633	0.625	0.582	-0.279
ILSTS 008	129-159	4	1.60	0.455	0.378	0.374	0.319	-0.217
ILSTS 095	201-219	6	2.63	0.745	0.626	0.619	0.561	-0.203
ILSTS 036	126-170	5	2.33	0.468	0.577	0.571	0.542	0.179
Mean	-	6.30	4.05	0.620	0.690	0.682	0.643	0.092

n_o = Observed no. of alleles; n_e = effective no. of alleles; PIC=Polymorphism Information Content.

Production performance

South Kanara buffaloes are moderate milk producers and normally give two to seven litres of milk daily. Some animals in villages reach a peak yield of more than 10 litres per day, however. The average daily milk yield was 3.9±0.3 litres (n=48) as reported by the farmers. The length of lactation varied from 210 to more than 360 days with an average of 313.6±10.2 days. The lactation milk yield varied from 420 to 2520 litres with a mean of 1 206.8±110.1 litres (n=44). South Kanara buffaloes have relatively long productive life spans as demonstrated by animals with more than five calvings commonly found in the villages. Age at first calving and calving interval varied from 30 to 60 months and 12 to 36 months respectively. The average age at first calving was estimated to be 41.4±1.9 months (n=38) and the mean calving interval was 543.4±51.3 days (n=36).

Figure 4. South Kanara bull.

Figure 5. South Kanara she-buffalo.

Figure 6. South Kanara males in wet fields operations.

Figure 7. South Kanara working buffalo.

Utility

South Kanara buffaloes are dual purpose animals used for milk production as well as agricultural operations in wet fields. They are better suited than are local cattle to ploughing and puddling the wet fields meant for paddy cultivation. They are active, fast moving, hardy and can work continuously for four to six hours in the wet fields. Although both males and females are used for the purpose, males are preferred (Figures 6 and 7).

Genetic characterization using microsatellite markers

All 10 microsatellite loci amplified successfully in the samples from South Kanara buffaloes and produced definite banding patterns from which individual genotypes could be ascertained (Figure 8). Different measures of genetic variation estimated in South Kanara buffaloes are presented in table 3. Across the 10 microsatellites studied, a total of 63 alleles were identified. The mean observed number of alleles (6.3) was marginally

lower than that of other Indian buffaloes as reported by Kumar *et al.* (2006).

Eight of the 10 loci with the exception of ILSTS 008 and ILSTS 073 had Polymorphism Information Content (PIC) values of more than 0.5, suggesting that they are informative for population genetic analysis. (Botstein *et al.*1980). Observed heterozygosity varied between zero (ILSTS 073) to one (ILSTS 058) and the mean observed heterozygosity of 10 loci was less than average expected heterozygosity (0.69). The mean observed heterozygosity of South Kanara buffalo population is higher than that of Marathwada (Kathiravan *et al.*, 2008), Bhadawari and Tarai (Arora *et al.*, 2004) buffaloes while it is slightly lower or comparable to that of other Indian buffalo breeds (Kumar *et al.*, 2006). The average observed heterozygosity estimation in this study thus shows that South Kanara buffaloes are harbouring a good amount of genetic variation.

The test for Hardy-Weinberg equilibrium (HWE) showed that all the 10 loci deviated significantly (Table 4). Departure from HWE is mostly due to heterozygote deficiency which may result from one or more of the following reasons:

1. presence of null alleles;
2. small sample size; and
3. Wahlund effect i.e. presence of fewer heterozygotes in a population than predicted on account of population subdivision.

In farm animal species, the prevalence of sire lines selected for economic traits leads to increased consanguinity. Such a breeding system produces reduced heterozygosity within a sub-population in a breed. However in our case, although selection and use of extensive A.I. are absent, the availability of very few breeding bulls in the tract might have contributed to increased consanguinity. This is further supported by the estimated mean value of F_{IS} in the population which was positive and equal to 0.09. Thus, the shortage of breeding bulls in the population and confinement of these buffaloes to a small geographical area could be the possible reasons for the deficiency of heterozygotes.

Table 4. Test for Hardy-Weinberg equilibrium at 10 microsatellite loci in South Kanara buffaloes

Locus	No. of observations	DF	Chi Square	P-value
ILSTS 017	48	21	38.14	0.012
ILSTS 073	48	3	103.51	0.000
ILSTS 052	48	45	64.39	0.030
HEL 013	48	15	36.36	0.002
ILSTS 061	48	28	68.79	0.000
ILSTS 058	47	45	63.61	0.035
ILSTS 026	45	6	18.60	0.004
ILSTS 008	44	6	19.34	0.000
ILSTS 095	47	15	48.02	0.000
ILSTS 036	47	10	20.24	0.027

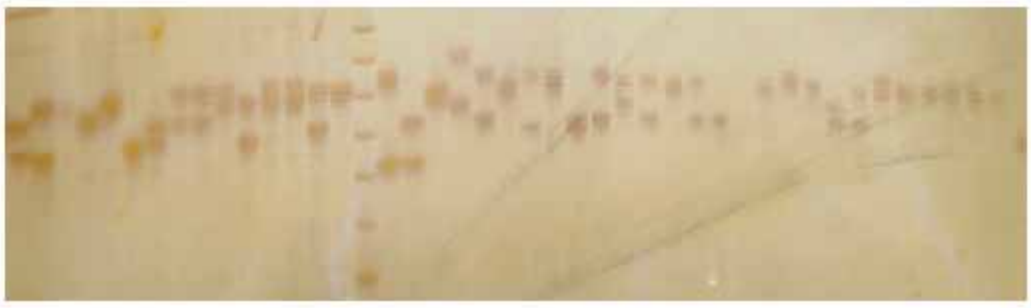

Figure 8. Resolution of genotypes at microsatellite locus ILSTS 058 in a silver stained Urea-PAGE gel.

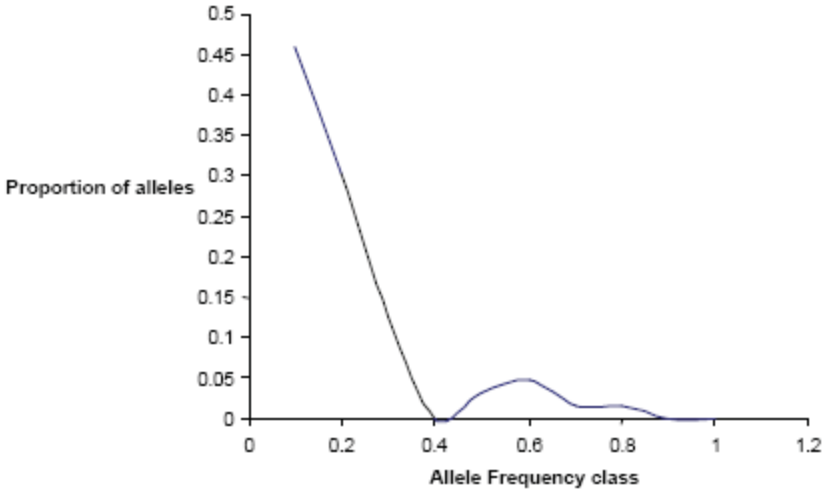

Figure 9. Normal L-shaped curve of distribution of allelic proportions in different allele frequency classes indicating absence of recent bottleneck in South Kanara buffaloes.

The test for BOTTLENECK did not show any significant reduction of effective population size in the recent past. The allele frequency spectrum visualized by the qualitative graphical method of Cornuet and Luikart (1996) is shown in the figure 9. The distribution followed the normal L-shaped form suggesting that the breed had not encountered a genetic bottleneck in the recent past.

Conclusion

South Kanara buffaloes are hardy, dual purpose animals reared for both milk and draught purposes. These buffaloes are able to thrive well in low input systems forming an integral part in the livelihood of farmers in the region. Sufficient genetic diversity was found to exist in the South Kanara buffalo population as revealed by microsatellite data, however steps need to be taken for the genetic improvement as well as conservation of this precious germplasm of the country.

Acknowledgement

The authors are grateful to Dr. R. Raveendra, Deputy Director, Department of Animal Husbandry and Veterinary Services, Shimoga and to Dr. M.G. Govindaiah, Dean, Veterinary College, Shimoga, Karnataka for their help and cooperation during the study.

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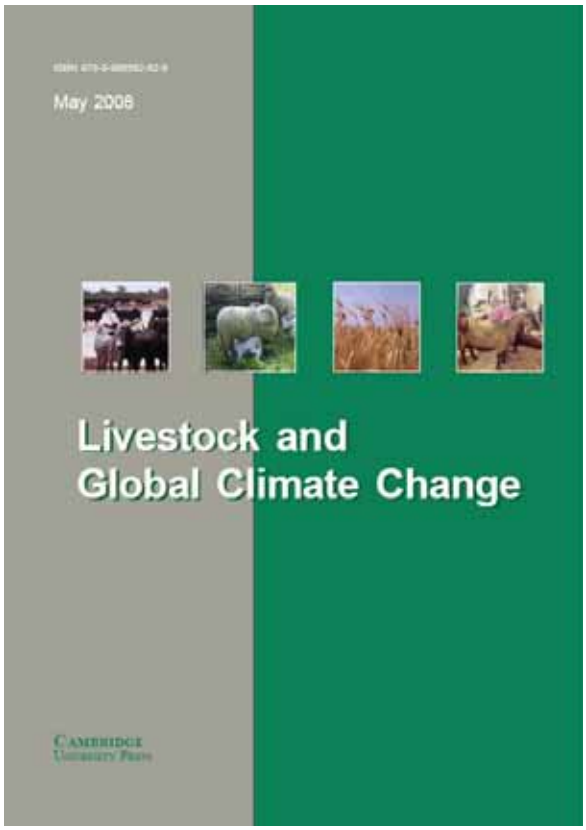
Livestock and Global Climate Change

Rowlinson, P., M. Steele and A. Nefzaoui (Eds)
Proc. of an International Conference held in Hammamet, Tunisia, 17-20 May, 2008
Cambridge University Press.
Published in 2008, pp. 216
ISBN 978-0-906562-62-8

The Proceedings include summaries of 75 theatre presentations and 23 posters. They come under five topics namely: Mitigation, Adaptation, Animal Health, Coping and Strategy - Management Tool, Coping and Mitigation Strategies - Nutritional Tool, and Coping Strategies - Socioeconomic Impact. The papers cover predictions of climate change as it may affect livestock production; the contribution that livestock production makes to these changes; how livestock production can help to mitigate them; how global supply of livestock products will be affected by climate change; how livestock production systems must adapt; and finally which future scientific priorities help address these issues. Extensive areas including production, health, breeding, nutrition, drought, agropastoral and sylvopastoral systems, climate models etc are also discussed. The lack of basic research in all fields related to climate change adaptation and mitigation in developing countries is marked. Differences between farms and countries in the amount of greenhouse gas per unit product are considerable, pointing to high mitigation potential even in standard agricultural practices.

Animal genetic resources were directly discussed in three presentations. These presentations entertain the possibility of changes in species and breed portfolios to adapt to climate changes, e.g. towards camelid and zebu in warmer drier climates, and at the breed level if genetic change could keep pace with the change in climate. Animal genetic diversity and breeding are important for both, climate change adaptation and mitigation. In view of a lack of hard data relevant to the topic, two of these papers used scenarios to anticipate future developments, and one concludes "Regardless of the specific direction of change, the four potential scenarios identified above (livestock product demand increase, breed portfolio change, gene pool reduction and livestock emissions importance) raise policy issues/concerns and have particular policy implications associated with them". The Conference has compiled the state of the art knowledge in highly specialized academic fields, and it served the purpose of arousing interest in an issue where little information is available to draw definitive plans of action.

Copy of the publication is freely available at: *www.bsas.org.uk/downloads/LGCC_procdings.pdf*



Lithuanian horses

Ministry of Agriculture of the Republic of Lithuania
Bertasius M., V. Girininkiene, L. Klimka, V. Macijauskiene, T. Petreikis, S. Svetlauskas & R. Sveistiene (Eds)
Published in 2008, pp. 213
ISBN: 978-9955-23-181-3

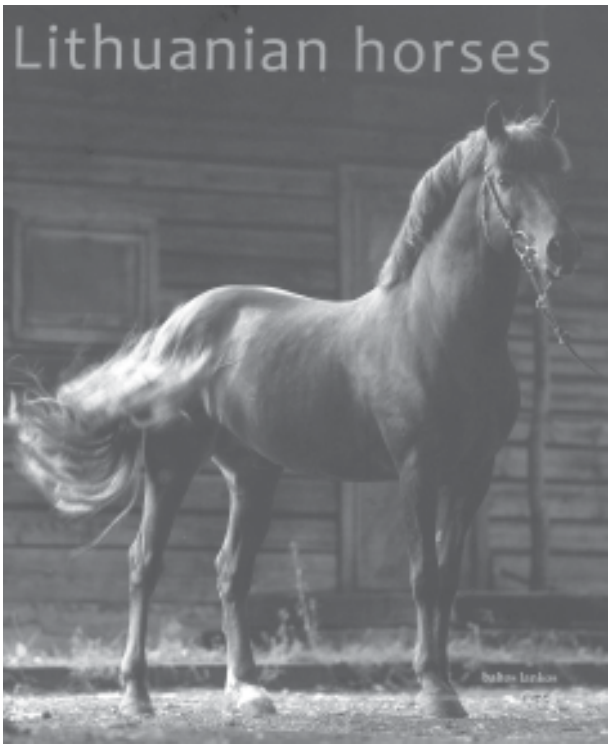
Horses are shrouded in a special aura in Lithuania. For centuries, horse breeding in the villages was linked to a number of customs in the belief that they guaranteed success. .

Lithuanians have always been thankful for their horses, as friends, helpers in hard work in the fields, and transport, and also in protecting their land from foreign invaders. Archaeologists have found burial grounds where a buried horse rests in a stately manner together with its rider, perhaps having brought ancestors back from the battlefield. This shows that Lithuanians were not only a nation of farmers, but also a nation of horsemen.

With urbanization, the role of the horse has changed dramatically, and you will see horses performing difficult agricultural work less and less often. But it still remains closer to Lithuanians than other animals do. This is shown not only by the growing numbers of horses in stables that specialise in rearing them, but also by the growing numbers of horses on farms.

Local breeds of horses are a historical and cultural feature of the country, and also a priceless gene pool. The Lithuanians take care of their breeds by protecting and fostering them. Some breeds are even recognized internationally as protected breeds. It can be said that Lithuanian horses are part of Lithuanian's cultural heritage: Most people have heard something about an old Lithuanian horse breed called •emaitukas. Through •emaitukas gave the beginning for three breeds, Trakehner, Lithuanian Heavy Draught Horses and •emaitukas the heavy type; all these breeds were on the edge of the extinct many times.

This book illuminates the common history of Lithuania and a horse in various aspects. The appearance of •emaitukas and other Lithuanian horse breeds, their diffusion, the condition of equestrian sports and horse-breeding perspectives are reviewed in this book. Particularly rich in pictures, this publication summarises the evolution of the Lithuanian local horse breeds with the parallel description of the evolution of the countries, from the agricultural uses of horses in the old times to leisure and holidays in our days. This publication shows what a pleasure it is for people today, living in urban cities, to communicate with the horse, a wonderful eclectic creature adaptable to the various necessities of man.



Managing breeds for a secure future - strategies for breeders and breed associations

D. Phillip Sponenberg and Donald E. Bixby (Eds)
The American Livestock Breeds Conservancy
P.O. Box 477, Pittsboro, North Carolina 27312 USA
Published in 2007, pp. 209
ISBN 1-887316-07-8

"Managing Breeds for a Secure Future" tackles the challenges of maintaining genetic diversity in species and breeds of livestock and poultry. It is both a theoretical exposition and a practical user's guide. Strategies that secure standardized breeds and landraces are outlined and developed. Many examples demonstrate the practical application of the theory so that breeders can apply the principles to their herds and flocks.

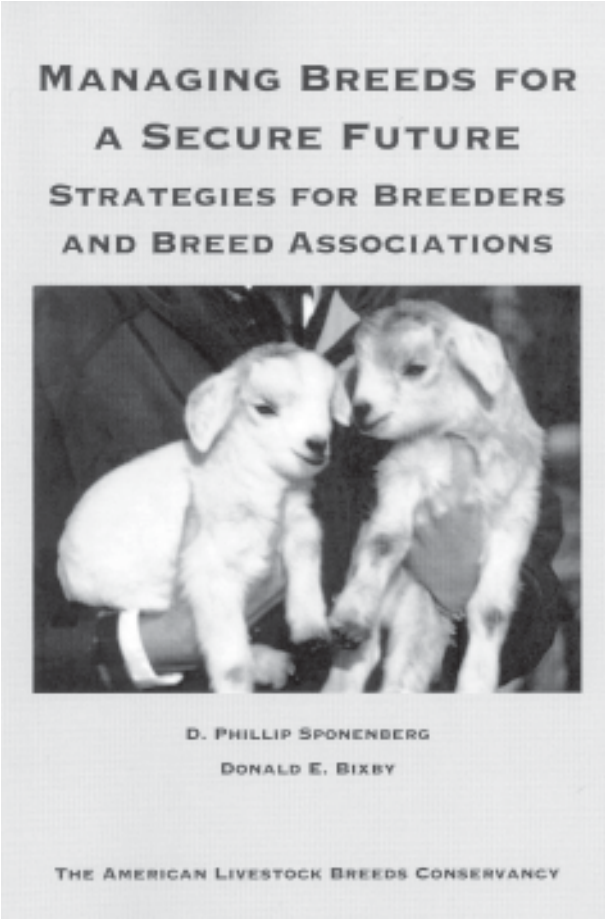
The book, in soft cover, provides information useful to all levels of breeders. Key points are emphasized and examples help beginning breeders. Crisp, detailed explanations of techniques and strategies provide the fine points needed by master breeders. The book addresses the complex political and human aspect of saving rare breeds. Associations are alerted to potential obstacles and pitfalls, and all members are informed of responsibilities.

Breed association leaders and members, breed stewards, conservation organizations, teachers, researchers and students will find this book an excellent resource, text, and handbook. Breed stewards of all levels of experience will find themselves returning to this book again and again.

Considering that the Authors have been the nation's leaders in protecting this valuable resource for our children and their heirs at the American Livestock Breeds Conservancy, this book provides a great service to that cause, with succinct strategies for protecting our food future and respecting our farming past.

Intellect, passion, and action are choreographed seamlessly in a dance to conserve livestock breeds. Each step necessary for breed continuity and its unique regional traditions is outlined and illustrated with interesting examples. This book is a comprehensive guide to proper and practical breed conservation.

A thought provoking and vital reference for any person and every breed association. The gene pools of domestic agriculture are evaporating gene puddles. Diversified agriculture systems and the keepers of our "warehouse " of agricultural knowledge are disappearing. How can individual breeders and breed associations contribute to a sustainable and diverse agriculture system? What are the principles, how can these principles be put into practice? The Authors have tackled these issues over many decades and have presented their knowledge, experience, and prescriptions in this valuable book. Breeders and associations are well served by this guide.



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, under the Global Strategy for the Management of Farm Animal Genetic Resources. 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.

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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.

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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.

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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.
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  FAO. 1996. Domestic Animal Diversity Information System, *http://www.fao.org/dad-is/*, FAO, Rome, Italy.

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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, d'après les recommandation de la Stratégie mondiale pour la gestion des ressources génétiques des animaux domestiques. 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

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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.

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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, siguiendo la Estrategia Mundial para la Gestión de los Recursos Genéticos de los Animales Domésticos. 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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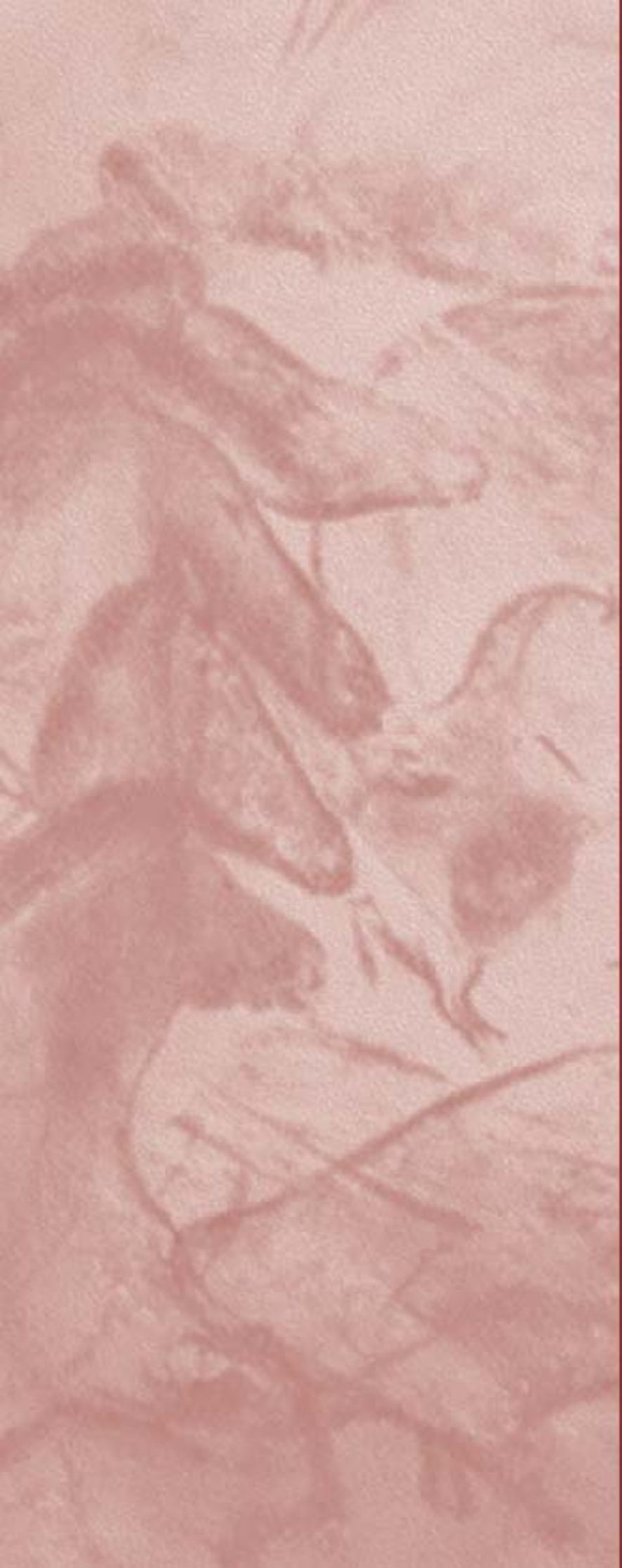
Gracias por su colaboración



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