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Animal Genetic Resources, 2015, 57, ii. © Food and Agriculture Organization of the United Nations, 2015
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Editorial

Dear reader,

With this issue of the journal, the editorial board bids a last farewell to Professor Salah Galal. We were deeply saddened by the news of Salah's passing. Our thoughts are with his wife and family. Salah served as editor of our journal for many years. We got to know him as a kind and knowledgeable team player, who was always available to assist his colleagues in case of need. After his retirement he remained active as a university professor, sharing his passion for animal genetic resources with his students. We shall miss him.

This issue features 13 articles, again with strong focus on the phenotypic and genetic characterization of local livestock breeds. However, it also includes an assessment of indicators for describing the risk status of breeds, an assessment of institutional capacities in animal genetic resources management and a paper on the possible impact of cross-breeding on the environment.

The papers published in this issue support the key findings of *The Second Report on the State of the World's Animal Genetic Resources for Food and Agriculture*, which will be launched in December 2015. The second report serves as an update of the first report, published in 2007, and was prepared based on information provided in 129 country reports, 15 reports from international organizations, 4 reports from regional focal points and networks for animal genetic resources management and inputs from 150 authors and reviewers. It provides a comprehensive overview of the management of animal genetic resources, focusing particularly on changes since 2007 when the first report was published and the Global Plan of Action for Animal Genetic Resources was adopted. The key findings of the second report are as follows: (1) the roles and values of animal genetic resources remain diverse, particularly in the livelihoods of poor people; (2) livestock diversity facilitates the adaptation of production systems to future challenges and is a source of resilience in the face of greater climatic variability; (3) the adaptations of specific species and breeds to specific environmental challenges need to be better understood; (4) the impact of many livestock-sector trends on animal genetic resources and their management is increasing; (5) the world's livestock diversity remains at risk; (6) the assessment of threats to animal genetic resources needs to be improved; (7) institutional frameworks for the management of animal genetic resources need to be strengthened; (8) establishing effective livestock breeding programmes remains challenging in many countries, particularly in the low-input production systems of the developing world; (9) conservation programmes for animal genetic resources have become more widespread, but their coverage remains patchy; (10) emerging technologies are creating new opportunities and challenges in animal genetic resources management; (11) livestock diversity and the sustainable management of animal genetic resources are acquiring a greater foothold on policy agendas. The analysis presented in the report suggests that the strategic priorities for action set out in the Global Plan of Action for Animal Genetic Resources remain relevant.

I kindly invite the readership of the journal to have a look at *The Second Report on the State of the World's Animal Genetic Resources for Food and Agriculture.* The online version will be made available in pdf format at http://www.fao.org/3/a-i4787e/index.html. You will find it in e-book formats in FAO's e-book collection at http://www.fao.org/publications/e-book-collection/en/.

Yours sincerely,

Roswitha Baumung

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Editorial

Cher lecteur,

Avec ce volume du journal, le comité de rédaction tient à rendre un dernier hommage au professeur Salah Galal. La nouvelle de son décès nous a profondément attristés. Sa femme et sa famille sont dans nos pensées. Salah a servi comme rédacteur du journal pendant de nombreuses années, au cours desquelles nous avons pu connaître sa facette de collaborateur aimable et instruit, toujours prêt à aider ses collègues si nécessaire. Après sa retraite, il est resté actif en tant que professeur d'université et a continué à partager avec ses élèves sa passion pour les ressources zoogénétiques. Il va nous manquer.

Ce volume contient 13 articles. De nouveau, l'accent est mis sur la caractérisation phénotypique et génétique des races locales de bétail. Cependant, ce volume comprend également une évaluation des indicateurs pour la détermination de l'état de risque des races, une évaluation des capacités institutionnelles pour la gestion des ressources zoogénétiques et un article sur le possible impact des croisements sur l'environnement.

Les articles publiés dans ce volume soutiennent les résultats-clés du *Deuxième Rapport sur L'État des Ressources Zoogénétiques pour l'Alimentation et l'Agriculture dans le Monde*, qui sera présenté en décembre 2015. Ce deuxième rapport, qui sert de mise à jour du premier (publié en 2007), a été préparé sur la base des informations fournies par 129 rapports nationaux, 15 rapports d'organisations internationales, 4 rapports de centres de coordination et réseaux régionaux pour la gestion des ressources zoogénétiques et avec les contributions de 150 auteurs et relecteurs. Le rapport donne un aperçu exhaustif de la gestion des ressources zoogénétiques, avec un accent particulier porté sur les changements survenus depuis 2007, lorsque le premier rapport a été publié et le Plan d'Action Mondial pour les Ressources Zoogénétiques a été adopté. Les résultats-clés du deuxième rapport sont les suivants: (1) les rôles et la valeur des ressources zoogénétiques restent divers, notamment dans les modes de vie des populations pauvres; (2) la diversité des animaux d'élevage rend plus facile l'adaptation des systèmes de production aux défis futurs et représente une source de résistance face à une plus grande variabilité climatique; (3) il s'avère nécessaire de mieux comprendre les adaptations de certaines espèces et races à des défis environnementaux précis; (4) l'impact des évolutions du secteur de l'élevage sur les ressources zoogénétiques et leur gestion s'est accru; (5) la diversité des animaux d'élevage reste menacée dans le monde; (6) une meilleure évaluation des menaces pour les ressources zoogénétiques est nécessaire; (7) il est nécessaire de renforcer les cadres institutionnels pour la gestion des ressources zoogénétiques; (8) la mise en place de programmes efficaces d'amélioration demeure toujours un défi difficile à relever pour de nombreux pays, surtout dans les systèmes de production à faible intensité d'intrants du monde en développement; (9) les programmes pour la conservation des ressources zoogénétiques se sont généralisés mais leur portée demeure inégale; (10) les technologies émergentes créent de nouvelles opportunités et défis dans la gestion des ressources zoogénétiques; (11) la diversité des animaux d'élevage et la gestion durable des ressources zoogénétiques bénéficient d'une position de plus en plus affermie dans les programmes politiques. L'analyse présentée dans le rapport suggère que les priorités stratégiques d'action énoncées dans le Plan d'Action Mondial pour les Ressources Zoogénétiques sont toujours valides.

Je voudrais inviter les lecteurs du journal à jeter un coup d'œil au *Deuxième Rapport sur L'État des Ressources Zoogénétiques pour l'Alimentation et l'Agriculture dans le Monde*. La version en ligne sera disponible en format PDF sur http://www.fao.org/3/a-i4787e/index.html. Vous le trouverez en format de livre électronique dans la bibliothèque de livres électroniques de la FAO sur http://www.fao.org/publications/fao-e-book-collection/fr/.

Cordialement,

Roswitha Baumung

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Editorial

Estimado lector,

Con este volumen de la revista, la junta editorial rinde un último homenaje al profesor Salah Galal. La noticia de su fallecimiento nos entristeció profundamente. Su mujer y su familia están presentes en nuestros pensamientos. Salah ejerció como redactor de nuestra revista durante muchos años, a lo largo de los cuales llegamos a conocer su faceta de colaborador amable y culto, siempre dispuesto a ayudar a los compañeros en caso de necesidad. Tras su jubilación, permaneció activo como profesor universitario, compartiendo con sus alumnos su pasión por los recursos zoogenéticos. Lo echaremos de menos.

Este volumen contiene 13 artículos, de nuevo con un marcado acento puesto en la caracterización fenotípica y genética de las razas ganaderas locales. No obstante, también incluye una evaluación de los indicadores para la determinación de la situación de riesgo de las razas, una evaluación de las capacidades institucionales para la gestión de los recursos zoogenéticos y un artículo sobre el posible impacto de los cruzamientos sobre el medio ambiente.

Los artículos publicados en este volumen sostienen los resultados clave del *Segundo Informe sobre la Situación de los Recursos Zoogenéticos Mundiales para la Alimentación y la Agricultura*, que será presentado en diciembre de 2015. Este segundo informe, que sirve como una actualización del primero (publicado en 2007), ha sido preparado de acuerdo con la información proporcionada por 129 informes nacionales, 15 informes de organismos internacionales, 4 informes de centros de coordinación y redes regionales para la gestión de los recursos zoogenéticos y con las aportaciones de 150 autores y revisores. El informe ofrece una exhaustiva visión de conjunto sobre la gestión de los recursos zoogenéticos, haciendo particularmente hincapié en los cambios acontecidos desde 2007, año en que se publicó el primer informe y se adoptó el Plan de Acción Mundial sobre los Recursos Zoogenéticos. Los resultados clave del segundo informe son los siguientes: (1) los roles y el valor de los recursos zoogenéticos siguen siendo diversos, sobre todo en los modos de vida de los pueblos pobres; (2) la diversidad del ganado facilita la adaptación de los sistemas de producción a los desafíos futuros y es una fuente de resistencia frente a una mayor variabilidad climática; (3) se hace necesario entender mejor las adaptaciones de determinadas especies y razas a ciertos desafíos ambientales; (4) se está acentuando el impacto de las evoluciones del sector ganadero sobre los recursos zoogenéticos y su gestión; (5) la diversidad ganadera mundial sigue estando amenazada; (6) es necesaria una mejor evaluación de las amenazas a los recursos zoogenéticos; (7) es necesario reforzar los marcos institucionales para la gestión de los recursos zoogenéticos; (8) el establecimiento de programas de mejora eficaces sigue representando un reto exigente para muchos países, sobre todo en los sistemas de producción de bajos insumos del mundo en desarrollo; (9) los programas para la conservación de los recursos zoogenéticos se han generalizado pero su alcance sigue siendo desigual; (10) las tecnologías emergentes están dando lugar a nuevas oportunidades y retos en la gestión de los recursos zoogenéticos; (11) la diversidad del ganado y la gestión sostenible de los recursos zoogenéticos gozan de una posición cada vez más afianzada en las agendas políticas. El análisis presentado en el informe sugiere que las prioridades estratégicas para la acción fijadas en el Plan de Acción Mundial sobre los Recursos Zoogenéticos siguen vigentes.

Quisiera invitar amablemente a los lectores de la revista a echar un vistazo al *Segundo Informe sobre la Situación de los Recursos Zoogenéticos Mundiales para la Alimentación y la Agricultura*. La versión online estará disponible en formato pdf en http://www.fao.org/3/a-i4787e/index.html. Lo encontrarán en formato de libro electrónico en la colección de libros electrónicos de la FAO en http://www.fao.org/publications/e-book-collection/es/.

Atentamente,

Roswitha Baumung

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Is cross-breeding of cattle beneficial for the environment? The case of mixed farming systems in Central Java, Indonesia

T.S.M. Widi[1,2]*, H.M.J. Udo[1], K. Oldenbroek[3], I.G.S. Budisatria[2], E. Baliarti[2], T.C. Viets[1] and A.J. van der Zijpp[1]

[1]*Animal Production Systems Group, Department of Animal Sciences, Wageningen University, PO Box 338, 6700 AH Wageningen, The Netherlands;* [2]*Centre for Genetic Resources, PO Box 16, 6700 AA Wageningen, The Netherlands;* [3]*Department of Animal Production, Faculty of Animal Science, Universitas Gadjah Mada, Jl. Fauna no 3, Kampus Bulaksumur UGM, Yogyakarta, Indonesia*

Summary

Cross-breeding with European beef breeds has become a standard approach for the intensification of smallholder cattle production in Indonesia. This study assessed the environmental impact of cross-breeding, in terms of Global Warming Potential (GWP) and land use. We sampled 90 local Ongole and 162 cross-bred (Simmental × Ongole) cattle farms in four study areas. Expressed per kilogram of live weight of young stock produced, GWP (26.9 kg CO_2–equivalents) and land use (34.2 m^2) of farms with Ongole breeding stock were not significantly different from the GWP (28.9 kg CO_2–equivalents) and land use (37.4 m^2) of cross-bred farms. Cross-bred young stock grew faster, but in general cross-bred cattle required more feed. In the current smallholder production system, the dominant cross-breeding practice of using Simmental semen on Ongole and F_1 cross-bred cows does not result in lower greenhouse gas emissions or land use per kilogram of live weight produced compared with farms with Ongole cows. The advantage from the faster growth of cross-breds is counteracted by the higher emissions from feed production for cross-breds.

Keywords: *cross-breeding, Indonesia, life cycle assessment, mixed farming systems, multi-functionality, Ongole, Simmental*

Résumé

Le croisement avec des races européennes de bovins à viande est devenu un procédé standard dans le but d'intensifier la production bovine des petits propriétaires de l'Indonésie. Cette étude a évalué l'impact environnemental du croisement en termes de potentiel de réchauffement global (PRG) et d'utilisation de la terre. Les mesures ont été effectuées dans 90 exploitations de bovins locaux Ongole et dans 162 exploitations de bovins croisés (Simmental × Ongole) de quatre zones d'étude. Exprimés par kilogramme de poids vif de jeune bétail élevé, le PRG (26,9 kg d'équivalents de CO_2) et les terres employées (34,2 m^2) dans les exploitations ayant des reproducteurs Ongole n'ont pas différé significativement du PRG (28,9 kg d'équivalents de CO_2) et des terres employées (37,4 m^2) dans les exploitations à bovins croisés. Le jeune bétail croisé a grandi plus rapidement mais, en général, les bovins croisés ont eu besoin de plus d'aliments. Dans le système actuel de production des petits propriétaires, la pratique généralisée du croisement, en inséminant les vaches Ongole et les croisées F1 avec du sperme Simmental, n'entraîne pas une moindre émission de gaz à effet de serre ni un moindre besoin de terres, par kilogramme de poids vif produit, par rapport aux exploitations de vaches Ongole. L'avantage de la croissance plus rapide des bovins croisés est atténué par les plus grandes émissions du système de production des aliments destinés au bétail croisé.

Mots-clés: *croisement, systèmes d'agriculture mixtes, Ongole, Simmental, Analyse du Cycle de Vie, multifonctionnalité, Indonésie*

Resumen

El cruzamiento con razas europeas de ganado bovino de carne se ha convertido en un procedimiento estándar para intensificar la producción de ganado bovino de los pequeños propietarios de Indonesia. Este estudio evaluó el impacto ambiental del cruzamiento en términos de potencial de calentamiento global (PCG) y de uso de la tierra. Se muestrearon 90 explotaciones de ganado local Ongole y otras 162 de ganado bovino cruzado (Simmental × Ongole) en cuatro zonas de estudio. Expresados por kilogramo de peso vivo de ganado joven producido, el PCG (26,9 kg de equivalentes de CO_2) y la tierra empleada (34,2 m^2) en las granjas con reproductores Ongole no difirieron significativamente del PCG (28,9 kg de equivalentes de CO_2) y la tierra empleada (37,4 m^2) en las explotaciones con ganado cruzado. El ganado joven cruzado creció más rápidamente pero, en términos generales, el ganado cruzado necesitó más alimento. En el sistema actual de producción de los pequeños propietarios, la práctica dominante del cruzamiento, consistente en utilizar semen Simmental para cubrir vacas Ongole y cruzadas F1, no conlleva una menor emisión de gases con efecto invernadero ni una menor necesidad de terreno, por kilogramo de peso vivo producido, en comparación con las explotaciones de vacas Ongole. La ventaja del crecimiento más rápido de los ejemplares cruzados se ve mitigada por las mayores emisiones del sistema de producción de alimentos para el ganado cruzado.

* Correspondence to: T.S.M. Widi, Animal Production Systems Group, Wageningen University, PO Box 338, 6700 AH Wageningen, The Netherlands. email: widi.tsm@ugm.ac.id

Palabras clave: *cruzamiento, sistemas mixtos de explotación, Ongole, Simmental, Análisis del Ciclo de Vida, multifuncionalidad, Indonesia*

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1. Introduction

Intensification of livestock production is widely promoted as a strategy to meet the increasing demand for animal source foods and to improve the livelihoods of smallholder livestock farmers (Delgado *et al*., 2000; Otte and Upton, 2005; Pica-Ciamarra, 2007). Intensification of livestock production is also seen as an important way of reducing the environmental impact of livestock, in particular in smallholder production systems (Steinfeld *et al.*, 2006; Gerber *et al.*, 2013). Various global studies suggest that intensification of livestock production will reduce emissions of greenhouse gasses (GHG) per unit of production (Steinfeld *et al.*, 2006; Gerber *et al.*, 2013). Intensification is also expected to reduce the pressure on land, resulting in less cultivation of natural areas and destruction of woodlands (Steinfeld *et al.*, 2006).

In resource-poor environments, cross-breeding with breeds selected for high production has become a standard intensification approach for cattle husbandry. Field studies on the impact of intensification through cross-breeding have mainly been undertaken for dairy cattle. These studies showed that smallholder dairying using cross-breds resulted in economic gains for the households involved (McDermott *et al.*, 2010; Samdup *et al.*, 2010; Udo *et al.*, 2011), although it was not feasible for really resource-poor households (Udo *et al.*, 2011). Weiler *et al.* (2014) showed, however, that intensification of dairy farming does not necessarily lead to lower emissions per kilogram of milk produced. Consideration of how off-farm feed production contributes to environmental impact is particularly important. Production levels may be higher in more intensive production systems but more feed supplements are also being used.

Little is known about the impact of the intensification of beef cattle systems in smallholder settings on GHG emissions. Wall, Simm, and Moran, 2009 and Scholtz *et al.* (2012) suggest that genetic improvement and cross-breeding may be sustainable ways of reducing the carbon footprint of beef cattle, but no results from field studies support this hypothesis. Intensification will require increased use of inputs, which may offset any beneficial impact of increased production on the environmental impact per unit of production.

In Indonesia, cross-breeding with European breeds has been promoted as a strategy to intensify its beef production. It is implemented throughout the country, regardless of differences in agro-ecology, of which the variation in available feed resources is a main element (Widi *et al.*, 2015). About 90 percent of cattle in Indonesia are owned by smallholder farmers with fewer than five head of cattle per farm and about 0.1–0.4 ha of crop land. The population pressure in the main island Java means that all agricultural land is used for cropping. As a consequence, the cattle management systems are predominantly based on cut-and-carry (stall) feeding (Palte, 1989).

In Java, cross-breeding is mainly practised by using Simmental semen on the local Ongole population (Widi *et al.*, 2015). Indonesian farmers, in common with smallholders in developing countries, keep cattle not only for meat production, but also for financial security, draught power, manure for cropping and social status (Widi, 2004). Comparisons of cross-bred and Ongole cattle production systems in different agro-ecological zones in Central Java have shown that the reasons for keeping cattle are similar for both systems (Widi *et al.*, 2015). Reproductive performances were not different between the two types of breeding stock. But at comparable ages, cross-bred cows and progeny reached approximately 25 and 17 percent heavier body weights than Ongole cows and progeny. Cross-bred cattle fetched higher sale prices, but they were fed more supplementary feed (Widi *et al.*, 2015). Consequently, no differences in the gross margins from cattle keeping were observed between farms with Ongole cattle and farms with cross-bred cattle within the same agro-ecological zone (Widi *et al.*, 2015).

Is intensification through cross-breeding indeed beneficial for the environment? There is a lack of field studies to substantiate the claims about the environmental benefits of intensification. Life cycle assessment (LCA) is commonly used to assess the environmental impact of producing livestock products (de Vries and de Boer, 2010; de Boer *et al.*, 2011). Environmental impacts from beef cattle production have mainly been estimated for intensive systems in Europe and America (Casey and Holden, 2006; de Vries and de Boer, 2010; Nguyen, Hermansen and Mogensen, 2010). In such studies the impacts are generally expressed per unit of meat produced. In resource-poor cattle keeping systems, the different livelihood functions should be included when assessing impacts per unit of production and mitigation opportunities (Weiler *et al.*, 2014). This will not only give a more realistic picture of the impacts but will also reflect farmers' realities when considering mitigation options. The objective of this study was to assess the environmental impact, in terms of GWP and land use, of Ongole and cross-bred beef cattle production systems in different agro-ecological zones in Central Java. This was achieved by applying the LCA methodology.

2. Materials and methods

2.1. Study areas

The study areas were situated in the southern part of Central Java. They represented two agro-ecological zones, the uplands and the lowlands, with three different rainfall patterns. Wet lowlands, wet uplands and dry uplands could be distinguished. The study areas differ in topography, soil types, soil fertility and agro-climatic conditions. Wet lowlands (lower than 100 m above sea level; annual rainfall of 2 400–3 000 mm; BPS, 2009) have fertile soils and are characterized by irrigated farming systems with paddy and maize as the main crops. Wet uplands (higher than 500 m above sea level with annual rainfall of 3 000–3 600 mm; BPS, 2009) also have fertile soils and are characterized by both irrigated and rain-fed farming systems, with paddy fields, horticulture and forest. Dry uplands (higher than 500 m above sea level) have less fertile soils and low annual rainfall (1 800–2 400 mm; BPS, 2009). This zone has rain-fed farming systems with mainly cassava and dry land paddy.

Wet lowlands were divided into wet lowlands I, located in Yogyakarta Province, where cross-breeding is broadly applied, and wet lowlands II, located in Central Java Province, where cross-breeding is less frequently applied. Wet lowlands II is a traditional breeding area of local cattle (Ongole, in Indonesia called *Peranakan Ongole*, PO). In this area, the local government allocated several districts (an administration unit within an area) for maintaining Ongole cattle.

All farms apply stall-feeding. The feed resources for cattle production are mainly cut native grasses and crop by-products. Rice straw is more frequently available in the lowlands than in the uplands. Supplementary feeds, such as wheat bran, fresh cassava, dried cassava, cassava waste, tofu (soybean curd) waste and soybean hulls are available locally. Cassava and legumes are available more frequently in the dry uplands. Rice bran is produced by the local milling factories. Compounded concentrates are usually produced by feed mill companies, which are located outside the study areas, particularly in areas where dairy farming is practised. Compounded concentrates are distributed to cooperatives and local shops selling farming supplies.

Most smallholder farmers in Central Java keep cattle for capital savings and additional income and to produce manure, which is beneficial for their crops. Farmers consider capital savings as security to be able to meet unexpected or large expenses. They consider income as the cash they receive from the sale of progeny (Widi *et al.*, 2015). They usually sell calves after weaning, which is around 7 months, until approximately 1 year of age. The smallholder farmers can be regarded as cattle breeders, they sell animals to traders and middle men. These intermediaries sell stock to other farmers, feedlots or butchers. Butchers either slaughter the animals immediately or fatten them for several months before slaughtering. The farmers store the manure in or close to the barns for several months and utilize all manure to fertilize soils for crop production.

2.2. Data collection

We sampled data from mixed farms owning cattle for 10 years or longer and owning at least one cow. In total, 252 farms were purposively selected, for monitoring inputs, outputs and on-farm resource flows: 56 (17 Ongole and 39 cross-bred) farms in wet lowlands I, 63 (31 Ongole and 32 cross-bred) farms in wet lowlands II, 59 (12 Ongole and 47 cross-bred) farms in wet uplands and 74 (30 Ongole and 44 cross-bred) farms in dry uplands (Widi *et al.*, 2015). Farmers could not distinguish subsequent cross-bred generations.

LCA calculations were based on the inputs and outputs of the cattle component of the study farms during the period from January 2011 until January 2012. Feed was the major input. Many different feeds were offered to the cattle. The feeds were categorized as fresh forages, dry forages and supplementary feeds. The proportions of the different fresh forages were estimated by separating the fresh forage into its components. Feed inputs were calculated based on farmers' estimates and direct observation of the types and amounts of feeds offered to each individual animal during 1 year. The estimates of the types and amounts of fresh forages offered were recorded by farmers each day. Trained enumerators ($n = 8$) checked the farm recording once a month. Young animals, approximately 6–12 months, were fed only fresh forages, and it was assumed that they get a half portion compared with adult animals. The amounts of dry forages and supplementary feeds that were bought were estimated from the amounts purchased. These estimates were translated into kilograms of dry matter (DM) and crude protein (CP) intake per animal, applying the feed composition tables of Hartadi, Reksohadiprodjo and Tillman (2005) for feeds available in Central Java.

Weights of cows, other adult stock (e.g. bulls and heifers) and young stock were estimated by the enumerators by measuring the chest girth using a measurement tape that transformed the chest girth in centimetres into live weight in kilograms (developed by FHK Ogawa Seki Co. Ltd, Tokyo, Japan) (Widi *et al.*, 2015).

In the LCA procedures, the emissions were allocated to the relative economic values of the different functions. The measurement of economic values took place over a period of 1.5 years (January 2011–July 2012), to ensure that the participating farms produced young stock in that period. The first author recorded, through monthly visits to the sample farms, farmers' inputs and outputs of cattle keeping during this period.

2.3. LCA procedures

An LCA is usually divided into four steps: goal and scope definition, inventory analysis, impact assessment and interpretation (ISO 14040, 1997; ISO 14041, 1998; ISO 14042, 2000 and ISO 14043, 2000). The first step of an LCA includes the definition of the system boundary, the "Functional Unit" (FU) to which environmental impacts are allocated, the method of allocation and the impact categories to be analysed.

The system boundary of the LCA determines which processes of a production system shall be included within the LCA. The system boundary of the cattle component in Ongole and cross-bred farms is shown in Figure 1. We assessed all processes up to the farm-gate, including the cattle (enteric fermentation), cut-and-carry forages and supplementary feeds. Transportation of forages by trucks was only found in the dry uplands area. Emissions for manure were not assigned to the cattle component, as all manure was used for cropping (Figure 1).

Given the system boundary, we computed the emissions of the main GHG: carbon dioxide (CO_2), methane (CH_4) and nitrous oxide (N_2O). The method used to calculate GHG emissions from enteric fermentation was based on the intergovernmental panel on climate change (IPCC) good practice guidance, Tier 2 approach (IPCC, 2006). We considered emissions under the current production conditions. Global warming potential and land use were assigned to all the feeds offered to the cattle on the farms on a yearly basis. Ecoinvent data 2.2 allowed us to compute the GWP and land use for each feed ingredient (Ecoinvent 2.2, available at http://pre-sustanability.com). If recent yield data were not available in Ecoinvent 2.2, we used production data from the FAO statistical database, and computed GWP and land use per feed ingredient using Simapro7.3 (Simapro 7.3, available at http://pre-sustanability.com).

2.4. Allocation procedures

The FU in a LCA analysis should represent the main function of the analysed system. Because of the multi-functionality of cattle keeping in the study areas, two allocation approaches were used: (i) allocation to live weight of young stock produced in the farms, and (ii) allocation to live weight of young stock produced taking into account the other functions of cattle keeping. ISO 14044 (2006) provides guidelines on how to allocate the environmental impact of a process or production system in the case of multiple functions. In this study we used economic allocation, which implies the allocation of GWP and land use to the different functions based on their economic values. When crop by-products were used as feed, economic allocation was applied based on the economic value of the crop for human food consumption and the value of its by-products for animal feed.

2.5. Economic allocation to the different functions of cattle keeping

Live weight of young stock sold has a direct market value, whereas young stock not sold represent an opportunity value. The economic value of cattle as a means of finance and insurance and the use of manure as fertilizer can only be assessed indirectly.

The economic value of live weight produced was calculated as follows:

$$LC_k: \; SC_k \times \text{head price}$$

where LC_k is the total economic value of live weight produced during 1 year in Indonesian Rupiah (IDR), SC_k is the number of cattle produced in one year (head) and head price is the cattle price (IDR), which is determined by body weight estimation.

The head prices of cattle sold were provided by the individual farmers. Village traders or middle men buy cattle from farmers. Prices are based on exterior appearance of the cattle. We interviewed farmers regarding the price of young stock produced at the farms. The opportunity values

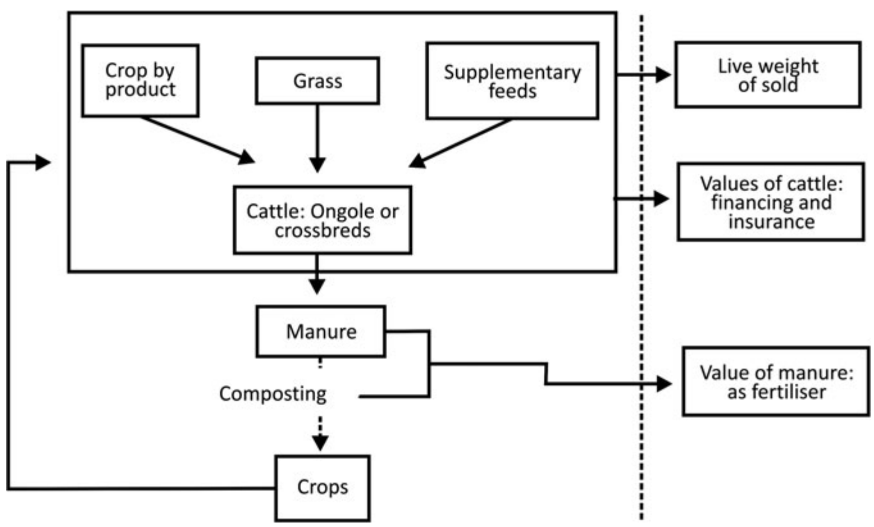

Figure 1. System boundaries for the life cycle assessment (LCA) of local and cross-bred cattle production systems.

of weaners still present on the farms were based on estimates of the farmers or traders.

The economic value of manure used as fertilizer was estimated based on synthetic N fertiliser equivalents, in this case urea ($CO(NH_2)_2$), which was the common fertilizer that farmers used. The economic value of manure used was calculated as follows:

$$\text{MANURE} : N_{\text{manure}} \times \text{ fertilizer price},$$

where, MANURE is the total economic value of manure used as fertilizer during 1 year (IDR), N_{manure} is kilograms N in manure used as fertilizer and fertilizer price is economic value of N in urea ($CO(NH_2)_2$) expressed as (IDR/kg N). Manure production in terms of kilograms per day (kg d^{-1}) of DM was calculated by multiplying the estimated weight of fresh manure produced per animal per day and the DM content of fresh manure. We assumed that an adult Ongole produces 15 $\text{kg d}^{-1}$of fresh manure and an adult cross-bred 20 kg d^{-1} and young stock produces half of these amounts, and that the DM content is 15 percent (Pertiwinigrum, personal communication). We assumed that cattle manure has a N content of 1.7 percent, based on Moore and Gamroth (1993) and that 50 percent of N was lost during storage (Moore and Gamroth, 1993). The price of fertilizer (urea) was estimated at 1 600 IDR per kilogram in 2011, and therefore we estimated the price of N at 3 478 IDR per kilogram (N content of urea is 46 percent, Hartadi, Reksohadiprodjo and Tillman (2005)).

Estimation of the intangible benefits of cattle was based on Bosman, Moll and Udo (1997), Moll (2005) and Moll, Staal and Ibrahim (2007). The intangible benefit from financing is related to not having to pay interest for borrowing money from a bank or an informal money lender when an animal is sold (Moll, 2005; Moll, Staal and Ibrahim (2007)). The benefit of financing was estimated as:

$$F_k : \ LC_k \times f$$

where F_k is benefit of financing, LC_k is total, economic value of live cattle sold in a farm in 1 year (IDR) and f is financing factor. The total economic value of live cattle sold, LC_k, refers to the direct economic value of the cattle. The formal interest rate of credit in the study areas was 12 percent (Bank BNI Yogyakarta, 2013, personal communication).

Bosman, Moll and Udo (1997) described the intangible insurance benefit of livestock as the economic value of the stock as insurance for the household, i.e. to pay premium in case of health insurance or another type of insurance. The intangible insurance benefit was estimated as:

$$I_k : \ SF_k \times s$$

where I_k is insurance benefit, SF_k is number of cattle on farm multiply by price per head (IDR), and s is insurance factor. The factor s was set at 9 percent (Asuransi Prudential – Yogyakarta, 2003, personal communication). This represents the human health insurance premium that would have to be paid for health insurance.

2.6. Impact assessment

The impact categories considered were GWP and land use. The carbon footprint, GWP in CO_2-equivalents (CO_2-eq) per kilogram animal product, is widely used to assess the climate change impact of cattle (Steinfeld *et al.*, 2006; Gerber *et al.*, 2013). In Java, land use is very much under pressure as almost all agricultural land is used for crop production. Grazing lands have disappeared and cattle are kept in a cut-and-carry management system. To assess the GWP of Ongole and cross-bred cattle farms, emissions of CO_2, CH_4 and N_2O were summed based on their equivalence factors in terms of kilograms of CO_2-equivalents: 1 for CO_2, 25 for CH_4 and 298 for N_2O (IPCC, 2007). Land used for producing the different types of feed was expressed in square metres (m^2) (Phong, de Boer and Udo, 2011). Interpretation of the results is based on the FU, live weight produced in the study period.

We compared the emission intensities and farm characteristics of the 25th percentile of Ongole farms, representing farms with lower emission intensities, with the emission intensities and farm management characteristics of all the other Ongole farms. The same analysis was conducted for cross-bred farms. This analysis was conducted to explore why some farms had lower emission intensities than others, analogous with Gerber *et al.* (2013).

2.7. Data analysis

One-way ANOVA was performed to analyse the variation in GWP and land use per kilogram live weight produced among areas, with breed nested within areas (Ott and Longnecker, 2010). The model was simplified to compare breeds within areas, because for most parameters no interaction was found between breed and area (Widi *et al.*, 2015).

3. Results

3.1. Characteristics of Ongole and cross-bred cattle farms

Table 1 presents the farm characteristics for the four study areas. Land size was not significantly different between the two types of farms within the four study areas. Most of the land was used for crop production. Farmers usually planted forages along the boundaries of their fields. Cut-and-carry feeding was practised in all study areas. Forages were collected from the fields, riversides, roadsides, forest edges and backyards. Supplementary feeds were offered irregularly. In wet lowlands II, rice bran was only offered during the rice harvesting period, because farmers utilized the by-product of their own harvested rice, whereas in the

Table 1. Characteristics of farms with Ongole and cross-bred cattle in the four study areas in Central Java.

	Area/Breed								
	Wet lowlands I ($n = 56$)		Wet lowlands II ($n = 63$)		Wet uplands ($n = 59$)		Dry uplands ($n = 74$)		***P* value***
	Ongole ($n = 17$) Mean ± SD	Cross-bred ($n = 39$) Mean ± SD	Ongole ($n = 31$) Mean ± SD	Cross-bred ($n = 32$) Mean ± SD	Ongole ($n = 12$) Mean ± SD	Cross-bred ($n = 47$) Mean ± SD	Ongole ($n = 30$) Mean ± SD	Cross-bred ($n = 44$) Mean ± SD	
Land size (ha)[ns]	0.13 ± 0.13	0.14 ± 0.09	0.36 ± 0. 80	0.21 ± 0.12	0.17 ± 0.06	0.16 ± 0.16	0.44 ± 0.29	0.55 ± 0.50	0.00
Crops	Paddy, maize, soybeans, shallots, groundnut, soybean, cassava, sweet potato and horticulture		Paddy, maize, cassava, sweet potato, groundnut, mung beans, fruits and horticulture		Paddy, cassava, maize, groundnut, fruits and horticulture		Paddy, maize, cassava and groundnut		
Feeds offered to cattle									
Fresh forages	*Pennisetumpurpureum*, *Panicum maximum*, maize foliage, native grass and fresh groundnut haulm		*Pennisetumpurpureum*, *Panicum maximum*, native grass, maize foliage, rice stalk and groundnut haulm		*Pennisetumpurpureum*, *Panicum maximum*, maize foliage, native grass, groundnut haulm and cassava leaves		*Pennisetumpurpureum*, *Panicum maximum*, maize foliage, native grass, groundnut haulm and legumes		
Dry forages	Rice straw		Rice straw		Rice straw		Rice and maize straw		
Supplementary feeds	Rice bran, wheat bran, concentrates[1] and tofu waste		Rice bran and fresh cassava		Rice bran, tofu waste, concentrates[1] and soybean hulls		Rice bran, fresh and dried cassava and cassava waste		

[ns]There were no significant differences between breeds within area and in all areas ($P < 0.05$).
**P* value for differences between areas.
[1]Concentrate composition: rice bran, palm kernel meal, cassava meal, maize cob, molasses and urea.

other areas rice bran was offered independent of the harvesting period.

Table 2 presents the inventory results for cattle herds, feeding practices and manure estimates for Ongole and cross-bred farms. The total number of cattle did not differ between Ongole (2.4) and cross-bred (2.6) farms within the four study areas. The amounts of the different feed types fed differed significantly among areas. More fresh forages were fed on wet uplands farms than in the other three areas. More dry forages were fed on wet lowlands II and wet uplands farms than in the other two areas and less supplementary feeds were fed in wet lowlands II than in the other three areas. Overall, the amounts fed of fresh forages, dry forages and concentrates were significantly higher for cross-bred farms than for Ongole farms. In wet lowlands I the amount of fresh forages fed hardly differed between Ongole and cross-bred farms, but the amount of concentrates fed was significantly higher for cross-bred farms (680 kg per farm per year or cross-bred farms vs 280 kg for Ongole farms). Overall, live weight produced was also significantly higher for cross-bred farms (149 kg) than for Ongole farms (117 kg). In all areas, cross-bred farms produced more kilograms of live weight of young stock than Ongole farms, but the variation between farms was high, so the differences between breeds within areas were only significant in wet lowlands II.

3.2. Economic allocation of the multiple functions for Ongole and cross-bred cattle farms

Cattle have multiple economic functions. Table 3 shows the relative contributions of the different functions that could be quantified. The biggest contribution was from live cattle produced; this accounted for 71.8 percent of total value for Ongole cattle and 71.4 percent for cross-bred cattle. The contribution of live weight produced was not significantly different ($P < 0.05$) between the two types of cattle farms within the different study areas. The insurance function of cattle comprised 18 percent of the total value of Ongole cattle, and 19 percent of the total value of cross-bred cattle. The additional two functions, which were quantified contributed little to the total value of cattle, an average contribution of 8.1 percent for financing and 1.1 percent for manure used as fertilizer.

3.3. Global warming potential of Ongole and cross-bred cattle production systems

Table 4 shows the total GWP and the GWP per kilogram of live weight produced for the cattle component of the two farm types in the four study areas. Ongole farms tended to have a significantly lower GWP than cross-bred farms (4 000 vs 5 600 kg CO_2-eq per year, $P < 0.05$). On average, 76 percent of GWP was due to methane emissions from enteric fermentation. The remaining 24 percent came from feeds and transport of forages. Use of fresh home-produced forages in cross-bred farms resulted in

Table 2. Composition of the cattle herd, feeding practices and manure produced for Ongole and cross-bred farms in the four study areas in Central Java, January 2011–January 2012.

	Area/Breed								Average		*P value
	Wet lowlands I ($n=56$)		Wet lowlands II ($n=63$)		Wet uplands ($n=59$)		Dry uplands ($n=37$)		Ongole ($n=90$)	Cross-bred ($n=162$)	
	Ongole ($n=17$) Mean ± SD	Cross-bred ($n=39$) Mean ± SD	Ongole ($n=31$) Mean ± SD	Cross-bred ($n=32$) Mean ± SD	Ongole ($n=12$) Mean ± SD	Cross-bred ($n=47$) Mean ± SD	Ongole ($n=30$) Mean ± SD	Cross-bred ($n=44$) Mean ± SD	Mean ± SD	Mean ± SD	
Number of cattle kept											
Cow (head)	$1.41^a \pm 0.62$	$1.23^a \pm 0.49$	$1.13^a \pm 0.62$	$1.53^b \pm 0.84$	$1.42^a \pm 0.67$	$1.45^a \pm 0.58$	$1.07^a \pm 0.25$	$1.48^a \pm 1.36$	$1.20^a \pm 0.55$	$1.42^b \pm 0.89$	0.73
Heifer (head)	$0.35^a \pm 0.49$	$0.31^a \pm 0.52$	$0.32^a \pm 0.54$	$0.16^a \pm 0.45$	$0.58^a \pm 0.67$	$0.09^b \pm 0.35$	$0.07^a \pm 0.254$	$0.23^a \pm 0.48$	$0.28^a \pm 0.50$	$0.19^a \pm 0.45$	0.25
Male (head)^{ns}	0.12 ± 0.33	0.13 ± 0.41	0.13 ± 0.34	0.06 ± 0.25	0.33 ± 0.65	0.19 ± 0.54	0.03 ± 0.83	0.09 ± 0.36	0.12 ± 0.36	0.12 ± 0.41	0.15
Calf (head)^{ns}	0.76 ± 0.66	0.74 ± 0.82	0.68 ± 0.65	0.84 ± 0.92	0.83 ± 0.58	0.87 ± 0.77	0.87 ± 0.73	1.05 ± 1.14	0.78 ± 0.67	0.88 ± 0.92	0.38
Total cattle (head)^{ns}	2.6 ± 1.0	2.4 ± 1.0	2.3 ± 0.8	2.6 ± 1.5	3.2 ± 1.1	2.6 ± 0.9	2.0 ± 0.7	2.8 ± 2.4	2.4 ± 0.9	2.6 ± 1.6	0.70
Total cattle (TLU)^{1ns}	$2.3^a \pm 0.9$	$2.1^a \pm 0.8$	$2.0^a \pm 0.7$	$2.3^a \pm 1.3$	$2.8^a \pm 1.0$	$2.3^b \pm 0.8$	$1.7^a \pm 0.5$	$2.4^a \pm 2.0$	$2.1^a \pm 0.8$	$2.3^a \pm 1.3$	0.62
Amount of feed offered											
Fresh forage (000 kg/farm/year)	$20.1^a \pm 0.8$	$21.9^a \pm 0.8$	$16.9^a \pm 0.8$	$24.1^b \pm 1.2$	$27.1^a \pm 0.9$	$25.6^a \pm 0.9$	$14.4^a \pm 0.5$	$23.9^b \pm 0.2$	$18.0^a \pm 0.8$	$24.0^b \pm 1.3$	0.02
Dry forage (000 kg/farm/year)	$2.1^a \pm 0.9$	$2.1^a \pm 1.2$	$2.8^a \pm 1.3$	$3.9^a \pm 2.7$	$4.0^a \pm 0.4$	$3.0^a \pm 1.7$	$1.84^a \pm 0.6$	$3.7^b \pm 3.8$	$2.5^a \pm 1.4$	$3.1^b \pm 2.6$	0.01
Supplementary feed (000 kg/farm/year)	$0.28^a \pm 0.25$	$0.68^b \pm 0.44$	$0.13^a \pm 0.09$	$0.37^b \pm 0.35$	$0.56^a \pm 0.45$	$0.60^a \pm 0.42$	$0.36^a \pm 0.20$	$0.71^a \pm 1.24$	$0.29^a \pm 0.27$	$0.60^b \pm 0.74$	0.01
Live weight of produced cattle (kg/farm/year)	$139^a \pm 64.4$	$161^a \pm 56.6$	$116^a \pm 28.3$	$141^b \pm 56.5$	$128^a \pm 45.8$	$150^a \pm 50.2$	$100^a \pm 25.2$	$142^b \pm 101.9$	$117^a \pm 41.2$	$149^b \pm 70.2$	0.00
Manure produced (000 kg/farm/year)	$12.8^a \pm 5.2$	$14.0^a \pm 5.2$	$9.9^a \pm 3.4$	$15.1^b \pm 8.4$	$16.2^a \pm 6.1$	$15.0^a \pm 5.3$	$8.7^a \pm 2.5$	$15.9^b \pm 13.1$	$10.9^a \pm 4.7$	$15.0^b \pm 8.6$	0.22

^{a,b}Different superscripts indicate significant differences between breeds within area and in all areas ($P < 0.05$).
^{ns}There were no significant differences between breeds within area and in all areas ($P < 0.05$).
*P value for differences between areas.
[1]TLU, Tropical livestock unit; adult cattle are equal to 1 cattle TLU and cattle younger than 1 year are equal to 0.6 cattle TLU (FAO, 2013).

Table 3. Economic allocation of the multiple functions (IDR/year) and allocation factor (%) for Ongole and cross-bred farms in the four study areas in Central Java, January 2011–July 2012

Cattle function	Area/Breed								Average		*P value
	Wet lowlands I ($n = 56$)		Wet lowlands II ($n = 63$)		Wet uplands ($n = 59$)		Dry uplands ($n = 74$)		Ongole ($n = 90$)	Cross-bred ($n = 162$)	
	Ongole ($n = 17$) Mean ± SD	Cross-bred ($n = 39$) Mean ± SD	Ongole ($n = 31$) Mean ± SD	Cross-bred ($n = 32$) Mean ± SD	Ongole ($n = 12$) Mean ± SD	Cross-bred ($n = 47$) Mean ± SD	Ongole ($n = 30$) Mean ± SD	Cross-bred ($n = 44$) Mean ± SD	Mean ± SD	Mean ± SD	
Live weight produced (million IDR)	$3.93^{a} \pm 1.5$	$4.91^{b} \pm 1.5$	$2.91^{a} \pm 0.93$	$3.62^{b} \pm 1.31$	$3.43^{a} \pm 1.30$	$5.09^{b} \pm 2.01$	$3.02^{a} \pm 0.73$	$4.76^{b} \pm 3.79$	$3.21^{a} \pm 1.10$	$4.67^{b} \pm 2.48$	0.01
Financing (million IDR)	$0.44^{a} \pm 0.15$	$0.54^{b} \pm 0.15$	$0.33^{a} \pm 0.07$	$0.43^{b} \pm 0.13$	$0.34^{a} \pm 0.13$	$0.51^{a} \pm 0.20$	$0.33^{b} \pm 0.07$	$0.54^{b} \pm 0.41$	$0.36^{a} \pm 0.11$	$0.52^{b} \pm 0.26$	0.01
Manure (million IDR)	$0.06^{a} \pm 0.02$	$0.06^{a} \pm 0.02$	$0.04^{a} \pm 0.01$	$0.06^{b} \pm 0.04$	$0.07^{a} \pm 0.03$	$0.07^{a} \pm 0.02$	$0.04^{a} \pm 0.01$	$0.06^{b} \pm 0.06$	$0.05^{a} \pm 0.02$	$0.07^{b} \pm 0.04$	0.19
Insurance (million IDR)	$1.10^{a} \pm 0.51$	$0.97^{a} \pm 0.05$	$0.68^{a} \pm 0.33$	$1.16^{b} \pm 0.70$	$1.30^{a} \pm 0.59$	$1.43^{a} \pm 0.61$	$0.70^{a} \pm 0.24$	$1.30^{b} \pm 1.17$	$0.8^{a} \pm 0.5$	$1.2^{b} \pm 0.8$	0.01
Total value[1] (million IDR)	$5.53^{a} \pm 1.84$	$6.49^{a} \pm 1.82$	$3.96^{a} \pm 0.97$	$5.27^{b} \pm 1.70$	$5.22^{a} \pm 1.94$	$7.16^{a} \pm 2.44$	$4.10^{a} \pm 0.55$	$6.68^{b} \pm 0.51$	$4.47^{a} \pm 1.45$	$6.49^{b} \pm 3.21$	0.00
Allocation factor[2](%)	$70.8^{a} \pm 7.2$	$75.3^{b} \pm 7.5$	$72.8^{a} \pm 8.2$	$68.8^{a} \pm 9.3$	$66.0^{a} \pm 5.6$	$70.7^{b} \pm 7.2$	$73.7^{a} \pm 3.6$	$70.9^{a} \pm 8.4$	$71.8^{a} \pm 6.8$	$71.4^{a} \pm 8.1$	0.02

IDR, Indonesian Rupiah.
[a,b]Different superscripts indicate significant differences between breeds within area and in all areas ($P < 0.05$).
*P value for differences between areas.
[1]Total value = live weight produced + financing + manure + insurance.
[2]Allocation factor = (live cattle sold/total value) × 100.

Table 4. Global warming potential (GWP) of Ongole and cross-bred cattle production systems in the four study areas in Central Java, January 2011–January 2012

	Area/Breed								Average		*P value
	Wet lowlands I ($n = 56$)		Wet lowlands II ($n = 63$)		Wet uplands ($n = 59$)		Dry uplands ($n = 74$)		Ongole ($n = 90$)	Crossbred ($n = 162$)	
	Ongole ($n = 17$) Mean ± SD	Cross-bred ($n = 39$) Mean ± SD	Ongole ($n = 31$) Mean ± SD	Cross-bred ($n = 39$) Mean ± SD	Ongole ($n = 12$) Mean ± SD	Cross-bred ($n = 47$) Mean ± SD	Ongole ($n = 30$) Mean ± SD	Cross-bred ($n = 44$) Mean ± SD	Mean ± SD	Mean ± SD	
Total GWP (000 kg CO_2 –eq) in 1 year	$4.3^{a} \pm 1.6$	$5.0^{a} \pm 1.8$	$3.6^{a} \pm 1.3$	$5.3^{b} \pm 2.9$	$5.2^{a} \pm 1.9$	$5.3^{a} \pm 1.7$	$3.7^{a} \pm 1.3$	$6.7^{b} \pm 5.9$	$4.0^{a} \pm 1.5$	$5.6^{b} \pm 3.6$	0.24
On farm cattle	$3.4^{a} \pm 1.3$	$3.9^{a} \pm 1.4$	$2.9^{a} \pm 1.0$	$4.2^{b} \pm 2.4$	$3.8^{a} \pm 1.4$	$4.1^{a} \pm 1.4$	$2.5^{a} \pm 1.0$	$4.5^{b} \pm 3.8$	$3.0^{a} \pm 1.2$	$4.2^{b} \pm 2.5$	0.70
Forage	$0.4^{a} \pm 0.2$	$0.5^{a} \pm 0.2$	$0.2^{a} \pm 0.1$	$0.3^{a} \pm 0.2$	$0.6^{a} \pm 0.2$	$0.5^{a} \pm 0.2$	$0.6^{a} \pm 0.2$	$1.1^{b} \pm 0.9$	$0.4^{a} \pm 0.2$	$0.6^{b} \pm 0.5$	0.00
Supplementary feed	$0.1^{a} \pm 0.1$	$0.4^{b} \pm 0.2$	$0.07^{a} \pm 0.04$	$0.2^{b} \pm 0.2$	$0.3^{a} \pm 0.4$	$0.3^{a} \pm 0.2$	$0.2^{a} \pm 0.1$	$0.4^{a} \pm 0.6$	$0.2^{a} \pm 0.19$	$0.3^{b} \pm 0.4$	0.01
Rice straw	$0.3^{a} \pm 0.1$	$0.3^{a} \pm 0.2$	$0.4^{a} \pm 0.2$	$0.5^{a} \pm 0.4$	$0.6^{a} \pm 0.3$	$0.4^{a} \pm 0.2$	$0.3^{a} \pm 0.1$	$0.5^{b} \pm 0.5$	$0.6^{a} \pm 0.2$	$0.4^{b} \pm 0.4$	0.10
Transportation of forage (off-farm)	0.0 ± 0.0	0.0 ± 0.0	0.0 ± 0.0	0.0 ± 0.0	0.0 ± 0.0	0.0 ± 0.0	$0.1^{a} \pm 0.0$	$0.2^{b} \pm 0.2$	$0.04^{a} \pm 0.06$	$0.06^{a} \pm 0.1$	0.00
Without allocation GWP/FU (kg CO2 –eq per kg LW)[1]	$35.9^{a} \pm 16.2$	$35.9^{a} \pm 18.7$	$35.9^{a} \pm 24.9$	$43.6^{a} \pm 23.4$	$44.8^{a} \pm 15.1$	$38.6^{a} \pm 14.7$	$40.6^{a} \pm 17.6$	$50.9^{a} \pm 24.9$	$38.7^{a} \pm 18.1$	$42.3^{a} \pm 21.6$	0.02
With allocation GWP/FU (CO_2 –eq per kg LW)[1]	$24.8^{a} \pm 10.2$	$26.2^{a} \pm 12.1$	$24.7^{a} \pm 10.4$	$28.0^{a} \pm 13.2$	$29.1^{a} \pm 8.9$	$26.5^{a} \pm 7.9$	$29.5^{a} \pm 11.8$	$34.3^{a} \pm 11.2$	$26.9^{a} \pm 10.8$	$28.9^{a} \pm 11.4$	0.00

FU, functional unit; LW, live weight.
[a,b]Different superscripts indicate significant differences between breeds within area and in all areas ($P < 0.05$).
[ns]There were no significant differences between breeds within area and in all areas ($P < 0.05$).
*P value of differences between areas.
[1]Without or with allocation to different livelihood functions.

significantly higher GWP per farm compared with Ongole farms. Among areas, emissions from the use of forages were significantly higher in the dry uplands than in other areas ($P < 0.05$). Most of the forages in the dry uplands were native grasses.

Ongole and cross-bred cattle did not have a significantly different impact in terms of GWP per kilogram of live weight produced. When all the GWP was allocated to live weight produced, the average GWP per kilogram of live weight produced was 38.7 kg CO_2-eq for Ongole farms and 42.3 kg CO_2-eq for cross-bred farms. The GWP per kilogram of live weight based on economic allocation to the different functions of cattle averaged 26.9 kg CO_2-eq for Ongole cattle farms and 28.9 kg CO_2-eq for cross-bred farms (Table 4).

The 25th percentile of Ongole farms with the lowest emission intensities had a 46 percent lower GWP per kilogram live weight produced than the other farms (Table 5). The result for cross-bred farms was similar with 45 percent lower GWP per kilogram live weight. The 25th percentile of both farm types owned fewer animals (1.6 vs 2.1 for Ongole farms, and 1.6 vs 2.3 for cross-bred farms), but produced more kilograms of live weight (169 kg vs 100 kg for Ongole farms and 238 kg vs120 kg for cross-bred farms) (Table 5). The amount of feed offered per animal (kg DM/head per day) was higher for the 25th percentile of farms compared with all the other farms for Ongole farms (10.0 vs 8.3 kg d^{-1}) and cross-bred farms (12.0 vs 10.0 kg d^{-1}). Calving interval (days) was significantly shorter for the 25th percentile of farms than for the other farms for both Ongole farms (377 vs 469 days) and cross-bred farms (404 vs 472 days). Body condition scores for the 25th percentile of farms were also higher than on the other farms for both Ongole (3.0 vs 2.4) and cross-bred farms (3.1 vs 2.8).

Table 5. Comparison of cattle management characteristics between the 25th percentile of farms with lowest Global warming potential (GWP) per kg live weight produced and all other farms for Ongole (a.) and cross-bred farms (b.), January 2011–January 2012.

No.	Variable	25th percentile ($n = 22$)	others ($n = 68$)
	a. Ongole farms		
1.	GWP (kg CO_2-eq per kg live weight produced)	$14.3^a \pm 2.0$	$31.0^b \pm 9.2$
2.	Dry matter (DM) per cow (kg/head/day)	$10.0^a \pm 0.4$	$8.3^b \pm 0.7$
3.	Body weight produced (kg)	$169.1^a \pm 47.5$	$99.5^b \pm 18.6$
4.	Calving interval (days)	$377.3^a \pm 4.2$	$469.1^b \pm 45.8$
5	Body condition score	$3.0^a \pm 0.0$	$2.4^b \pm 0.4$
	b. Cross-bred farms		
1.	GWP (kg CO_2-eq per kg live weight produced)	$14.9^a \pm 2.9$	$33.4^b \pm 9.2$
2.	Dry matter (DM) per cow (kg/head/day)	$12.0^a \pm 0.9$	$10.0^b \pm 0.7$
3.	Body weight produced (kg)	$237.8^a \pm 85.6$	$119.5^b \pm 26.7$
4.	Calving interval (days)	$404.1^a \pm 45.7$	$471.6^b \pm 52.6$
5	Body condition score	$3.1^a \pm 0.5$	$2.8^b \pm 0.4$

[a,b]Different superscript indicates a significant difference between the 25th percentile and the other farms.

3.4. Land use in Ongole and cross-bred cattle production systems

Table 6 shows the land use per farm and per kilogram live weight for the cattle component of Ongole and cross-bred farms in the four study areas. In all areas the land use (off-farm and on-farm land use) for the cattle component of Ongole cattle farms tended to be lower than for cross-bred cattle farms. In the wet lowlands II and dry uplands, this difference was significant ($P < 0.05$). Overall this parameter was also significantly lower ($P < 0.05$) for Ongole farms, 5 339 m^2 compared with 7 467 m^2 for cross-bred farms. Table 6 shows that nearly all of this land use (96 percent) was for fresh forage production. The land use for producing supplementary feeds (0.1 m^2 for Ongole farms and 0.2 m^2 for cross-bred farms) was significantly higher for cross-bred farms than for Ongole farms. The amount of land required to produce 1 kg of live weight was slightly higher for cross-bred cattle (37.4 m^2) than for Ongole cattle (34.2 m^2) (Table 6). Among areas, the wet lowlands I and wet uplands showed higher ($P < 0.05$) total land use and land use per kilogram live weight produced than the other two areas, both without and with economic allocation to the different livelihoods functions. More home-produced forage is used in these areas.

4. Discussion

4.1. Methodology: multi-functionality

In this study, the cattle were components of mixed farming systems and served multiple functions that were linked to each other. Including the various functions of cattle in our LCA calculations resulted in approximately 30 percent lower emissions per unit of live weight produced compared with the calculations in which multiple functions were not considered. The estimate for the insurance function of cattle was relatively small (approximately 20 percent) relative to the total value of cattle. This is in contrast with the finding of Widi *et al.* (2015) that farmers regarded “saving” as the most important motive for keeping cattle When farmers need cash for big expenses, they sell one of their cattle. It seems likely that our method of valuing the insurance function of cattle still underestimates the true value of this function of keeping cattle in Indonesia. The function of security will remain important in the future, as farmers regard cattle as an attractive way to accumulate capital (Widi *et al.*, 2015).

Farmers considered manure as the third most important motive for keeping cattle (Widi *et al.*, 2015). Our estimation of the economic value of manure (1.1 percent of the total economic value of cattle keeping) seems to

Table 6. Land use (LU) of Ongole and cross-bred cattle production systems in the four study areas in Central Java, January 2011–January 2012

	Area/Breed										
	Wet lowlands I ($n = 56$)		Wet lowlands II ($n = 63$)		Wet uplands ($n = 59$)		Dry uplands ($n = 74$)		Average		*P value
	Ongole ($n = 17$)	Cross-bred ($n = 39$)	Ongole ($n = 31$)	Cross-bred ($n = 39$)	Ongole ($n = 12$)	Cross-bred ($n = 47$)	Ongole ($n = 30$)	Cross-bred ($n = 44$)	Ongole ($n = 90$)	Cross-bred ($n = 162$)	
	Mean ± SD	Mean ± SD	Mean ± SD	Mean ± SD	Mean ± SD	Mean ± SD	Mean ± SD	Mean ± SD	Mean ± SD	Mean ± SD	
Total LU (000 m^2)	$7.8^{a} \pm 2.8$	$8.1^{a} \pm 2.9$	$3.8^{a} \pm 1.6$	$5.4^{b} \pm 2.8$	$9.2^{a} \pm 3.1$	$8.7^{a} \pm 3.0$	$4.3^{a} \pm 1.4$	$7.1^{b} \pm 5.8$	$5.3^{a} \pm 2.7$	$7.5^{b} \pm 4.0$	0.00
Forage	$7.2^{a} \pm 2.8$	$7.8^{a} \pm 2.7$	$3.7^{a} \pm 1.5$	$5.2^{b} \pm 2.8$	$9.0^{a} \pm 3.0$	$8.5^{a} \pm 2.9$	$4.0^{a} \pm 1.3$	$6.7^{b} \pm 5.4$	$5.1^{a} \pm 2.8$	$7.2^{b} \pm 3.8$	0.00
Supplementary feed	$0.05^{a} \pm 0.04$	$0.17^{b} \pm 0.23$	$0.02^{a} \pm 0.01$	$0.07^{b} \pm 0.06$	$0.1^{a} \pm 0.08$	$0.1^{a} \pm 0.07$	$0.2^{a} \pm 0.1$	$0.3^{a} \pm 0.3$	$0.1^{a} \pm 0.1$	$0.2^{b} \pm 0.2$	0.00
Rice straw	$0.07^{a} \pm 0.03$	$0.07^{a} \pm 0.04$	$0.09^{a} \pm 0.05$	$0.13^{a} \pm 0.09$	$0.14^{a} \pm 0.08$	$0.10^{a} \pm 0.06$	$0.06^{a} \pm 0.02$	$0.13^{a} \pm 0.13$	$0.09^{a} \pm 0.05$	$0.11^{b} \pm 0.09$	0.10
Without allocation LU/FU (m^2/kg LW)[1]	$57.4^{a} \pm 23.7$	$55.7^{a} \pm 26.9$	$37.5^{a} \pm 23.5$	$43.3^{a} \pm 23.4$	$78.0^{a} \pm 29.2$	$61.7^{a} \pm 4.1$	$46.0^{a} \pm 19.5$	$53.6^{a} \pm 28.0$	$49.5^{a} \pm 26.3$	$54.4^{a} \pm 26.3$	0.00
With allocation LU/FU (m^2/kg LW)[1]	$39.6^{a} \pm 14.6$	$40.7^{a} \pm 17.0$	$25.7^{a} \pm 12.2$	$27.9^{a} \pm 11.8$	$50.6^{a} \pm 18.1$	$42.3^{a} \pm 13.1$	$33.4^{a} \pm 12.9$	$36.1^{a} \pm 12.3$	$34.2^{a} \pm 15.8$	$37.4^{a} \pm 14.6$	0.00

FU, functional unit; LW, live weight.
[a,b]Different superscripts indicate significant differences between breeds within area and in all areas ($P < 0.05$).
**P* value of differences between areas.
[1]Without or with allocation to different livelihood functions.

underestimate its real value. This estimate was based only on the synthetic fertilizer N-equivalent and therefore excludes the *P* and *K* values of manure, and the positive effects of manure on soil organic matter and water-holding capacity (Hiernaux and Diawara, 2014). Manure production will be valued higher in the future because farmers appreciate its effect on soil fertility and structure and because of the rising cost of fertilizers.

4.2. The effect of cross-breeding on GWP and land use

Global studies have estimated that emission intensities for beef are highest in developing regions, e.g. South Asia, sub-Saharan Africa, Latin America and the Caribbean, and East and Southeast Asia (Gerber *et al.*, 2013). Gerber *et al.* (2013) mention that the high emissions in these regions are largely caused by low feed digestibility (leading to higher enteric and manure emissions), poorer animal husbandry and lower slaughter weights (slow growth rates leading to more emissions per kilogram of meat produced), and higher age at slaughter (longer life leading to more emissions).

It is difficult to compare our results with the other studies in the literature because the FU differs. Our results are expressed as GWP per kilogram of live weight produced because the weaners were sold to other farmers as breeding stock or to feedlot companies for fattening. Other studies in the literature use a different FU, especially kilogram of carcass weight. Our estimates of 27–29 kg CO_2-equivalents per kilogram of live weight are slightly higher compared with the estimate of 46 kg CO_2-equivalents per kilogram carcass weight (equivalent to 23 kg CO_2-eq per kilogram live weight at slaughter) in South Asia of Gerber *et al.* (2013). Suckler beef systems in Ireland, UK and Canada have much lower emissions, ranging from 5.6 to11.2 kg CO_2-equivalents per kilogram of live weight produced (de Vries and de Boer, 2010).

The global call for the intensification of livestock production to improve productivity in order to reduce GHG emission intensities (Steinfeld *et al.*, 2006; Herrero *et al.*, 2010; Gerber *et al.*, 2013) is not supported by the results of our field research on the environmental impact of cross-breeding in mixed farming systems of Central Java. The postulated paradigm that breeding strategies, such as cross-breeding, can reduce the carbon footprint of cattle production (Scholtz *et al.*, 2012) is not straightforward in complex mixed farming systems. In our case, intensification through cross-breeding resulted in increased production: 25 percent higher body weights for adult cross-bred cows and 14–19 percent higher body weights for weaners compared with local Ongole cattle (Widi *et al.*, 2015). However there were no differences in GWP per kilogram live weight produced between local Ongole and cross-bred cattle production systems. Cross-breds required more feed; they were fed more forages, which were collected from the farm and communal sources or bought, and more supplementary feeds, such as rice bran, pollard, compound concentrates, tofu (soybean curd) waste, and soybean hulls (Table 2). We did not measure feed efficiencies (Net Feed Intake: feed intake compared with theoretical feed use) of cross-bred and Ongole animals, but feed intake estimates (Widi *et al.*, 2015) indicated that DM and CP intakes per kg metabolic body weight were higher for cross-breds than for Ongole cows. In Australia, progeny of Brahman (*Bos indicus*) cows bred by British (*Bos taurus*) sire breeds were the least efficient in feed use, whereas purebred Brahmans were the most efficient (Moore, Johnston and Burrow, 2015). Cross-breds showed faster growth rates, but may be feed efficiency of Ongole stock was better. The advantage from the faster growth of cross-breds in terms of reduced GWP per kilogram live weight produced is counteracted by the higher emissions from feed production for cross-breds. Thus the expectation was that local breeds in the local production systems would have higher emissions per unit product than “improved” breeds, in this case cross-bred of Ongole and Simmental cattle, was not substantiated.

Cross-breeding did not result in lower land use. The Ongole and cross-bred beef cattle farms in the study areas had the same land use, approximately 36 m^2 per kilogram of live weight produced. Forages contributed the most to total land use. The use of supplementary feeds was low. Crop by-products, such as rice bran and maize cobs, have a low value. Therefore only a small fraction of land use for crops is allocated to crop by-products for beef production.

Cross-breeding is not done in a systematic way; Simmental semen is used irrespective of the cross-bred generation of the female animals. The majority of cross-bred farmers keep F_1 stock, however, this is gradually changing towards F_2 stock. Farmers do not prefer to upgrade to higher levels of Simmental (Widi *et al.*, 2015). The current cross-breeding practices have not improved the environmental performance of cattle production in Central Java. However, our estimates do not include the impact of cross-breeding on the final fattening stage. This fattening is often done by butchers, large scale farmers (>50 heads) or feedlots (>1 000 heads). Their feeding practices are comparable with those of the smallholders in the present study. The only component in the cross-breeding strategy is the use of exotic semen. Farmers do not receive any assistance in feeding and breeding management. Thus, cross-breeding has not changed the farming systems in the study areas; herd sizes and management practices did not differ between farms with cross-bred or Ongole breeding stock. Cross-breeding has also not affected the motives for keeping cattle, which were similar between Ongole and cross-bred cattle farms (Widi *et al.*, 2015).

Increasing animal productivity requires both better quality and greater quantities of feed (Steinfeld *et al.*, 2006; Gerber *et al.*, 2013). Growing more feed crops might conflict with other land uses, given the limited availability of land in Java. A current regulation stipulates that farmers are not allowed to plant non-food crops on productive lands (Setneg, 1999). Farmers do not have sufficient cash to buy more forages and supplements. These constraints suggest that there is little scope to increase the quality and quantity of feed. Nevertheless, there is large heterogeneity among farmers; the coefficients of variation for the overall emission intensities and land use are approximately 40–45 percent. The driving force behind the differences between farmers is the difference in kilograms of live weight produced. The 25th percentiles of Ongole and cross-bred farms with the lowest GWP per kilogram live weight produced fed their animals more in terms of DM compared with other farms. They also had lower calving intervals and higher body condition scores for their cows, indicating that they managed their animals in a more efficient way (Table 4).

4.3. Conservation of genetic resources and the relation with emissions and land use

In Indonesia, the policy of cross-breeding and the increasing demand for meat are putting considerable pressure on local farm animal genetic resources. Policies that promote cross-breeding run concurrently with more recent policies promoting breeding programmes for local cattle (Widi *et al.*, 2015). This paradox is also found in the international literature. There is a large global literature on livestock biodiversity and the need for conserving local farm animal genetic resources (Hall, 2004; FAO, 2007, 2010a). On the other hand, the global literature considers local ruminant breeds as less efficient in their potential for mitigating GHG emissions than improved breeds. Local ruminant breeds are expected to have higher emission intensities than improved breeds as they are usually fed roughages and crop residues only, and have low outputs (Steinfeld *et al.*, 2006; FAO, 2010b). Hoffmann (2010) expressed concern that the pressure to reduce GHG emissions from ruminants may disadvantage local breeds. In two of the study areas, wet lowlands II and dry uplands, the local government has started a “Return to Ongole” breeding programme. Our results indicate that the promotion of local breeds does not necessarily conflict with efforts to reduce the intensity of GHG emissions from cattle keeping in mixed farms in Java.

5. Conclusions

Cross-breeding (as a tool for intensification) was not more efficient in mitigating GHG emissions and reducing land use per kilogram of live weight produced than local breeds in the current smallholder farming systems in Central Java. The biggest contribution to GWP was from enteric fermentation, which is closely related to the low quality of feeds available. The advantage from the faster growth of cross-breds in terms of GWP and land use per kilogram live weight produced was counteracted by the higher emissions from feed production for cross-breds.

Cross-breeding has not changed current cattle keeping practices. Only exotic semen is provided; sustainable cross-breeding will require assistance in terms of feeding and breeding management. This could improve environmental performance, as the farms with lower emission intensities had, on average, lower calving intervals and higher body condition scores.

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Statement of interest

The work reported in this manuscript is not being considered for scientific publication elsewhere. The authors declare that there are no conflicts of interest related to this manuscript.

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On-farm phenotypic characterization of Mursi cattle in its production environment in South Omo Zone, Southwest Ethiopia

Endashaw Terefe[1], Tadelle Dessie[2], Aynalem Haile[3], Wudyalew Mulatu[2] and Okeyo Mwai[4]

[1]Arsi University, College of Agriculture and Environmental Science, P.O. Box 193, Asella, Ethiopia; [2]International Livestock Research Institute (ILRI), P.O. Box 5689, Addis Ababa, Ethiopia; [3]International Center for Agricultural Research in the Dry Areas (ICARDA), P.O. Box 5689, Addis Ababa, Ethiopia; [4]International Livestock Research Institute (ILRI), P.O. Box 30709, Nairobi, Kenya

Summary
This study was conducted to characterize the morphological peculiarities and performance characteristics of Mursi cattle in its production environment managed by Bodi and Mursi pastoral communities in Southern Ethiopia. A structured questionnaire survey, group discussion, cattle morphological measurements and morphological descriptions were used to collect data. One hundred and two household heads were selected to administer the questionnaire and 201 adult cattle were selected for morphological description and body measurements. The Mursi cattle population was found to have variable coat colour type (85.9 percent) and coat colour pattern (51.3 percent). Body length, chest girth, withers height, rump width and rump length of Mursi cattle were 122.1 ± 0.9, 144.5 ± 0.9, 113 ± 0.1.1, 36.9 ± 0.3 and 20.4 ± 0.3 cm, respectively. Morphological measurements of most linear traits show no difference in the two locations but all measurements vary ($P < 0.001$) between males and females. Estimated age at first calving was 4.6 years and was significantly ($P < 0.0001$) higher in the Mursi area, while the calving interval (14.5 months) and cow reproductive life (14.2 years) were the same in both locations. Average daily milk yield (2.1 litres) and lactation length (7.8 months) of Mursi cattle in the two locations were similar. Cattle production was constrained by high disease prevalence, seasonal feed availability, and water shortage, with frequent drought. Trypanosomosis, black leg, anthrax and skin diseases are major cattle diseases reported in the two study areas. Because of its peculiar morphological characteristics, including large body frame, higher production performance, and survivability in the harsh environment, the Mursi cattle can be used as an alternative genetic resource for production improvement programs.

Keywords: *body measurement, breed characterization, Mursi cattle, morphological description*

Résumé
Cette étude a été menée dans le but de caractériser les particularités morphologiques et les performances productives des bovins Mursi dans son milieu de production, géré par les communautés pastorales Bodi et Mursi dans le Sud de l'Éthiopie. Un questionnaire structuré, un groupe de discussion et des mesures et des descriptions morphologiques des bovins ont été utilisés pour la collecte des données. Cent-deux chefs de famille ont été sélectionnés pour le questionnaire alors que 201 animaux adultes ont été choisis pour la description morphologique et les mesures corporelles. Il a été observé que la population bovine Mursi présente des couleurs (85,9 pour cent) et des motifs de la robe (51,3 pour cent) variés. La longueur du corps, le périmètre thoracique, la hauteur au garrot et la largeur et la longueur de la croupe chez les bovins Mursi ont été de 122,1 ± 0,9, 144,5 ± 0,9, 113 ± 0,1, 36,9 ± 0,3 et 20,4 ± 0,3 cm, respectivement. Aucune différence n'a été décelée entre les deux zones pour ce qui est de la plupart des mesures linéaires mais toutes les mesures ont varié ($P < 0.001$) entre mâles et femelles. L'âge estimé à la première mise bas a été de 4,6 ans et a été significativement ($P < 0.0001$) plus élevé dans le territoire Mursi, alors que l'intervalle entre mises bas (14,5 mois) et la vie reproductive des vaches (14,2 ans) ont été les mêmes dans les deux zones. La production moyenne journalière de lait (2,1 litres) et la durée de la lactation (7,8 mois) ont été similaires pour les bovins Mursi des deux territoires. La production du bétail a été limitée par une prévalence élevée de maladies, par la variation saisonnière dans la disponibilité en aliments et par le manque d'eau, dû aux fréquentes sécheresses. La trypanosomiase, le charbon symptomatique, la fièvre charbonneuse et les maladies cutanées ont été les principales maladies identifiées chez les bovins des deux zones étudiées. En raison de leurs caractéristiques morphologiques particulières, parmi lesquelles leur grand format corporel, leurs plus grandes performances productives et leur capacité de survie en milieu hostile, les bovins Mursi peuvent être utilisés comme une ressource génétique alternative dans les programmes d'amélioration de la production.

Mots-clés: *bovins Mursi, description morphologique, mesure corporelle, caractérisation raciale*

Resumen
Este estudio fue llevado a cabo con el fin de caracterizar las peculiaridades morfológicas y los rendimientos productivos del ganado bovino Mursi en su ambiente de producción, gestionado por las comunidades pastoriles Bodi y Mursi en el Sur de Etiopía. Para la toma de los datos, se emplearon un cuestionario estructurado, un grupo de debate y medidas y descripciones morfológicas del ganado. Ciento

Correspondence to: Endashaw Terefe, Arsi University, College of Agriculture and Environmental Science, P. O. Box 193, Asella, Ethiopia. email: endashawterefe1@gmail.com

dos cabezas de familia fueron escogidos para el cuestionario mientras que se seleccionaron 201 animales adultos para la descripción morfológica y las medidas corporales. Se observó que la población bovina Mursi presenta colores (85,9 por ciento) y patrones de color de la capa (51,3 por ciento) variables. La longitud corporal, la circunferencia torácica, la altura a la cruz y la anchura y la longitud de la grupa en el ganado bovino Mursi fueron, respectivamente, de 122,1 ± 0,9, 144,5 ± 0,9, 113 ± 0,1, 36,9 ± 0,3 y 20,4 ± 0,3 cm. No se detectaron diferencias entre las dos ubicaciones para la mayoría de los parámetros lineales, si bien todas las medidas variaron ($P < 0.001$) entre machos y hembras. La edad al primer parto estimada fue de 4,6 años y fue significativamente ($P < 0.0001$) mayor en el área Mursi, mientras que el intervalo entre partos (14,5 meses) y la vida reproductiva de las vacas (14,2 años) fueron iguales en ambas localizaciones. La producción media diaria de leche (2,1 litros) y la duración de la lactación (7,8 meses) fueron similares entre las dos áreas para el ganado Mursi. La producción del ganado se vio limitada por la alta prevalencia de enfermedades, por la variabilidad estacional en la disponibilidad de alimento y por la escasez de agua, debida a las frecuentes sequías. La tripanosomiasis, el carbunco sintomático, el ántrax y las enfermedades cutáneas fueron las principales enfermedades identificadas en el ganado bovino en las dos áreas de estudio. Debido a sus peculiares características morfológicas, entre las cuales se incluye su gran formato corporal, su mayor rendimiento productivo y su capacidad para sobrevivir en un ambiente hostil, el ganado bovino Mursi puede ser utilizado como un recurso genético alternativo en los programas para la mejora de la producción.

Palabras clave: *ganado bovino Mursi, descripción morfológica, medida corporal, caracterización racial*

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Introduction

Ethiopia is home to diverse cattle genetic resources that are adapted to and distributed in different agro-ecological zones of the country. As a result, cattle production is one of the main components of agricultural activities in all parts of the country. For smallholder farmers and pastoralists, cattle play multiple roles as source of food, income and serve as an asset and security against risks (Terefe *et al*., 2012). The multi-function of cattle genetic resources in the country is identified through production system and breed characterization studies in their natural production environment (FAO, 2012).

So far, several cattle breed studies have been conducted in Ethiopia to identify the available cattle genetic resources, and describe their phenotypic and genetic diversity, husbandry practices, production systems and breed performances (Albero and Haile Mariam, 1982a, 1982b; Rege, 1999; Rege and Tawah, 1999; Ayalew *et al*., 2004). These early breed identification and characterization studies in the country classified the available cattle genetic resources into five major groups viz, Large East African Zebu, Small East African Zebu, Senga, Zenga and the Taurine (humpless shorthorn) breeds (Rege, 1999; Rege and Tawah, 1999). These major breed groups were further classified into more than 32 breeds/ecotypes (DAGRIS, 2007). Furthermore, molecular characterization has shown high genetic diversity between and within breeds/ populations (Zerabruk *et al*., 2012).

The Mursi cattle breed is classified as Small East African Zebu in the Abyssinian Shorthorn subgroup (Rege and Tawah, 1999). This breed group is believed to have descended from zebu cattle that were introduced into Africa (FAO, 2007). The Mursi cattle breed has a relatively large body size compared with other breeds of the subgroup (Rege and Tawah, 1999). The large body size is due to some ancestral linkage with the Large East African Zebu subgroup. The ancestral linkage might be due to geographical proximity of the breed distribution, human migration, long-distance pastoralist travel in search of pasture and water for their cattle, and markets (Fedlu *et al*., 2007).

The Mursi and Bodi pastoral communities keep the Mursi cattle in the Southwestern rangelands, South Omo zone (Rege, 1999). The pastoralists prefer the breed due to its perceived relative trypanotolerance (that is, its ability to survive and produce under trypanosomosis challenge) in trypanosomosis epidemic areas (Terefe *et al*., 2015), where there is little veterinary services. The study reported here is part of a project, which designed to study phenotypic characterization and trypanosomosis prevalence in Mursi cattle breed in its production environment. Therefore, this paper reports the morphological characteristics, production and reproduction performance, and identifies the major production constraints of Mursi cattle in Southwestern Ethiopia.

Materials and method

Study area

The study was conducted in Southern Nations Nationalities and Peoples Regional State, South Omo Administrative Zone in Salamago *Wereda*, Southwest Ethiopia. It is 870 km to the southwest of Addis Ababa and located in between 6°19′ and 7°10′N latitude, and 15°12′ and 22°25′E longitude with total land area of 451.12 square km. The *Wereda* has two major agro-climatic zones; the midland that covers 33 percent of the total land and the rest 67 percent of the area is low land. The mean annual temperature was recorded to be 29 °C (ranges from 20 to 37.5 °C). The average altitude of the Wereda is 971 m and receives bimodal rainfall, in which the long rainy season is in the months of March to June, while the short rainy season occurs in the months of August to October. Scattered woodland, savanna grass and large grassland plains dominate the vegetation type of the study area. *Acacia, Combretum* and *Grewia* are common woody plant species, whereas *Cynodon, Brachiaria, Heteropogon, Cymbopogon, Aristida* and *Chloris*are common herbaceous grass species found in the study area (Tesfaye, 2008). Two locations, Mursi and Bodi areas, where the Mursi and Bodi pastoral communities live, respectively, were selected for this study. The two pastoral communities keep the Mursi cattle breed and share common territorial boundary and the locations also characterized by tsetse fly infested area, where trypanosome is prevalent (Terefe *et al*., 2015).

Sampling and data collection

Two hundred and one animals (28 males and 173 females) were selected from the Bodi and Mursi pastoral communities' household herd for morphological description and body measurements. The morphological characteristics such as coat colour pattern, coat colour type, horn type, horn orientation, horn shape, hump size, hump orientation, hump position and temperament were recorded according to FAO cattle morphological characteristics descriptor manual (FAO, 2012) and Ayalew and Rowlands (2004). Basic temperament of an animal was described in docile, moderately tractable and aggressive during handling for body measuring and blood sampling. Body measurements (body length, chest girth, height at wither, rump length, rump width, tail length and other traits) were made on adult animals using graduated measuring tape to 0.5 cm precision. One hundred and two heads of household (43 from *Bodi* and 59 from *Mursi* pastoral communities) were selected for questionnaire survey. Structured questionnaires were designed to collect data communities' responses on cattle performance, feed resource and utilization, major cattle production constraints and disease challenges that impede cattle production in the area. Additional information such as cattle management, major cattle production constraints and information how the community cope seasonal problems were collected through group discussion with community elders.

Data analysis

Data on physical body measurements were analysed using general linear model procedure of SAS (SAS®, Cary, North Carolina) in which sex of cattle and locations were fitted as explanatory fixed effects while body length, chest girth, withers height and other measured traits were response variables. Descriptive statistics was employed to analyse data on reproductive performance (age at first mating, age at first calving, calving interval and reproductive lifespan) and productive performance (daily milk yield and lactation length). Independent sample *t*-test was employed to compare the significance level of the two locations. Frequency statistics were used to analyse body morphology such as coat colour type and coat colour pattern, horn shape and orientation, hump size and orientation, udder size and animal temperament.

The morphological variability, that is, variability in coat colour, coat colour pattern, hump size, hump orientation, horn nature, horn orientation and shape, and temperament of individuals in the population was analysed using the coefficient of unalikablity. This measures the within-population variability of categorical variables on a scale from 0 to 1. The higher the value, the more unalike the qualitative variables are. The coefficient of unalikablity (u_2) is calculated using the following formula and is equal to one minus the sum of square of the proportion (P_i) of each category response (Kader and Perry, 2007).

$$\boldsymbol{u}_2 = 1 - \sum_i p_i^2$$

Rank indices of major cattle production constraints were calculated as the sum of weighted number of response for criterion (n times number of response criterion ranked 1st + $n - 1$ times number of response ranked 2nd + ⋯ + 1 times number of response ranked nth) given to a criteria divided by the total sum of responses under each rank (n times total response ranked 1st + $n - 1$ times total response ranked 2nd + ⋯ + 1 times total response ranked nth) for overall criteria; where n is the number constraints to be ranked.

Result and discussion

Morphological characteristics of Mursi cattle

Qualitative body description

Qualitative body description of Mursi cattle population show variable coat colour pattern and colour types among individual cattle (Figure 1). The most commonly observed coat colour patterns were plain (64.1 percent), pied (25.6 percent) and spotted (10.3 percent) with different colour combinations and were similar in the two study locations. Males predominantly have plain coat colour (68 percent) and while the rest 32 percent possess pied coat colour. Similarly most (63.5 percent) of the female cattle population were of plain coat colour, while 24.7 percent were pied and 11.8 percent of spotted coat colour patterns.

The dominant plain coat colours of Mursi cattle breed were 22.6 percent red, 18.5 percent white and 11.3 percent black, while the rest 14.4 percent were different colour types such as grey, brown and fawn. The pied coat colour are variable, in which white is found to be dominant colour that covers most part of animals' body with red, black or brown combination (14.3 percent). Black dominated black-white or black-red pied coat colour comprises 8.2 percent in proportion. A dominant red colour with white combination made up the lowest proportion (8.2 percent) of the total population. The remaining 2.5 percent of the population consists of different coat colour

Figure 1. Variable coat colour types and colour patterns of a Mursi cattle herd.

combinations (Table 1). Rege and Tawah (1999) also reported high coat colour variability for the breed. The variable coat colour probably helps the breed to adapt the very hostile environment through avoiding effects of radiation and heat stress (Olson *et al.*, 2003) and some colours do not attract the tsetse fly, preventing it landing, and this averts the fly biting the animal (Makokha *et al.*, 2006).

Particular morphological characteristics of Mursi cattle breed include its shiny and smooth hair type with large curved horns (Figures 1–3). Of the total population, 69.4 percent possess straight horns and some, (22.8 percent) possess forward oriented horns. The common horn shape is curved (82.4 percent), while some possess straight upward (15.0 percent) and most of the cattle (57.7 percent) have artificially modified horns. Artificial horn modification is manipulation of cattle horn from an early age to give the horn special shape desired by the owners. Horn modification is usually done through fastening the horn with a knotted rope to give a curved and twisted shape. The tips of the two horns come close together and form circular shape through time (Figures 3A & B). The purposes of horn modification are to give the animal a special look, ease identification of ownership and to protect the cattle from harming each other or humans. It also provides ease of restraint during milking, blood collection, or medication.

The cattle breed is also characterized by its thoracic hump, which is distinctive characteristic feature of zebu cattle. Most (97.4 percent) of the cattle in the population possess an erect hump, while 2.6 percent have a laterally drooped hump. The hump size of the cattle was variable; most of the animals, (64.2 percent), possess a small hump, whereas the rest (22.3 and 13.5 percent) have medium and large humps, respectively. The male cattle have large (48 percent) and medium (44 percent) humps, whereas, the highest proportion of female cattle (72.6 percent) possess a small hump. As in other indigenous zebu cattle, the udder size of most cows (63.3 percent) is small, whereas, a few cows (32.0 percent) possess medium udder size and only 4.7 percent have a large udder size. Concerning the temperament of Mursi cattle, 75.5 percent of the animals were found to be very docile, while 19.4 percent were moderate and the rest 5.1 percent were very aggressive (Table 2). Male cattle were observed more aggressive than females. The pastoral communities in the two locations used cattle as a source of milk and blood for consumption (Terefe *et al.*, 2012), and as a result, animals with good temperament are preferable for easy handling or restraining during milking, blood collection and medication. Therefore, docile cattle remain in the herd through long-term selection for docility.

The morphological unalikability analysis indicated that the cattle breed is very variable. From these morphological traits, 85.9 percent of the population was unlikeable in coat colour type, while, 51.3 percent of the population differs in coat colour pattern. Similarly, the variability of individuals due to hump and udder size was variable with unalikablity coefficient of 0.52 and 0.49, respectively. Lower unalikablity coefficient was observed for hump orientation (0.05) and temperament (0.39) of the population. The variability of the cattle breed due to horn nature (0.49), orientation (0.46)

Table 1. Colour pattern and colour type (%) of Mursi cattle in the Bodi and Mursi pastoral areas of South Omo zone, Southwest Ethiopia.

Colour pattern and type		Overall	Location		Animal sex	
			Bodi	Mursi	Male	Female
Coat colour pattern	Plain	64.1	64	64.1	68	63.5
	Pied	25.6	26	25.5	32	24.7
	Spotted	10.3	10	10.3	0	11.8
Coat colour type	Red	22.6	12	26.2	20	22.9
	White	18.5	20	17.9	20	18.2
	Black	11.3	14	10.3	8	11.8
	Brown	2.6	4	2.8	0	2.9
	Grey	7.7	6	7.6	4	8.2
	Roan	4.1	4	4.1	12	2.9
	Whit dominant red, black or brown	14.3	16	13.9	16	14.1
	Black dominant white or red	8.2	12	6.9	12	7.7
	Red dominant white	8.2	8	7.6	8	7.6
	Other colours	2.5	4	2.8	0	3.6

Figure 2. Coat colour type and colour pattern of a typical Mursi cows (a and b).

Figure 3. Typical Mursi bull with alternative (a) pied coat colour and (b) modified horn types.

Table 2. Body description (%) of Mursi cattle in the Bodi and Mursi pastoral areas of South Omo zone, Southwest Ethiopia.

Cattle body description		Overall	Location		Animal sex	
			Bodi	Mursi	Male	Female
Horn nature	Natural	42.3	52	38.9	48	41.4
	Modified	57.7	48	61.1	52	58.6
Horn orientation	Lateral	5.7	8.0	4.9	12	4.8
	Forward	22.8	20.0	23.8	24	22.6
	Straight	69.4	70	69.2	64	70.2
	Drooping	2.1	2	2.1	0	2.4
Horn shape	Scurs	2.6	2	2.8	4	2.4
	Straight upward	15.0	18	14.0	20	14.3
	Curved	82.4	80	83.2	76	83.3
Hump size	Large	13.5	12.2	13.9	48	8.3
	Medium	22.3	12.3	25.7	44	19.1
	Small	64.2	75.5	60.4	8	72.6
Hump orientation	Drooping	2.6	8	0.7	12	1.2
	Erect	97.4	92	99.3	88	98.8
Udder size	Small	63.3	88.1	55.0	–	63.3
	Medium	32.0	11.9	38.9	–	32.0
	Large	4.7	0	6.1	–	4.7
Temperament	Docile	75.5	64	79.5	69.2	76.5
	Moderately tractable	19.4	32	15.0	23.1	18.8
	Aggressive /Wild	5.1	4.0	5.5	7.7	4.7

Table 3. Least square means and standard error of body measurements (cm) of adult Mursi cattle in the Bodi and Mursi pastoral areas of South Omo zone, Southwest Ethiopia.

Measured traits	Over all	CV%	Location			Sex		
			Bodi	Mursi	SL	Female	Male	SL
Body length	122.1 ± 0.9	7.6	121.5 ± 1.4	122.7 ± 1.0	ns	114.9 ± 0.8	129.3 ± 1.7	***
Chest girth	144.5 ± 0.9	6.02	142.1 ± 1.3	146.8 ± 0.9	***	134.3 ± 0.7	154.6 ± 1.6	***
Height at wither	113.0 ± 1.1	9.65	112.6 ± 1.6	113.3 ± 1.2	ns	104.6 ± 0.9	121.3 ± 1.9	***
Rump width	36.9 ± 0.3	8.4	37.8 ± 0.5	36.0 ± 0.3	***	35.0 ± 0.3	38.8 ± 0.6	***
Rump length	20.4 ± 0.3	12.28	20.2 ± 0.4	20.7 ± 0.3	ns	18.4 ± 0.2	22.4 ± 0.5	***
Tail length	75.0 ± 0.6	8.04	73.4 ± 0.9	76.5 ± 0.7	***	72.1 ± 0.5	77.9 ± 1.1	***
Canon bone length	19.6 ± 0.2	8.91	19.6 ± 0.3	19.6 ± 0.2	ns	18.9 ± 0.2	20.3 ± 0.3	***
Canon bone circum.	15.1 ± 0.1	9.16	15.0 ± 0.2	15.2 ± 0.2	ns	13.5 ± 0.1	16.7 ± 0.35	***
Ear length	18.6 ± 0.3	13.19	18.9 ± 0.4	18.3 ± 0.3	ns	18.3 ± 0.2	18.9 ± 0.5	ns
Horn length	30.8 ± 1.1	31.71	28.0 ± 1.5	33.5 ± 1.1	***	27.0 ± 0.8	34.5 ± 1.9	***
Face length	39.3 ± 0.3	5.86	38.9 ± 0.4	39.6 ± 0.3	ns	37.4 ± 0.2	41.2 ± 0.5	***
Dewlap width	17.1 ± 0.3	19.83	17.0 ± 0.5	17.2 ± 0.4	ns	14.7 ± 0.3	19.5 ± 0.6	***
Tail length	75.0 ± 0.6	8.04	73.4 ± 0.9	76.5 ± 0.7	***	72.1 ± 0.5	77.9 ± 1.1	***
Teat length	5.2 ± 0.3	25.3	5.6 ± 0.6	4.9 ± 0.4	**	–	–	–

SL = significance level; ns = non-significant; ** significant at $P < 0.01$; *** significant at $P < 0.001$.

and shape (0.29) may not be genetic but rather it might arise from horn modification made by individual cattle owners in the two communities (Table 2). The high coat colour variability observed in the population implies the existence of heterogeneity within the breed. This multiple coat colour and colour pattern variations come from preferential selection of the pastoral communities toward animals with variable coat colour pattern (Terefe *et al.*, 2012) and uncontrolled mating.

Quantitative body measurement

The overall least-square means and standard error of body length, chest girth and height at withers were 122.1 ± 0.9, 144.5 ± 0.9 and 113.0 ± 1.1 cm, respectively (Table 3). The measurements were significantly different ($P < 0.001$) between the male and female populations. No significant differences in body length and height at wither were observed between the cattle from the two locations. However, there were significant differences ($P < 0.001$) in chest girth, rump width, tail and horn length observed in Bodi and Mursi areas. Canon bone length and cannon bone circumference were 19.6 ± 0.2 and 15.1 ± 0.1 cm, respectively. Similarly, ear, horn, face, dewlap width and tail length measurements were 18.6 ± 0.3, 30.8 ± 1.1, 39.3 ± 0.3, 17.1 ± 0.3 and 75.0 ± 0.6 cm, respectively. The teat length of cows was 5.2 ± 0.3 cm and longer ($P < 0.01$) cows in the Bodi (5.6 ± 0.6 cm) than in the Mursi (4.9 ± 0.4 cm) areas. The significant differences of some measured body morphological traits of cattle between the two locations might be due to within breed variability, which has been seen in most cattle breeds in Ethiopia using molecular studies (Fedlu *et al.*, 2007). As a comparison with other cattle breed characterization results, the body measurements of Mursi cattle breed were superior to those of Kereyu cattle (Garoma, 2006) and Abigar (Nuer) cattle breeds (Minuye, 2009) under pastoral management system in Ethiopia, but its body frame is comparable with the Boran (Rege, 1999) and Ogaden cattle breeds (Mekuriaw, Ayalew and Hegde, 2009). Similarly, this breed was found to be superior to the taurine Sheko cattle breed, which survive and produce in trypanosome prevalent area (Ayalew, 2001).

Performance characteristics of Mursi cattle

Reproductive performance

The mean age at first breeding of male and female cattle were reported to be 3.6 and 3.4 years, respectively (Table 4). The average age at first calving (AFC) of the female Mursi cow was 4.6 years and it was significantly ($P < 0.001$) lower in the Bodi (4.3 years) than in the Mursi (4.9 years) herds. The calving interval (CI) of Mursi cow was found to be 14.5 months and did not differ in the two pastoral communities. However, no notable cattle husbandry practices were observed in the Bodi pastoral communities that led heifers to have a lower AFC (Terefe *et al.*, 2012).

AFC and CI of Mursi cattle breed is similar to that reported by Tesfaye (2008) on the same breed. As a result, AFC of Mursi cattle in this study was similar to Kereyu cattle (Garoma, 2006) and Borana (Rege, 1999) cattle breeds under pastoral management. However, the CI was lower than in Ogaden cattle managed on station farm (Mekuriaw, Ayalew and Hegde, 2009), and Abigar cattle under pastoral management (Minuye, 2009). The lower CI in the Mursi cattle might be due to breed difference or uncontrolled breeding practice (Terefe *et al.*, 2012). Similar to the Sheko cattle breed, which was reported as a trypanosome tolerant breed in Ethiopia (Lemecha *et al.*, 2006), the Mursi cattle inhabit a trypanosome epidemic area, and the two breeds have similar reproductive performances such as AFC and CI (Taye, Ayalew and Hegde, 2007). The lower CI produces more calves per cow, which increases herd size that grants the production

Table 4. Mean and standard deviation of reproductive performance of Mursi cattle in the Bodi and Mursi pastoral areas of South Omo zone, Southwest Ethiopia.

Reproductive traits	Location			*t*-value	*P*-value*
	Bodi	Mursi	Overall		
Age at first service (year)	3.4(0.7)	3.6(0.6)	3.4(0.7)	1.59	0.115
Age at first calving (year)	4.3(0.6)	4.9(0.8)	4.6(0.8)	4.00	0.0001
Calving interval (month)	14.8(5.3)	14.2(4.0)	14.5(4.5)	0.55	0.582
Female reproductive life (year)	13.5(3.2)	14.6(2.9)	14.2(3.1)	1.697	0.093
Total calves born per cow lifetime	10.6(2.7)	11.4(1.7)	11.0(2.2)	1.71	0.091
Age at first mating of male (year)	3.4(0.7)	3.7(0.6)	3.6(0.7)	1.89	0.062
Male reproductive life (year)	14.2(4.3)	14.1(3.5)	14.1(3.8)	0.053	0.958

*Significant at $P < 0.05$.

of more milk from a larger number of cows in pastoral communities.

The mean reproductive lifetime of Mursi cow was reported to be 14.2 years. Within this reproductive lifetime, the mean number of calves born per cow was estimated to 11 calves (Table 4). The mean reproductive lifetime of Mursi cow is the same as the turine Sheko cattle breed (Taye, Ayalew and Hegde, 2007); however, the number of calves born in a lifetime of the Sheko cow is eight calves and is lower than the Mursi cow. The large number of calves per cow in Mursi cattle might be due to breed and management differences, with Mursi cattle being managed in open grazing compared with the restricted feeding management of Sheko cattle (Taye, Ayalew and Hegde, 2007). This uncontrolled breeding results all season reproduction of cattle as compared with the controlled breeding system (Mekonnen *et al.*, 2012), which results in a large number of calves produced in a herd that can raise household herd size for sustainable milk production (Terefe *et al.*, 2012).

Milk production performance

Cow milking frequency in the two pastoral communities was reported two times as twice a day, in the morning and evening after grazing. The interviewees estimated the amount of milk produced per cow per day in their herd by recalling the apparent milk yield in spite of cows' lactation stage and andty. The daily milk yield reported here is the amount excluding suckled by the calf. As a result, the daily milk production of Mursi cow does not exceed two "*bakacha*", local wooden milking container measuring on average an equivalent of 1.5 litres. The mean daily milk produced per cow for human purpose was estimated to be 2.1 litres and the amount produced in the two pastoral communities did not differ ($P > 0.05$). The Mursi cow produce a higher quantity of milk compared with Kereyou (Garoma, 2006), and Abigar (Minuye, 2009) cattle, which are adapted in trypanosome free area of the country and are managed under pastoral management system. However, the milk yield was similar to that of Sheko cattle breed (2.3 litres) which is adapted to trypanosome prevalent area of Southwest Ethiopia (Taye, Ayalew and Hegde, 2007). Similarly, the average lactation length of Mursi cow was estimated to be 7.8 months and did not significantly vary in the two locations. From the mean daily milk yield and lactation length, the lactation yield of Mursi cow was estimated to be 453.4 litres (Table 5).

Cattle management practices

Feed and feeding management

Natural pasture is the most common source for cattle grazing in the rainy season of the two locations. Beside to natural pasture, tree leaves and shrubs are used as cattle feed in rainy and dry periods (Table 6). In the two locations, 92.1 percent of the respondents said that the cattle feeding system is free grazing on communal grazing land. This system is a common feeding practice of cattle and other livestock in pastoral production system in the country. Some pastoral communities in the Mursi areas practice both free grazing and tethering, so that cattle that could

Table 5. Mean and standard deviation of milk production performance of Mursi cattle ($N = 102$) in the Bodi and Mursi pastoral areas of South Omo zone, Southwest Ethiopia

Milk production traits	Locations			*t*-value	*P*-value*
	Bodi	Mursi	Overall		
Lactation length (months)	7.9(2.4)	7.7(2.5)	7.8(2.4)	0.452	0.652
Daily milk yield (litre)	2.1(0.7)	2.2(0.4)	2.1(0.6)	0.499	0.659
Lactation milk yield (litre)	455.7(1.6)	451(1.4)	453.4(1.5)	0.105	0.917

*Significant at $P < 0.05$.

Table 6. Response (%) on feed resource and feeding management in the Bodi and Mursi pastoral communities in the Bodi and Mursi pastoral areas of South Omo zone, Southwest Ethiopia.

Feed resource and utilization		Location		
		Bodi	Mursi	Overall
Feed source in rainy season	Natural pasture	100	98.5	100
	Tree/shrub leaf	67.5	88.1	79.4
Feed source in dry season	Natural pasture	83.7	86.4	85.3
	Tree/shrub leaf	86.0	79.6	82.4
Grazing methods	Free grazing	97.7	86.4	92.1
	Free grazing and tethering	0	13.6	7.9
Seasonal feed shortage	Yes	90.7	88.1	89.2
	No	9.3	11.9	10.8

not move long distances, such as calves are usually tethered on grazing areas near to the homestead.

The majority of the pastoral communities (89.2 percent) responded that there is frequent seasonal feed shortage in quality and quantity in the two locations. This marked seasonal variation of feed resources is due seasonal variation in rainfall distribution (Tolera and Abebe, 2007). The problem is aggravated by absence of feed conservation practices by the pastoral communities for the dry season and frequent droughts due to prolonged dry periods. The communities usually solve seasonal cattle feed shortages by trekking their cattle to the Omo River and grazing on the flood-recessed area. However, sufficient feed is available in the wet season and cattle graze close to human housing, whereas in dry season, animals travel long distances and sometimes the communities shift their location during an extended dry period to areas where grazing is available. They do not provide supplemental feeds for cattle of any production status and age groups that are able to graze on natural pasture. However, a few respondents reported that they provide cut grass to calves and sick cattle, which are unable to move long distances.

Cattle health management

Disease is one of the major constraints of animal farming. The diseases identified from local naming in this study were based on their clinical signs and symptoms. According to the respondents, trypanosomosis, blackleg, anthrax and skin diseases were the major challenges to cattle production in the two pastoral areas (Table 7). Ticks and mangemites were the observed external parasites and where a critical problem in the area. The communities report that Contagious Bovine Pleuropneumonia (CBPP) and Pasteurellosis were the main cattle diseases that cause significant losses through cattle death and reduction of production.

The communities use traditional medication to prevent and treat cattle diseases. Local herbs are used to treat sick animals. Moreover, they usually smoke the barns to protect

Table 7. Response (%) on major cattle diseases in the Bodi and Mursi pastoral areas of South Omo zone, Southwest Ethiopia.

Major cattle disease	Locations		
	Bodi	Mursi	Overall
Trypanosomosis	100	100	100
Black leg	93.0	86.4	89.2
Anthrax	74.7	84.4	81.4
Contagious Bovine Pleuropneumonia	39.5	22.0	29.4
Pasteurellosis	23.3	18.6	20.6
Internal and external parasites	46.5	79.7	65.7
Skin disease	51.2	88.1	72.6
Mastitis	14.0	16.9	15.7
Poisonous plants	7.0	5.1	5.9

cattle from tsetse fly biting. The communities move their cattle away from tsetse fly infested areas when there is a high infestation during the wet season. Animals are watered at noon when tsetse flies become inactive and hide under vegetation to protect themselves from the intense heat (FAO, 1982).

Major cattle production constraints

The main cattle production constraints reported by the Bodi communities were disease and parasite (rank index of 0.27), seasonal feed (0.26) and water (0.22) shortages (Figure 4). While the Mursi pastoralist ranked water shortage (0.35) as their first priority problem and feed (0.33) and animal disease (0.11) were second and third in their area. The Bodi communities settle along the *Gura* a river where water is available for livestock and human consumption, while the Mursi people live far from a water source and state this as the community's primary problem. Water and feed shortage due to erratic rainfall were the major challenges to cattle production in the two study locations, mainly in the Mursi area. The prolonged absence of rainfall in the area leads to drought that causes animal

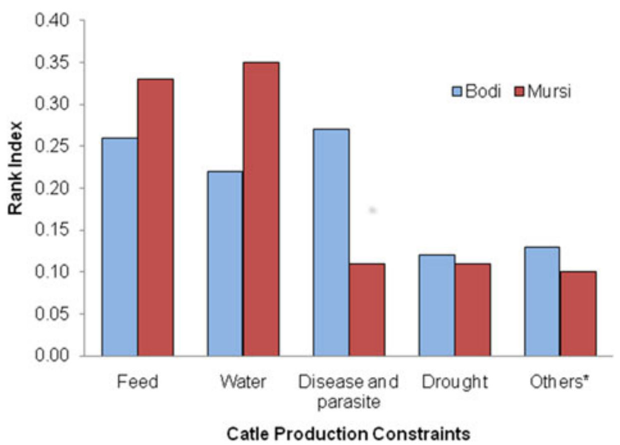

Figure 4. Rank indices of major cattle production constraints in Bodi and Mursi pastoral communities in South Omo Zone, Southwest Ethiopia. (*Other production constraints include veterinary services, wild predators, infrastructure such as Market and roads, theft and conflicts that result in cattle raiding.)

disease outbreaks and results in high cattle mortality. To cope with these problems, the communities move their herd to areas where pasture and water are available and usually cause conflict with neighbouring ethnic groups due to the sharing of resources and can result in theft and raiding of cattle.

Inadequate or complete absence of veterinary services in the area, absence of livestock markets and roads were identified as the major production constraints in the Bodi and Mursi pastoral communities. Absence of market in the areas limited the availability of production inputs such as veterinary supplies, sale of animals and animal products, which influence herd growth, productivity, and general livelihood of the pastoral communities. *Hana* and *Jinka*, the Salamago Wereda and South Omo zone administrative towns, respectively, are the only two small marketing places where the Bodi and Mursi communities have to travel long distances for marketing. In these markets, the communities sell their animals and purchase food grains especially in the long dry season. During this period, the communities' consume mainly a grain-based diet since milk production is low and not sufficient for household consumption. Therefore, the communities have to travel a long distance to sell their cattle in distant markets and even in some worse drought seasons, they exchange live animals for food grains (Terefe *et al*., 2012).

Disease and parasite prevalence were among the listed main constraint that hindered cattle production in the Bodi and Mursi communities. This high disease and parasitic problem in the area might arise from the presence of different wild animals in the area that share common national park ecosystem with the livestock (Bengis, 2003). Besides being a disease and parasite reservoir, the wild animals are potential predators of livestock and are challenges to cattle production in the areas. This is because the communities graze their cattle in the national parks in dry season when grazing pasture is scarce. This situation is common for most pastoral areas that inhabit and share national park boundaries (Gegner, 2002) and these cause significant losses in cattle numbers.

Conclusion

The Mursi cattle breed shows morphological variability. This variability indicates absence of directional selection towards particular objective traits. However, the breed shows peculiar morphological characteristics that enable the separation of Mursi cattle from other breeds and ecotypes. On the other hand, the morphological variability may have contributed to its survival and production in the hot and humid environment where trypanosome is highly prevalent.

The long and large body frame of Mursi cattle compared to some breeds in the country means it could be a genetic resource to use in improvement programs. It provides an option to maximize beef production to satisfy the ever-increasing demand. The breed produces a higher quantity of milk compared with other indigenous cattle breeds that are managed under pastoral management system. The breed can also be used as a potential genetic resource to improve milk production through implementing appropriate breeding strategy in the pastoral production system. With this genetic potential, introducing the breed to a smallholder mixed production system, increases cattle genetic resource for alternate breed improvement in the country.

Even though the breed survives and produces through tolerating the existing hostile environment and trypanosomosis challenge, cattle production in the area is constrained by prevalent disease, seasonal feed and water shortages, and frequent drought. Absence of frequent vaccination and treatment of cattle in such hostile environment make the area potential to harbouring epidemic diseases and parasites that cause loss of cattle number. Therefore, alleviating these constraints should increase the productivity of Mursi cattle in their natural environment.

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Phenotypic and genetic parameters for milk yield in traditional *Nublang* cattle *(Bos indicus)* of Bhutan

Jigme Dorji[1], Dhendup[2] and Iona M. MacLeod[3]

[1]*National Biodiversity Centre, Serbithang, Ministry of Agriculture and Forests, Bhutan;* [2]*Department of Livestock, National Nublang Breeding Farm, Tashiyangphu, Bhutan;* [3]*Melbourne School of Land and Environment, University of Melbourne, Victoria, Australia*

Summary

The Nublang is a unique dual-purpose breed of *Bos indicus* cattle found in Bhutan. They have been crossed with Mithun (*Bos frontalis*) and *Bos taurus* breeds in an effort to improve milk production leading to a decline in the population of purebred Nublang. An alternative to crossbreeding would be the genetic improvement of milk yield within purebred Nublang, thus allowing conservation and sustainable utilization of the pure breed. It is important to measure the genetic variability (heritability) of milk yield to assess the potential for genetic improvement within Nublang. Therefore this study estimated phenotypic and genetic parameters of milk yield using 2 052 test day milk yields from 66 cows recorded from 1997 to 2013 in the National Nublang Farm, Tashiyangphu. The average daily milk yield (DMY) was 2.12 ± 0.7 litres (N 2 052, range: 0.3–5.0 L, CV: 34 percent). Parity, month in milk and year all had a significant effect on DMY ($P < 0.05$). The average lactation milk yield (LMY) was 519.2 ± 151 L (N: 261, range: 115–881.7, CV: 29.1 percent) and average lactation length was 239 days. LMY was significantly influenced by parity ($P < 0.05$) and season of calving. The heritability of DMY and LMY was 0.22 ± 0.16 and 0.13 ± 0.20, respectively. The repeatability estimates were 0.45 ± 0.05 and 0.49 ± 0.08 for DMY and LMY, respectively. Overall the heritability and repeatability estimates of milk yields indicate potential for genetic improvement of milk yield in Nublang cattle through selection. However, it is recommended that a larger dataset is generated to enable more precise estimates of genetic parameters.

Keywords: *breed conservation, genetic improvement, heritability, repeatability*

Résumé

La race Nublang est une race unique de bovins *Bos indicus*, à double aptitude, élevée au Bhoutan. Elle a été croisée avec le gayal (*Bos frontalis*), ainsi qu'avec des races de *Bos taurus*, dans le but d'améliorer la production laitière, ce qui a mené à une réduction de la population d'individus purs de race Nublang. Une alternative au croisement pourrait être l'amélioration génétique de la production laitière au sein du cheptel de pure race Nublang, ce qui permettrait la conservation et l'utilisation durable de la race dans sa pureté. Il s'avère important de mesurer la variabilité génétique (l'héritabilité) de la production laitière afin d'évaluer le potentiel d'amélioration génétique au sein de la race Nublang. Ainsi, cette étude a estimé des paramètres phénotypiques et génétiques de la production laitière à partir des données de 2 052 contrôles laitiers journaliers effectués sur 66 vaches de 1997 à 2013 à la Ferme Nationale Nublang, à Tashiyangphu. La production moyenne quotidienne de lait (PMQL) a été de 2.12 ± 0.7 litres ($n = 2\,052$, intervalle: 0.3–5.0l, coefficient de variation: 34 pour cent). L'ordre de mise bas, le mois de lactation et l'année ont tous eu un effet significatif ($P < 0.05$) sur la PMQL. La production moyenne de lait par lactation (PMLL) a été de 519.2 ± 151 litres ($n = 261$, intervalle: 115–881.7 l, coefficient de variation: 29,1 pour cent) et la durée moyenne de la lactation a été de 239 jours. La PMLL a été significativement affectée par l'ordre de mise bas ($P < 0.05$) et par la saison de naissance des veaux. L'héritabilité de la PMQL et de la PMLL a été de 0.22 ± 0.16 et 0.13 ± 0.20, respectivement. La répétabilité estimée a été de 0.45 ± 0.05 et 0.49 ± 0.08 pour la PMQL et la PMLL, respectivement. Dans l'ensemble, l'héritabilité et la répétabilité estimées pour les productions de lait suggèrent un potentiel d'amélioration génétique de la production laitière des bovins Nublang au travers de la sélection. Cependant, il est recommandé de générer un plus grand ensemble de données, afin d'obtenir des estimations plus précises des paramètres génétiques.

Mots-clés: *conservation de races, amélioration génétique, héritabilité, répétabilité*

Resumen

La raza Nublang es una raza singular de ganado bovino *Bos indicus* de aptitud doble, que se halla en Bhután. Ha sido cruzada con gayal (*Bos frontalis*) así como con razas de *Bos taurus*, en un intento por mejorar la producción de leche, lo que ha llevado a una reducción de la población de ejemplares puros de Nublang. Una alternativa al cruzamiento sería la mejora genética de la producción lechera dentro de la cabaña de pura raza Nublang, permitiendo así la conservación y la utilización sostenible de la raza en pureza. Resulta importante medir la variabilidad genética (la heredabilidad) de la producción lechera para evaluar el potencial de mejora genética dentro de la raza Nublang. Así, este estudio estimó parámetros fenotípicos y genéticos de la producción lechera a partir de los datos de 2 052 controles lecheros diarios de 66 vacas, registrados entre 1997 y 2013 en la Granja Nacional Nublang, en Tashiyangphu. La producción media diaria de leche (PMDL) fue de 2.12 ± 0.7 litros ($n = 2\,052$, intervalo: 0.3–5.0 l, coeficiente de variación: 34 por ciento). El número de parto, el mes de lactación y el año tuvieron todos un efecto significativo ($P < 0.05$) sobre la PMDL. La producción media de leche por

Correspondence to: J. Dorji, National Biodiversity Centre, Serbithang, Ministry of Agriculture and Forests, Bhutan. email: jigmedorjik@gmail.com

lactación (PMLL) fue de 519.2 ± 151 litros (n = 261, intervalo: 115–881.7 l, coeficiente de variación: 29,1 por ciento) y la duración media de la lactación fue de 239 días. La PMLL se vio significativamente afectada por el número de parto (P<0.05) y por la estación en que nacían las crías. La heredabilidad de la PMDL y la PMLL fue de 0.22 ± 0.16 y 0.13 ± 0.20, respectivamente. La repetibilidad estimada fue de 0.45 ± 0.05 y 0.49 ± 0.08 para la PMDL y la PMLL, respectivamente. En general, la heredabilidad y la repetibilidad estimadas para las producciones de leche dejan entrever un potencial de mejora genética de la producción lechera del ganado Nublang a través de la selección. No obstante, se recomienda generar un mayor conjunto de datos, que permita obtener unas estimaciones más precisas de los parámetros genéticos.

Palabras clave: *conservación de razas, mejora genética, heredabilidad, repetibilidad*

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Introduction

The Nublang is a dual-purpose breed (milk and draft) of *Bos indicus* cattle. It is a genetically unique breed (Dorji *et al*., 2003; Sharma *et al*., 2013) that evolved from crossing of humpless cattle (*Bos taurus*) from Tibet and humped cattle (*B. indicus*) from India (Dorji *et al*., 2010). They are highly adapted to harsh and varied environments ranging from sub-tropical to cool temperate climate and between an altitude range of 200–3 000 m asl. They are also relatively tolerant to some local ecto-parasites and diseases (DAD-IS, 2014).

Nublang cattle are central to household nutrition and subsistence agriculture prevalent in remote and rural areas of Bhutan. They are found throughout the country with the most concentrated populations in the districts of Haa, Chukha and Samtse. They are also in the Indian states of Sikkim and Darjeeling district of West Bengal where they are known as Siri. In the past, their number symbolized the wealth of the family. They used to be sacrificed during annual household rituals and construction of new houses. They are also worshipped by Hindu communities in Bhutan as a Goddess of Wealth (Arbenz and Tshering, 2000).

The milk yield of Nublang cattle is low and for this reason, they were traditionally crossbred with Mithun (*Bos frontalis)* to produce Jatsham (F1 female progeny) for better milk yield (Dorji, Tshering and Rai, 2009). From the 1960s onwards they have also been extensively crossed with high yielding *B. taurus* breeds (Jersey and Brown Swiss cattle). Consequently, the quality and population size of purebred Nublang has declined (RNRRC Jakar, 2008). Currently the purebred Nublang population constitutes <35 percent of total cattle population of 298 916 in the country (DoL, 2013). However, the current population is classified as "breed not at risk" (DAD-IS, 2014).

Genetic parameter estimates are specific to a trait, population and environment where measured and it is not appropriate to generalize them to other populations. Although heritability (h^2) and repeatability (r) estimates for milk production traits have been extensively reported for temperate and tropical dairy breeds, they are lacking for Nublang cattle. This paucity is likely due to the lack of a functional herd recording system for this breed.

Therefore, this study assessed the phenotypic variation and genetic parameters for milk yield in *Nublang* cattle to gain insights into the potential for improving milk yield through selective breeding, towards conservation and sustainable utilization of the breed.

Materials and methods

Data and milk recording

Milk yields and pedigree records of Nublang cows from the National Nublang Breeding Farm, Tashiyangphu, Bhutan were used for the study. The farm was established in 1994 for conservation of purebred Nublang. The animals were maintained on kikuyu grass (*Pennisetum clandestinum*) pasture in the summer and fed its hay and silage during winter. Supplementary feeding of 1 kg of concentrate feed mixture in summer and 2 kg during the winter were provided to the milking cows irrespective of level of production. Both artificial insemination and natural service were used on the farm and calving occurred year round.

The final clean data consisted of 2 052 test day (TD) milk yields of 66 milking cows over a period from 1997 to 2013. These cows were sired by 18 bulls: ten sires with less than three daughters and eight sires with three to ten daughters. TD milk yields were recorded monthly on the 30th day of each month except for the 28th in February. Cows were milked in morning and evening and, immediately prior to milking, their calves were allowed to suckle from one udder quarter to initiate the milk let-down reflex and removed from their mother. TD milk yield was the sum of morning and evening milk yields. The average number of cows lactating per year was 15.

Total lactation milk yield (LMY) for each cow was estimated from TD milk yields and the interval in days between subsequent milk recordings using the Test Interval Method (ICAR, 2009). Overall there were 261 lactation records (average of four lactations per cow) available considering only lactation with TD records of four and above for calculation of LMY:

$$\mathrm{LMY} = I_0 M_1 + \frac{I_1{}^*(M_1 + M_2)}{2} + \frac{I_2{}^*(M_2 + M_3)}{2} \ldots\ldots \frac{I_{n-1}{}^*(M_{n-1} + M_n)}{2} + I_n M_n$$

where

LMY is the estimated total milk yield for the lactation period of $(I_{0\,+} I_1 + I_3 + \cdots + I_n)$; I_1, I_2, I_{n-1} are the intervals, in days, between TD recording dates; I_0 is the interval, in days, between the lactation period start date and the first recording date; I_n is the interval, in days, between the last recording date and the end of the lactation period.

M_1, M_2, M_n are milk yields in litre, given to one decimal place of the milk yielded in the 24 h of the recording day. That is, M_1 is the milk yield for TD_1, M_2 for TD_2, etc.

Data analysis

Phenotypic analyses of the data were done using univariate GLM in Statistical package for Social Sciences (SPSS, 2007). The final statistical model used for this analysis was;

$$\mathrm{DMY}_{ijklm} = \mu + \mathrm{Par}_i + \mathrm{TD}n_j + \mathrm{Sea\_}r_k + \mathrm{Year}_i + e_{ijklm}$$

where

DMY_{ijklm}, the observation of daily milk yield on the mth cow that on ith parity, jth TDn, kth season and lth year; μ the overall mean; Par_i the ith parity subclasses ($i = 1$ to ≥ 6); TDn_j the jth month in milk ($j = 1$ to ≥ 9); $\mathrm{Sea\_}r_k$ the kth season of milk recording (k = spring, March–May; summer, June–August; autumn, September–November; and winter, December–February).

Year_l the lth year ($i = 1997$–2013); e_{ijklm} the residual associated with y_{ijklm}.

Where there were few observations within a factor level, these levels were combined: this included combining parity_7, parity_8 and parity_9 with parity_6 as $\mathrm{parity}_{\geq 6}$ and TD_9, TD_{10} and TD_{11} into $TD_{\geq 9}$.

The factors fitted for LMY were number of TD records per lactation (NTD) with six levels (4 to ≥9), as well as parity and season of calving (sea_c) with levels as described for DMY. Wherever a factor had a significant effect, a pairwise comparison of level means was carried out using least significant difference (LSD) (SPSS, 2007).

Estimation of variance components and genetic parameters

The variance components of DMY and LMY were estimated using an Average Information Restricted Maximum Likelihood mixed model procedure with ASReml statistical package version 3 (Gilmour *et al.*, 2009) using the following univariate linear repeated measure animal model;

$$\mathbf{y} = \mathbf{X}\mathbf{b} + \mathbf{Z}_1\mathbf{a} + \mathbf{Z}_2\mathbf{p} + \mathbf{e}$$

where

y the phenotypic repeat measures of the trait (DMY, LMY) where TD milk yields were treated as repeated measures of DMY; **b** the vector of fixed effects; **a** the vector of random additive genetic effects for all animals, assumed to be distributed as N $(0,{}^2{}_g\mathbf{A})$ where **A** is the pedigree relationship matrix and $\sigma^2{}_g$ is the additive genetic variance; **p** the vector of permanent environmental effects (PE) for all animals with milk records, and; e the vector of residual effects.

The matrices **X** and **Z** are design matrices that associate observations to particular fixed or random effects, respectively.

The final model for DMY included fixed effects (parity, TD_n and sea_r) and random effects of additive genetic effects, permanent environment and residuals. Similarly the fixed effects for LMY included parity, NTD and sea_c, and random effects as for DMY. The variance components from these models were used for estimation of heritability and repeatability using standard formula from Falconer and Mackay (1996) in ASReml software package.

Results

The mean DMY of Nublang cows in the farm was 2.12 ± 0.7 litres (N = 2 052, range 0.3–5.0 litres). The mean LMY was 519.2 ± 151.4 litres (N = 261, range 115–881.7 litres) with an average lactation length of 239.6 days. The variation in these traits, as indicated by the coefficient of variations (DMY 34 percent, LMY 29.1 percent), is high. Parity, season and stage of lactation (TD_n) significantly affected DMY ($P < 0.05$). For example, least-squares mean DMY in the first parity was 1.84 ± 0.04 litres and increased thereafter to peak in the fourth parity (2.37 ± 0.04 litres) (Table 1). Mean DMY was highest in summer (2.40 ± 0.03) and lowest in winter (1.81 ± 0.04) ($P < 0.05$). For stage of lactation, (as measured by the TD_n), DMY peaked on TD_2 (2.54 ± 0.04) and then declined gradually up to $TD_{\geq 9}$ (1.70 ± 0.07) (Figure 1). The effect of interaction between parity and TD_n, parity and year, and season and year were significant ($P < 0.05$).

Total lactation milk yields were significantly affected by parity and NTD ($P < 0.05$). It was highest in the fourth parity (572.5 ± 20.90 litres) and lowest in the first parity (411.6 ± 19.68 litres) (Table 1). The LMY of spring calvers (456.3 ± 14.70 litres) was significantly low compared to other seasons. As expected, NTD and LMY are highly correlated because an increasing number of TD milk yields per lactation corresponds to a longer lactation and therefore

Table 1. Least-squares means and standard error (SE) of DMY and LMY of Nublang cows.

Effects	DMY			LMY		
	N (NC)	Mean	SE	N (NC)	Mean	SE
Parity						
1	492 (60)	1.76[a]	0.03	59 (59)	411.60[b]	19.68
2	396 (51)	2.04[b]	0.03	60 (60)	472.70[c]	18.88
3	354 (46)	2.24[d]	0.03	51 (51)	537.60[a]	18.69
4	292 (37)	2.37[c]	0.04	37 (37)	572.50[a]	20.90
5	228 (29)	2.33[cd]	0.04	29 (29)	522.50[ac]	25.33
≥6	290 (37)	2.16[d]	0.04	38 (22)	463.40[bc]	24.64
Season*						
Spring	435 (59)	2.10[a]	0.03	92 (42)	456.30[a]	14.70
Summer	448 (65)	2.40[b]	0.03	45 (26)	510.40[b]	20.21
Autumn	590 (66)	2.16[a]	0.03	55 (29)	502.80[b]	17.80
Winter	578 (62)	1.81[c]	0.03	69 (46)	511.80[b]	16.01

N, no. of observations; NC, no. of cows; DMY, daily milk yield; LMY, lactation milk yield.
*Season = season during milk recording for DMY (Sea_r); season of calving for LMY (Sea_c).
[a,b,c,d]Least-squares mean within a column group with different letters differ significantly ($P < 0.05$).

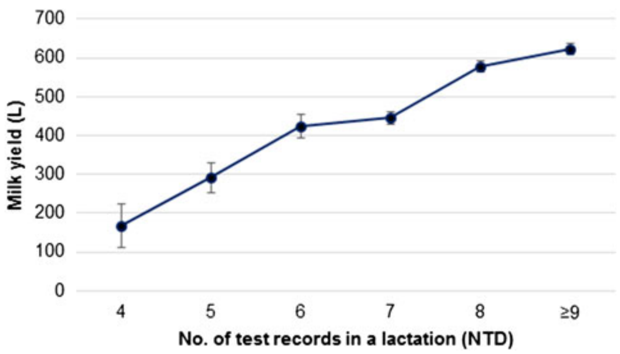

Figure 2. LSM Lactation milk yield of Nublang cows by number of test records in a lactation.

a higher LMY (Figure 2). The effect of interaction between parity and NTD was significant ($P < 0.05$) among other factors.

The h^2 estimates for DMY and LMY were 0.22 ± 0.16 and 0.13 ± 0.20, respectively. The repeatability of DMY and LMY were 0.44 ± 0.05 and 0.49 ± 0.08, respectively.

Discussion

Milk yield

The milk yield of Nublang in this study is low compared with its crossbreds with Jersey (4.9 litres) and Brown Swiss cattle (4.3 litres) in the country (Tamang and Dorji, in press). Further, it is lower than some of the other *B. indicus* tropical dairy breeds; Sahiwal (1 200–1 800 kg) (Bajwa *et al.*, 2004) and Tharparkar (2 179 litres) (Gahlot, Pant and Kachawaha, 2000) but comparable to the dual purpose Ongole breed of cattle (675 litres) (Gaur, Kaushik and Garg, 2002). Within the Nublang breed, the milk yield in this study was similar to that found in Tamang and Perkins (2005) (2.2 litres). However, there is wide variation in reported milk yields of Nublang; 1.5 litres (Arebenz and Tshering, 2000), (2.5 litres) Phanchung and Roden (1996) and 5.0 litres (Dorji *et al.*, 2005) which is similar to the range observed across cows in the present study. It is likely that the differences between studies may be attributed to the differences in animal management, environment, sampling methodology and genetic merit of the animals. Overall, the milk yield in Nublang cattle is low yet highly variable reflecting a similar pattern seen in other *B. indicus* breeds in general (Syrstad, 1993).

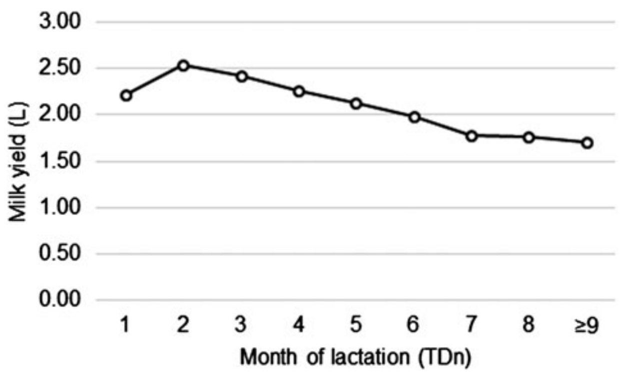

Figure 1. LSM Daily milk yield of Nublang cows by stages of lactation.

Within a lactation, peak yield occurred around TD_2 which is within 2 months from date of calving. In other *B. indicus* breeds, peak milk yield was observed in about 1 month post calving in Tharparkar (Balbir, Pankaj, and Pathodiya, 2011) and about 7 weeks into milk in Sahiwal (Dongre and Gandhi, 2014). The increase in milk yield from first to fourth parity in this study is in line with a number of studies (Rekik *et al.* 2003; Gradiz *et al.* 2009; Amasaib *et al.* 2011; Jingar *et al.* 2014), which according to Gradiz *et al.* (2009), is a consequence of the increasing development of the udder, increase in body size, increase in feed intake and possibly improved partitioning of energy into milk production.

The seasonal variation in milk yields with higher yields in summer in this study is in agreement with Rekik *et al.* (2003), where animals were mainly maintained on pasture in summer and conserved fodder in winter. Such seasonal variation may be capitalized upon to produce more milk by planning breeding programs to coincide with availability of high-quality fodder in summer to increase milk production. Scheduling mating programmes when cows are in good condition and most likely to become pregnant should be considered. Although breeding occurred all year round in this study, the number of calvings in spring (95) was higher than other seasons (45–69). This may be due to better conception rates in summer due to availability of quality fodder and better nutrition.

Genetic parameters

The h^2 estimates for milk yield in this study suggest a moderate additive genetic effect on milk production, although standard errors were large. They suggest that genetic progress can be made by selection for these traits. The estimates were within the range for other *B. indicus* cattle (0.05–0.40) reviewed by Rehman *et al*. (2013). The low accuracy of the estimates may be attributed to smaller datasets as in Eid *et al*. (2012) and Bilal *et al*. (2008) and inaccurate recording of milk yield or errors in pedigree records (Javed, Mohiuddin and Ahktar, 2001). However, for better accuracy of estimates, analysis of a larger dataset is recommended.

The medium repeatability estimates in this study are within the range reported for Sahiwal cattle (0.13–0.50) reviewed by Rehman *et al*. (2013). This suggests that information from first parity could be used as a reasonable prediction of future milk yields, thereby hastening the process of selection and genetic gain. This is useful information for bull selection where breeding value for milk yield would generally be evaluated through the time-consuming process of progeny testing.

Conclusions

The results of the present study indicate potential for genetic improvement of milk production within the Nublang breed. However, for better accuracy of heritability estimates, computation using a larger dataset of Nublang cattle is recommended in future. Performance recording of Nublang cows in villages in addition to the government farm is suggested for obtaining adequately large datasets.

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Statement of interest

The authors do not have any conflict of interest that will influence the judgment and potentiality of being biased. Further, the authors did not have any financial arrangements or connections pertinent to submitted manuscript.

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Creole cattle from northwestern Mexico has high genetic diversity in the locus DRB3.2

I.G. Fernández[1,2], I. Leyva-Baca[1], F. Rodríguez-Almeida[1], R. Ulloa-Arvizu[3], J.G. Ríos-Ramírez[1], A. Gayosso-Vázquez[3] and R.A. Alonso-Morales[3]

[1]*Universidad Autónoma de Chihuahua, Chihuahua, Chihuahua, México;* [2]*Universidad Autónoma Agraria Antonio Narro, Torreón, Coahuila, México;* [3]*Universidad Nacional Autónoma de México, D.F., México*

Summary

The objective of this study was to determine the genetic diversity of creole cattle in northwestern Mexico using the BoLA-DRB3.2 locus of the Major Histocompatibility Complex (MHC). A total of 56 creole cattle were sampled from five communities; in the state of Chihuahua (Cerocahui, Guadalupe y Calvo and Cuauhtémoc) and in the state of Baja California Sur (La Paz and Mulegé). The BoLA-DRB3.2 locus was genotyped by PCR-RFLP assay. Thirty-nine alleles were identified, out of which 14 had not been previously reported. The average level of inbreeding in all populations analyzed was $F_{IS} = 0.09$ ($P < 0.0001$), but only two populations (Cerocahui and Guadalupe y Calvo) showed an excess of homozygotes ($P < 0.05$). The breed differentiation in all populations studied was $F_{SC} = 0.068$ ($P < 0.0001$). The smallest genetic distance was between La Paz and Mulegé (0.022); but Mulegé presented smaller distances (0.028–0.053) with the populations of La Paz (0.071–0.083) and with Chihuahua. Baja California Sur populations are grouped in a separate branch than Chihuahua populations. We conclude that creole cattle from Baja California Sur and Chihuahua show high genetic diversity in the locus BoLA-DRB3.2.

Keywords: *allelic richness, BoLA-DRB3.2 locus, creole cattle, genetic diversity, PCR-RFLP*

Résumé

L'objectif de l'étude était de déterminer la diversité génétique des bovins créoles originaires du Nord-Ouest du Mexique en utilisant le locus DRB3.2 du complexe majeur d'histocompatibilité (MHC). Des échantillons de sang de 56 bovins créoles dans cinq endroits de l'État de Chihuahua (Cerocahui, Guadalupe y Calvo et Cuauhtémoc) et dans l'État de Baja California Sur (La Paz et Mulegé) ont été prélevés. Le locus BoLA-DRB3.2 a été génotypé en utilisant la technique PCR-RFLP. Trente-neuf allèles ont été identifiés, dont 14 avaient déjà été signalés. La différenciation génétique des populations étudiées était de $F_{SC} = 0{,}068$ ($P < 0.0001$). Le niveau moyen de consanguinité dans les populations analysées était de $F_{IS} = 0.09$ ($P < 0.0001$) mais seulement deux populations (Cerocahui et Guadalupe y Calvo) ont présenté un excès d'homozygotes ($P < 0.05$). La distance génétique la plus petite s'est observée entre La Paz et Mulegé (0.022); mais aussi, Mulegé a présenté de plus courtes distances (0.028–0.053) avec les populations de La Paz (0.071–0.083) et Chihuahua. Les populations de Baja California Sur sont regroupées dans une branche distincte des populations de Chihuahua. Nous concluons que le locus BoLA-DRB3.2 possède une grande diversité génétique chez les bovins créoles originaires de Chihuahua et Baja California Sur.

Mots-clés: *diversité génétique, locus BoLA-DRB3.2, le bétail criollo, PCR-RFLP, richesse allélique*

Resumen

El objetivo del presente estudio fue determinar la diversidad genética del bovino criollo del noroeste de México utilizando el locus DRB3.2 del Complejo Principal de Histocompatibilidad (MHC). Se tomaron muestras sanguíneas de cincuenta y seis bovinos criollos en cinco localidades; en el estado de Chihuahua (Cerocahui, Guadalupe y Calvo y Cuauhtémoc) y en el estado de Baja California Sur (La Paz y Mulegé). El locus BoLA-DRB3.2 fue genotipificado mediante la técnica PCR-RFLP. Se identificaron 39 alelos, de los cuales 14 alelos no habían sido reportados previamente. El nivel de consanguinidad promedio en todas las poblaciones analizadas fue $F_{IS} = 0.09$ ($P < 0.0001$) pero sólo dos poblaciones (Cerocahui y Guadalupe y Calvo) presentaron exceso de homocigosis ($P < 0.05$). La diferenciación genética entre las poblaciones estudiadas fue F_{SC} 0.068 ($P < 0.0001$). Las distancias genéticas más cortas fueron entre La Paz y Mulegé (0.022); además, la población de Mulegé presentó las distancias genéticas más cortas (0.028–0.053) con las poblaciones de La Paz (0.071–0.083) y con Chihuahua. Las poblaciones de Baja California se agruparon en una rama aparte de las poblaciones de Chihuahua. Se concluye que los bovinos criollos de Chihuahua y Baja de California mostraron alta diversidad genética en el locus BoLA-DRB3.2.

Palabras clave: *diversidad genética, locus BoLA-DRB3.2, ganado criollo, PCR-RFLP, riqueza alélica*

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Introduction

Cattle populations from some of the Latin American countries has its origin from populations brought to America by Christopher Columbus since its second expedition (1 493)

Correspondence to: I.G. Fernández, Universidad Autónoma Agraria Antonio Narro, Torreón, Coahuila, México. email: ilda.fernandez@uaaan.mx

from the Iberian peninsula, mainly from Andalucia and Extremadura and from Canary Islands which had cattle from Portugal and Africa (Rouse, 1977; de Alba, 1987; Primo, 1992). Later in 1 521 the cattle arrived to Mexico at several places along the Mexican Gulf coast from Cuba, Haiti and Jamaica. It is known that by 1 565 the cattle arrived on the Nayarit Pacific coast, reaching the Baja California peninsula in 1 670 (Rouse, 1977). Currently these cattle are known as creoles, chinampos or local domestic cattle breeds. These creoles breeds are composed of non-selected populations raised in traditional production systems and they seem to be well adapted to a wide range of environments, showing high levels of phenotypic variability (Ulloa-Arvizu *et al.*, 2008; Espinoza Villavicencio, Guevara Franco and Palacios Espinoza, 2009). Mexican creole cattle have been characterized using molecular markers like short tandem repeats (STRs), mitochondrial D-Loop, Y-chromosome and single-nucleotide polimorphism (SNPs) (Fernández *et al.*, 2008; Ulloa-Arvizu *et al.*, 2008; Ginja *et al.*, 2009; Delgado *et al.*, 2012), and more recently, Giovambattista *et al.* (2013) reported the range of variation at the Major Histocompatibility Complex (MHC) DRB3.2 locus in South America Creole cattle breeds. The MHC is a phenomenal resource of the immunological system for the recognition of antigen peptides from pathogens to mount a proper immune response. The MHC codifies class I and II molecules. MHC class I receptors capture and present intracellular antigens to cytotoxic T-cells and MHC class II receptors capture and present intracellular antigens to helper T-cells. High variability of MHC is present at nucleotide level that translates in a heterodimeric cell surface α and β receptors with broader recognition capabilities of foreign peptides to be presented to T-cells to initiate an immune response (Male *et al.*, 2013). Particularly, the exon 2 of the β-chain of the MHC class II receptor called bovine lymphocyte antigen DRB 3.2 (BoLA-DRB3.2) (Lewin, 1989; Kelm *et al.*, 1997), is a suitable gene candidate to study genetic variability in cattle populations. Thus, documenting variability of the DRB3.2 will provide a broader insight of immunogenomic diversity, population dynamics and better understanding of allele frequencies of the DRB3.2 within Mexican creole cattle. In Mexico, creole cattle populations are mostly distributed in isolated areas limited by natural barriers (seas, rivers, semi-desert and mountains). Previous studies have shown that Mexican creole cattle populations have high genetic diversity because of mean number of alleles reported: 5.5–10.8 and 10.2–13.6 (Fernández *et al.*, 2008; Ulloa-Arvizu *et al.*, 2008). The objective of this study was to determine the genetic diversity in populations of creole cattle in two regions of northwestern Mexico based on the polymorphism of the locus BoLA-DRB3.2.

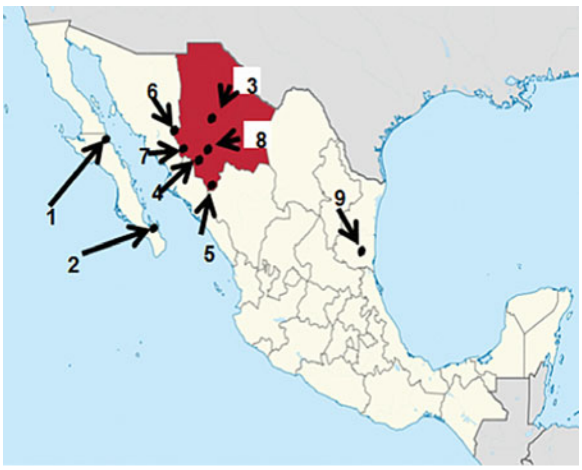

Figure 1. Geographic location of the populations in the actual study and those reported previously by Fernández *et al.* (2008). 1) Mulegé, 2) La Paz, 3) Cuauhtémoc, 4) Cerocahui, 5) Guadalupe y Calvo, 6) Moris, 7) Chínipas, 8) Guachochi and 9) Tamaulipas.

Materials and methods

Sampling areas

Blood samples were obtained from creole cattle (*Bos taurus*) from two northwestern states of Mexico: Chihuahua and Baja California Sur. In Chihuahua, creole cattle is mainly concentrated in the Western Mountain Range with approximately 45 000 heads of cattle; while creole cattle from Baja California Sur, held approximately 33 000 cattle in two semiarid regions (SAGARPA, 2014). Three populations were sampled in Chihuahua: Cerocahui ($n = 10$), Guadalupe y Calvo ($n = 11$) and Cuauhtémoc ($n = 16$), and two towns in Baja California Sur: La Paz ($n = 10$) and Mulegé ($n = 9$) (Figure 1). Animals were randomly chosen in several herds in each locality that included both sexes. Verbal verification of no relationship between sampled creoles was confirmed.

Polymerase chain reaction-restriction fragment length polimorphism (PCR-RFLP) of BoLA-DRB3

The methodology of DNA extraction and the conditions of PCR, cloning and digestion of amplicons were described by Fernández *et al.* (2008). The second exon of the BoLA-DRB (284 pb) was amplified by PCR. For this purpose, a pair of oligonucleotides previously described by van Eijk, Stewart-Haynes and Lewin (1992) (HL030: 5′-ATCCTCTCTCTGCAGCACATTTCC-3′ and HL032: 5′-TCGCCGCTGCACAGTGAAACTCTC-3′) were used. The amplification of the BoLA-DRB3.2 gene was performed in a single PCR reaction rather than two subsequent hemi-nested reactions as originally proposed by van Eijk, Stewart-Haynes and Lewin (1992).

Allele nomenclature with PCR-RFLP patterns proposed by Davies *et al.* (1994) was used. The corresponding PCR-RFLP patterns are also comparable with those previously reported by van Eijk, Stewart-Haynes and Lewin (1992), Gelhaus *et al.* (1995), Gilliespie *et al.* (1999), Maillard *et al.* (1999), da Mota *et al.* (2002), Martínez *et al*. (2005), Behl *et al.* (2007), Sadeghi *et al.* (2008), Fernández *et al.* (2008) and Pashmi *et al.* (2009). Cattle BoLA-DRB nomenclature with alleles names, DBR3-RFLP, and their local names are described in the IPD (2003) website (http://www.ebi.ac.uk/cgi-bin/ipd/mhc/view_nomenclature.cgi?bola.drb3). With the advent of new molecular techniques like capillary sequencing, the nucleotide sequences of BoLA genes can be read out more precisely for allele identification and comparison. However, for laboratories with limited access to novel technologies, the classical molecular biology techniques like PCR-RFLP continue to be a useful tool for BoLA-DRB3.2 genotyping, because of its affordability and, relatively easy to perform. The novel BOLA-DRB3 alleles described in this study were designated by PCR-RFLP patterns.

Statistical analyses

In order to have a wider view of the genetic diversity among creole populations of northwestern Mexico, allele frequencies of three populations of Chihuahua state (Chínipas, Guachochi and Moris) and one from Tamaulipas state, previously reported by Fernández *et al.* (2008), were included (Table 1).

Calculation of the allele frequencies, observed heterozygosities (Ho) and unbiased expected heterozygosities (He) were carried out using the GENEPOP v.4.0.10 program (Raymond and Rousset, 1995). The amount of inbreeding within population (F_{IS}), was estimated according to Weir and Cockerham (1984), measuring the heterozygote deficit/excess. The exact test for population differentiation according to Raymond and Rousset (1995) was applied. Statistical significance was measured by the Markov Chains method (Guo and Thompson, 1992). A first approach to within-breed diversity was ascertained by calculating the mean number of alleles, observed and unbiased expected estimates of heterozygosity per population (Nei, 1973), and their standard deviations. Allelic richness (Rt) was estimated as a measure of the number of alleles independent of sample size, hence allowing comparisons among different sample sizes. Computations were carried out using FSTAT v. 2.9.3.2 (Goudet, 2001). After defining groups of breeds by geographic region (Baja California Sur, Chihuahua and Tamaulipas) and by location of origin, a hierarchical analysis of variance was carried out, which allowed the partitioning of the total genetic variance into components owing to interindividual and interbreed differences. Variance components were used to compute fixation index. The interpretation of population structure by *F*-statistics was tested using a non-parametric permutation approach as described by Excoffier, Smouse and Quattro (1992). Computations were carried out using an Analysis of Molecular Variance (AMOVA) procedure (Excoffier, Laval and Schneider, 2005). Genetic divergence among breeds was estimated through a commonly used genetic distance measure; Reynolds genetic distances (Reynolds, Weir and Cockerham, 1983). A NeighborNet (Huson and Bryant, 2006) was constructed from Reynolds genetic distances to graphically represent the relationships between breeds, as well as, to depict evidence of admixture.

Results

Thirty nine alleles were identified in the creoles from Chihuahua and Baja California Sur. The alleles and allelic frequencies are shown in Table 1. The creoles from Chihuahua and Baja California Sur presented 14 previously unreported alleles. For creoles from Cuauhtémoc the cutting patterns detected were: jab, jnn, qab y qbb. In Cerocahui four alleles were detected: cab, cba, rda and rba. In Guadalupe y Calvo three alleles were detected: jad, lbd and qbd. In Mulegé population three alleles were detected: jaa, nab and pba. The restriction digestion patterns more frequently were: qaa (0.27), qba (0.25), naa (0.20), jaa (0.1) and fbb (0.111) for Guadalupe y Calvo, Cuauhtémoc, Cerocahui, Mulegé and La Paz, respectively. Allele DRB3.2*28 was detected only in Baja California Sur populations with high frequency (>0.15). Allele DRB3.2*23 was detected in all populations analyzed. In Mulegé population this allele showed high frequency (0.111). Alleles DRB3.2*16, DRB3.2*24 and DRB3.2*50 were only detected in creoles from Chihuahua.

Genetic diversity and genetic differentiation

The DBR3 gene shows high genetic diversity He > 0.89 in all populations studied. Mulegé population had the highest genetic diversity (He = 0.988 and Rt = 12) and the lowest value was observed in Cuauhtémoc population (He = 0.898; Table 2). Guadalupe y Calvo population show an excess of homozygotes and registered a value of F_{IS} = 0.3. Only this population did not show Hardy–Weinberg equilibrium ($P < 0.01$). *F*-statistics and AMOVA assessed the population structure of Baja California Sur and Chihuahua, having two and six populations each (Table 3). These results suggest that the apparent levels of breed differentiation was moderate, with F_{SC} values indicating that approximately 6.8 percent of the total genetic variation corresponded to differences between populations ($P < 0.0001$), while the remaining 93.2 percent corresponded to differences among individuals. Among Baja California Sur and Chihuahua populations did not differ significantly $F_{CT} = 0.025$ ($P = 0.14$). In metapopulation level (nine subpopulations), a high value of F_{IT} = 0.173 ($P < 0.0001$) was detected. The F_{IS} index had average value of 0.09 ($P < 0.0001$) in all the populations analyzed (Table 3).

Genetic distances

The Reynolds genetic distances among the different populations, studied (Table 4) ranged from 0.022 for La Paz/Mulegé pair to 0.083 for La Paz/Guadalupe y Calvo

Table 1. Allele frequencies of locus DBR3.2 in creole cattle populations from Chihuahua (Cuauhtémoc, Cerocahui, Guadalupe y Calvo, Moris, Chínipas and Guachochi), Baja California Sur (Mulegé and La Paz) and Tamaulipas, Mexico.

Allele	La Paz	Mulegé	Cerocahui	Cuauhtémoc	Guadalupe y Calvo	Chínipas[1]	Guachochi[1]	Moris[1]	Tamaulipas[1]
DRB3.2*06									0.010
DRB3.2*08	0.01								
DRB3.2*09	0.05								
DRB3.2*10	0.01					0.10	0.071		
DRB3.2*13									0.010
DRB3.2*15	0.05				0.050		0.071	0.077	0.049
DRB3.2*16				0.031	0.136	0.05			
DRB3.2*17									0.049
DRB3.2*18									0.049
DRB3.2*19							0.107	0.115	0.020
DRB3.2*20	0.10	0.056		0.094					0.020
DRB3.2*22									0.290
DRB3.2*23	0.05	0.111	0.05	0.031	0.091	0.10		0.058	0.206
DRB3.2*24			0.10	0.094		0.15	0.393	0.423	0.176
DRB3.2*25					0.045				
DRB3.2*28	0.15	0.167							0.010
DRB3.2*32		0.056							0.010
DRB3.2*35			0.05						
DRB3.2*36	0.05								
DRB3.2*37	0.02								
DRB3.2*40									0.020
DRB3.2*50				0.100				0.036	
caa			0.05						
dba									0.200
dbb									0.010
fbb	0.10					0.05	0.071		
gba									0.010
gbb								0.038	
ibb						0.10		0.135	0.020
ibe						0.05			
jbb				0.094		0.05		0.019	
kbd									0.010
laa	0.05				0.045				
mab									0.010
mbb		0.056							0.010
naa			0.20		0.091	0.05			0.020
nbd						0.05		0.019	0.010
nbe									0.020
obd									0.010
sba							0.071		0.010
seb								0.019	
taa									0.010
tbb									0.039
tbd									0.010
ubb									0.010
ubd									0.010
vbd									0.020
xbb							0.071	0.058	
cab			0.05						
cba			0.05						
ibd							0.071	0.019	
rbd						0.10			
sbd							0.036	0.019	0.010
tba		0.056	0.05			0.05			0.069
vad						0.05			
jaa		0.111							
jab				0.031					
jad					0.045				
jba		0.056		0.125					
jnn				0.031					
lbd					0.091				
nab		0.056							
pba		0.111							
qaa		0.056		0.062	0.273				
qab				0.031					
qba		0.111		0.250	0.136				
qbb				0.125					
qbd					0.045				
raa			0.15						
rba			0.15						

New alleles found in this study are in bold.
[1]Allele frequencies reported by Fernández *et al*. (2008).

Table 2. Number of individuals per population (N) and genetic diversity statistics in nine Mexican creole cattle populations from Chihuahua, Baja California Sur and Tamaulipas, Mexico.

Population	N	Nt	NE	Rt	Nu	Nu > 0.1	Ho	He	F_{IS}
La Paz	10	11	8.7	10.5	0	0	1.000	0.928	−0.078
Mulegé	9	12	10.1	12.0	3	2	0.889	0.988	0.073
Cerocahui	10	10	8.3	10.4	5	2	0.800	0.933	0.143*
Cuauhtémoc	16	12	7.8	9.4	1	1	0.938	0.898	−0.044
Guadalupe y Calvo	11	10	6.9	9.2	3	0	0.636	0.909	0.300**
Chínipas	10	14	11.8	13.1	3	1	0.900	0.967	0.069
Guachochi	14	10	5	8.5	0	0	0.643	0.838	0.233*
Moris	26	12	4.4	7.5	2	0	0.731	0.790	0.075
Tamaulipas	51	34	10.8	11.4	16	0	0.628	0.919	0.317**

Nt, number of alleles; NE, effective number of alleles; Rt, allelic richness per population based on minimum sample size of nine diploid individuals; Nu, new alleles and with frequency >0.1 (Nu > 0.1); Ho, observed heterozygosity; He, expected heterozygosity; F_{IS}, within-population inbreeding coefficient. *($P < 0.05$); **($P < 0.01$); Hardy–Weinberg disequilibrium deviations estimated.

Table 3. Partitioning of genetic variability among the different sources of variation with breeds grouped by States from Chihuahua and Baja California Sur, Mexico.

Source of variation	Degrees of freedom	Sum of squares	Variance components	Percentage of variation	Fixation index
Among States	1	1.929	0.01209	2.47	$F_{SC} = 0.068$
Among populations within State	6	8.073	0.03251	6.70	$F_{IS} = 0.090$
Among individuals within populations	98	47.08	0.03977	8.20	$F_{IT} = 0.173$
Within individuals	106	42.50	0.4009	82.64	$F_{CT} = 0.025$

The following States were defined as creoles from Baja California (La Paz and Mulegé) and from Chihuahua (Cerocahui, Guadalupe y Calvo, Cuauhtémoc, Chínipas, Guachochi and Moris).

Table 4. Pair wise population Reynolds genetic distances values among nine creole cattle populations from Chihuahua (Cuauhtémoc, Cerocahui, Guadalupe y Calvo, Moris, Chínipas and Guachochi), Baja California Sur (Mulegé and La Paz), and Tamaulipas, Mexico[1].

	La Paz	Mulegé	Cerocahui	Cuauhtémoc	Chínipas	Guadalupe y Calvo	Guachochi	Moris	Tamaulipas
La Paz	0.0000								
Mulegé	0.0221	0.0000							
Cerocahui	0.0712	0.0533	0.0000						
Cuauhtémoc	0.0780	0.0291	0.0808	0.0000					
Chínipas	0.0313	0.0282	0.0238	0.0486	0.0000				
Guadalupe y Calvo	0.0834	0.0370	0.0701	0.0479	0.0526	0.0000			
Guachochi	0.1103	0.1168	0.0873	0.1071	0.0342	0.1479	0.0000		
Moris	0.1514	0.1404	0.1136	0.1280	0.0447	0.1718	0.0004	0.0000	
Tamaulipas	0.0635	0.0374	0.0454	0.0711	0.0052	0.0769	0.0532	0.0570	0.0000

[1] $P < 0.05$.

($P < 0.05$). When these were compared with the populations reported by Fernández *et al.* (2008), Moris population shows the largest genetic distances (0.11–0.17). Chínipas population appears with shorter genetic distances (0.023–0.052). In Figure 2 it is shown a dendrogram where Mulegé and La Paz (Baja California Sur) populations are located in the same branch. While creoles from Cuauhtémoc and Guadalupe y Calvo (Chihuahua) formed a population group near to creoles from Baja California Sur. A second group was formed by the creoles from Moris and Guachochi (Chihuahua). Among them and not grouped are the creoles from Cerocahui and Chínipas (Chihuahua). While creoles from Tamaulipas are located between Chihuahua populations.

Discussion

Our results indicate that the creoles from Baja California Sur and Chihuahua showed high polymorphism at the locus DRB3.2, given the high number of observed alleles, which is consistent with the other described populations of creole cattle (Giovambattista *et al.*, 1996, 2013; Postiglioni *et al.*, 2002; Kelly *et al.*, 2003; Ripoli *et al.*, 2004;

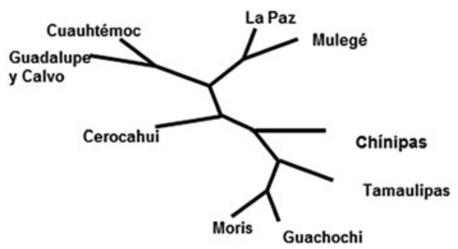

Figure 2. Dendrogram showing nine populations of creole cattle from Chihuahua, Baja California Sur and Tamaulipas, Mexico.

Martínez *et al.*, 2005). Allele DRB3.2*23 was observed in all populations of creoles analyzed in this study (La Paz, Mulegé, Cerocahui, Cuauhtémoc and Guadalupe y Calvo) as well as in creole populations reported by Fernández *et al.* (2008). This means that 90 percent of populations from Baja California Sur, Chihuahua and Tamaulipas share the DRB3.2*23 allele. While allele DRB3.2*24 was only detected in Cerocahui and Cuauhtémoc. This means that altogether 67 percent of the nine populations studied share DRB3.2*24 allele. Likewise, DRB3.2*23 and DRB3.2*24 alleles were observed in creoles from Argentina and Colombia (Giovambattista *et al.*, 1996; Martínez *et al.*, 2005; Baltian *et al.*, 2012). Creole cattle have the special ability of surviving in extreme climates and resisting to diseases. The phenotype of the Mexican Creole cattle shows a small frame animal that allows them to adapt to harsh environments allowing them to survive with limited pasture and water. Moreover, Mexican creole cattle constitutes the only type of livestock production system in some of the most marginalized and isolated rural communities of Mexico as a source of milk, meat and as a draft and load animals for agricultural purposes (Ríos Ramírez *et al.*, 1998). For example, Martínez *et al.* (2006) associated the DRB3.2*23 allele with a reduction in the number of ticks on cattle F_2 (Gyr x Holstein). In fact, a positive association of DRB3.2*23 allele with resistance to mastitis in Holstein cows was found (Yoshida *et al.*, 2008; Baltian *et al.*, 2012). Meanwhile, Dietz *et al.* (1997) associated the DRB3.2*24 allele with the neutrophil count and increased serum IgG_2 in Holstein cattle. While the Norwegian Red race DRB3.2*24 allele contributed to mastitis resistance (Kulberg *et al.*, 2007). The high frequency detected in the DRB3.2*23 and DRB3.2*24 alleles from multiple breeds, suggest a favourable effect conferring resistance to certain diseases. Creole cattle from Guadalupe y Calvo, Cuauhtémoc, Cerocahui, Mulegé and La Paz, showed a high frequency in the following alleles: qaa, qba, naa, jaa and fbb, respectively. These high frequencies may be the combination of a founder effect, bottleneck and natural selection. However, selection for advantageous mutations cannot explain the unusually high degree of polymorphism and is rather attributable to an overdominant selection (Hughes and Nei, 1989). This study detected a high value on the number of effective alleles in the populations studied. Creoles from Mulegé showed 12 total alleles, with a high affective value of 10.1, while creoles from Tamaulipas had the highest number of total alleles and only 10.8 effective alleles. Guachochi population did not observe unique alleles, while Cerocahui population observed the largest number of them. This suggests that creoles from Cerocahui possess the highest genetic diversity. Sixteen unique alleles were detected with frequencies <0.1 in creoles from Tamaulipas, while frequencies ≥0.1 were found in creoles from Mulegé, Cuauhtémoc, Chínipas and Cerocahui. These results show the high degree of genetic diversity in populations of creoles from Baja California Sur and Chihuahua, followed by creoles from Tamaulipas. The level of inbreeding determined by AMOVA was high ($F_{IT} = 0.17$), which is overestimated, since it is due to Wahlund effect when the population subdivision is not considered. However, the average inbreeding estimated by subpopulations was $F_{IS} = 0.09$. Indeed two populations had an excess of homozygotes which indicates that the effective population size is small, suggesting bottlenecks and geographic isolation. In addition, two populations showed deficiency homozygotes (Cuauhtémoc and La Paz). In fact, in La Paz homozygous animals were found. In this study a large number (64–100 percent) of heterozygous animals were observed. Dendrogram results are in agreement with the geographic location of some of the populations studied. Creoles from Mulegé and La Paz (Baja California Sur) are located in a separate node; these isolated populations are geographically located between the Pacific Ocean and the Gulf of California, while creoles from Chínipas and Cerocahui (Chihuahua) are located on separate nodes. These animals are located in deep canyons of the Western Mountain Range where roads are inaccessible. This independence suggested little gene flow, while populations of Cuauhtémoc and Guadalupe y Calvo, Moris and Guachochi suggest more genetic exchange. In fact, these populations are geographically located in areas with roads more accessible to communication, which probably influenced the exchange of sires and females. Creoles from Tamaulipas are located on a separate node among Chihuahua populations.

Conclusions

Creole cattle from Baja California Sur and Chihuahua in Mexico showed high genetic diversity. Fourteen new haplotypes were detected, of which some had relatively high frequencies that could be the result of the combination of a founder and multiple bottleneck effect and natural selection. Populations from Baja California and Chihuahua were located in different branches in dendrogram; which coincides with the geographic location of the populations studied. Inbreeding was detected in two cattle populations, suggesting the need for appropriate measures to be taken to avoid its negative effects. The results presented in this study may be used to promotion and to assist all stakeholders in the implementation of conservation measures and breeding programs adjusted to the specific characteristics of each cattle population.

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Declaration of interest

The authors declare that there is no conflict of interests.

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Current situation and diversity of indigenous cattle breeds of Saudi Arabia

R.M. Al-Atiyat, R.S. Aljumaah, A.M. Abudabos, A.A. Alghamdi, A.S. Alharthi, H.S. AlJooan and M.N. Alotybi

Animal Production Department, King Saud University, Kingdom of Saudi Arabia

Summary

This study aims to evaluate the current situation and diversity of indigenous cattle breeds in the Kingdom of Saudi Arabia (KSA). A survey was executed in five regions of the KSA. We recorded population sizes, phenotypes and rearing conditions. Taurine *Bos taurus* and zebu *Bos indicus* populations were found. The zebu cattle include two breeds; the Hassawi and the Janobi. The Hassawi breed was found in the eastern region and it is in decreasing number. It may become extinct soon in the absence of conservation plan. Janobi remains common with thousand animals in the south-western part of the country. Only one indigenous taurine cow, showing no phenotypic evidence of zebu introgression, was found in the Central region of KSA (Najd Plateau). This cow might be the last pure indigenous Saudi Arabia taurine animal and therefore, the breed is now close to extinction. We advocate the urgency to design conservation plan for the indigenous livestock of the KSA and to complement these with phenotypic as well as genotypic information.

Keywords: *Taurine (Bos taurus), Zebu (Bos indicus), livestock conservation, Saudi Arabia*

Résumé

Le but de cette étude a été d'évaluer la situation et la diversité actuelles des races bovines autochtones du Royaume d'Arabie Saoudite (RAS). Une enquête a été menée dans cinq régions du RAS. La taille des populations, les phénotypes et les pratiques d'élevage ont été étudiés. Des populations de bovins (Bos taurus) et de zébus (Bos indicus) ont été rencontrées. Les zébus comprenaient deux races: Hassawi et Janobi. La race Hassawi, dont les effectifs sont en régression, se trouvait dans la région orientale. Cette race pourrait s'éteindre bientôt en l'absence d'un plan de conservation. La race Janobi reste une race assez courante avec mille animaux dans la partie sud-ouest du pays. La seule race bovine autochtone n'ayant pas présenté d'indices phénotypiques de l'introgression du zébu a été trouvée dans la région centrale du RAS (plateau du Nejd). Il pourrait s'agir de la dernière race pure de bovins autochtones de l'Arabie Saoudite. Ainsi, la race est actuellement menacée d'extinction. Nous insistons sur l'urgence de concevoir un plan de conservation pour les animaux d'élevage autochtones du RAS et d'obtenir plus de données phénotypiques et génétiques de ces races.

Mots-clés: *bovins (Bos taurus), zébu (Bos indicus), conservation des animaux d'élevage, Arabie Saoudite*

Resumen

Este estudio pretende evaluar la situación y la diversidad actuales de las razas autóctonas de ganado bovino del Reino de Arabia Saudita (RAS). Se llevó a cabo una encuesta en cinco regiones del RAS. Se observaron los tamaños de población, los fenotipos y las condiciones de cría. Se encontraron poblaciones de ganado vacuno (Bos taurus) y de cebú (Bos indicus). Los cebúes incluían dos razas: Hassawi y Janobi. La raza Hassawi, cuyo censo está disminuyendo, fue encontrada en la región oriental. Esta raza podría extinguirse pronto en ausencia de un plan de conservación. La raza Janobi sigue siendo una raza bastante común con un censo de mil animales en la parte Suroeste del país. La única raza autóctona de ganado vacuno que no presentó indicios fenotípicos de introgresión del cebú fue encontrada en la región central del RAS (meseta de Nechd). Podría tratarse de la última raza autóctona pura de ganado bovino de Arabia Saudita. Así, la raza está en la actualidad en peligro de extinción. Insistimos sobre la urgencia de diseñar un plan de conservación para el ganado autóctono del RAS y de recabar más información fenotípica, así como genética, para estas razas.

Palabras clave: *ganado vacuno (Bos taurus), cebú (Bos indicus), conservación de razas ganaderas, Arabia Saudita*

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Introduction

The Kingdom of Saudi Arabia (KSA) enacted its first strategic plan of action for conserving its biodiversity in 2005 after becoming a signatory to the Convention in Biological Diversity (CBD) in 2001 (NCW, 2005). The plan emphasizes that indigenous breeds of livestock are part of the biodiversity of the Kingdom and that they represent invaluable commodities (e.g. protein sources) in a context where KSA depends on imported animal products to meet the increasing demands from local consumers.

Correspondence to: R.M. Al-Atiyat, Animal Production Department, King Saud University, Kingdom of Saudi Arabia. email: ralatiyat@ksu.edu.sa, raedatiyat@gmail.com

Accordingly these genetic resources must be conserved. Several regulations and measures have been put in place to prevent endangered livestock and wildlife to become extinct. For example, the establishment of the National Committee of Medical and Bioethics, approved by a royal decree, regulating research involving human and animals, including endangered species, subjects (KACST, 2010) and the creation of the King Abdul Aziz Arabian Horses Center, a success story in maintaining and conserving indigenous Arabian horses in KSA.

The loss of indigenous livestock breeds means a loss of well-adapted animals to local environments and production conditions at a time where the production systems are facing the challenge of climate changes and where sustainability is increasingly becoming an important characteristic of all livestock production systems. The indigenous (locally called Baladi) cattle of KSA are well-adapted to local environment of dry areas and they are thought to be resistant to tropical diseases (Mason and Maule, 1960; ACSAD, 1988). Until now the population size of these cattle population has been poorly documented. It is has been reported that the numbers of the indigenous cattle reared in traditional systems have declined from 130 136 head in the year 2008 to 102 438 head in 2012 (MOA, 2013). At the opposite, cattle censuses have showed sharp increase for exotic cattle in specialized dairy farms (MOA, 2013).

Indigenous cattle remain the common breed in traditional production systems. Most of them are reared in southwest part of KSA and they belong to a breed called Janobi. In the East region of KSA, there is another group of indigenous cattle described earlier in the literature, called Hassawi (Mohammed, 1997; Al-Shami, 2003). These two populations have been described as Indian zebu type of cattle (ACSAD, 1988), whereas indigenous taurine cattle have reported to be reared in the Central and West regions of KSA. However, to the best of our knowledge, they are no scientific literature regarding these indigenous Saudi taurine cattle.

The objective of this study was to assess and to document the current situation, phenotypic diversity and origin of indigenous cattle across all regions of KSA, in a context of changes in agricultural practices and increasing importation of exotic breeds.

Materials and methods

A stratified random sampling survey was used to search for the presence of indigenous cattle population phenotypically distinct and/or representing different ecotypes. The survey was conducted in rural areas across the five recognized regions of KSA (North, East, Central, West and South (Figure 1). Their topography includes plains, mountains, deserts and plateaus. The climate of KSA is a desert climate characterized by extreme heat during the day, and low temperature at night. The weather is rather temperate in the North and the south-north heights and humid at the coastal region. In the East, along the Arabian Gulf, there is a low-lying region called Al-Hasa. The survey was done in collaboration with the Ministry of Agriculture personnel. The stratification survey involved dividing the existing cattle population into groups before recording the description and characteristics of the breed. The survey was designed to capture phenotypic, reproduction and breeding parameters data, geographic location, the presumed origin of the populations and any catastrophic event that has occurred (Table 1).

Census data of cows, bulls, heifers and bullocks were also collected to estimate population size in each region. In the

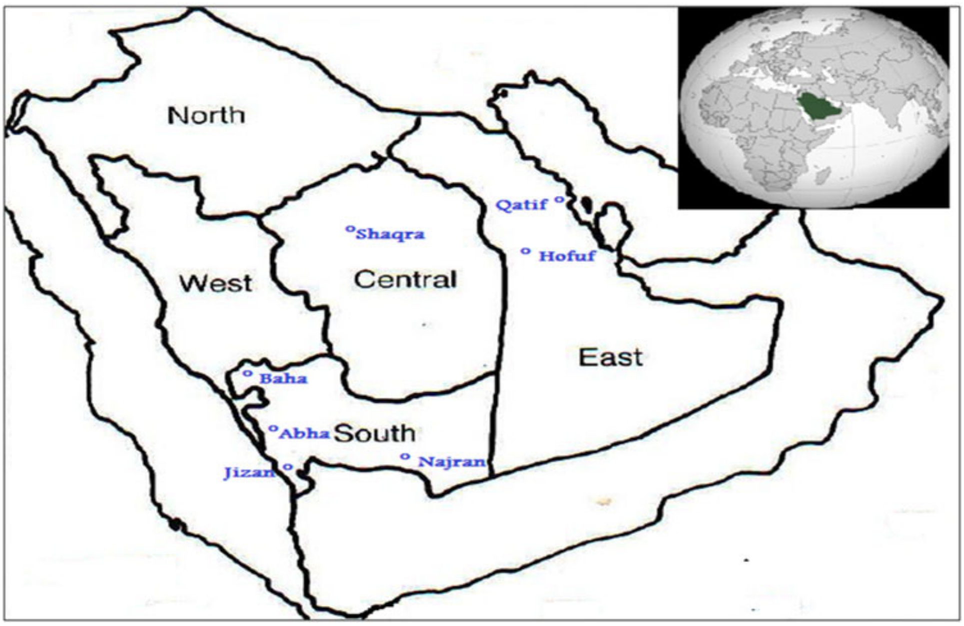

Figure 1. Map of Kingdom of Saudi Arabia where indigenous cattle were surveyed: Qatif and Hofuf in East region, Shaqra in Central region and Baha, Abha, Jizan and Najran in South region.

Table 1. Reproduction and breeding parameters recorded during our census for the three Saudi Arabian indigenous cattle breeds.

Reproduction and breeding parameters	Cattle breed		
	Saudi taurine	Hassawi	Janobi
Reproduction parameters			
Maximum parity size (calf)[1]	1	2	1
Mean parity size (calf)	1	1.05	1
Sex ratio at birth (male:female) (%)	–	45:55	46:54
Female maximum breeding age (year)	10	12	10
Male maximum breeding age (year)	–	7	7
Adult males (Bulls) (%)	–	~9	~6
Adult breeding females (Cows) (%)	100	~48	~52
Cows produce first progeny in a year (%)[2]	100	100	100
Live time Mortality for all classes (%)[3]	–	5%	–
Mating and breeding parameters			
Females are in the breeding pool (%)[4]	100	91	94
Males are in the breeding pool (%)	0	9	6
Number of mates/successful sire (times)	–	3–5	4–6
Replacement	No	Yes	Yes
Gene flow from other farm	No	Yes	Yes
Catastrophes			
Exotic breed competition (%)	100%	25	25
Drought	–	10	40
Endemic Diseases (%)	–	50	20

[1]The annual maximum number of progeny per cow; when single is listed 1 and twin listed 2.
[2]The ratio is calculated from number of cows entering the herd for the first time, to those out of them produced first progeny.
[3]Measure of death rate in the entire population. It is calculated from number of animal deaths in the entire studied population.
[4]The breeding pool is defined as sum of number of the breeding male and breeding female.

South region, the indigenous cattle are reared in herds in remote areas, while in the East region, the census data were estimated based on surveying all cattle at farm levels. Table 2 shows the results from six Hassawi cattle farms surveyed in the East region. Effective population size (N_e) was estimated for Hassawi cattle population based on the number of breeding males (N_m) and breeding females (N_f) found at the farms as $N_e = 4(N_m \times N_f)/(N_m + N_f)$ (Falconer, 1989) (Table 1). In addition, phenotypic and production parameters of the cattle were also surveyed during sampling whenever available. In the Central region only two farms with a total of 13 indigenous cattle, were found. The survey team found no indigenous cattle in the North region. Finally, in southern and western regions, seven farms were surveyed. The number of surveyed cattle in each farm ranged from 8 to 22 heads. The linear body measurements were taken for mature cows and bulls when the standing naturally with head raised and weight on all four feet. Body length was measured from the point of the shoulder to the pin bone, height at withers from the ground level to the highest point of withers, head length from poll to nose, head width for distance between the temples, ear length from the base of the ear to its tip, horn length from the horn base to the tip, hump height from the base of the hump to its highest point and tail length from the base of the tail to its tip. Colour of coat was recorded visually.

Results

Saudi indigenous cattle were found in three out of the five KSA regions surveyed during the year 2014. The results showed that two worldwide species of cattle, taurine (*Bos taurus*) and zebu (*Bos indicus*), were found in KSA.

Saudi Taurine cattle (*Bos taurus*)

A single phenotypically pure indigenous taurine cattle was found in the Central region of KSA. The geographic area of finding is in agreement with evidences of indigenous

Table 2. Total (N) and effective (N_e) population size of Hassawi cattle in the East region of Kingdom of Saudi Arabia in the year 2014.

Farm no	Province	Cow	Bull	Heifer	Bullock	N	N_e
1	Al-Hasa	8	1	3	3	15	
2	Al-Hasa	3	1	2	1	7	
3	Al-Hasa	8	1	2	4	15	21.1
4	Al-Hasa	3	1	1	1	6	
5	Al-Qatif	18	1	13	8	40	
6	Al-Qatif	3	1	2	1	7	
	Tota	43	6	23	18	90	

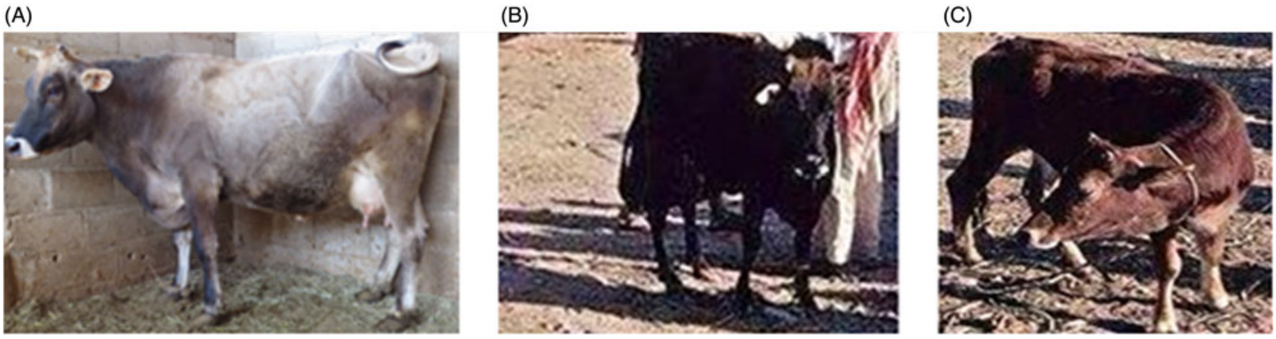

Figure 2. Photos of Saudi Arabian taurine cattle reared in (Central Region). (A) Indigenous cow in 2014, (B) and (C) indigenous cow in 1976.

taurine presence of this region in the past. More particularly this unique pure taurine female (10 years old) was found in Shaqra city (Figure 2A). This Saudi taurine cow matched with available historical information, phenotypic records and images of the pure Saudi breed that lived in the region few decades ago (Figure 2B, C). For example, its phenotype and morphology matched with available images (R. S. Aljumaah., personal communication, 2014) of cows reared in the same region taken in 1976. Based on these evidences, we consider this cow as a pure individual of Saudi taurine cattle from the Central region and the only one found during our survey. This pure indigenous Saudi taurine was characterized by a small body size, a varied coat colour from black to brown, small horn and legs (Figure 2). This cow might be the last individual of this breed left and therefore, in the absence of any taurine bull, we consider the breed as extinct.

Saudi Indian cattle (*Bos indicus*)

The zebu cattle *Bos indicus*, were found and they are classified into two breeds. These are Hassawi and Janobi cattle breeds found in the East and South regions, respectively. Both breeds have close morphological and production traits. Both breeds are considered as indigenous by the local people.

Hassawi cattle breed

Hassawi cattle were found in the East region of KSA around the Hofuf and Qatif cities close to the Arabian Gulf (Figure 1). Hassawi cattle were found in six small farms with numbers between 6 and 40 heads per herd (Table 2). Five of them were surveyed in Hofuf city (Al-Hasa area). In total, 90 heads of cattle were surveyed (Table 2). Hassawi cattle are therefore reared into small numbers under small-scale traditional farms. The N_e for this population, combining data from both areas is 21.1. Our census number shows a sharp and continuous decrease in comparison with previous years. If the decreasing trend continues (Table 2), Hassawi cattle could become extinct in the next coming few years.

Outcomes from the surveys indicate that the main purpose of rearing Hassawi cattle is to provide milk for household consumption. The milk yield of this breed is low likely following a low inputs management system with poor quality and scarcity of feed rather than a low genetic potential, but further studies are needed here. Calf meat of this breed was preferred over other livestock's meat by local people. Their reasonable conformation, growth rate, meat yield and other good carcass traits are appreciated by the local farmers. The herds are usually kept under a sedentary production system (in permanent confinement) with separated barns for cows, heifers, bulls and bullocks as well as calves (Figure 3). The feed was green fodder and hay with supplements of low-quality date palm. Calves were kept in separate barns and allowed to suckle their mothers twice a day (Figure 3D). The dominant breeding plan is to keep at least one mature bull selected from the herd to be the sire of heifers and cows.

The Hassawi breed was phenotypic homogenous and exhibited little variations in body dimensions and colour. The measured traits of body length, height at wither and mature weight were 180 and 165 cm, 158 and 150 cm, and 215 and 175 kg for mature bull and cow, respectively. It might be considered that body size of Hassawi cattle was medium. The body coat colour varied from dark brown to red with short hair and some pigments. The head length and width were 60 and 46 cm, 35 and 21 cm for mature bull and cow, respectively. The head is small in relation to the body size with long and triangular face. In addition, they have medium size erected ears. The bulls have small horns, whereas females have vestigial horn or are hornless. They have a little dewlap. The hump is clearly visible in bulls (Figure 3H) but defined in cows (Figure 3I). The tail is long and markedly advanced on the back. The udder is small with small teats (Figure 3A). The mature cows have a fair body depth and short width at the chest and flanks (Figure 3A). The body condition score was considered low (less than 3) with ribs easily seen. The legs are long and light with fine bones (Figure 3G, L, M). The overall mortality rate was estimated to be relatively low, namely less than 5 percent a year.

Janobi cattle breed

The second breed of Saudi zebu cattle was found in the South and West regions of KSA. They are called Janobi, which means in Arabic language southern. The surveyed areas in these regions covered four main provinces;

Figure 3. Hassawi zebu cattle from Hofuf and Qatif Provinces in the East Region of KSA (photographs taken in April 2014).

Figure 4. Janobi Zebu cattle. Baha city (A, B, C, D, E, F) and Abha city (G) both in the South region of KSA (photographs taken in April 2014).

Baha, Abha, Jizan and Najran (Figure 4). In general, this cattle breed is unevenly distributed over the entire South and West regions of KSA (Figure 4), but mostly in Jizan and Najran. Herd size ranges from five to a few hundred heads. They are kept in pastoral to sedentary productions systems. Most of Janobi cattle herds found in Baha and Abha are reared under the pastoral system (Figure 4A) with mature cows grazing pastures, rangeland and side-roads. The herds at Jizan and Najran are kept under the sedentary system with animals confined in barns. Both production systems are characterized by poor and traditional inputs. The population size of this breed is assumed to be in the order of a few thousands with therefore no endangerment or threats of extinction. The breed exhibits wide variation in body conformation and coat colour. They are reared in harsh environmental conditions, which prevail in most parts of the region. Janobi breed is maintained in a low input production system with very old traditional and unimproved practices (Figure 4A, B). Furthermore, the survey indicates that this breed is kept for its ability to produce milk for household consumption under the harsh condition of heat stress and feed scarcity characteristic of the region. Compared with the Hassawi breed, given the bigger sizes of udder and teats, the Janobi breed has more potential to be developed as a local indigenous milk breed (Figure 4B, E, F).

There were no dominant breeding practices noticeable all over the studied south-west region. Most farmers usually keep at least one family-based selected bull from same herd to be the sire of heifers and cows regardless of any inbreeding considerations. The bulls were usually kept in permanent confinement with separated barn. Newly born calves with their mothers for suckling were also kept separately (Figure 4C). The feeding plan is grazing whenever it is available during the year. Supplements of green fodder, hay and other vegetable leftovers are given.

The average measured traits of body length, width and height at wither were 138, 66 and 135, and 133, 65 and 130 cm for mature bull and cow, respectively. The head length and width were 55.2 and 32, and 31.6 and 23.7 cm for mature bull and cow, respectively. The body size could generally be assumed to be medium for mature females and males. The head is long and medium in size in relation to the body size. They have medium size erected ears for both sexes. The bulls have medium straight horns of 15 cm on average length, whereas females have either rudimentary or small straight horns. Both mature sexes have an obvious dewlap (Figure 5A, F and 5B, D). The hump is clearly seen in bulls (20 cm in length and 35 in width) and cows (10 cm in length and 20 in width). In general, body score were reasonably good with fair chest and flanks flatted over seen ribs. The legs are strong and long with noticed bones, suggesting that the animals have ability to walk long distances (Figures 4 and 5). The tail is long and markedly advanced on the back. As indicated above, despite smaller body conformations than Hassawi individuals, the udder and its teats are bigger than those of Hassawi. As a consequence, milk production in this breed might show good potential considering the low input production system, in which they are kept. Last but not the least variation at phenotypic and performance traits support a broad genetic base for the breed (Figures 4 and 5). For example, the Janobi cattle exhibited wide variations in body coat colour (Figures 4 and 5). The body coat colour varied from creamy

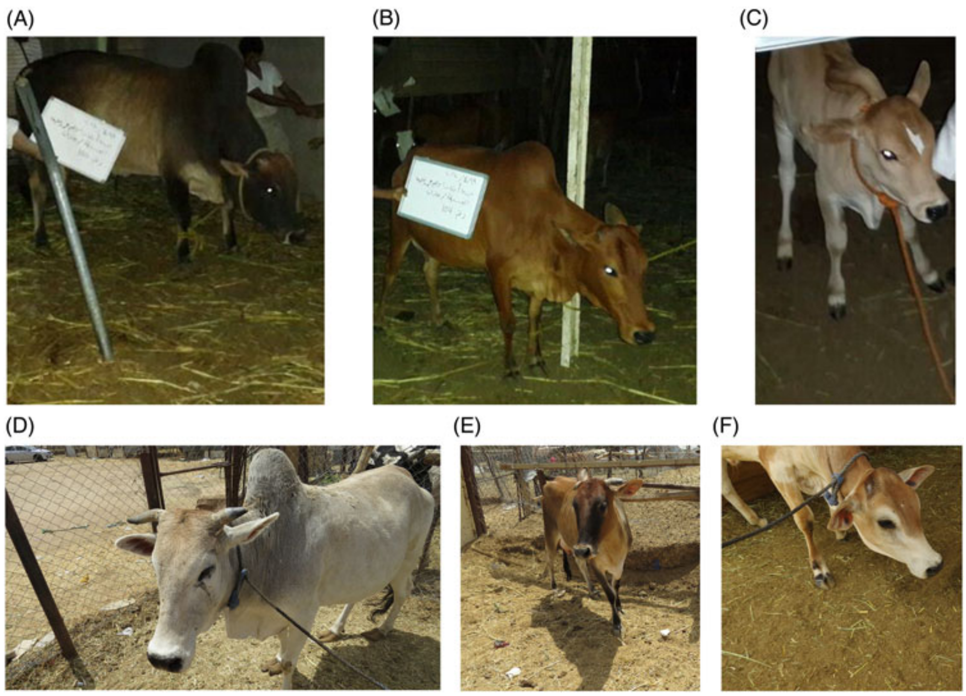

Figure 5. Janobi zebu cattle taken in Jizan city (A, B, C) and in Najran D, E, F in the South region of KSA (photographs taken in April 2014).

to black. The reddish coat colour was dominant in most of the herds from Baha down to Najran (Figures 4 and 5). In addition, the body coat was characterized by short hair. Pigmentations were noticed in different parts of the body.

Rearing indigenous cattle along with exotic cattle

During the survey, we observed in several cases the presence of an exotic bull within the herd, which is used in mating with indigenous cows. This F1 cross-breeding is considered as the main threat for the conservation of the genetic diversity of indigenous Saudi cattle population. The farmers practice cross-breeding mating or even breed replacement with exotic breed in order to improve milk production.

There was a case where an exotic Brown Swiss bull was used for breeding a herd of 20 females in order to produce heavier calves (Figure 6A). It was in the same farm where the last pure Saudi Arabian taurine cow was found (Shaqra city). The exotic bull was allowed to mate with all taurine × zebu hybrid females present in the farm as well as the last pure indigenous cow (Figure 6A). In a Hassawi cattle herd an exotic bull was allowed to mate with the indigenous Hassawi heifers (Figure 6B-I). In addition, a hybrid Hassawi–Friesian heifer was produced by crossing indigenous Hassawi cow with the presence of Holstein–Friesian bull in order to improve milk yield while keeping the adaptive environmental traits of the Hassawi (Figure 6B-II). Finally, a similar situation was observed for the Janobi breed with exotic bulls reared along Janobi cows in different farms in the South and West regions. For example, exotic Somali beef bulls were imported for meat consumption and used as terminal sire with local Janobi cows for better meat yield (Figure 6C-I), while Holstein–Friesian bulls were used to produce hybrid cows in the same breed (Figure 6C-II).

Discussion

Our survey was performed in accordance to Ericson (1965) recommendation sampling each subpopulation independently within an overall population. We found indigenous cattle in 3 out of the 5 regions of the KSA. The survey indicates that two main cattle species (taurine, zebu) (Grubb, 2005) are present, although today we were only able to record a single indigenous taurine cow. We also found exotic European taurine as well as exotic zebu breed. The taurine cattle were found in the Central region, whereas zebu cattle belong to two breeds (Hassawi and Janobi) found in the East and South regions, respectively. Both Zebu breeds have variable morphological and

Figure 6. Photographs illustrating cross-breeding of indigenous Saudi cattle with exotic. (A–I) Represent the pure indigenous Saudi taurine cow II. Represent exotic Brown Swiss bull III. Represent a hybrid offspring cow. (B) Images of an exotic beef bull and indigenous Hassawi heifers (I) hybrid Hassawi–Friesian heifer (II). (C) Somali bullocks allowed to breed with Janobi indigenous heifers in Baha city (I). Hybrid Janobi–Friesian heifer in Najran (II).

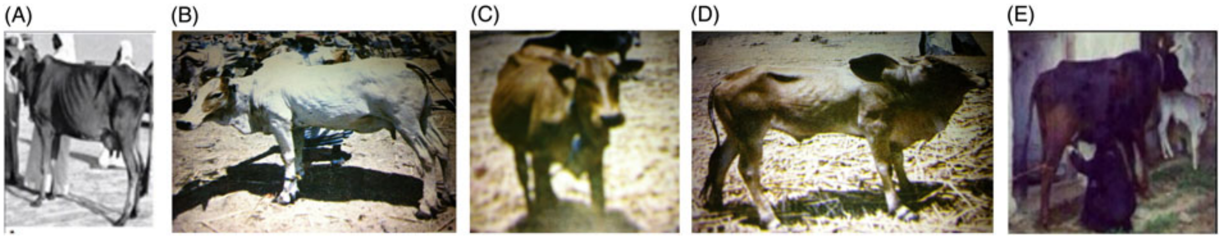

Figure 7. Ancient images of Saudi Arabian Zebu indigenous cattle (A) Hassawi cow, cattle market in Hofuf (1976), (B) Janobi cow from Jizan city (1985), (C). Janobi cow from Najran (1985). (D) Janobi bull from Abha city (1985) and (E) Janobi cow from Baha city (1985).

production traits, and it is of our opinion that they should definitively be considered as two distinct breeds. Although in the past some reports have lumped them as one breed, even though morphological and production differences were reported (ACSAD, 1988).

We consider the taurine cattle in KSA now virtually extinct as only one 10-year old female was found; although it remains possible more animals could be present in areas and regions not covered in this study. The extinction of a breed is considered when either sexes or one of them disappeared (FAO, 2000). The observations from the current survey indicated that these indigenous taurines are characterized by low milk production, a likely slow growth rate and a small body size. It should be noted that our survey does not allow us to distinguish between the possible low genetic potential of the breed as milk producers and the consequence of low management inputs in a production system where indigenous cattle are kept under harsh environmental conditions. Moreover, the introduction of exotic breeds in 1970s which lead to many hybrid animals with different proportion of exotic genetic background and with, based on our observation, no obvious loss of fitness is further complicating the issue.

There are hardly any available studies or reports regarding indigenous Saudi taurine cattle. A study aimed at surveying the presence of coccidian parasites reported that 205 indigenous domestic cattle *Bos taurus* from five regions of KSA were examined in 1985 (Kasim and Al-Shawa, 1985). It suggests that the number of Saudi taurine was at least a few hundred in the 1980s.

The endangerment level is a function of the downward trend in the number of breeding animals at a country or geographical level (FAO, 1995; Al-Atiyat, 2009). The number of breeding animals is the most common assessing system of endangerment of any species or breed (1995). In fact, there are more assessing system commonly used (DGFZ, 1991; European Commission, 1992; EAAP, 2005). The FAO (1995) system is the most commonly used. It states that if N_e is less than 82 then the breed is at a critical and endangered level. Using these criteria, following the results of Table 2 for the Hassawi cattle breed, the breed has reached the critical level of endangerment and it may face extinction in the near future. Their overall N_e was 21.1 which is much less than the reported critical N_e value.

Hassawi cattle are kept in small numbers on some small-scale traditional farms in the Eastern province of the KSA. In fact, the breed has been previously described in the literature (Mohammed, 1997; Al-Shami, 2003). Census number shows sharp and continuous decrease over the last years (MOA, 2013). The major threat is the culling of the cattle as a result of endemic tuberculosis outbreaks. Due to this and other anticipating threats (e.g. feed scarcity and cross-breeding practices), Hassawi cattle breed may become extinct in the coming few years, and thus their potential as indigenous genetic resources will be lost. Institutional support and conservation initiatives are needed for saving the breed. . It is worth mentioning that the only cattle market in the KSA was at Al-Hasa (Figure 7A). The cattle used to be flown in and out of the market from all nearby gulf countries. Hassawi cows seen in this market were phenotypically different from the cow of 1970s (Figure 7A).

Similarly, old images of indigenous cattle breed from different regions dating from the same period of Al-Hasa market pictures (in year 1976) matched with the present indigenous cattle photographs both in size, conformation and colour (Figure 7B–E).

The indigenous cattle of the KSA represent still today a source of valuable animal proteins in the form of milk and meat. Their importance and uniqueness comes from their adaptation to the local harsh environmental conditions including water scarcity, heat stress and endemic diseases. Nasher (1990) reported that indigenous cattle in Asir, in south-western KSA, were well-resistant to 13 parasite species. They also showed resistance to ticks infestation and tick-borne diseases.

We also observed an ancient rock art of wild and domesticated cattle in different regions of KSA during our cattle survey (Figure 8). Ancient drawing of what may be interpreted as domesticated cattle was first seen in caves in Al-Shouq valley in Abha city (Figure 8A, B). The most overwhelming cattle rock arts were seen in Najran province, at the site of the ancient citadel of Al-Okhdood and at Bir Hima (Figure 8 C, D, E). These ancient drawings are assumed to date from the period of 2500–1000 BC (Jennings *et al*., 2013; Olsen, 2013). Cattle are the most common representation of animals in more than 25 sites in the KSA (Jennings *et al*., 2013; Olsen, 2013). For example, Figure 8(F) shows engravings of goats (ibex or

Figure 8. Example of ancient rock art depicting domestic cattle in different sites in Kingdom of Saudi Arabia (KSA) dated around the first millennium period (BC or AD) (Jennings *et al*., 2013; Olsen, 2013). (A) and (B) Rock painting of humpless domesticated cattle drawn (Al-Shouq valley in Abhaa city south-western KSA). (C), (D) and (E) Cattle rock carving (ancient citadel of Al-Okhdood and Bir Hima sites in Najran in southern KSA. (F) and (G) Rocket carving of bovides in Northern KSA (Jennings *et al*., 2013). (H) Drawings of a taurine cows and bull (Soaaj Mountain near Qassim region on the Najad Plateau) and (I). t Pregnant taurine cows, (Soaaj Mountain near Qassim region on the Najad Plateau). Photo credits etc.

wild) and bovids (wild or domesticated cattle), on the right, including a large example with horns and head turned to one side. The second image shows equally a wild or domesticated bovid (Figure 8G). These two examples were reported by Jennings *et al*. (2013) in the Jubbah area of northern KSA. The presence of some piebald coats indicate that some of these bovids were domesticated animals (Figure 8G) (McCorriston and Martin, 2009). Furthermore, heritage drawings of mating Saudi taurine cows and bull indicate breeding in the Central region (Figure 8H). Another drawing was seen at the same place showing a likely pregnant taurine cow (Figure 8I). Both drawings were found in Soaj Mountain near the Qassim area on the Najad Plateau of the Central region.

These pictorial evidences emphasize that KSA was a habitat of wild, ancient and indigenous cattle and while the wild relatives became extinct in the past, our study shows that today their domesticated counterparts may follow the same path in the Kingdom. Once these valuable animal genetic resources are lost, the KSA will have to depend exclusively on imported cattle animal products, particularly meat, to meet increasing demand by consumers. Moreover, the loss of indigenous livestock breeds means the loss of important animal genetic resources well-adapted to local environments and production conditions. Urgent measures and interventions are now required. More particularly, it is recommended that the indigenous cattle of the KSA are further characterized at phenotypic and genotypic levels for implementing sustainable conservation plan.

Conclusions

The current status of indigenous cattle in KSA indicated the existence of two main separate types; taurine and zebu cattle. Saudi taurine cattle are currently considered under the threat of extinction or even extinct because they have disappeared in many regions where they had existed previously and only a single pure cow was found. On the other hand, the zebu cattle are in a better situation being found in large number. However, N_e of Hassawi zebu cattle breed has now reached the endangerment level of extinction as a result of continuous downward trend in number over the years. The Janobi cattle breed is still common and it is not in danger of extinction in the short-term. The threat of extinction exists due to the following for example disease outbreak and culling, cross-breeding and scarcity of food. Archaeological pictorial evidences indicate the presence of wild and domesticated cattle in the KSA in large number in the past. However, today the remaining indigenous cattle populations of the KSA are the modern legacy of the ancient pastorals societies. We recommend that in parallel to molecular and quantitative characterization studies, conservation plans must urgently be put in place to conserve these unique livestock genetic resources of the KSA.

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Conflict of Interest

The authors wish to state that there is no conflict of interest in regards to this manuscript.

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Pedigree analysis of the Afrikaner cattle breed

L. Pienaar[1,2], F.W.C. Neser[1], J.P. Grobler[1], M.M. Scholtz[1,2] and M.D. MacNeil[2,3]
[1]*University of the Free State, Bloemfontein 9300, South Africa;* [2]*ARC – Animal Production Institute, Private Bag X2, Irene 0062, South Africa;* [3]*Delta G, 145 Ice Cave Road, Miles City, MT 59301, USA*

Summary
The reduction of genetic variability in beef cattle has been extensively researched on a global scale. However, the genetic variability and inbreeding of indigenous cattle breeds of Southern Africa, referred to as Sanga cattle, has been less well characterized. Breeds of Sanga cattle include Afrikaner, Drakensberger and Nguni breeds. In recent years, the number of Afrikaner cattle and herds has decreased. Our objective was to determine the mean level of inbreeding (F), effective population size (N_e) and generation intervals of Afrikaner cattle using their recorded pedigree. A total of 244 718 records extending from 1940 until 2011 were analysed. The average inbreeding coefficient was 1.83 percent and the effective population size was 167.54. The average generation interval was calculated as 6.6 ± 3.9 years. Pedigree analysis on the Afrikaner cattle population yielded levels of inbreeding that appear to be both acceptable and manageable. By implication, the large N_e results in a low rate of change in F. Current results study can be utilized by farmers and the breeders' society to conserve the Afrikaner and utilize the breed to its full potential in the era of climate change.

Keywords: *Bos taurus africanus, effective population size, inbreeding coefficient, Sanga*

Résumé
La réduction de la variabilité génétique chez les bovins à viande a fait l'objet de nombreux travaux de recherche à l'échelle mondiale. Pourtant, la variabilité génétique et la consanguinité ont à peine été étudiées chez les races autochtones de bovins à viande du Sud de l'Afrique, regroupés sous le nom de Sanga. Parmi les races du rameau bovin Sanga, se trouvent les races Afrikaner, Drakensberger et Nguni. Ces dernières années, l'effectif de bovins Afrikaners et le nombre d'éleveurs de cette race ont diminué. Notre objectif a été de déterminer le niveau moyen de consanguinité (F), la taille effective de la population (N_e) et les intervalles générationnels des bovins Afrikaners, en se servant pour cela du registre généalogique de la race. Un total de 244 714 inscriptions faites de 1940 à 2011 ont été analysées. Le coefficient moyen de consanguinité et la taille effective de la population ont été respectivement de 1.83 pour cent et 167.54. L'intervalle générationnel moyen a été de 6.6 ± 3.9 ans, d'après les calculs. Les niveaux de consanguinité décelés par l'analyse généalogique de la population bovine Afrikaner semblent acceptables et maîtrisables. En fait, la grande taille N_e entraîne un faible taux de changement pour le coefficient F. Les résultats de cette étude peuvent être utiles à l'association d'éleveurs dans le but de conserver la race Afrikaner et de l'utiliser jusqu'à son plein potentiel à l'ère du changement climatique.

Mots-clés: *Bos taurus africanus, taille effective de population, coefficient de consanguinité, Sanga*

Resumen
La reducción de la variabilidad genética en el ganado vacuno de carne ha sido investigada ampliamente a nivel mundial. Sin embargo, la variabilidad genética y la endogamia de las razas autóctonas del ganado vacuno de carne del Sur de África, conocido como ganado Sanga, han sido estudiadas en mucha menor medida. Entre las razas de ganado bovino Sanga, se encuentran las razas Afrikáner, Drakensberger y Nguni. En los últimos años, el censo de ganado Afrikáner y el número de explotaciones que lo crían han disminuido. Nuestro objetivo fue el de determinar el nivel medio de endogamia (F), el tamaño efectivo de la población (N_e) y los intervalos generacionales del ganado Afrikáner, empleando para ello su registro genealógico. Se analizaron un total de 244 714 registros, que iban de 1940 a 2011. El coeficiente medio de endogamia fue de 1.83 por ciento y el tamaño efectivo de población fue de 167.54. El intervalo generacional medio ascendió, según los cálculos, a 6.6 ± 3.9 años. Los niveles de endogamia arrojados por el análisis genealógico de la población bovina Afrikáner parecen aceptables y manejables. En consonancia, el gran tamaño N_e conlleva una baja tasa de cambio en el coeficiente F. Los resultados del estudio actual pueden ser utilizados por los ganaderos y por la asociación de criadores para conservar la raza Afrikáner y emplearla hasta su pleno potencial en la era del cambio climático.

Palabras clave: *Bos taurus africanus, tamaño efectivo de población, coeficiente de endogamia, Sanga*

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Correspondence to: L. Pienaar, ARC – Animal Production Institute, Private Bag X2, Irene, South Africa. email: PienaarL@arc.agric.za

Introduction

Inbreeding occurs when mating of individuals that are more closely related than random individuals from a population (Falconer and Mackay, 1996). Inbreeding causes a reduction in genetic variability which in return is the basis of inbreeding depression which affects fitness-related traits such as fertility when recessive alleles are deleterious (Falconer and Mackay, 1996; Croquet *et al.*, 2007; Panetto *et al.*, 2010). In addition, genetic variation will ensure a capacity for long-term response to selection pressures, either through artificial or natural selection (Frankham, Ballou and Briscoe, 2002). Additionally, Vahlsten, Mäntysaari and Strandén (2004) emphasized the importance of monitoring the level and rate of inbreeding within a population across time. The reduction of genetic variability in beef cattle has been researched extensively (e.g. Cleveland *et al.*, 2005; Santana *et al.*, 2010; Piccoli *et al.*, 2014). Further, there have been numerous genetic analyses based on pedigree information in livestock species including dairy cattle (Maiwashe *et al.*, 2006; Mc Parland *et al.*, 2007), beef cattle (Gutiérrez *et al.*, 2003; Bouquet *et al.*, 2011; Steyn *et al.*, 2012a, 2012b), horses (Moureaux *et al.*, 1996; Vicente, Carolino and Gama, 2012) and sheep (Huby *et al.*, 2003; Maiwashe and Blackburn, 2004).

Relatively little work has been conducted to assess the degree of inbreeding in indigenous (Sanga) cattle of Southern Africa. These are breeds with unique characteristics and differ from the *Bos taurus* breeds. Meyer (1984) concluded that Sanga type cattle, with specific reference to the Afrikaner, have distinct genetic markers inherited from both *Bos indicus* and *B. taurus* cattle. The species name, *B. taurus africanus*, was proposed to show that Southern African Sanga cattle such as the Afrikaner and Nguni are distinct from other African taurine cattle (Meyer, 1984; Frisch *et al.*, 1997). Furthermore, Sanga cattle is known for its hardiness, adaptability to extreme environmental conditions, heat tolerance, disease- and external parasite resistance (Scholtz, 2010). The number of the Afrikaner cattle breed has decreased drastically over the past three decades from more than 27 000 seed stock females in 1980 (Bosman, 1994) to 6 000 in 2010 (Bergh and Havenga, 2011), mainly due to the increased popularity of composite breeds. Similarly, the number of registered herds has decreased from 355 to 66.

One method to ensure the future existence of the Afrikaner breed is through the maintenance of genetic variability. Therefore, it was imperative that a pedigree analysis be conducted on the Afrikaner to ensure the sustainable conservation (through avoiding inbreeding between close relatives and sourcing of genetic material from commercial herds) of this indigenous South African breed. Genetic variation is important for the adaptive potential of a population and can be utilized when faced with extreme environmental changes such as global warming.

Quantitative genetics based on pedigree analysis is an alternative measurement to the use of molecular genetic markers to determine the level of genetic variability and inbreeding within a livestock breed. Thus, the aim of the current study was to use pedigree data from the Afrikaner cattle breed to examine the pedigree structure of the breed, to determine the levels of inbreeding, effective population size (N_e), average relatedness (AR) and generation intervals. Parameters derived from the probability of gene origin, i.e. effective number of founders (f_e) and effective number of ancestors (f_a) were also investigated.

Materials and methods

Pedigree analysis was conducted using ENDOG v4.8 software (Gutiérrez and Goyache, 2005). A total of 244 718 individuals were used in this analysis, which included records from 1940 until 2011. Several analyses were carried out to determine the probability of gene origin, average coefficient of inbreeding, effective population size, AR coefficient and generation interval (Gutiérrez, Cervantes and Goyache, 2010).

Rates of inbreeding (F) were calculated using the regression of applicable values on the year of birth (Meuwissen and Lou, 1992). The individual increase in inbreeding (ΔF_i) was estimated using the individual inbreeding coefficient (F_i) as described by Gonzalez-Recio *et al.* (2007) and modified by Gutiérrez, Cervantes and Goyache (2009). Effective population size (N_e) can be defined as the number of animals used for breeding which would lead to an increase in inbreeding if the contribution of all breeding animals were equal. The "realized effective size" was calculated according to Cervantes *et al.* (2008). AR is the probability that an allele belongs to a specific animal when it was randomly selected from the total population within the pedigree. The interpretation of AR consequently is the depiction of animal in the whole of pedigree, irrespective of the information provided for its individual pedigree (Gutiérrez, Cervantes and Goyache, 2010). The generation interval was calculated as the average age of the parents at the birth of their offspring that replaced them (Falconer and MacKay, 1996). The parameter f_e can be defined as the number of contributing founders that would be expected to produce the same level of genetic diversity as the population under investigation. For a given number of founders, the more equal the genetic contribution of each founder, the greater the number of effective founders that will be identified. Boichard, Maignel and Verrier (1997) defined f_a as the minimum number of ancestors (including both founders and non-founders) which demonstrates the complete diversity of the population being studied. The information provided by f_e is complemented by f_a given that these parameters account for the losses of the genetic variation that was produced by the uneven number of reproductive animals which produced bottlenecks (Gutiérrez and Goyache, 2005). This parameter, pedigree completeness, indicates the degree of depth of the pedigree. It was measured in complete generation equivalents (CGE). CGE can be defined as the degree of pedigree information of an animal. Three traced generations are computed by ENDOG for each animal in the pedigree: (i) fully traced generations – defined as the individuals separating the progeny of the furthest generation, which is where the second generation of ancestors of the specific individual are identified. Generation 0 are the founders of the population, which are the ancestors whose parents are both unknown; (ii) maximum amount of generations traced – defined as the amount of generations which separate the individual from its outermost ancestor; (iii) equivalent complete generations – estimates the pedigree of each individual as the sum over all known ancestors of the terms $(1/2)^n$. The amount of generations which separates the individual from each identified ancestor is represented by *n* (Maignel, Boichard and Verrier, 1996; Boichard *et al.*, 1997).

Results

Parameters characterizing the genetic variability of the Afrikaner breed are presented in Table 1. The original dataset contained 244 718 animals. The reference population, where both parents are known for an animal, contained 203 821 animals. The effective population size of the founder animals was 396.16 animals.

The effective numbers of founders (f_e) and ancestors (f_a) were 288 and 226, respectively. The fact that a gap that exists between f_e (288) and f_a (226) implies the existence of a bottleneck. Furthermore, when the ratio between f_e and f_a (f_e/f_a) is 1.27. The ideal ratio should be one. The larger the ratio, the more severe the effect of the bottleneck is (Boichard *et al.*, 1997; Mokhtari *et al.*, 2013). The results from the current study thus do indicate a bottleneck, but the bottleneck was not large enough to have a big effect on the Afrikaner population. The fact that the value of N_e for the current study is still 167.54, also indicates that the effect of the bottleneck was not severe. The effective population size (N_e) was also calculated via two other methods using the ENDOG software, namely complete generations and equivalent generations and values of 61.67 and 87.48 were obtained. Although the latter two

Table 1. Parameters characterizing the probability of gene origin in the Afrikaner cattle breed.

Item	Total
Original dataset	244 718
Reference population (animal with both parents known)	203 821
Effective population size of founder animals	396.16
Number of ancestors contributing to reference population	21 263
Effective number of founders (f_e)	288
Effective number of ancestors (f_a)	226
Number of ancestors explaining 50 percent of genetic variability	201
Number of founder herds in reference population (f_h)	528
Effective number of founder herds for the reference population	35.2
Mean *AR* (%)	0.44
Maximum number of generations	4.42
Number of complete generations	1.86
Number of equivalent generations	2.81
Effective population size (N_e)	167.54
Mean inbreeding (%)	1.83

Table 2. Levels of inbreeding in the Afrikaner breed.

Number of animals (*N*)	Level of inbreeding (%)
4	>40
230	30–39.9
3 144	20–29.9
11 666	10–19.9
13 140	6–9.9
35 820	1–5.9
20 134	<1.0

N_e's are smaller, they are still within the acceptable limits as indicated in the discussion below.

A total of 21 263 ancestors were recorded which contributed to the reference population. A total of 201 ancestors explained 50 percent of the genetic variability of the reference group. The mean inbreeding value was calculated as 1.83 percent with an *AR* of 0.44.

The number of animals at each level of inbreeding was calculated (Table 2). There are only four animals which are more than 40 percent inbred. A total of 84 138 animals were inbred to some degree, implying that 160 576 animals showed no levels of inbreeding. Matings between the close relatives were also observed in the study where a total of 67 matings between full sibs (brother and sister) were recorded, which presents 0.03 percent of the population under study. Furthermore, mating between half sibs (half-brother and sister or brother and half-sister) was recorded in a total of 8 607 cases, which amounts to 3.52 percent. Finally, mating between parent and offspring (mother and son or father and daughter) was recorded in 1.17 percent of the records within the dataset, accounting for 2 856 animals.

The increase in inbreeding and the *AR* per generation are illustrated in Figure 1. A maximum of 14 generations was detected. Generations 0–2 showed no levels of inbreeding. From generations 2 to 6, there was a steady increase in inbreeding of ±1 percentage unit per generation. Until generation 12, inbreeding levels were constant with minimal to no increase of inbreeding for the six generations. From generations 12 to 14, a sharp increase in inbreeding was observed. One explanation for this may be the drastic decrease in the number animals and herds. *AR* per generation followed a similar trend compared with the levels of inbreeding. Generations 0–3 displayed a minimum to no increase in relatedness. From generations 3 to 6, a gradual increase was observed. From there on, a constant relatedness level was observed with a slight increase from generations 13 to 14.

The most recent ancestral generation, calculated from all the animals in the dataset, were 87 percent complete. The second ancestral generations for dam and sire lines were on average 69.9 and 73.9 percent complete, respectively. For the third generation, the pedigree completeness decreased to the lowest percentage, at 48.4 percent.

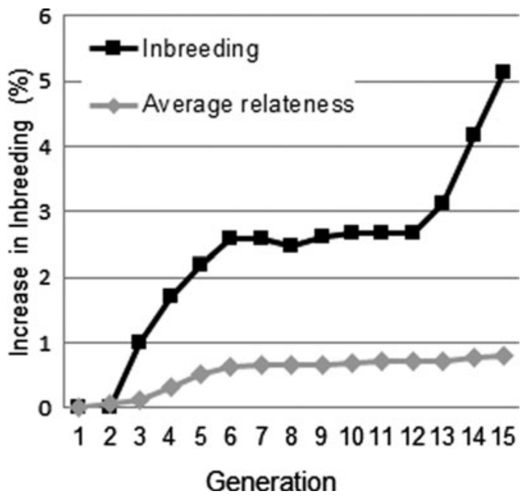

Figure 1. Increase in inbreeding and *AR* for each generation.

The average generation interval for the whole population was calculated as 6.6 ± 3.9 years. Furthermore, the generation interval estimated for the four different gametic pathways was as follows: dam to son: 6.712 ± 3.653 years; dam to daughter: 6.615 ± 3.514 years; sire to son: 6.507 ± 4.704 years and sire to daughter: 6.489 ± 4.146 years.

The numbers of animals used to calculate the level of inbreeding per year for the whole pedigree data and inbred animals are presented in Figure 2. In 1981, there was a sharp increase in the number of animals used in the analysis for both inbred animals and all pedigree data used. The reason for this sharp rise in the number of animals was driven by the society to register more animals.

The mean inbreeding level per year for the whole pedigree data and the mean inbreeding level per year for inbred animals are presented in Figure 3. The proportion of animals that were inbred in 1970 was very low; therefore their average inbreeding level was high. The opposite happened in 2011, where a larger proportion of animals were inbred, translating into a lower level of inbreeding. From 1970 to 1979, the inbreeding level for all animals showed an increase of 0.94 percent; onwards from 1980 until 2011 all inbreeding levels were above 1 percent. A stable increase in inbreeding levels was visible from 1978 to 1988 and from there on constant levels followed. The year with the highest inbreeding level was 1996, with an average of 2.79 percent. Along with the number of inbred animals increasing, the number of generations of inbred animals also increased; therefore, the level of inbreeding effectively decreased over time. Consequently, the level of inbreeding for the inbred animals showed a constant decrease as the number of generations used in analysis increased.

Discussion

When the entire dataset was considered, a total of 34.4 percent of animals were, to some degree, inbred. The average inbreeding coefficient for the whole population was 1.83 percent. The value of N_e for the current study is 167.54. The observed high N_e of the Afrikaner may be the result of a project involving introgression of Bonsmara genes into the Afrikaner breed by a number of breeders to improve its performance. Following the introgression, line breeding was implemented to a certain degree. This project allowed the *AR* to also stay constant over generations since line breeding was used to breed pure Afrikaner animals, but however caused an increase in inbreeding since a smaller number of pure Afrikaner animals were available. This estimate N_e of the Afrikaner is similar to that of the Nguni cattle that was estimated to be 168 (Matjuda, 2012). The N_e reported here is greater than the minimum of 50–100 recommended by the FAO

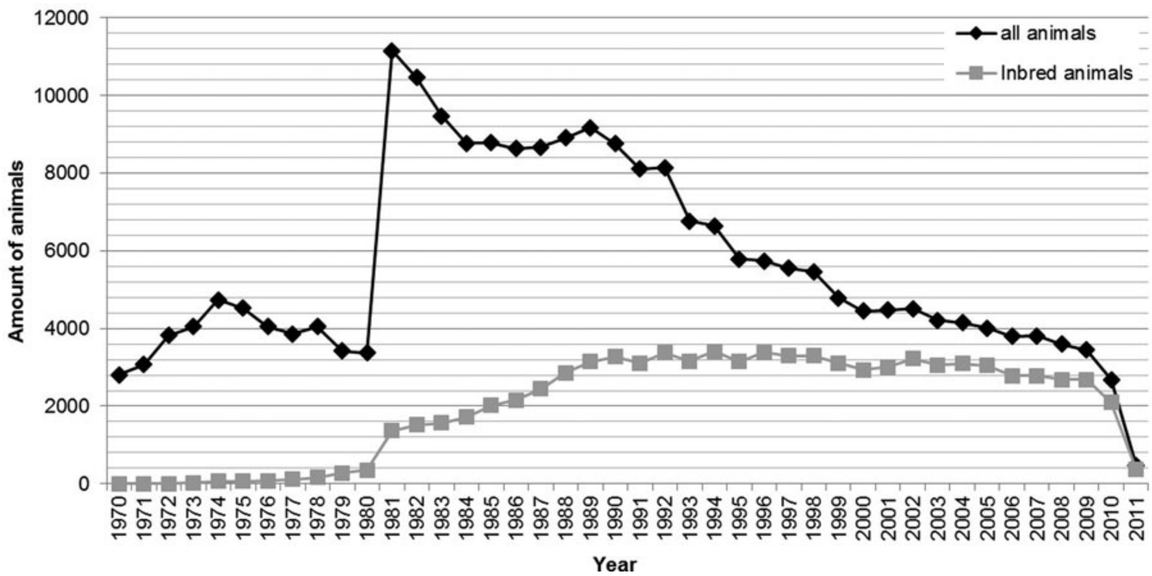

Figure 2. Number of animals used to calculate the level of inbreeding per year for the whole pedigree data and inbred animals.

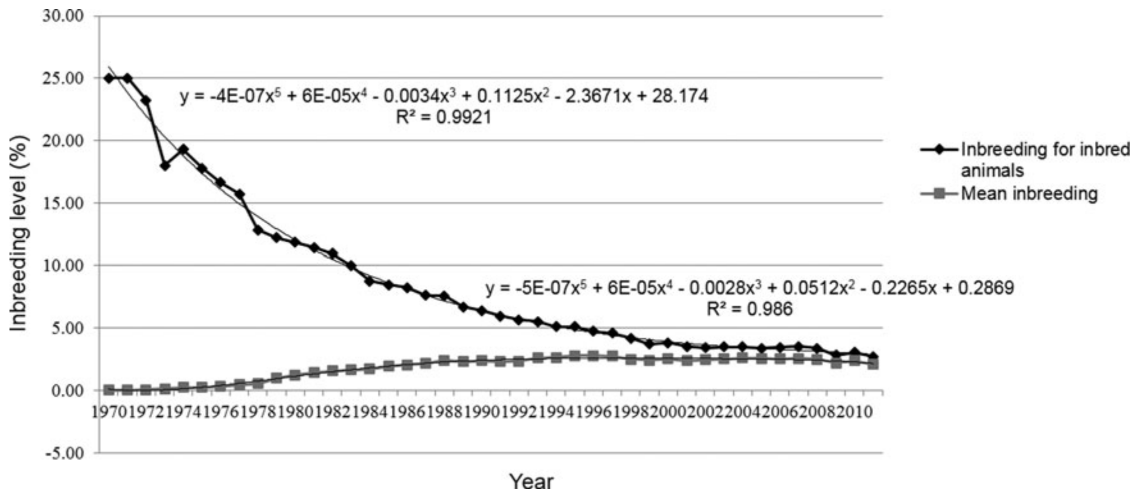

Figure 3. Mean inbreeding level per year for whole pedigree data and mean inbreeding level per year for inbred animals

(1998) and within the 25–255 range of effective population size that was suggested as being critical for maintaining fitness by Meuwissen and Woolliams (1994). The N_e estimate of the Afrikaner was large when compared with some international breeds. Mc Parland *et al.* (2007) estimated N_e sizes of 64, 127 and 75 for Irish Herefords-, Simmental- and Holstein–Friesian breeds, respectively, whereas that of Italian beef cattle breeds were in the range from 122 to 138 (Bozzi *et al.*, 2006). Estimates of N_e for Danish dairy cattle populations ranged from 49 to 157 (Sørensen, Sørensen and Berg, 2004). Pedigree analysis on the Afrikaner cattle population yielded levels of inbreeding that appear to be at acceptable and manageable levels, especially when compared with international breeds such as the Holstein–Friesian.

The comparatively low levels of inbreeding observed in Afrikaner cattle could be due to random mating processes or outcrossing that were induced within the herds. The introgression project may have contributed to keep inbreeding in the Afrikaner population at low levels. As an additional consequence, the relatedness between the animals decreased. The Afrikaner cattle population in study has an acceptable level for the estimated effective population size. The low inbreeding levels confirm the relatively high effective population size. The implication of a high effective population size is that more animals are available for the selection, whereas inbreeding can be contained.

Conclusions

Pedigree analysis on the Afrikaner cattle population yielded levels of inbreeding that appear to be at acceptable and manageable levels. The inbreeding of the Afrikaner breed has been low even though the number of animals has decreased due to the popularity of exotic and composite breeds found in South Africa. The current study provided useful results than can be utilized by farmers and the Afrikaner Breeders' Society. The results of this study indicate that there is sufficient variation within the Afrikaner breed of cattle that will allow it to expand into the diverse markets that exist both within and beyond the boundaries of South Africa, especially in the era of climate change. The results also indicate that the breed is in a favourable position to continue countering the undesirable effects of inbreeding.

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Morphometrical and production traits of Bengal sheep in West Bengal, India

Sandip Banerjee
School of Animal and Range Sciences, Hawassa University, Ethiopia

Summary
The study was conducted to phenotypically characterize the Bengal (Desi) sheep in some purposively selected villages of Nadia and Murshidabad districts of West Bengal, India. The Bengal sheep is reared as mutton sheep and has not been studied or characterized. Qualitative (coat colour and tail type) and quantitative (height at withers, height at rump, chest circumference, paunch girth, oblique body length, head length, head width, ear length, horn length, shoulder width, ear width, pelvic width, canon length, length of the fore leg, length of the hind leg, fore canon circumference, neck circumference, neck length, body weight) traits were included in the study. Phenotypic traits indicated that the sheep is of a small, thin tailed type adapted to grazing in water logged areas and lowly to moderately prolific. The structural indices indicate that the sheep is forward aligned, robust and rectangular in shape; it is well balanced and adapted for humid climates. The wool is coarse and hairy type, used for making blankets and durries. The reproductive parameters indicate that the age at first service was 295 days for ewes and 252 days for rams while the age at first lambing averaged around 425 days. Conservation efforts and genetic characterization are needed to maintain the breed purity and further studies regarding the carcass and mutton quality traits need to be carried out

Keywords: *Bengal sheep, morphometrical characterization, reproduction, structural indices wool quality, West Bengal, India*

Résumé
L'étude a été menée dans le but de caractériser phénotypiquement les moutons du Bengale (Desi) dans certains villages sélectionnés intentionnellement dans les districts de Nadia et Murshidabad en Bengale Occidental, Inde. Les moutons du Bengale sont élevés pour sa viande et n'ont pas été étudiés ou caractérisés. Cette étude comprend aussi bien des paramètres qualitatifs (couleur de la robe et type de queue) que quantitatifs (hauteur au garrot, hauteur à la croupe, périmètre thoracique, tour du ventre, longueur latérale du corps, longueur et largeur de la tête, longueur des oreilles, longueur des cornes, largeur des épaules, largeur des oreilles, largeur du bassin, longueur des canons, longueur des pattes avant et arrière, tour des canons antérieurs, tour et longueur du cou, poids corporel). D'après les paramètres phénotypiques, il s'agit de moutons de petite taille à queue fine adaptés au pâturage dans des zones inondées et avec une prolificité moyenne – faible. Les indices structuraux révèlent que les moutons présentent un corps nivelé, dirigé vers l'avant, de constitution robuste et forme rectangulaire. Ce sont des animaux équilibrés et adaptés aux climats humides. La laine, grossière et avec des mèches, est utilisée pour la confection de couvertures et tapis. D'après les paramètres reproductifs, l'âge à la première saillie a été de 295 jours pour les brebis et de 252 jours pour les béliers alors qu'en moyenne l'âge à la première mise bas a été d'environ 425 jours. Les efforts de conservation et de caractérisation génétique s'avèrent nécessaires pour maintenir la pureté de la race. En outre, il faudra mener, dans le futur, des études d'évaluation de la qualité de la carcasse et de la viande.

Mots-clés: *moutons du Bengale, caractérisation morphométrique, indices structuraux, qualité de la laine, reproduction, Bengale Occidental, Inde*

Resumen
El estudio fue llevado a cabo con el fin de caracterizar fenotípicamente el ganado ovino Bengala (Desi) en algunos pueblos seleccionados intencionadamente en los distritos de Nadia y Murshidabad en Bengala Occidental, India. El ganado ovino Bengala se cría por su carne y no ha sido estudiado o caracterizado. En este estudio se incluyeron parámetros cualitativos (color de la capa y tipo de cola) y cuantitativos (altura a la cruz, altura a la grupa, circunferencia torácica, contorno de la panza, longitud lateral del cuerpo, longitud y anchura de la cabeza, longitud de las orejas, longitud de los cuernos, anchura entre espaldas, anchura de las orejas, anchura de la pelvis, longitud de las cañas, longitud de las patas delanteras y traseras, circunferencia de las cañas delanteras, circunferencia y longitud del cuello, peso corporal). Los rasgos fenotípicos indicaron que se trata de ovejas de pequeño tamaño con cola fina adaptadas al pastoreo en áreas inundadas y con una prolificidad media-baja. Los índices estructurales muestran que las ovejas presentan un cuerpo nivelado dirigido hacia delante con constitución robusta y forma rectangular. Son animales equilibrados y adaptados a los climas húmedos. La lana, basta y con mechones, se utiliza para la confección de mantas y alfombras. De acuerdo con los parámetros reproductivos, la edad al primer servicio fue de 295 días para las ovejas y de 252 días para los carneros mientras que la edad media al primer parto rondó los 425 días. Los esfuerzos para la conservación y la caracterización genética son necesarios para mantener la pureza de la raza. Asimismo, son precisos futuros estudios que evalúen parámetros de calidad de la canal y de la carne.

Correspondence to: S. Banerjee, B-1/87, Kalyani, Nadia West Bengal, 741235, India. emails: sansoma2003@yahoo.co.in, sansoma2003@gmail.com

Palabras clave: *ganado ovino Bengala, caracterización morfométrica, índices estructurales, calidad de la lana, reproducción, Bengala Occidental, India*

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Introduction

The need for characterization of livestock breeds is a cornerstone for understanding their uniqueness and ability to thrive under various agro climates. The "phenotype" of an animal is the resultant of the genetics and its peerless blending with the environment where it thrives. The phenotype is further subjected to the social and aesthetic relationships of the owners and the aim for which they were developed (Boettcher, Ajmone-Marsan and Lenstra, 2010). Phenotypic characterization is all the more important for livestock that can thrive well under changing climatic conditions and in unfavourable places (FAO, 2015). "Phenotypic characterization of livestock generally refers to the process of identifying distinct breed populations and describing their external and production characteristics within a given production environment", FAO (2012). In many developing nations there is a lack of information on the population fragmentation, sub populations and geographically isolated populations. Generally such populations/breeds/types are generally reported to as non-descript/ traditional, as information on the inventories of these population are by and large non-existent. However, over the years new breeds are being identified (e.g. Banerjee and Banerjee, 2004, Wuletaw *et al.*, 2008). Thus, in such regions it becomes necessary to phenotypically characterize the livestock before applying advanced characterization techniques (FAO, 2012). Such evolutions are generally based on several criteria viz. the reasons for their domestication, migrations, genetic and geographical isolations, uniqueness of their products, selective breeding's and admixture of populations. The attempts to phenotypically classify the sheep population have been made in the past in India, however the animals were limited to single populations (Yadav *et al.*, 2013). The sheep breeds reared in the area are colloquially known as Desi bhada (native sheep). The conservation efforts of Bengal sheep has to be initiated as the breeding tract of sheep adjoins with that of the Dumka (Chottanagpuri) sheep reared in the adjoining state of Jharkhand and hence there are chances of the breed losing its niches because of the crossing with the Dumka sheep. Trading of Dumka sheep (to be further sold for mutton to the metros) takes place in large numbers in the studied districts. Thus, breeding between Bengal and Chottanagpuri sheep breeds cannot be ruled out however the respondents are well aware of the phenotypic attributes of the two types.

The study was thus, conducted to phenotypically characterize the Bengal breed of sheep. The Bengal sheep is reared primarily as a mutton sheep with very little value being given to its coarse fleece. Phenotypic as well as genetic characterization of Bengal sheep has yet to be carried out and the breed is not mentioned in the list of Indian sheep breeds. Furthermore the data was used to calculate some important morphometrical indices besides studying some important reproductive and wool quality parameters of the sheep.

Materials and Methods

The state of West Bengal is situated between 85° 50′ and 89° 50′ E longitude and 21° 38′ and 27° 10′ N latitude in the eastern part of India. Although, the state has varied agro climatic conditions, the breeding tract of Bengal sheep is by and large hot and humid. There are two distinct sheep breeds reared in the state viz. Garole and Bengal, while two more sheep breeds Sahabadi and Dumka have their breeding tract which extends from the adjacent states of Bihar and Jharkhand to the bordering districts of West Bengal. Garole sheep is reared in the coastal districts of 24 Parganas (South), Midnapur (East), some parts of 24 Parganas (North), and northern districts of Jalpaiguri and Cooch Behar, Banerjee, Galloway and Davis (2011). The breeding tract of Bengal sheep extends from the districts of Uttar Dinajpur (25°11′ N to 26°49′ N latitude and 87° 49′ E to 90°00′ E longitude), DakshinDinajpur (26°35′ 15″ N to 25°10′ 55″ N latitude and 89°00′30″ E to 87° 48′ 37″ E longitude) Malda (24°40′20″ N to 25° 32′08″ N latitude and 88°28′10″ E to 87°45′50″ E longitude), Murshidabad (24° 50′20″ N to 23°43′30″ N latitude and 88° 46′00″ E to 87° 49′17″ E longitude) and Nadia (22° 53″ and 24°11″ N latitude and 88°09″ and 88°48″ E longitude) and adjoining districts of Bangladesh. The present study was initiated to characterize the Bengal breed of sheep from diverse populations reared in two districts (Murshidabad and Nadia) of the state of West Bengal.

The study was conducted in some purposively selected villages of Murshidabad and Nadia districts of West Bengal, (Table 1). The villages were selected based on the population of the Bengal sheep they have, the respondents too were selected purposively, villagers who had been rearing sheep for more than 5 years were identified, and later 50 percent of the identified villagers were randomly selected for the study. Prior to the study the villagers were made to understand the purpose of the study in local language. A semi structured questionnaire was prepared which was later pretested on a few respondents and modified

Table 1. Some geographical parameters of the studied locations and the sheep population of the area.

District	Block	Panchayat	Households surveyed	Annual temperature (°C)	Relative humidity (%)	Meters above mean sea level	Sheep population	Indigenous sheep population (district)	Reference
Murshidabad	Bharatpur- 1	Amlai	20	15.6–35 (winter–summer)	58–80	19	2 491	113 918	DARH (2006a)
	Khargram	Moregram	22				3 895		
	Burwan	Sahora	25				2 914		
	Sagardighi	Balia	25				4 493		
	Beldanga-2	Rampara-1	20				2 449		
Nadia	Nakashipara	Birpur-1	22	15.6–35 (winter–summer)	58–80	14	1 364	12 696	DARH (2006b)
	Nabadwip	Sawarupgunj	25				706		
	Tehatta-2	Palsunda-2	20				270		
	Haringhata	Birohi-1	22				97		

accordingly. The questioner was then translated to Bengali (the local language spoken in the area) for their better understanding. The questions were asked to all the family members who are engaged in ovine husbandry. The numbers of households surveyed per village are presented in Table 1. Separate questionnaire was also developed, pretested and translated in Bengali for those engaged in trading of the sheep and fleece collectors. The numbers of traders and fleece collectors at Beldanga (Murshidabad) and Nakashipara (Nadia) livestock markets were 17; 11 and 14; 9, respectively.

The sheep in the study area are housed in makeshift houses often made of bamboo and mud while in some places the sheep are housed in the verandas adjoining the houses of their owners; this is done in order to minimize predatory and theft related losses (Figure 1). Some of the respondents also rear the sheep along with other livestock, this is done especially when the flock size is diverse and moderately large (Figure 2). The Bengal sheep are reared under semi-intensive system of management and are rarely provided any supplementary feed. These sheep are often seen grazing in marshy lands (Figure 3).The most common grasses on the natural pastures are *Cynodon dactylon, Urochloa mutica* while the farmers at times may provide leaves of *Artocarpus heterophyllus, Musa paradisiacal, Leucaena leucocephala, Magnifera indica and Bambusa tulda*. The leaves are provided when there is lack of grazing facilities or when the sheep are unable to go for grazing which is common during the heavy monsoon rains. Vegetable peels and rice gruel are at times provided to the ewes with lambs at foot that are unable to go for grazing or those nursing many lambs.

The sheep droppings are used to manure kitchen gardens. The day to day husbandry activities (cleaning the house, caring for the lambs) of the sheep are carried out by the females and children of the household. The morphometrical measurements considered in the study were, Height at withers (HW), Height at rump (HR), Chest circumference (CC) , Paunch girth (PG), Oblique body length (OL), Head length (HDL), Head width (HDW), Ear length (EL), Horn

Figure 1. Sheep housed in a veranda.

Figure 2. Sheep housed with cattle.

length(HoL), Shoulder width (SW), Ear width (EW), Pelvic width (PW), Canon length (CL), Length of the fore leg (FL), Length of the hind leg (HL), Abdomen girth (AG), Fore canon circumference (CAC), Neck circumference (NC), Neck length (NL) and Body weight, (BW, assessed using a suspended balance with an error margin of ±100 g). The methods used for the measurements were carried out according to the procedures reported by Macjowski and Zieba (1982) and presented in Table 2. The age of the sheep was estimated using their dentition (Charray, Humbert and Leif, 1992) and also the respondents recall method although the study encompassed only adult sheep (aged more than 1 year). The morphometric indices, were calculated from the phenotypic measurements (Table 3). The wool quality parameters (staple length, crimp, percentage of fibre and average fibre diameter (hairy, hetero and wooly), scouring yield and wool wax were assessed according to the methods suggested by Dagur (1996), von Bergen (1963) and Bureau of Indian Standard (BIS, 1989). The fibres were collected according to the methods suggested by Pokhrana *et al.* (1974). The fibre diameter was assessed using ocular micrometre using a magnification of 40X through a monocular microscope.

Figure 3. Bengal sheep grazing on marshy lands.

The data were analysed statistically using SPSS v 12 (2003) (for Windows). The data were analysed using descriptive statistics (Mean ± SD) and the means were compared using Duncan's Multiple Range test, the values were considered significant ($P < 0.05$).

Results and Discussions

General husbandry practices

The results of the study indicated that average flock size was 4.5 ± 2.5 heads, respondents having flocks as large as 25 heads in the area. Most of the rearers were small and marginal farmers besides; some landless labourers too were among the respondents. The average flock size are in consonance with the findings of Bose, Duttagupta

Table 2. Method of assessing different morphometrical measurements.

Traits	Measurements
Height at withers	Distance from the highest point of the wither to the ground
Height at rump	Distance from the highest point of the rump to the ground
Chest circumference	The circumference of the chest at the widest point
Paunch girth	The circumference at the widest point of the abdomen just behind the last ribs
Body length	Distance from the point of the shoulder to the pin bone
Length of head	Distance between the midpoint of the two polls and the muzzle
Head width	Width between the two polls
Ear length	The length of the external ear from the base to the tip
Horn length	The length of the horn from the polls to the tip
Shoulder width	Width of the thorax at the widest point just behind the elbow
Ear width	Width of the broadest part of the external ear
Pelvic width	The widest point between the two pelvic bones
Height at sternum	Height of the highest point of the sternum taken from the floor, taken using a scale.
Canon length and circumference	Length of the metatarsus and its circumference at the widest point
Fore and Hind leg length	Fore leg length comprises of the length of the humerus, radius and ulna, carpals and metacarpals, to the tip of the hoof while the hind leg length comprises the length of the femur, tibia and fibula, tarsals, metatarsals, to the tip of the hoof
Neck length and circumference	Length of the cervical vertebrae from the atlas vertebrae till prior of the first thoracic, while the circumference of the neck at its widest part

Table 3. Methods of calculating the structural indices.

Indices	Measurements
Height index[1]	Height at withers/body length × 100
Over increase index[1]	Height at rump/height at withers × 100
Height slope[2]	Wither height – rump height
Length index[2]	Body length/wither height
Body Weight: index[2]	Body length × chest depth × (hip width + chest width)/2)
Index of compaction[3]	Chest circumference/height at withers × 100
Index of chest compression[3]	Chest circumference/body length × 100
Cephalic index[4]	Head width × 100/Head length
Body index[4]	Body length × 100/Chest girth(When this measure is > 0.90, the animal is longiline; between 0.86 and 0.88 is medigline, and < 0.85, it is brevigline)
Dactyl thorax index[4]	CC/HG. The DTI may not be more than 10.5 in light animals, up to 10.8 in intermediary; up to 11.0 in light meat animals and up to 11.5 in heavy meat type. This index also indicates thoracic development
Weight[4]	HG^3*80. Weight above 45 kg correspond to large or hypermetric animals, between 35 and 55 kg medium or eumetric animal and < 35 kg, small or elipometric animals
Transverse pelvic[4]	Pelvic width × 100 /Height at rump
Metacarpal coastal[4]	Cannon bone circumference × 100/rib distance
Body ratio[4]	Height at withers/Height at Rump. If the withers are lower than the rump, the animal is low in front and vice versa
Compact index [4]	(Weight/Height at Sterum)/100; indicates how compact the animal is. Meat type animals have values above 3.15. Values close to 2.75 indicate dual purpose and close to 2.60 indicate animals more suitable for milk
Compact index[4]	Weight/(Height at sternum-1)/100. This index also indicates the aptitude of the animal. Values above 9.5 indicate meat type animals from 8.0 to 9.5 indicates animals suitable for dual purpose and from 6.0 to 7.75 indicates milk type animals
Pectoral Index[5]	((Height at Sternum + Height at Rump)/2)/height at withers. When the back height is less than the sternum height, the animal is considered “far from ground”
Thoracic development[5]	Chest circumference /Height at sternum. This indicates thoracic development of the animal, with values above 1.2 indicating animals with good thoracic development
Conformation index[5]	Chest $circumference^2$/Height at sternum. The greater the index, the more robust the animal, also called Baron & Crevat

[1]Alderson, 1999.
[2]Szabolcs *et al.* (2007).
[3]Marković, Marković and Radonjić (2012).
[4]Edilberto *et al.* (2011).
[5]Concepta *et al.* (2008).

and Maitra (1999) and Banerjee (2003), Biswas (2010) for sheep flocks reared in Sunderban region of West Bengal.

The Bengal sheep seem to be quite tolerant towards fleece and foot rot as they are often seen grazing in the marshy land unsuitable for agricultural operations (Figure 3). The trait is similar to that of Garole sheep as has been reported by Banerjee and Banerjee (2000), Banerjee *et al.* (2011). Children and family elders (who are unable to participate in agricultural operations) are traditionally entrusted to overlook the grazing of the sheep; the findings are in agreement with the observations of Saddullah (2000). However, now a days professional grazers locally known as “rakhals” (Figure 4), are employed by most of the farmers to take care of the grazing. The respondents reported that the body condition and productivity of the sheep can improve substantially if they are provided with some sort of supplementary feed. The rearers however are generally not able to provide them with the necessary supplements owing to lack of financial resources. Salim *et al.* (2002) too indicated that native sheep of Bangladesh responded well to concentrate supplement which helped in improving both their productive and reproductive traits. It has also been observed that many of the sheep in the study areas suffer from mineral and vitamin deficiencies as has been reported earlier by Banerjee and Banerjee (2004) and Banerjee (2005) who reported zinc and also copper deficiency in sheep reared in Nadia district of West Bengal.

The respondents also indicated that the most commonly occurring diseases in the area are diarrhoea (in the summer and monsoon season) followed by respiratory distress (of unknown origin). These diseases occur mostly among the lambs (during the monsoon and winter seasons) leading to high mortality. Helminth infestation too is common, infected sheep usually become weak and debilitated, the observations are in accordance with the findings of Bose *et al.* (1999) and Hassan and Talukder (2011).

The rearers mostly rely on ethno veterinary medicines (77.5 percent of the respondents) which are locally available and relatively cheap. When the sheep are too sick they prefer to sell them to the butchers at a relatively cheap price. It was also observed that few respondents avail the services of the veterinary clinics; the primary reason was the high cost and non-availability of the medicines. Hence, the rearers mostly use ethno veterinary medicines; the use of ethno veterinary medicines have also been reported by Amin *et al.* (2010) and Ghosh (2008). The respondents reported that if the sheep are allowed to graze on natural pastures they rarely fall ill. The sheep are able to graze on the naturally growing

Figure 4. Professional grazers with sheep.

Figure 5. Watering point for Bengal sheep.

medicinal herbs. The respondents also reported that the livestock often fall ill when their normal grazing schedule is disturbed which often corresponds to the monsoon season. The findings are in accordance with those of Banerjee and Banerjee (2004), Villalba *et al.* (2010) and Villalba and Landau (2012) who reported that if provided a choice livestock occasionally consume medicinal plants which grow along with the pasture grasses. The medicinal plants which were once commonly available are now rarely seen in the grazing areas. The natural pastures are mostly degraded and overgrazed or have been overrun by many invasive species of grasses; the observations are in accordance with those of Erenstein *et al.* (2007) and Dixit *et al.* (2013). One of the reasons for high incidences of helminth infestation can be attributed to consumption of water from stagnant pools and other water bodies (Figure 5).

The respondents indicated that the sheep are sold only when they are sick, barren, old or when the family is in need of cash. The respondents also indicated that they prefer not to sell the lambs until they are 6 months old. The price of a ram is decided by the family head who usually sell them directly to the weekly market locally known as “haat”. The sheep passes through several hands by the time it reaches the butchers. However, there are instances when the primary collectors (middlemen) purchase the animals at the farm gate; in such instances the price paid is usually lower than that of the markets. The middlemen collect anything from three to 20 rams (Figure 6) and sell to the nearby livestock markets from where the traders further purchase the sheep to be transported to metros like Kolkata; the observations are in accordance with the findings of Bose *et al.* (1999). The study also indicated that unlike the bucks the rams are rarely castrated. The sheep change hand three to four times before they are ultimately sold to the butchers, the transportation of the animals are not only stressful but also at times lead to mortality, this in turn affects the quality of the carcass (meat) and skin; the observations are in accordance with the reports of Sagar and Biswas (2008), Viroji Rao, Thammi Raju, and Ravindra Reddy (2008), SA PPLPP (2011).

The price of the sheep is decided by visual assessment of its body weight and mutual consent of the seller and the buyer. The average price of a yearling ram (body weight (BW) 14.5 ± 1.5 kg) of the rams of Bengal breed at Beldanga and Nakashipara livestock market as on August 2014 was estimated to be Rs. 1 950 (US\$1 = Rs. 60.00) while the farmers generally receive Rs. 1 570, respectively. The price of ewes is generally less (15–20 percent) compared with that of the rams. The prices of the sheep fluctuate erratically between seasons and are

Figure 6. Sheep collected by middlemen for sale.

significantly influenced by festivals and disease outbreak; the findings are in accordance with that of Saddullah (2000).

The predominant coat colour of Bengal sheep (Figures 7 and 8) are cream, brown, mixed (brown/ black and cream) and black. Around 65 percent of the sheep had cream coat colour. The observations are in accordance with the reports of Pervage *et al.* (2009) for Barind sheep from Bangladesh. The Bengal sheep is of thin and short tailed type, the tail length varies from 8.5 to 10.2 cm averaging around 9.2 cm for both ewes and rams. The tail length values are in close agreement with the findings of Sharma *et al.* (1999), Banerjee (2003) for Garole sheep and to those reported by Hassan and Talukder (2011) for Barind sheep of Bangladesh. The average HW of rams (Table 4) are similar to that of the Garole sheep (Banerjee and Banerjee, 2000, Sahana, Gupta and Nivsarkar, 2001 and Banerjee, 2003) and Barind sheep of Bangladesh Pervage *et al.* (2009). The results indicated there was a variation ($P < 0.05$) between locations. The rams reared in Nakashipara (N) had significantly lower values (*r* age groups 1 and 2) when compared with those reared at Khargram (K) and Sagardighi (S). While the HR values were higher among the rams reared at K and S for the same age groups.. The CG was lower ($P < 0.05$), among the rams reared at K in comparison with those reared in N. The PG was lower in rams reared in K and N (age group1) and in K (age groups 2 and 3). The HdL, HdW, EL of the rams did not vary ($P < 0.05$) across the locations studied. The BL was lowest in the rams reared in S (age groups 2 and 3). The HW, CC, PG and BL values find consonance with the observations of Barind sheep (Pervage *et al.*, 2009 and Hassan and Talukder, 2011) and Garole sheep (Banerjee, 2003). The horn length (HoL) was lower ($P < 0.05$) for the rams reared in N and S (age group1) while lower ($P < 0.05$) values were observed in rams reared in K and S (age group 3). The SW was lower ($P < 0.05$) among the rams reared in K and S (age group 3). The PW too varied ($P < 0.05$) among the rams (age group 1 and 3) with lower values observed among those reared in S. The CL was lower ($P < 0.05$) among the rams (age group 1) and reared in S, while it did not vary significantly across the locations for rams of other age groups. The fore leg length (FL) too varied ($P < 0.05$) among the rams reared in the different locations and also across age groups, the values were lowest (age group 1 and 2) among the rams reared in K while it was lowest for those reared in S for age group 3. The hind leg length (HL) too varied ($P < 0.05$) among the rams reared at the different locations; it was lower ($P < 0.05$) among those reared at K, across all the age groups. The BW of the rams did not vary ($P < 0.05$) across the different locations (within a particular age category). The BW of the rams are in close accordance with those reported by Pervage *et al.* (2009) for Barind sheep of Bangladesh but lower than those reported by Hassan and Talukder (2011).

Figure 7. Coat colours of Bengal sheep.

The results pertaining to the morphometrical traits of the ewes are presented in Table 5. The results indicated that the HW did not vary among the ewes reared in the three locations (age group 1), while it varied ($P < 0.05$) across the locations. The ewes reared at K and S had lower values (age group 2) while it was lower among the ewes reared at K (age group 3). The HR varied among the ewes reared in the three locations and across the different age groups. Lower values were observed among the ewes reared in K (age group 1) and in K and S (age groups 2 and 3), respectively. The CC and PG too varied across the study areas, lower values were observed among the ewes reared at K (age groups 1 and 2). The BL too varied ($P < 0.05$), across the three locations and also across the age groups. The ewes at K had lower values (age group 1), while for age groups 2 and 3 it was lower among the ewes reared in S. The HDL and HDW too varied ($P < 0.05$), across the study areas and among the age groups. The BL was lower among the ewes reared in K (age groups 1 and 2). The SW too indicated variation ($P < 0.05$) across locations and also across different age groups. It was lower among the ewes raised in K (age groups 1 and 2) and in S (age group 3). The PW too varied ($P < 0.05$), across locations and also among age groups .The values being lower among ewes reared at K and S (age groups 1 and 2). The FL and HL were lower ($P < 0.05$) among the ewes reared at K and S. The NCM and NL too varied ($P < 0.05$) among the ewes of age group 3. The NCM being lower for those reared at S and N. The NL was lower among the ewes raised at K and N, respectively.

It was observed that 9.2 percent of the sheep had rudimentary earlobes. Similar observations too have been reported by Bose *et al.* (1999), Banerjee and Banerjee (2000) and Banerjee (2003) in Garole sheep. The rams are horned while the ewes are polled. The horns are oriented upward, and backward, the whorl is open type, the average HoL are similar to those reported by Pervage *et al.* (2009) for Barindsheep.

Table 4. Values (Mean ± SD) of some morphometrical measurements of rams of Bengal breed across the various locations and age groups.

Age group traits	1			2			3		
Observations	Khargram 27	Sagardighi 22	Nakashipara 26	Khargram 22	Sagardighi 25	Nakashipara 19	Khargram 18	Sagardighi 20	Nakashipara 22
HW	44.1 ± 1.2^{b}	43.6 ± 4.8^{b}	41.2 ± 0.2^{a}	45.2 ± 1.5^{b}	45.1 ± 1.4^{b}	42.5 ± 0.6^{a}	$47.8.5 \pm 1.1$	47.9 ± 0.7	46.5 ± 0.3
HR	48.8 ± 1.9^{b}	46 ± 3.7^{b}	42.0 ± 1.0^{a}	48.2 ± 1.5	48.0 ± 0.4	49.0 ± 0.6	50.2 ± 1.2	49.2 ± 1.8	50.7 ± 0.9
CC	55.9 ± 3.3^{a}	57.8 ± 1.7^{ab}	62.3 ± 1.0^{b}	58.8 ± 1.5^{a}	60.8 ± 0.8^{ab}	66.3 ± 0.9^{b}	74 ± 0.8	75.3 ± 1.2	73.1 ± 0.8
PG	49.2 ± 6.7^{a}	52.1 ± 2.5^{b}	50.8 ± 4.3^{a}	57.9 ± 1.9^{a}	59.6 ± 1.5^{ab}	63.1 ± 0.8^{b}	61.0 ± 14^{a}	64 ± 1.6^{b}	65.3 ± 1.1^{b}
HS	30.1 ± 1.4	27 ± 0.6	26.7 ± 1.0	29.2 ± 1.2	28.7 ± 0.8	30.1 ± 1.9	31.8 ± 1.1	30.9 ± 0.8	32.5 ± 1.3
BL	42.4 ± 0.7	40.0 ± 2.4	42.5 ± 2.3	46.7 ± 0.6^{b}	44.8 ± 0.2^{a}	46.1 ± 0.8^{b}	49.9 ± 2.0^{ab}	47 ± 1.3^{a}	51.6 ± 1.2^{b}
HDL	14.2 ± 2.0	14.5 ± 0.6	14.7 ± 1.8	15.9 ± 2.2	15.4 ± 0.8	16.7 ± 0.6	16.2 ± 0.4	17.0 ± 1.1	17.2 ± 1.2
HDW	7.9 ± 1.5	8.8 ± 1.1	8.9 ± 0.8	9.2 ± 1.3	9.4 ± 1.9	9.8 ± 0.7	10.2 ± 0.8	9.9 ± 1.2	9.9 ± 0.5
EL	3.6 ± 1.5	4.3 ± 2.2	3.9 ± 1.8	5.2 ± 1.3	4.6 ± 1.1	4.9 ± 2.1	4.5 ± 1.6	4.9 ± 1.1	5.5 ± 0.6
HoL	6.2 ± 1.3^{b}	5.2 ± 2.1^{a}	4.9 ± 1.3^{a}	4.5 ± 1.1	5.1 ± 0.9	4.5 ± 0.7	6.5 ± 1.2	5.9 ± 2.1	6.5 ± 1.5
SW	12.8 ± 1.7	11.4 ± 1.7	11.8 ± 1.6	13.2 ± 1.3	14.1 ± 0.7	14.6 ± 1.7	15.5 ± 1.6^{a}	16.1 ± 1.3^{a}	18.5 ± 1.4^{b}
EW	3.3 ± 0.8	3.8 ± 1.3	4.6 ± 1.4	4.2 ± 1.3	4.1 ± 0.9	3.8 ± 0.8	4.1 ± 0.4	4.4 ± 1.4	4.7 ± 1.2
PW	13.6 ± 1.8^{ab}	11.5 ± 1.6^{a}	14.1 ± 1.2^{b}	15.5 ± 1.1	15.1 ± 1.7	15.5 ± 1.8	15.4 ± 1.5^{b}	14 ± 1.3^{a}	15.3 ± 1.4^{b}
CL	6.9 ± 2.3^{a}	7.4 ± 2.7^{ab}	8.5 ± 1.2^{b}	10.5 ± 1.5	$10.6 \pm .0.5$	$9.3 \pm .0.6$	9.2 ± 1.3	9.0 ± 0.3	10.1 ± 0.5
FL	37.8 ± 0.8^{a}	45.6 ± 2.2^{b}	44.4 ± 0.3^{b}	44.0 ± 1.3^{a}	45.7 ± 0.1^{ab}	47.2 ± 0.8^{b}	48.5 ± 1.1^{b}	46.5 ± 1.3^{a}	49.3 ± 2.3^{b}
HL	39.4 ± 1.8^{a}	48.6 ± 1.9^{b}	49.2 ± 1.6^{b}	48.1 ± 1.6^{a}	51.9 ± 1.5^{b}	50.1 ± 1.8^{b}	51.1 ± 1.0^{a}	50.6 ± 1.3^{a}	55.8 ± 1.6^{b}
CAC	6.4 ± 1.1	6.6 ± 0.5	6.0 ± 0.8	6.2 ± 1.1^{a}	7.0 ± 1.6^{ab}	7.8 ± 0.8^{b}	6.8 ± 1.2^{a}	7.3 ± 1.0^{b}	7.9 ± 0.6^{c}
NCM	14.2 ± 2.5	14.7 ± 1.2	15.7 ± 1.8	15.5 ± 0.9	15.9 ± 1.1	16.0 ± 0.2	16.6 ± 1.0	16.5 ± 1.0	16.3 ± 1.4
NL	13.7 ± 0.5	14.6 ± 0.6	14.9 ± 0.5	15.6 ± 0.4	15.2 ± 0.3	15.5 ± 0.4	15.5 ± 0.3	16.1 ± 0.4	16.2 ± 0.3
BW	16.9 ± 0.5	15.2 ± 1.9	17.4 ± 2.1	20.4 ± 1.2	19.1 ± 2.8	18.2 ± 2.0	22.9 ± 0.2	25.0 ± 1.8	22.8 ± 1.6

^{a,b,c}values across rows in a particular age groups are significantly different ($P < 0.05$), (>1 but <2 years, 1), (>2 but <3 years, 2) and (>3 but <4 years, 3).

HW, height at withers; HR, height at rump; CC, chest circumference; PG, paunch girth; BL, body length; HDL, head length; HDW, head width; EL, ear length; HoL, horn length; SW, shoulder width; EW, ear width; PW, pelvic width; CL, canon length; FL, length of the fore leg; HL, length of the hind leg; CAC, fore canon circumference, NCM, neck circumference, NL, neck length; BW, body weight; All values in cms and BW (kgs).

Table 5. Values (Mean ± SD) of some morphometrical measurements of ewes of Bengal breed across the various locations and age groups.

Age group traits	1			2			3		
Observations	**Khargram 60**	**Sagardighi 59**	**Nakashipara 55**	**Khargram 39**	**Sagardighi 40**	**Nakashipara 45**	**Khargram 50**	**Sagardighi 45**	**Nakashipara 37**
HW	38.2 ± 2.3	38.4 ± 1.3	39.8 ± 1.1	38.0 ± 2.5^{a}	38.7 ± 0.5^{a}	41.6 ± 3.0^{b}	42.6 ± 2.9^{a}	43.5 ± 0.6^{ab}	44.6 ± 0.3^{b}
HR	40.7 ± 2.5^{a}	38.6 ± 1.3^{b}	40.3 ± 1.2^{b}	38.7 ± 2.8^{a}	39.2 ± 0.6^{a}	42.2 ± 2.9^{b}	45.2 ± 1.7	45.4 ± 1.6	46 ± 1.3
CC	59.3 ± 0.7^{a}	62.8 ± 1.8^{b}	65.1 ± 1.6^{c}	68.1 ± 1.4^{a}	65.2 ± 1.9^{a}	69.5 ± 1.8^{b}	71.3 ± 1.9	69.4 ± 2.9	73.6 ± 1.7
PG	54 ± 1.6^{a}	55.4 ± 3.7^{a}	59.4 ± 2.7^{b}	54 ± 1.9^{a}	59.2 ± 1.1^{b}	61 ± 1.7^{c}	63.3 ± 1.6	61.5 ± 0.5	64.5 ± 0.9
BL	42.6 ± 1.0^{a}	45.1 ± 0.5^{a}	41.4 ± 0.6^{b}	43.1 ± 1.6^{b}	44.8 ± 1.0^{a}	49.4 ± 1.7^{b}	50.4 ± 0.5^{b}	47.6 ± 0.7^{a}	50.8 ± 0.7^{b}
HS	25.2 ± 0.6	26.1 ± 1.2	25.9 ± 0.5	26.1 ± 0.7	27.2 ± 0.5	26.9 ± 1.2	27.6 ± 1.1	27.8 ± 1.2	28.2 ± 0.5
HDL	13.6 ± 0.7^{a}	14.6 ± 1.6^{b}	14.5 ± 1.2^{b}	13.9 ± 1.7^{a}	15.4 ± 1.3^{ab}	14.6 ± 1.2^{b}	14.1 ± 1.1	15.9 ± 1.4	15.7 ± 1.2
HDW	7.9 ± 1.9^{a}	8.0 ± 0.3^{b}	7.3 ± 1.3^{a}	8.2 ± 1.0^{a}	8.3 ± 0.8^{c}	8.2 ± 1.0^{b}	8.5 ± 0.12	8.2 ± 0.7	8.6 ± 0.5
EL	3.3 ± 1.1	3.9 ± 0.5	3.7 ± 0.8	4.2 ± 0.3	4.5 ± 0.5	4.5 ± 0.4	4.2 ± 1.3	3.5 ± 1.3	5.1 ± 0.8
SW	11.5 ± 0.8^{a}	10.9 ± 0.8^{a}	12.7 ± 1.1^{b}	12.3 ± 2.1^{a}	12.6 ± 1.0^{a}	13.9 ± 3.0^{b}	14.5 ± 1.2^{b}	14.4 ± 2.1^{a}	15.3 ± 1.3^{b}
EW	3.6 ± 0.5	3.9 ± 1.4	4.1 ± 1.1	4.1 ± 1.0	4.0 ± 0.8	3.6 ± 0.5	3.9 ± 0.2	4.1 ± 0.5	4.3 ± 1.0
PW	9.8 ± 0.8^{a}	9.3 ± 1.4^{a}	12.3 ± 0.2^{b}	12.0 ± 0.3^{b}	11.0 ± 0.3^{a}	13.0 ± 2.7^{b}	14.3 ± 1.2	13.6 ± 2.4	12.9 ± 1.2
CL	9.1 ± 1.5	9.5 ± 0.2	8.6 ± 0.1	9.5 ± 0.3	9.6 ± 1.3	9.9 ± 0.9	11.3 ± 1.1	11.2 ± 0.8	10.8 ± 1.6
FL	40.6 ± 0.3^{a}	39.7 ± 1.0^{a}	40.8 ± 1.8^{b}	42.3 ± 1.4^{a}	42.8 ± 1.5^{a}	43.6 ± 2.0^{b}	41.1 ± 1.8^{a}	41.9 ± 1.8^{a}	42.8 ± 1.3^{b}
HL	42.3 ± 0.4^{a}	43.6 ± 1.1^{a}	42.5 ± 0.5^{b}	44.5 ± 0.8^{a}	45.8 ± 1.2^{a}	43.2 ± 1.3^{b}	46.8 ± 1.4^{a}	46.9 ± 1.8^{a}	49.8 ± 2.7^{b}
CAC	6.2 ± 1.0	6.8 ± 0.6	6.4 ± 0.2^{a}	6.3 ± 0.4^{a}	8.4 ± 1.8^{b}	7 ± 0.6	6.8 ± 0.4	6.7 ± 0.6	6.7 ± 0.6
NCM	13.8 ± 0.4	13.5 ± 0.7	14.4 ± 0.5	14.9 ± 1.7	13.6 ± 2.3	14.8 ± 0.8	16 ± 0.6^{b}	14.5 ± 2.7^{a}	14.9 ± 1.8^{a}
NL	12.9 ± 0.2	13.8 ± 0.2	14.9 ± 1.9	14.8 ± 0.8	15.1 ± 2.1	15.1 ± 1.2	15.8 ± 1.3^{a}	14.7 ± 1.2^{b}	13.2 ± 0.3^{a}
BW	14.5 ± 1.5^{a}	16.1 ± 0.9^{b}	16.0 ± 1.6^{b}	17.1 ± 1.5	18.3 ± 0.5	19.7 ± 0.5	19.1 ± 1.4	23.4 ± 1.6	20.9 ± 1.3

^{a,b,c} values across rows in a particular age age groups are significantly different ($P < 0.05$), (>1 but <2 years, 1), (>2 but <3 years, 2) and (>3 but <4 years, 3).

HW, height at withers; HR, height at rump; CC, chest circumference; PG, paunch girth; BL, body length; HDL, head length; HDW, head width; EL, ear length; HL, horn Length; SW, shoulder width; EW, ear width; PW, pelvic width; CL, canon length; FL, length of the fore leg; HL, length of the hind leg; CAC, fore canon circumference; NCM, neck circumference; NL, neck length; BW, body weight. All values in cms and BW (kgs).

The results of the structural indices were calculated from the morphometrical traits with an aim to assess the functionalities of relationship that is attributed to some of the morphomerical traits. The values pertaining to the structural indices are presented in Table 6. It can be inferred from the results of the height index (HI) that the HW irrespective of the sexes is more or less similar to their BL. The results from the over increase index (OlI) indicates that the hind region are higher than the front. Thus, it can be inferred that the breed is not unbalanced. Studies by Edilberto *et al.* (2011) indicate that a balanced animal is known to have better production and health especially in uneven terrains.

The length index (LI) indicates that the sheep is longiline (>0.9) type, Edilberto *et al.* (2011). The height slope (HS) indicate that the slope is forward aligned. The body weight index (BWI) indicates that the sheep is mostly eumetric i.e. medium type of animals Edilberto *et al.* (2011). The index of compaction (IC) values is lower than those reported by Marković, Marković and Radonjić (2012) for Sora sheep. The IC values differed between sexes with values lower among the rams the difference may be attributed to higher CC in the ewes. The index of chest compaction (ICC) indicated that the body is more compact as the CC values are higher than the BL in both the sexes, indicating short but deep and rectangular shaped animals. The cephalic index (CeI) indicates the braquicephalic tendency in the breed. The body index (BI) indicates that the breed is breviline and sublongiline type. The dactyl thorax index (DTI) indicates that the breed is of intermediate to light type Edilberto *et al.* (2011). The BW of the rams and ewes indicate that the breed is of small orelipometric type as the values are mostly below 35 kg, Edilberto *et al.* (2011). The transverse pelvic (TrP) values indicate that the PW is less than the HR indicating that the ewes will have less chance of dystocia. The metacarpal coastal (MCC) are similar to those reported by Edilberto *et al.* (2011) for Creole goats. The body ratio (BR) indicates that the Bengal sheep is low in the front. The results for the compact index (CI-1) indicate that the Bengal sheep is primarily suited for meat type as the value for the trait is above 3.15, Edilberto *et al.* (2011). However, the results of the CI-2 indicate that the aptitude of the sheep and it is more of a dual type breed. The thoracic development (TD) values indicate that the Bengal sheep has a well-developed thoracic area while the conformation index values (CI) indicates that the Bengal sheep is a robust animal.

The HS varied between the locations and among the rams of the different age groups, the rams reared at N had lower values (age group 1), while higher values were observed among those reared at N (age group 3). The ICC too varied across the rams of different age groups and across the locations. The IC values too varied ($P < 0.05$), across the locations and across the age groups (1 and 2). Lower values were observed among the rams reared at K and S; the trend was similar for other traits viz. weight (W), TrP and relative body index (RBI). The TD values too differed for $P < 0.05$, across the study areas (age group 1), the rams reared at K having lower values. The result pertaining to CI too varied with $P < 0.05$ among the rams of all the age groups and was lowest among those reared at K.

The results pertaining to the structural index values of the ewes presented in Table 7 indicate that the HS values varied among the ewes of age group 1 the values were lower ($P < 0.05$) among those raised at S and N. The length index (LI) was lower ($P < 0.05$) among the ewes reared in K and N (age group 3). The CI indicates that the trait too varied ($P < 0.05$) among the ewes reared at the different locations and was lower among those raised at K, S and N for age groups 1, 2 and 3, respectively.

The fleece quality parameters (Mean ± SD) were assessed from 75 sheep and from both the sexes. The average staple length (SL) of the fleece was observed to be 7.4 ± 1.3 cms, finding consonance with the observations of Banerjee (2003, 2009; Garole sheep), Arora and Garg (1997; Jaisalmeri, Patanwadi, Hissardale, Deccani, Nali, Rampur Bushair and Pugal sheep), Gopalakrishnan and Morleymohanlal (1985; Magra sheep), Hassan and Talukder (2011; Barind sheep). The SL was higher than those reported by Pan and Sahoo (2003) in Garole sheep. The average numbers of crimp (3.3 ± 1.5/inch) finds similarity with the observations of Banerjee (2003, 2009), Hassan and Talukder (2011). The fleece is predominantly of hairy distantly followed by wooly and hetero types, respectively, (72.2 ± 1.8; 18.3 ± 1.2 and 9.5 ± 2.0) percent the findings are close to the reports of Hassan and Talukder (2011) for Jamuna, Barind and Coastal sheep breeds, respectively. The average hairy, hetero and wooly fibre diameters were 122.5 ± 10.2, 65.3 ± 32.1 and 49.7 ± 10.2 µm, respectively, similar values were reported by Banerjee (2003, 2009) in Garole sheep.

The scouring yield and wax content were assessed as 70.2 ± 5.5 and 2.9 ± 0.2 percent, respectively, the values were similar to those reported by Banerjee (2003, 2009). The fleece is traded for making coarse blankets and durries by some traders in the region. The price per clipping from an adult sheep is Rs. 25 (US$ = Rs. 60.00). The average clipping yield is estimated to vary between 350 and 500 g averaging to about 435 ± 50.2 g. The findings are in accordance with the findings of Banerjee (2003), Pan and Sahoo (2003), Pan *et al.* (2004), Hassan and Talukder (2011) and Banerjee *et al.* (2009). The variation in quality parameters may be attributed to genetic and non-genetic parameters, viz. nutrition and climate, the findings are in accordance with those of Smith and Purvis (2009), Sohail, Muhammad and Muhammad (2010) and Muhammad *et al.* (2012).

Reproductive parameters of Bengal sheep

The results pertaining to some reproductive traits of Bengal sheep indicated that the age at first service (AFS) was 295 days among the ewes and 252 days among the

Table 6. Values (Mean ± SE) of morphometrical indices of rams of Bengal breed across different locations and age groups.

Age group traits	1			2			3		
Observations	**Khargram 27**	**Sagardighi 22**	**Nakashipara 26**	**Khargram 22**	**Sagardighi 25**	**Nakashipara 19**	**Khargram 18**	**Sagardighi 20**	**Nakashipara 22**
HI	104.0 ± 5.1	109.1 ± 1.2	96.94 ± 1.7	96.8 ± 4.1	100.7 ± 5.1	92.2 ± 5.4	95.8 ± 2.9	101.9 ± 2.1	90.1 ± 1.4
OII	110.6 ± 2.9	105.5 ± 4.3	101.9 ± 5.2	105.9 ± 8.2	106.4 ± 4.6	115.3 ± 3.6	105.0 ± 5.2	102.7 ± 1.9	109.0 ± 3.7
HS	−4.7 ± 0.3[c]	−2.4 ± 0.02[b]	−0.8 ± 0.05[a]	−3.0 ± 0.01[a]	−2.9 ± 0.03[a]	−6.5 ± 0.06[b]	−2.4 ± 0.05[b]	−1.3 ± 0.02[a]	−4.2 ± 0.03[c]
LI	0.96 ± 0.02	0.91 ± 0.05	1.03 ± 0.07	1.03 ± 0.04	0.99 ± 0.03	1.08 ± 0.09	1.04 ± 0.02	0.98 ± 0.03	1.10 ± 0.02
BWI	38.3 ± 0.1	34.8 ± 0.3	42.2 ± 0.11	45.1 ± 0.12	42.3 ± 0.12	42.8 ± .0.4	47.9 ± 0.12	52.2 ± 0.13	49.0 ± 0.17
IC	126 ± 2.2[a]	132 ± 2.6[a]	151 ± 1.8[b]	130 ± 1.5[a]	134.8 ± 1.9[a]	156.0 ± 2.5[b]	154.8 ± 1.9	157.2 ± 2.2	157.2 ± 1.9
ICC	131.8 ± 1.7[a]	144.5 ± 1.3[b]	146.5 ± 2.3[b]	125.9 ± 2.9[a]	135.7 ± 1.5[b]	143.8 ± 2.2[c]	148.3 ± 1.7[b]	160.2 ± 1.4[c]	141.6 ± 2.4[a]
CeI	55.6 ± 0.7[a]	60.7 ± 1.6[a]	70.5 ± 0.5[b]	58.0 ± 2.1	61.0 ± 1.7	58.7 ± 1.9	63.0 ± 2.6	58.9 ± 3.4	57.5 ± 5.5
BI	75.8 ± 3.5	76.7 ± 3.9	68.2 ± 4.3	79.4 ± 2.4	73.5 ± 2.4	69.5 ± 2.6	67.3 ± 4.1	62.4 ± 2.1	70.1 ± 3.3
DTI	8.73 ± 0.7	8.75 ± 1.2	10.4 ± 1.4	9.5 ± 0.8	8.7 ± 0.6	8.5 ± 0.4	11.0 ± 1.6	10.3 ± 1.1	9.3 ± 0.9
W	13.9 ± 2.0[a]	15.4 ± 1.3[a]	19.34 ± 0.8[b]	16.3 ± 0.5[a]	18.0 ± 0.7[a]	23.3 ± 2.1[b]	32.4 ± 3.5	34.15 ± 1.9	31.2 ± 1.8
TrP	27.9 ± 1.6[a]	24.8 ± 0.8[a]	33.6 ± 1.9[b]	32.15 ± 1.4	31.4 ± 2.1	31.6 ± 1.5	30.67 ± 1.1	28.45 ± 1.4	30.2 ± 1.6
MCC	50.0 ± 2.7	57.8 ± 1.5	50.8 ± 2.3	47.0 ± 1.4	49.6 ± 2.4	53.4 ± 1.6	44.0 ± 2.1	45.3 ± 1.8	42.7 ± 2.4
BR	61.7 ± 1.2	58.3 ± 2.4	63.5 ± 3.3	60.6 ± 2.4	59.8 ± 1.9	61.4 ± 1.2	63.3 ± 2.2	62.8 ± 1.9	64.1 ± 2.1
CI-1	5.6 ± 0.8	5.6 ± 0.5	6.5 ± 0.41	7.0 ± 0.51	6.65 ± 0.4	6.04 ± 0.21	7.2 ± 0.2	8.1 ± 0.3	7.01 ± 0.14
CI-2	5.8 ± 0.05	5.8 ± 0.06	6.8 ± 0.01	7.2 ± 0.09	6.9 ± 0.04	6.2 ± 0.01	7.4 ± 0.05	8.4 ± 0.03	7.2 ± 0.04
PI	0.9 ± 0.02	0.83 ± 0.03	0.83 ± 0.02	0.85 ± 0.01	0.85 ± 0.04	0.93 ± 0.01	0.85 ± 0.03	0.84 ± 0.04	0.89 ± 0.07
TD	1.86 ± 0.03[a]	2.14 ± 0.4[b]	2.33 ± 0.04[b]	2.01 ± 0.09	2.11 ± 0.05	2.2 ± 0.07	2.32 ± 0.03	2.43 ± 0.2	2.25 ± 0.03
CI	103.8 ± 0.7[a]	123.7 ± 1.8[b]	145.4 ± 0.9[c]	118.4 ± 1.9[a]	128.4 ± 1.3[b]	146.02 ± 0.7[c]	172.2 ± 1.0[a]	183.1 ± 0.9[b]	164.2 ± 1.4[a]

[a,b,c]values across rows of a particular age group are significantly different ($P < 0.05$), (>1 but < 2 years, 1), (>2 but <3 years,2) and (>3 but <4 years, 3).

HI, height index; OII, over increase index; HS, height slope; LI, length index; BWI, body weight index; IC, index of compaction. ICC, index of chest compression; Cel, cephalic index; BI, body index; DTI, dactyl thorax index; W, weight; TrP, transverse pelvic; MCC, metacarpal coastal; BR, body ratio; CI-1, compact index-1; CI-2, compact index-2; PI, pectoral index; TD, thoracic development; CI, conformation index.

Table 7. Values (Mean ± SE) of morphometrical indices of rams of Bengal breed across different locations and age groups.

Age group traits	1			2			2		
Observations	Khargram 60	Sagardighi 59	Nakashipara 55	Khargram 39	Sagardighi 40	Nakashipara 45	Khargram 50	Sagardighi 45	Nakashipara 37
HI	89.7 ± 2.2	85.1 ± 2.1	96.13 ± 3.1	88.2 ± 2.9	86.4 ± 3.2	84.2 ± 1.7	84.5 ± 2.1	91.4 ± 2.7	87.8 ± 4.7
OII	95.9 ± 4.9	100.5 ± 4.7	101.2 ± 5.1	101.8 ± 3.1	101.3 ± 2.1	101.4 ± 2.4	106.1 ± 1.2	104.4 ± 3.1	103.1 ± 2.9
HS	−2.5 ± 0.8[b]	−0.2 ± 0.01[a]	−0.5 ± 0.03[a]	−0.7 ± 0.03	−0.5 ± 0.01	−0.6 ± 0.02	−2.6 ± 0.05	−1.9 ± 0.05	−1.4 ± 0.02
LI	1.11 ± 0.02	1.17 ± 0.06	1.04 ± 0.03	1.13 ± 0.02	1.16 ± 0.04	1.18 ± 0.08	1.18 ± 0.04	1.1 ± 0.03	1.14 ± 0.05
BWI	37.95 ± 2.1	41.92 ± 2.9	40.2 ± 3.4	45.0 ± 2.4	47.3 ± 3.2	47.3 ± 4.1	44.8 ± 2.1[a]	53.8 ± 1.7[b]	46.8 ± 3.2[a]
IC	155.2 ± 2.7	163.5 ± 5.2	163.5 ± 2.9	179.2 ± 3.4	168.4 ± 4.2	167.1 ± 4.1	167.4 ± 4.9	159.5 ± 5.3	165.0 ± 4.4
ICC	139.2 ± 2.3[a]	139.2 ± 1.6[a]	157.2 ± 2.2[b]	158.0 ± 1.7[c]	145.5 ± 1.4[b]	140.7 ± 1.9[a]	141.4 ± 2.1	145.8 ± 1.3	144.9 ± 1.7
CeI	58.1 ± 3.2	54.8 ± 3.0	50.3 ± 2.1	58.9 ± 1.4	54.0 ± 2.8	56.2 ± 2.1	60.3 ± 1.8	51.6 ± 1.4	54.8 ± 1.9
BI	71.8 ± 5.2	71.8 ± 3.1	63.6 ± 2.4	63.3 ± 2.2	68.7 ± 4.1	71.1 ± 5.4	70.6 ± 5.1	68.6 ± 2.9	69.0 ± 4.1
DTI	9.56 ± 1.2	9.2 ± 0.4	10.2 ± 2.4	10.8 ± 0.5	7.7 ± 0.4	9.9 ± 0.8	10.4 ± 2.1	10.3 ± 0.8	10.9 ± 1.1
W-2	16.7 ± 1.2	19.8 ± 0.8	22.1 ± 1.3	25.3 ± 1.8	22.2 ± 1.2	26.8 ± 3.1	29.0 ± 1.8	26.7 ± 2.1	31.8 ± 1.7
TrP	24.1 ± 1.2	24.1 ± 1.5	30.5 ± 2.4	31.0 ± 1.4	28.1 ± 1.9	31.0 ± 1.5	31.6 ± 1.7	30.0 ± 2.2	28.04 ± 2.2
MCC	53.9 ± 2.0	62.4 ± 2.9	50.4 ± 1.4	51.2 ± 1.6	66.6 ± 1.3	50.3 ± 2.4	46.9 ± 2.1	46.5 ± 1.8	43.8 ± 2.2
BR	0.62 ± 0.05	0.68 ± 0.02	0.64 ± 0.06	0.67 ± 0.03	0.69 ± 0.01	0.64 ± 0.07	0.61 ± 0.01	0.61 ± 0.05	0.61 ± 0.04
CI-1	5.75 ± 0.3	6.16 ± 0.2	6.2 ± 0.06	6.5 ± 0.03	6.7 ± 0.4	7.3 ± 0.5	6.92 ± 0.1	8.41 ± 0.2	7.41 ± 0.8
CI-2	6.74 ± 0.2	6.15 ± 0.09	6.2 ± 0.3	6.54 ± 0.08	6.71 ± 0.06	7.3 ± 0.2	6.91 ± 0.04	8.4 ± 0.05	7.4 ± 0.03
PI	0.86 ± 0.03	0.84 ± 0.01	0.83 ± 0.06	0.85 ± 0.08	0.86 ± 0.04	0.83 ± 0.01	0.85 ± 0.04	0.84 ± 0.07	0.83 ± 0.04
TD	2.35 ± 0.05	2.40 ± 0.01	2.50 ± 0.07	2.61 ± 0.02	2.4 ± 0.05	2.58 ± 0.05	2.58 ± 0.03	2.50 ± 0.05	2.61 ± 0.04
CI	139.5 ± 2.6[a]	151.1 ± 2.1[b]	163.6 ± 1.8[b]	177.7 ± 1.5[b]	156.3 ± 1.7[a]	179.5 ± 1.2[b]	184.2 ± 1.1[b]	173.2 ± 2.4[b]	147.5 ± 2.3[a]

[a,b,c]Values across rows of a particular age group are significantly different ($P < 0.05$), (>1 but < 2 years, 1), (>2 but <3 years,2) and (>3 but <4 years, 3).

HI, height index; OII, over increase index; HS, height slope; LI, length index; BWI, body weight index; IC, index of compaction; ICC, index of chest compression; Cel, cephalic index; BI, body index; DTI, dactyl thorax index; W, weight; TrP, transverse pelvic; MCC, metacarpal coastal; BR, body ratio; CI-1, compact index-1; CI-2, compact index-2; PI, pectoral index; TD, thoracic development; CI, conformation index.

Figure 8. Ram and ewe of Bengal breed.

rams. The age at first lambing (AFL) was 425 days. The average age at first lambing was similar to that reported by Pervage *et al.* (2009). Bengal breed are low to moderately prolific (Figure 9) and the questionnaire results indicated that nearly 40 percent of the ewes had history of twinning, however the survivability of the lambs was also low which can be attributed to poor nutrition of the ewe and also due to prevailing diseases. The rams mature earlier than the ewes which in accordance with the reports of Taylor (1968).The age at sexual maturity (days) and lambing interval for the ewes are higher than those reported by Hassan and Talukder (2011) but lower than those reported by Pervage *et al.* (2009) The variation may be attributed to management and the type of nutrition available to the ewes, reproductive parameters are influenced of both intrinsic and extrinsic factors while the former relates to the genotype the latter is influenced by the non-genetic (environmental factors), Bronson (1989), Rosa and Bryant (2003) and Ungerfeld and Bielli (2012). The reproductive parameters are also influenced by temperature, nutrition, social influences, lambing date and lactation period, Forcada and Abecia (2006) and Scaramuzzi and Martin (2008). The respondents indicated that the ewe's lamb thrice in 2 years is similar to those of Garole sheep (Banerjee, 2003).

Figure 9. A ewe with her triplets.

Conclusion

The results indicate that Bengal sheep play an important role in the rural economy and a large section of the population is dependent on the husbandry and trade of these breeds. The sheep are reared as a source of savings by the small, marginal and landless farmers, the findings are inconsonance with the reports of Saddullah (2000) and SA PPLPP (2011). The demand of mutton is on a rise while the numbers of sheep reared per household have lessened, this is primarily because of lack of grazing land, intensification of agriculture and migration of the working hands (Banerjee, 2009). As regards the wool, the farmers are unaware of its use and hence lose an opportunity of value addition and thereby earning some extra income.

There is panmectic breeding between the breeds thus the breed purity is being compromised in the areas of the present study. Hence, immediate steps are to be taken for the conservation of Bengal sheep.

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Effect of slaughter age on meat quality of Chamarito lambs

M. Pascual-Alonso[1], L. Aguayo-Ulloa[1], G.C. Miranda-de la Lama[2], S. Alierta[1], J.L. Olleta[1], M.M. Campo[1], M. Villarroel[3] and G.A. María[1]

[1]Department of Animal Production and Food Science, Faculty of Veterinary Medicine, University of Zaragoza, Miguel Servet 177, E-50013, (50013) Zaragoza, Spain; [2]Group of Animal Welfare and Sustainable Livestock Production, Department of Food Science, Metropolitan Autonomous University, UAM-Lerma, State of México, México; [3]Department of Animal Science, E.T.S.I.A. Polytechnic University of Madrid, Madrid, Spain

Summary

Chamarito lamb was recognized as a quality brand in Spain in April 2010 and this meat is highly appreciated in the local market, but little is known about how a short fattening period may affect final product quality. Twenty lambs, ten from the Ternasco category and ten from the suckling lamb category, were slaughtered and their carcass characteristics compared. All animals were weighed at birth, weaning and before slaughter, and average daily gain was calculated. Cold carcasses were weighed and bruising score, carcass conformation and carcass fatness were noted. The left back of each carcass was separated for dissection. The meat pH, cooking and thawing losses, texture, colour and fatty acid composition were measured on M. *longissimus* samples. Production traits and meat quality variables were analysed fitting a one-way model with the fixed effect of mean lamb age at harvest. The conformation and degree of fatness of Ternasco-type lambs was not significantly different from suckling lambs but the pH values 24.00 hours post-mortem in muscle (pHult) of the former was slightly higher. The fatty acid profile of suckling lambs was more suitable for a healthy human diet.

Keywords: *Chamarito lamb, meat quality, productive traits, short fattening period, suckling lamb*

Résumé

Avec une chair très appréciée dans le marché local, l'agneau Chamarito a été reconnu avec un label de qualité en Avril 2010. Cependant, on sait peu sur la façon dont une courte période d'engraissement peut affecter la qualité du produit final. Dix agneaux d'un troupeau de race Chamarita ont été abattus dans la gamme de poids de la catégorie « Ternasco » et ont été comparés à dix autres agneaux de la catégorie « Cordero Lechal » (Agneau de Lait). Tous les animaux ont été pesés à la naissance, au sevrage et avant l'abattage, afin de calculer le gain moyen quotidien. Les carcasses froides ont été pesées et le degré de contusions, la conformation et l'état d'engraissement de la carcasse ont été évalués. L'épaule gauche a été séparée de chaque carcasse pour sa dissection. La valeur pH de la viande, les pertes par cuisson et par décongélation, la texture, la couleur et la composition en acides gras de la viande ont été évaluées sur des échantillons du muscle *longissimus*. Les caractéristiques productives et les paramètres de qualité de la viande, ajustés à un modèle unidirectionnel ayant l'âge de l'agneau comme effet, ont été analysés. Le poids de la carcasse froide a été utilisé comme covariable pour la viande et les paramètres de qualité de la carcasse. Aucune différence significative n'a été décelée pour la conformation et l'état d'engraissement entre les agneaux de type « Ternasco » et ceux de lait, bien que le pH a été légèrement plus élevé pour les premiers. Le profil en acides gras des agneaux allaités s'est avéré plus adapté à un régime alimentaire sain pour les humains.

Mots-clés: *agneaux de race Chamarita, agneaux de lait, engraissement court, performances productives, qualité de la viande*

Resumen

El cordero Chamarito fue reconocido con marca de calidad en abril de 2010 y es una carne muy apreciada en el mercado local, pero poco se sabe acerca de cómo un corto período de engorde puede afectar a la calidad del producto final. Diez corderos de un rebaño de raza Chamarita fueron sacrificados dentro del rango de peso de la categoría tipo Ternasco y se compararon con otros 10 de la categoría de cordero lechal. Todos los animales fueron pesados al nacer, en el momento del destete y antes del sacrificio, y se calculó la ganancia media diaria. Se pesaron las canales en frío y se evaluó el grado de contusiones, la conformación y el engrasamiento de la canal. La espalda izquierda de cada canal fue separada para su disección. El pH de la carne, las pérdidas por cocinado y descongelación, la textura, color y composición de ácidos grasos de la carne se evaluaron en muestras del músculo *longissimus.* Se analizaron las características productivas y las variables de calidad de la carne ajustadas a un modelo unidireccional con la edad del cordero como efecto. La carne y las variables de calidad de la canal fueron co-variadas con el peso de la canal fría. La conformación y grado de engrasamiento de corderos de tipo Ternasco no fue significativamente diferente de corderos lactantes pero el pHult de los primeros fue ligeramente superior. El perfil de ácidos grasos de corderos lactantes se adecuó más a una dieta humana sana.

Palabras clave: *corderos Chamaritos, lechales, cebo corto, caracteres productivos, calidad de la carne*

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Correspondence to: M. Pascual-Alonso, Department of Animal Production and Food Scvaience, Faculty of Veterinary Medicine, University of Zaragoza, Miguel Servet 177, E-50013, (50013) Zaragoza, Spain. email: mpascual@unizar.es

Introduction

Chamarita sheep are farmed in La Rioja (Spain) and are considered an Endangered Native Breed in the Official Catalogue of Spanish Livestock Breeds. In the past, Chamarito meat was either commercialized as suckling lamb (12–14 kg live weight) or the heavier Ternasco-type (20–22 kg live weight; Doménech *et al.*, 1992), but suckling lambs are now more preferred by consumers. After being officially recognized as a quality brand in April 2010, the production system complies with strict animal welfare and health programmes, sheep are pasture-fed extensively and lambs receive their mother's milk and are slaughtered under 13.5 kg (maximum 40 days old). Their meat is very tender and juicy with a pleasant, mild flavour (Warren, 2011).

In Mediterranean countries, consumers prefer meat from light lambs fed either milk or mainly concentrate diets (Vergara & Gallego, 1999; Sañudo *et al.*, 2006). Among light lambs, suckling lambs reared exclusively on maternal milk are the lightest on the market (Gorraiz *et al.*, 2000). Some authors report that increasing the carcass weight of suckling lambs has little influence on meat quality traits (Russo, Preziuso & Verità, 2003, Díaz *et al.*, 2005a), but others have found large differences in tissue composition and meat quality over a narrow range of carcass weights in light lambs (Sañudo, Sánchez & Alfonso, 1998; Díaz *et al.*, 2003). Carcass weight is one of the most important factor affecting carcass and meat quality (Sañudo *et al.*, 1992; Vergara & Gallego, 1999). Moreover, in meat production systems, a small increase in the slaughter weight of lambs may result in higher farmerś incomes.

In addition to carcass weight, diet may affect meat quality within a short range of slaughter weights. Most of the studies on lamb meat quality consider pH, colour, texture and water-holding capacity. More recently, there has also been an emphasis on the fatty acid profiles of lamb tissues, which appear to be strongly affected by dietary fat composition (Osorio *et al.*, 2008).

Although highly appreciated on the local market, little is known about the instrumental quality of *Chamarito* lamb meat, which makes it very difficult to be able to compare with other similar products or to improve production within or among farms. Thus, in this study we aimed to characterize the instrumental meat quality of commercial Chamarito lambs and compare those characteristics among lambs of two different ages.

Materials and methods

This study is a collaboration between the Autonomous Regions of Aragon and La Rioja (Spain). A flock of 50 Chamarita adult ewes and 45 lambs were transported from La Rioja to the Animal Experimentation Support Service (SAEA) of the University of Zaragoza, Aragón (41°41_N). All the sheep used were raised, transported and slaughtered according to present regulations of the European Community Commission (1986) for Scientific Procedure Establishments. All the protocols were approved by the Animal Experimentation Ethics Committee of the University of Zaragoza.

Animals

The flock of 50 Chamarita multiparous adult sheep were housed in pens during pregnancy and lactation at a density of 2 m^2/ewe. They were fed twice a day, in the morning between 08.00 and 08.30 hours and in the afternoon between 15.00 and 15.30 hours All ewes received pellet concentrate (11.5 MJ ME/kg DM and 15.5 percent crude protein; approximately 0.3 kg/ewe), and lucerne chaff (*Medicagosativa*) ad libitum. The pen was equipped with a metallic water trough (1.5 m × 0.60 m) and two metallic feeders (4.5 m × 0.80 m, 27 cm/ewe), and a lick stone for minerals.

Productive traits

Controlled natural mating was used. The resulting lambs were kept together in the same pen with their mothers (2 m^2/sheep and lamb). All animals had ad libitum access to water. Lambs were weighed at birth and at weaning. The pre-weaning average daily gain (AGD) was calculated as weaning weight− birth weight divided by the total milking period (30 days). Lambs subjected to a short fattening period were also weighed before slaughter.

Carcass and meat quality parameters

A total of 20 lambs were used to study carcass and meat quality. Ten were slaughtered within the weight range of the suckling lamb-type category and ten more within the weight range of the Ternasco-type category (Sañudo *et al.*, 1996), at an EU-approved abattoir in the city of Zaragoza. After overnight lairage, lambs were electrically stunned and dressed using standard commercial procedures. After slaughter, the carcasses were stored in cold rooms at 2 °C for 24.00 hours. Cold carcasses were weighed at 24.00 hours (at 1–2 °C) in the cold room. The extent of bruising on the carcasses was estimated visually using scale adapted from Miranda-de la Lama *et al.* (2009), with a score of 0 (no bruises), 1 (slight bruising), 2 (moderate bruising) or 3 (high bruising). The carcass conformation and fatness were scored according to the European classification system (European Union, 1993), the EUROP conformation scale (converted to a 15 point scale) and the carcass fatness scale (converted to a 15 point scale). To determine pH 24.00 hours of the *longissimus dorsi* muscle, we used a portable pH meter (fitted with a penetration electrode 52-00 from Crison), which was inserted into a small incision in the right loin (L2–L3 vertebrae). The pH meter was re-calibrated after every five samples, using two standard buffer solutions at pH 7.02 and 4.00. After chilling for 24.00 hours, carcasses were transferred to the Meat Laboratory at the Faculty of Veterinary Medicine of the University of Zaragoza without disrupting the cold chain.

The left back of each carcass was separated according to the standard cut method used for lamb carcasses defined by Boccard & Dumont (1955), vacuum packed and frozen at −20 °C until further dissection. The samples were thawed for 24.00 hours in a refrigerator (2–4 °C) in sealed plastic bags under a vacuum, before testing. After weighing, each piece was dissected into its components: subcutaneous fat, intermuscular fat, muscle, bone and waste (lymph, large blood vessels, nerves, tendons, ligaments and fascia of conjunctive tissue) according to the protocol described by Colomer-Rocher *et al.* (1988). Fatty prescapular deposits were also dissected and included as part of the total fat.

The *M. longissimus* was removed, wrapped and stored at −20°C. The loin was divided into three sections. The first section was wrapped, aged for 72.00 hours at 4 °C and then vacuum-packaged before being frozen and stored at −20 °C. The samples were thawed for 24.00 hours in a refrigerator (2–4 °C) in their sealed plastic bags under a vacuum before testing. Then the samples were weighed and heated in a water bath to an internal temperature of 70 °C and then cooled for 30 min under cold running water, analysing thawing losses (fresh weight-thawed weight) and cooking losses (thawed weight-cooked weight). Instrumental colour was evaluated using a Minolta CM 202 calibrated chromameter with a standard illuminant D65. A 10° observer with an aperture size of 2.54 cm, following the CIE $L^*a^*b^*$ system, measured the colour of fresh meat on the cut surface of the 13th thoracic vertebra of the *M. longissimus*. The colourimetric indices of chromaticity [chroma* = (a*2 + b*2)1/2, quantity of colour] and hue [h^* = 1/tan (b^*/a^*), real colour] were calculated. Final values were the average of three measurements. To perform the Warner–Bratzler test, samples were cooked in their vacuum-sealed plastic bags in a 75 °C water bath (GLF-D3006), until the internal temperature of the meat (measured with a penetration thermometer) reached 70 °C, then cooled for 30 min under flowing cold water. The samples were randomly allocated in two batches. The texture of the cooked meat was measured with a Warner–Bratzler device, using an Instron 4301 equipped with a Warner–Bratzler shear. To cut 1 cm^2 pieces (in the direction of the muscle fibres), we used a digital calibre MITUTOYO Series 500 (Mitutoyo Corporation, Aurora, IL, USA). For each animal, three measurements were taken. Maximum load, maximum stress and toughness were measured as described by Campo *et al.* (2000). The sample gauge was 10 mm, gauge length was 30 mm, load cell was 100 kg (minimum load level 0.001 kg), crosshead speed was 150 mm/min (high extension limit = 30 mm), and the sampling rate was 20 points/s.

The second section of *M. longissimus* was wrapped, aged for 72.00 hours at 4 °C and then vacuum-packaged before being frozen and stored at −20 °C for further determination of fatty acid composition. The samples were thawed for 24.00 hours in a refrigerator (2–4 °C) in their sealed plastic bags under vacuum before testing. The muscle tissue was blended using a small food processor. Duplicate 1 g samples were hydrolysed in 6 ml of 5 M KOH in methanol:water (1:1, v/v) at 60 °C. After acidification, the fatty acids and aldehydes were extracted in petroleum spirit (BP 40 ± 60 °C), methylated with a solution of diazomethane in diethyl ether and analysed on a 50 mm × 0.25 mm ID CP Sil 88 FAME column (Chrompack, UK) (Whittington *et al.*, 1986). Fatty acids were quantified using heneicosanoic acid methyl ester as internal standard added prior to saponification. Peaks were identified using standards where available (Sigma Chemical Co., Ltd, Poole, UK). Linearity of response was confirmed using GLC-50 monoenoic reference mixture (Superlco, Poole, UK) and on-column injection of test samples. The third section of *M. longissimus* was wrapped, aged for 72.00 hours at 4 °C and then vacuum-packaged before being frozen and stored at −20 °C for sensory analysis.

Data analysis

Data were analysed using the least squares methods of the GLM procedure using SAS/STAT (9.1 SAS Inst. Inc., Cary, NC, USA) by SAS (1998), fitting a one-way model with a fixed effect of type of lamb (suckling or Ternasco-type). A probability of $P < 0.05$ values was considered statistically significant.

Results and Discussion

The average weight of lambs (from both groups) at birth was 3.72 ± 0.18 kg. Average daily gain was 0.2 ± 0.008 kg during the milking period, resulting in a weaning weight of 10.97 ± 0.3 kg. The ADG of lambs fattened to the Ternasco-type category during the fattening period (30 days) was 0.15 ± 0.02 kg with a final weight of 16 ± 0.72 kg before slaughter.

Table 1 summarizes the results for carcass and meat quality traits in both types of lambs. According to the Order of September 18, 1975 (BOE, 1975), amended by the Order of September 24, 1987 (BOE, 1987), which sets the quality standards for ovine carcasses for the national market, suckling lambs must be fed mainly on milk, be less than 45 days old and have a carcass weight below 8 kg. In our study, suckling lambs were 30 days old when slaughtered, with an average carcass weight of 4.58 (±0.31) kg after 24.00 hours in the cold room, which is very similar to the type of lamb commercialized in La Rioja. On the other hand, animals with a short fattening period (30 days) were slaughtered at 60 days of age, with a carcass weight of 6.99 (± 0.27) kg. That product is new on the market in La Rioja and could be used as an alternative since it improves the performance of the production system by increasing individual lamb productivity. It is also a way

Table 1. Least square means (±SE) for carcass and meat quality traits in suckling and light Ternasco type Chamarito lambs.

	Suckling lambs	Fattened lambs
Carcass weight (kg)	4.58 ± 0.31	6.99 ± 0.27
Bruising score (0–3)	1.42 ± 0.33[a]	0.33 ± 0.29[b]
Conformation score	2.16 ± 0.25	2.2 ± 0.22
Fatness score	3.02 ± 0.46	1.82 ± 0.4
pH_{ult} (24.00 hours post mortem)	5.56 ± 0.02[a]	5.73 ± 0.02[b]
Thawing losses (g)	2.11 ± 0.77	2.79 ± 0.77
Cooking losses (g)	5.79 ± 0.36[a]	4.29 ± 0.36[b]
Meat colour		
Brightness (L)	47.82 ± .98[a]	43.86 ± 0.98[b]
Red index (a*)	13.91 ± 0.53[a]	15.35 ± 0.53[b]
Yellow index (b*)	5.83 ± 0.28	5.15 ± 0.28
Chroma* $C^* = (a^2 + b^2)1/2)$,	15.11 ± 0.55	16.19 ± 0.55
Hue* [$h^* = 1/\text{TAN}(b^*/a^*)$]	22.91 ± 0.96[a]	18.44 ± 0.96[b]
Meat texture by Warner–Bratzler		
Maximum load (kg)	3.16 ± 0.5	3.65 ± 0.5
Maximum stress (kg)	3.03 ± 0.52	3.63 ± 0.52
Toughness (kg/cm^2)	1.23 ± 0.33	1.85 ± 0.32

[a,b]Different letters (a,b) represent significant differences ($p < 0.05$) between groups.

of reducing stress since it dissociates the stress of pre-slaughter handling from weaning stress.

Carcass weight is the most important criterion to classify sheep (Miguélez *et al.*, 2007). It is a good indicator of the quality traits of the carcass (Hammond, 1932). The optimal slaughter weight varies with breed, type of feeding, sex, litter size and the number of lambings (Sañudo *et al.*, 1993, 1997; Sánchez *et al.* 1998; Vergara, Berruga & Gallego 2001; Diaz *et al.*, 2003; Gutiérrez, 2006). In this study, animals were selected for slaughter by age instead of by weight. The weaning and slaughtering of *Chamarito* lambs is very early compared with other breeds, which explains why the average weights recorded are lower than other suckling lambs such as "Lechazo de Castilla y Leon" with an average cold carcass weight of 5.5 kg (Sánchez *et al.*, 1998). The lambs are probably managed in this way since they are well adapted to a hard environment and may undergo pasture shortages. Later weaning may create serious competition between lambs and ewes for grazing resources. The establishment of a short fattening period could reduce those differences, improving the competitiveness of *Chamarito* lambs on the market. Another alternative to compensate for that loss of competitiveness would be to develop a brand that highlights the special characteristics of suckling *Chamarito*.

Carcass conformation is determined by general shape, degree of roundness and compactness (De Boer *et al.*, 1974). Breed is one of most important factors influencing carcass conformation in lambs (Miguélez *et al.*, 2007). For suckling lambs, "Lechazo de Castilla y León" the average carcass conformation is low (with a mean of 2.00 points, Sánchez *et al.*, 1998), and our results are very similar (average of 2.16). The degree of fatness of lamb carcasses is seen primarily on the outer and inner surfaces, in the loins, in the omentum and in the tail (García-Díez, 1990). Similarly to the conformation, the fatness of suckling *Chamarito* carcasses closely resembles the "Lechazo deCastilla y León", corresponding to a slight fat cover that is hardly noticeable at the extremities (Sánchez *et al.*, 1998). Miguélez *et al.* (2007) suggests that local breeds deposit more internal fat compared with more productive breeds. Carcasses of animals subjected to short fattening did not improve much in conformation or degree of fatness, and no significant differences were found between groups, contrary to what might be expected. That may be because the short fattening period does not allow enough time for the animals to adapt to new feeding and housing conditions after weaning. Animals may even lose some weight at the beginning of the fattening period due to weaning stress. Thirty days may not be enough to improve the performance at this stage of growth.

Regarding carcass bruising, it was significantly higher ($P \leq 0.05$) in suckling lambs compared with light Ternasco-type lambs. That may be because of the cumulative effect of weaning stress, pre-slaughter management and slaughter itself. Bruising produces colour changes in the carcass and is an important indicator in post-mortem examination, with commercial and animal welfare implications (Cooper & Cooper, 2007.) The transport used had few standardized divisions of space so it is possible that smaller animals had more space to move around and bump into walls.

The pH measured 24 hours post-slaughter is probably one of the most important commercial indicators of meat quality (Gregory, 2007). In our study, the pH values were always below 6.0, within the range of optimum commercial quality. The pH_{ult} of lambs fattened for 30 days was slightly higher than the suckling lambs (+3 percent, $P \leq 0.05$), but within a range of optimum meat quality. There is a tendency towards increased pH with age (Alexandrova *et al.*, 1996; Sañudo *et al.*, 1996), which coincides with our study. Some authors suggest it might be because of the increased susceptibility to management stress in older animals (Devine *et al.*, 1993).

Colour is one of the main criteria used by consumers to judge the quality of meat (Sañudo *et al.*, 1997). In our study, meat colour was also significantly different between different types of carcasses in terms of L* (lightness), which was higher in suckling lambs (+9 percent, $P \leq 0.05$), while a* (red index) was significantly higher in Ternasco-type lambs (+10.4 percent, $P \leq 0.05$) and hue* was 24.2 percent higher in suckling lambs ($P \leq 0.05$). Colour variables are generally affected by carcass weight (Field *et al.* 1990; Rashid & Faidhi, 1990; Sañudo *et al.*, 1996; Rousset-Akrim, Young, & Berdague, 1997), although colour evolution is not linear and at certain ages may remain stable (Alexandrova *et al.*, 1996). Changes in meat colour can also be related to diet: a diet based exclusively on milk produces paler meat with less pigment (Sañudo, Sánchez & Alfonso, 1998). Specifically, a^* values vary in relation to the amount of haemoglobin pigments, and therefore the lower content of suckling animals is probably related to the milk-based diet with low iron content (Sañudo *et al.*, 1996).

Cooking losses were higher in suckling lambs (+35 percent, $P \leq 0.05$), whereas no differences were found in thawing losses. In general, cooking losses are positively correlated with fatness (Kemp *et al.*, 1972; Babiker, El Khider, & Shafie, 1990). Regarding the texture, estimated by Warner–Bratzler, no significant differences were detected between the two types of lamb.

Table 2 shows the least square means (± SE) for dissection composition of the back (percentage of total weight) from suckling and light Ternasco type Chamarito lambs. The carcass has a large number of tissues which influence its quality, depending on their proportions. Those tissues are grouped from a functional standpoint into muscle, fat and bone. There were no significant differences in percentage of muscle, total fat, intermuscular fat or subcutaneous fat between types of lambs. However, the percentage of bone was significantly higher in fattened lambs (+11.7 percent, $P \leq 0.05$), as well as the proportion of waste (43.2 percent higher in fattened lambs, $P \leq 0.05$). Muscle tissue has the greatest economic value (Sañudo *et al.*, 1996) but the percentage of muscle was not significantly different among treatments. The percentage of muscle in suckling lambs was similar to that found in "Lechazos de Castilla y León" by Sánchez *et al.* (1998). There were no significant differences in fat percentage between types of lambs, which were very similar to Miguélez *et al.* (2007) for suckling lamb carcasses from different breeds. The differences in percentage of bone and waste may be because of the short duration of the fattening, increasing the percentage of bone and waste in relation to the amount of muscle and fat.

Finally, regarding fatty acid composition (Table 3), there were significant differences in both the ratio of the percentage of polyunsaturated fatty acids (PUFAs) vs saturated fatty acids (SFAs, P:S) and the ratio of the percentage of omega-6 vs the percentage of omega-3 fatty acids (n-6/n-3). Those two variables suggest that the fatty acid profile of suckling lamb meat is healthier for human consumption than fattened lambs. Suckling lambs had a P:S ratio of 0.43, while the recommended level is above 0.4 (Wood *et al.*, 2003), well above the 0.33 obtained for the fattened lambs. In the first stages of fattening the concentration of saturated relative to unsaturated fatty acids increases (Wood et al., 2003), since the majority of dietary PUFA is hydrogenated in the rumen leading to higher values for SFAs (Scollan *et al.*, 2001). Our results agree with Cifuni *et al.* (2000) who attributed the differences between lambs of different age to the differential development of tissues in young animals and different physiological condition and digestive capabilities of the animals being younger lambs characterized by a fatty acid profile more compatible with good health and nutrition of consumers. Moreover, there is evidence that an inappropriate n-6/n-3 ratio is a risk factor in cancer and coronary heart disease (Enser, 2001) and it should be lower than 4 (Wood *et al.*, 2003). The values obtained in this study for the fattened lambs exceed this limit, while suckling lambs showed a significantly lower ratio of 3.78. That difference between types of animals is sustained by the percentages of n-3 fatty acids,

Table 2. Least square means (±SE) for dissection composition (percentage of total weight) of the back from suckling and light Ternasco type Chamarito lambs.

	Suckling lambs	Fattened lambs
Dissection (%)		
Muscle	57.59 ± 1.69	54.45 ± 1.69
Total fat	14.83 ± 1.88	14.15 ± 1.88
Subcutaneous fat	6.19 ± 1.2	5.62 ± 1.2
Intermuscular fat	5.29 ± 0.53	5.32 ± 0.53
Bone	19.86 ± 0.65[a]	22.19 ± 0.65[b]
Waste	4.47 ± 0.42[a]	6.4 ± 0.42[b]

[a,b]Different letters (a,b) represent significant differences ($p < 0.05$) between groups.

Table 3. Least square means (±SE) for fatty acid composition (percentage of total fatty acids) of intramuscular fat from suckling and light Ternasco type Chamarito lambs.

Trait	Suckling lambs	Fattened lambs	aSE	*P*
C10:0	0.19	0.16	0.02	NS
C12:0 (lauric)	0.48	0.3	0.04	**
C14:0 (myristic)	4.55	4.45	0.35	NS
C15:0	0.48	0.43	0.02	NS
C16:0 (palmitic)	22.88	23.86	0.59	NS
C16:1 (palmitoleic)	1.46	1.99	0.1	**
C17:0	1.16	1.31	0.04	*
C17:1	0.58	0.75	0.02	***
C18:0 (stearic)	12.04	11.78	0.25	NS
C18:1 *n-9* (oleic)	29.38	32.71	0.68	**
C18:1 *n-9* trans	1.99	2.21	0.22	NS
C18:1 *n-11*	1.44	1.48	0.07	NS
C18:2 *n-6* (linoleic)	8.41	7.05	0.6	NS
C18:3 *n-3* (α-linolenic)	0.89	0.51	0.04	***
CLA	0.55	0.47	0.08	***
C20:3 *n-3*	0.28	0.18	0.03	*
C20:3 *n-6*	0.32	0.24	0.02	NS
C20:4*n-6* (arachidonic)	4.89	3.79	0.4	NS
C20:5 *n-3* DPA	0.7	0.42	0.05	**
C22:5 *n-3*	1.21	0.75	0.08	***
C22:6 *n-3* DHA	0.57	0.3	0.03	***
SFA	43.08	43.18	0.9	NS
MUFA	35.3	39.6	0.74	***
PUFA	18.13	14.04	1.18	*
n-6	13.9	11.34	1.1	NS
n-3	3.73	2.22	0.22	***
P:S	0.43	0.33	0.04	*
n-6:n3	3.78	5.08	0.27	*

NS, not significant; PUFA, polyunsaturated fatty acid; SFA, saturated fatty acid; MUFA: Monounsaturated fatty acid; DPA: Docosapentaenoic acid; DHA: Docosahexaenoic acid

[a]Means; SE: standard errors.

[*]Values between columns are significantly different (within trait) ($P < 0.05$).

which were higher in suckling lambs. This makes the PUFA percentage higher in suckling lambs, increasing the P:S ratio and the *n*-6/*n*-3 ratio. Our results agree with Cañeque *et al.* (2005), who found that this ratio, as well as some fatty acids such as palmitoleic (C16:1) and heptadecenoic (C17:1) acids, increased as carcass weight increased. That is especially the case for 18:3 and 20:5, related to the consumption of grass (Fisher *et al.*, 2000), which are higher in suckling lambs. In our study those fatty acids may have been transmitted via the ewe's milk, since they had access to lucerne chaff during the whole milking period. Those results agree with Díaz *et al.* (2005b) who found higher levels of *n*-6 fatty acids and therefore a high *n*-6/*n*-3 ratio in lambs with an exclusively concentrate based diet, but lambs fed grass had high levels of *n*-3 fatty acids and low *n*-6/*n*-3 ratios. Nevertheless, it remains necessary to explore the possibility of developing new feeding strategies for lactating ewes with by-products (e.g. from the wine industry) which may favour healthier fatty acid profile for human consumption, with particular reference to the *n*-6/*n*-3 ratio.

Conclusions

Meat from the *Chamarito* lamb is a distinct quality product with high potential in La Rioja and its surroundings. The quality of suckling Chamarito lamb meat is comparable to other recognized suckling lambs. Fattening lambs for 30 days (Ternasco-type lamb) did not have important effects on conformation or degree of fatness and the percentage of muscle and fat were similar to suckling lambs. However, the pH_{ult} of the heavier lambs was slightly higher, which may be because of the increased amount of or susceptibility to management stress. It appears that a short fattening period is not enough to improve the performance at that stage of autonomous growth. The fatty acid profile of suckling lambs was healthier for human consumption. Further studies are needed to ascertain whether lambs should be fattened further to increase individual productivity, but it could also have detrimental effects on the sustainability of the system and on differential characteristics compared with other lambs.

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Morphometric differentiation of Moroccan indigenous Draa goat based on multivariate analysis

M. Ibnelbachyr[1], I. Boujenane[2] and A. Chikhi[3]

[1]*Institut National de la Recherche Agronomique, Center of Errachidia, Morocco;* [2]*Department of Animal Production and Biotechnology, Institut Agronomique et Vétérinaire Hassan II, Rabat, Morocco;* [3]*Institut National de la Recherche Agronomique, Center of Kénitra, Morocco*

Summary
The Moroccan goat livestock is characterized by the existence of different phenotypes distributed among diverse geographic locations. The objective of this study was to analyse the morphometric traits that differentiate the Draa breed from the other local populations raised in areas close to its cradle zone. Eight morphometric measurements were taken on 287 goats in South-eastern and Southern Morocco. The variance analysis, fitting a model that included the random effect of animal and the fixed effects of population, gender and age of animal, was used. Mahalanobis distances were calculated between identified populations and an Unweighted Pairs Group Method Analysis tree was built. Draa goats had the highest height at withers (61.5 cm), heart girth (74.4 cm), body length (64.6 cm) and live body weight (27.2 kg). These morphometric traits varied significantly among populations as well as the age and the gender of animal. The most discriminating traits between the identified populations were the body length, the heart girth, the hair length, the horn length, the ear length and the live body weight. Draa animals had the largest genetic distances from the other populations and appeared more distinguished from them. This differentiation can contribute in defining the phenotypic standard of the breed and in orienting its genetic improvement programs in the future.

Keywords: *Goats, Morocco, Mahalanobis distances, phenotype*

Résumé
Le cheptel caprin marocain est caractérisé par l’existence de différents phénotypes répartis sur divers sites géographiques. L’objectif de cette étude était d’analyser les caractères morphométriques qui différencient la race Draa des autres populations locales élevées dans les zones limitrophes de son berceau. Huit mesures morphométriques ont été prises sur 287 animaux dans le Sud-Est et le Sud du Maroc. L’analyse de la variance, en utilisant un modèle qui comprenait l’effet aléatoire de l’animal et les effets fixes de la population, du sexe et l’âge de l’animal, a été utilisée. Les distances de Mahalanobis ont été calculées entre les populations identifiées et un dendrogramme UPGMA a été construit. Les caprins Draa avaient les valeurs les plus élevées pour la hauteur au garrot (61.5 cm), le tour de poitrine (74.4 cm), la longueur du corps (64.6 cm) et le poids vif (27.2 kg). Ces caractères variaient considérablement entre les populations et aussi selon l’âge et le sexe des animaux. Les caractères les plus discriminants entre les populations identifiées étaient la longueur du corps, le tour de poitrine, la longueur du poil, la longueur des cornes, la longueur des oreilles et le poids vif. Aussi, les animaux Draa ont eu les distances génétiques les plus élevées des autres populations et semblaient plus distingués d’eux. Cette différenciation peut contribuer à la définition du standard phénotypique de la race Draa et à orienter les programmes d’amélioration génétique dans l’avenir.

Mots-clés: *Caprins, Maroc, phénotype, distances de Mahalanobis*

Resumen
El ganado caprino marroquí se caracteriza por la existencia de diferentes fenotipos distribuidos en diversos sitios geográficos. El objetivo de este estudio fue analizar las características morfométricas que diferencian la raza Draa de otras poblaciones locales en las zonas cercanas de la cuna de la raza Draa (Valle de Draa, sureste de Marruecos). Ocho medidas morfológicas se tomaron sobre 287 animales en el sureste y el sur de Marruecos. El análisis de varianza, usando un modelo que incluyó el efecto aleatorio del animal et los efectos fijos de la popblacion, del sexo y de la edad de los animales, se utilizó. Las distancias genéticas se calcularon entre las poblaciones identificadas y un árbol UPGMA se construyó. Animales de raza Draa tuvieron la mayor alzada a la cruz (61.5 cm), circunferencia torácica (74.4 cm), longitud corporal (64.6 cm) y peso vivo (27.2 kg). Estos rasgos morfométricos variaron significativamente entre las poblaciones, así como la edad y el sexo del animal. Los rasgos más discriminantes entre las poblaciones identificadas fueron la longitud corporal, la circunferencia torácica, la longitud del pelo, la longitud de los cuernos, la longitud de la oreja y el peso vivo. Animales Draa tenían las distancias de Mahalanobis más grandes y aparecieron más distinguido de ellos. Esta diferenciación puede contribuir en la definición del estandard fenotípico de la raza y en la orientación de sus programas de mejoramiento genético en el futuro.

Correspondence to: M. Ibnelbachyr, Institut National de la Recherche Agronomique, Center of Errachidia, Errachidia, Morocco. email: m_ibnelbachyr@yahoo.fr

Palabras clave: *Caprino, Maruecos, fenotipo, distancias de Mahalanobis*

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Introduction

Phenotypic characterization refers to the population identification process and to the description of their characteristics and those of their production environment (FAO, 2012). The Global Action Plan for Animal Genetic Resources recognizes that "a better understanding of the characteristics of livestock breeds is necessary for guiding decision making in the development of farms and breeding programs" (FAO, 2007). In goats, the analysis of morphological traits was used in several studies for characterizing goat genetic resources (Dekhili *et al.*, 2013; Fantahun *et al.*, 2013), differentiating populations and breeds (Herrera *et al.*, 1996; Capote *et al.*, 1998; Yakubu and Salako, 2011; Pires *et al.*, 2012; Nafti *et al.*, 2014) and studying genetic distances and taxonomic trees (Machado *et al.*, 2000; Marichatou *et al.*, 2012).

The Moroccan goat livestock accounts more than 6.2 million heads and occupies the 13th position worldwide (http://faostat3.fao.org/browse/Q/QA/E). Only the goat of oases in Southern-East of Morocco, called Draa, has been considered as a breed (Hossaini-Hilali and Mouslih, 2002) and has been defined as a medium-sized goat with a fine and triangular head often polled (Ezzahiri *et al.*, 1989). The other populations have been classified according to their geographical site ("goat of the North") or their dominant coat colour ("black goat" called also "R'halia"). In the last decade, some subpopulations of black goat were described on the basis of slightly different morphologies and were officially called Atlas, Barcha and Ghazzalia.

This phenotypic description remains insufficient since it was not based on a statistical analysis of morphometric traits. Such analysis will contribute to define a morphological standard and to guide the genetic improvement programs in the future. Thus, the objective of this study was to characterize the Draa breed in comparison with other local populations using a multivariate analysis of morphometric traits.

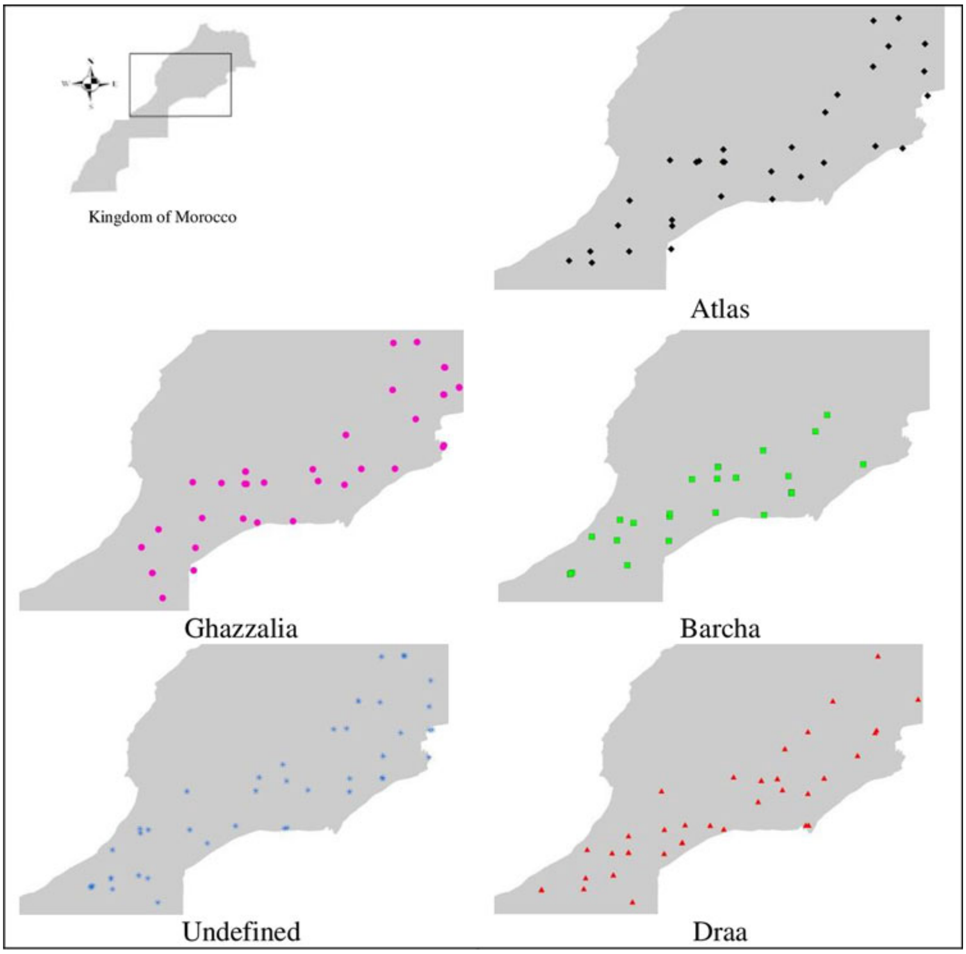

Figure 1. Sampled areas for each population located on the map of Morocco.

Figure 2. Draa does with different coat colour.

Figure 4. Barcha buck.

Figure 3. Atlas doe.

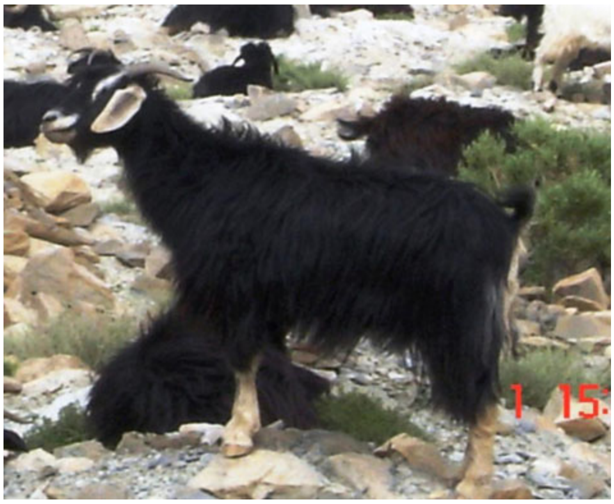

Figure 5. Ghazzalia doe.

Figure 6. Un-defined animals.

Materials and methods

Site of the study and data collection

The study was carried out in the cradle zone of Draa breed (Draa valley) and in the neighbouring areas that include other goat populations in the South-eastern and Southern Morocco (Figure 1). A sampling grid covering these areas was established on the basis of geo-referenced and uniform cells of 2 500 km^2. A total of 54 cells were sampled in which five adult animals were randomly selected from each of three different flocks in each cell. The gender of animals was recorded and their age was estimated from their dentition. Morphometric traits studied, as described by FAO (2011), were height at withers (HW), heart girth (HG), body length (BL), ischion circumference (IC), ear length (EL), horn length (HoL), hair length (HL) and body live weight (BW).

According to their dominant phenotype, the sampled animals were classified into five populations. The Draa breed has been defined and recognized as the goat of oasis area (Figure 2). The population called "Atlas" (A) was described as all black with a reddish glow (Figure 3) and the population called "Barcha" (B) is black with speckled ears and muzzle (Figure 4). The population called "Ghazzalia" (G) is also black, but scratched on the face, with ears, limbs and lower abdomen brown

Table 1. Least-squares means ± standard errors of morphometric traits taken in the five populations[1].

Fixed effects	HW (cm)[2]	HG (cm)	BL (cm)	IC (cm)	EL (cm)	HoL (cm)	HL (cm)	BW (kg)
Gender	***	***	NS	***	NS	***	*	***
Male	61.4 ± 0.9[a]	73.8 ± 1.2[a]	62.0 ± 1.2	8.37 ± 0.1[a]	16.9 ± 0.5	28.6 ± 1.2[a]	10.2 ± 0.8[a]	25.7 ± 1.0[a]
Female	56.7 ± 0.4[b]	67.9 ± 0.6[b]	60.9 ± 0.6	7.07 ± 0.1[b]	16.5 ± 0.2	17.0 ± 0.5[b]	8.56 ± 0.3[b]	21.3 ± 0.5[b]
Age	***	***	***	***	*	***	NS	***
Age ≤ 24	55.1 ± 0.7[c]	65.1 ± 1.0[c]	55.5 ± 1.0[b]	7.23 ± 0.1[b]	15.8 ± 0.4[b]	18.8 ± 0.9[b]	8.96 ± 0.6	18.0 ± 0.9[c]
24 < Age ≤ 36	57.9 ± 0.9[b]	71.0 ± 1.2[b]	63.1 ± 1.2[a]	7.82 ± 0.1[a]	16.5 ± 0.5[ab]	21.5 ± 1.3[b]	9.48 ± 0.7	24.1 ± 1.0[b]
Age > 36	64.1 ± 1.0[a]	76.4 ± 1.3[a]	65.8 ± 1.3[a]	8.11 ± 0.2[a]	17.8 ± 0.6[a]	28.1 ± 1.3[a]	9.75 ± 0.8	28.4 ± 1.1[a]
Population	***	***	***	NS	NS	NS	***	***
Draa	61.5 ± 0.6[a]	74.4 ± 0.8[a]	64.6 ± 0.9[a]	7.74 ± 0.1	17.1 ± 0.4	23.1 ± 1.0	3.7 ± 0.5[d]	27.2 ± 0.7[a]
Atlas	59.0 ± 0.8[b]	70.3 ± 1.1[b]	60.6 ± 1.1[b]	7.67 ± 0.1	16.2 ± 0.5	22.5 ± 1.0	10.9 ± 0.7[b]	22.3 ± 1.0[bc]
Barcha	58.2 ± 0.9[b]	69.5 ± 1.2[b]	58.9 ± 1.3[b]	7.75 ± 0.2	17.3 ± 0.5	23.1 ± 1.2	13.0 ± 0.8[a]	21.7 ± 1.1[bc]
Ghazzalia	57.8 ± 0.7[b]	69.4 ± 1.0[b]	61.6 ± 1.0[b]	7.75 ± 0.1	16.7 ± 0.4	23.1 ± 1.0	10.9 ± 0.6[b]	22.3 ± 0.9[bc]
Un-defined	58.7 ± 0.7[b]	70.5 ± 1.0[b]	61.6 ± 1.0[b]	7.68 ± 0.1	16.2 ± 0.4	23.0 ± 1.0	8.71 ± 0.6[c]	24.0 ± 0.9[c]

[1]Least-squares means within a column that have a different superscript are significantly different ($P < 0.05$).
NS, not significant ($P > 0.05$), *$P < 0.05$, ***$P < 0.001$.
[2]HW, height at withers; HG, heart girth; BL, body length; IC, ischion circumference; EL, ear length; HoL, horn length; HL, hair length; BW, body live weight.

Table 2. Correlation matrix of morphometric traits studied with *P*-value between brackets[1].

	HW	HG	BL	IC	EL	HoL	HL
HG	0.52 (<0.0001)						
BL	0.40 (<0.0001)	0.48 (<0.0001)					
IC	0.50 (<0.0001)	0.49 (<0.0001)	0.32 (<0.0001)				
EL	0.02 (0.5334)	−0.06 (0.0791)	−0.04 (0.1231)	0.05 (0.2134)			
HoL	0.37 (0.0445)	0.44 (0.0914)	0.15 (0.1527)	0.36 (<0.0001)	0.04 (0.1014)		
HL	−0.19 (0.0007)	−0.15 (<0.0001)	−0.10 (<0.0001)	−0.04 (0.4010)	0.06 (0.7143)	0.23 (<0.0001)	
BW	0.53 (<0.0001)	0.68 (<0.0001)	0.51 (<0.0001)	0.44 (<0.0001)	0.01 (0.0069)	0.01 (0.8075)	−0.14 (0.0007)

[1]HW, height at withers; HG, heart girth; BL, body length; IC, ischion circumference; EL, ear length; HoL, horn length; HL, hair length; BW, body live weight.

(Figure 5). The other phenotypes different from these were grouped as "Un-defined goats" (Figure 6). Thus, a total of 251 does and 36 bucks were sampled from Draa (85 animals), Atlas (50 animals), Barcha (31 animals), Ghazzalia (58 animals) and Un-defined goats (63 animals).

Statistical analyses

Statistical analyses were performed using SAS software, version 9.0 (Statistical Analysis System, 2002). The analysis of variance was performed using the Mixed procedure fitting a model that included the random effect of animal and the fixed effects of gender and age of animal. A canonical discriminant analysis was performed, using Candisc procedure, for determining morphometric traits most discriminating the populations. Then, the probabilities of including an individual in a population were determined using Discrim procedure based on the linear discriminant function that included the eight morphometric variables. Mahalanobis distances between studied populations were calculated (Mahalanobis, 1936) as used in several studies (Capote *et al*., 1998; Jimcy *et al*., 2011; Nafti *et al*., 2014). These distances were then used to construct a dendrogram using the Unweighted Pairs Group Method Analysis.

Results

Least-squares means and standard errors for morphometric traits are presented in Table 1. Only HW, HG, BL and BW varied significantly among populations. Draa animals had the highest HW (61.5 cm), HG (74.4 cm), BL (64.6 cm) and BW (27.2 kg), as well as the shortest HL (3.74 cm) ($P < 0.05$). For IC, EL and HoL the measurements were similar for the five populations ($P > 0.05$). Except HL, all morphometric traits increased significantly with the age of animal ($P < 0.05$). Also, males had the highest values for HW, HG, IC, HoL, HL and BW ($P < 0.05$). The correlations between the studied measurements were given in Table 2. The highest correlations varying between 0.15 and 0.68 were found among HW, HG, BL, IC, HoL and BW. Correlations among the other measurements varied from −0.18 to 0.07.

The canonical discriminant analysis allowed determining the morphometric traits most differentiating between the

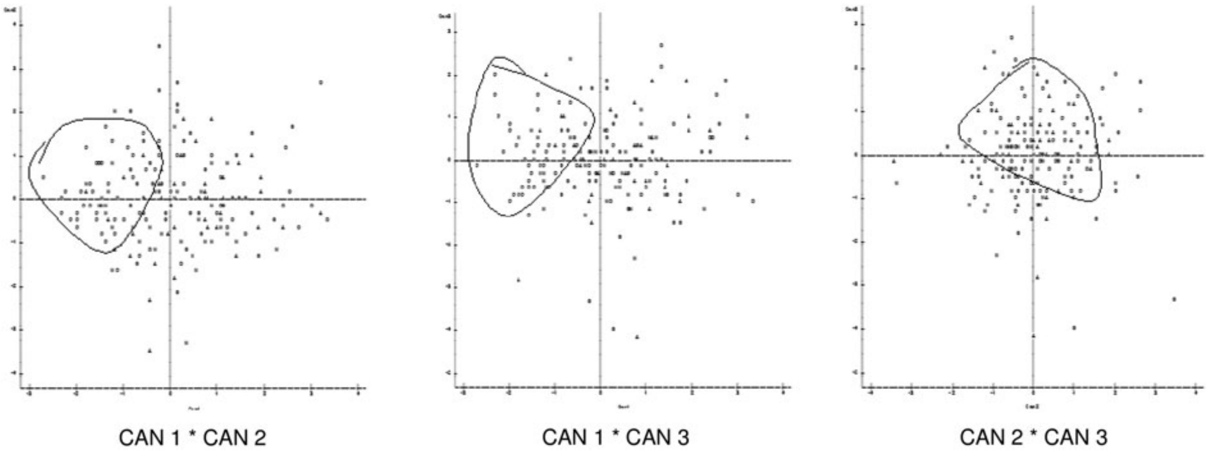

Figure 7. Graphical representation of all individuals according to canonical variables (Draa animals are circled).

Table 3. Mahalanobis distances between the studied populations on the basis of morphometric traits.

	Draa	Atlas	Barcha	Ghazzalia
Atlas	3.74 (***)			
Barcha	5.35 (***)	0.51 (NS)		
Ghazzalia	4.17 (***)	0.33 (NS)	0.76 (NS)	
Un-defined	1.95 (***)	0.49 (NS)	1.46 (***)	0.88 (**)

NS, not significant ($P > 0.05$), $^{**}P < 0.01$, $^{***}P < 0.001$.

identified populations. Thus, three canonical variables were fitted; the first (CAN 1) included HL (0.90) and HOL (0.54), the second (CAN 2) represented HG (0.70), BL (0.56) and BW (0.55) and the third (CAN 3) included EL (0.75) and IC (0.59). The graphical representation of all animals according to these canonical variables (Figure 7) showed that Draa animals tended to be isolated according to CAN 1 *CAN 2 and CAN 1 *CAN 3 plans because of having the highest HG, BL and BW and the shortest HL. Therefore, the most differentiating morphometric traits of Draa breed were HG, BL, BW, HL, EL, IC and HoL.

Mahalanobis distances between the five populations studied were calculated based on the eight morphological traits. These distances showed that the Draa breed had the greatest distance from the other populations (Table 3). The smallest distance of the Draa breed was from the "un-defined goats". The dendrogram of the five populations, built on the basis of the morphometric measurements (Figure 8), showed two main clusters. The first one was formed by Atlas and "Un-defined goats" and the second one by Barcha and Ghazzalia populations. Draa breed was located far from these two clusters.

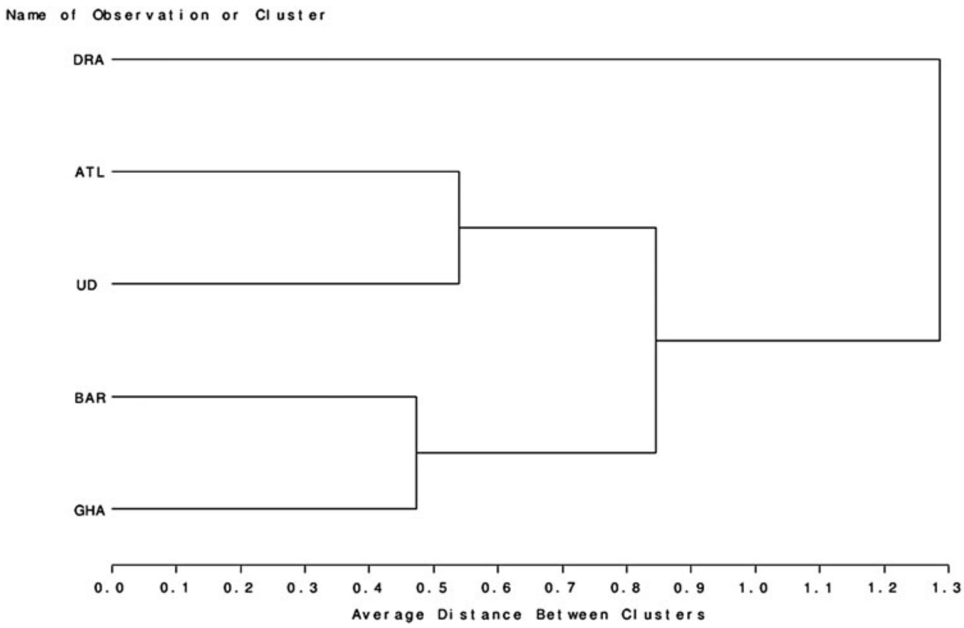

Figure 8. UPGMA tree based on pair-wise Mahalanobis distances of studied populations (DRA = Draa, ATL = Atlas, UD = Undefined, BAR = Barcha, GHA = Ghazzalia).

The discriminant analysis revealed that 88 individuals were misclassified in their own populations. These individuals correspond to 46.9 percent in Atlas, 38.7 percent in Barcha, 4.71 percent in Draa, 39.7 percent in Ghazzalia and 41.3 percent in Un-defined goats. Thus, the Draa breed showed the least assignment error; with only four individuals that were misclassified.

Discussion

The Draa breed was distinguished from the other populations. It had the highest HW, HG, BL and BW, as well as the shortest hair. These findings are in agreement with those already reported on the same breed (Ezzahiri *et al.*, 1989). The variability among populations may reflect some genetic differences and specific adaptation of each population to the environment conditions.

Compared with goats in the Canary Islands, from which the breed was suspected to be introduced, the Draa is less long, has almost the same HW but has a thin chest. Capote *et al.* (1998) reported that measurements' averages of Canary goats were 69.5–72.4; 66.2–71.7 and 92.6–97.1 cm, for BL, HW and HG, respectively. Moreover, Draa goats are similar to goats of Kerala in India (Jimcy *et al.*, 2011) for which HW varied from 62 to 71 cm, BL from 59 to 67 cm, HG from 67 to 75 cm and IC from 7 to 8 cm. However, it is not comparable with Andalusian goats whose morphometric measurements varied from 69 to 78, 71 to 81, 85 to 96 and 8 to 10 cm, for HW, BL, HG and IC, respectively (Herrera *et al.*, 1996).

Moreover, morphometric traits increased with the age, reflecting the development of animals' body with age. The same tendency was reported by Fantahun *et al.* (2013). Also, there was a certain sexual dimorphism in all studied traits, except in HL. This result is in accordance with those of Birteeb *et al.* (2012) and Yadav *et al.* (2013) who found that males had the highest value for all morphometric traits studied in Djallonke and Sahel sheep and in sheep of southern peninsular zone of India, respectively.

The most discriminating traits between the studied populations were BL, HG, HL, HoL EL and BW. These discriminating factors were almost similar to those reported in Andalusian goats (Herrera *et al.*, 1996) and in some goat breeds from the Bench Maji area in Ethiopia (Fantahun *et al.*, 2013). In the opposite, Nafti *et al.* (2014) found that only three morphological measurements (HL, EL and HW) were the most discriminant traits in goats of Tunisian oases.

Based on morphometric measurements, the Draa breed had the largest Mahalanobis distances to other populations. This result is consistent with Machado *et al.* (2000) who found a high genetic distance between Draa- and black-goat called "R'halia". Likewise, Nafti *et al.* (2014) reported a highest distance between Arbi Jerid and Serti Nefzawa goats in Tunisia and attributed this result to differences in body size. In fact, phenotypic divergence between breeds/populations might be partly attributed to differences in management practices, agro-climatic conditions and biophysical resources (Yadav *et al.*, 2013). Also, the different goat populations raised in Morocco appeared to bear specific adaptation, even when submitted to similar conditions and the difference between Draa- and black-goats support the hypothesis of different mechanisms of adaptation (Benjelloun *et al.*, 2015).

The tendency showed by the canonical discriminant analysis is illustrated by the dendrogram of the five populations on the basis of morphometric measurements. Thus, Atlas is closely related to the "Un-defined" goats, and Barcha is closely related to Ghazzalia populations. The Draa breed appears to be far from these four populations. Also, fewer Draa animals were erroneously assigned, indicating homogeneity and distinctiveness of Draa breed. A similar result was found between Florida breed and Andalusia goat populations (Herrera *et al.*, 1996).

Conclusions

The Draa goat breed is morphometrically differentiated and had the largest distances from the other local populations being raised in the neighbouring areas. This distinctiveness can contribute in defining the breed standard and in guiding the genetic improvement programs. However, it is recommended that this study be repeated in the future on a large scale and considering all different areas of Draa breed throughout the Draa valley. Also, more solid characterization tools are needed for further characterization.

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Caractérisation de l'élevage familial de la poule locale (*Gallus gallus*) dans la région de Trarza en Mauritanie

M. Ould Ahmed[1] and A. N'Daw[2]

[1]Département de Production et Santé Animales, Institut Supérieur d'Enseignement Technologique (ISET) de Rosso, Mauritanie; Unité de Recherche Génomes et Milieux, faculté des Sciences et Techniques (FST) de Nouakchott, Université des Sciences, Technologie et Médecine (USTM), Mauritanie; [2]Département des Sciences et Technologies des Aliments, Institut Supérieur d'Enseignement Technologique de Rosso, Mauritanie

Résumé

Cette étude a été entreprise dans trois villages de la région de Trarza en Mauritanie, afin de caractériser la poule locale. Dans les trois villages enquêtés tous les éleveurs ont été interviewés suivant un questionnaire rédigé en français et traduit oralement en *hassanya* ou en *poular* (langues nationales) si nécessaire. Au total, 56 ménages ont été enquêtés et 260 oiseaux (69 coqs et 191 poules) ont été pesés et mesurés. Il ressort de l'étude que l'aviculture familiale est une activité sous la responsabilité des femmes. Malgré son importance socio-économique, elle n'est pas considérée comme une activité principale chez les enquêtés. L'alimentation, la santé et la faible productivité des poules ont été déclarées comme les principales préoccupations des éleveurs. L'âge moyen des poules à l'entrée en ponte est de 6 mois. Le poids moyen des mâles est de 1324 ± 249 g. Celui des femelles est de 1028 ± 229 g. Le poids moyen pour les deux sexes confondus est de 1107 ± 268 g. Le poids moyen de l'œuf est de $31 \pm 4{,}81$ g. Le poids moyen de poussin d'un jour est de $26 \pm 6{,}03$ g. Toutes les mensurations corporelles considérées sont plus élevées significativement ($p < 0{,}05$) chez les mâles. La variabilité observée des caractères permet d'envisager des possibilités de sélection de souches répondant aux besoins des éleveurs. Chez la poule locale le plumage est très varié et présente plusieurs colorations.

Mots-clés: *poule locale, caractérisation, performances, diversité génétique, morphobiométrie, Mauritanie*

Summary

This study was conducted in three villages of the Trarza region of Mauritania. The purpose of this study was to describe the management of and to characterize the local chicken. In the three surveyed villages, all the breeders were interviewed according to a questionnaire drafted in French and translated orally into *hassanya* or *poular* (national languages) as necessary. 56 poultry breeders were surveyed. Measurements were carried out on 260 adult chickens with 191 females and 69 males. The results showed that family poultry rearing is an activity managed by women. In spite of its socioeconomic importance, it is not considered as a main activity among the farmers responding to the survey. Feed resources deficiencies, animal health and the low productivity of the chickens were declared as the main concerns of the breeders. The average age of females when they start to reproduce is 6 months. The average weight of males was 1324 ± 249 g. That of females was 1028 ± 229 g. The average weight for both sexes together was 1107 ± 268 g. The average weight of the egg was 31 ± 4.81 g. The average weight of a chick on any given day was 26 ± 6.03 g. All the considered physical measurements were significantly higher ($p < 0.05$) in males. The variability of characters observed offers possibilities for genetic improvement (selection or crossbreeding). In the local chicken, the plumage was highly varied and presented several tints.

Keywords: *local chicken, characterization, performances, genetic diversity, morphobiometry, Mauritania*

Resumen

Este estudio fue llevado a cabo en tres pueblos de la región de Trarza en Mauritania. El objetivo de este estudio fue caracterizar las gallinas locales y describir su manejo. En los tres pueblos objeto de estudio, todos los criadores fueron entrevistados de acuerdo con un cuestionario, que, en un primer momento, se redactó en francés pero que después se tradujo oralmente, sobre el terreno, a hassanía o a poular (lenguas nacionales) cuando fue necesario. En total, fueron entrevistados 56 criadores de gallinas. Las medidas fueron tomadas sobre 260 aves adultas (191 hembras y 69 machos). Los resultados mostraron que la avicultura familiar es una actividad a cargo de las mujeres. A pesar de su importancia socioeconómica, la avicultura no es considerada como una actividad principal por parte de los ganaderos que contestaron a la encuesta. La escasez de recursos alimenticios, el estado sanitario de los animales y la baja productividad de las aves fueron identificados como las principales preocupaciones de los criadores. De media, las hembras se inician en la reproducción a los 6 meses. El peso medio de los machos fue de 1324 ± 249 g, mientras que el de las hembras fue de 1028 ± 229 g. El peso medio de las aves, independientemente del sexo, fue de 1107 ± 268 g. El peso medio del huevo y el peso medio del pollito de 1 día ascendieron,

Correspondence to: M. Ould Ahmed, Département de Production et Santé Animales, Institut Supérieur d'Enseignement Technologique (ISET) de Rosso, Mauritanie; Unité de Recherche Génomes et Milieux, faculté des Sciences et Techniques (FST) de Nouakchott, Université des Sciences, Technologie et Médecine (USTM), Mauritanie. email : ouldahmedmohamed@yahoo.fr

respectivamente, a 31 ± 4,81 y 26 ± 6,03 g. Todas las medidas físicas consideradas alcanzaron valores significativamente mayores ($p < 0,05$) en los machos. La variabilidad observada en los caracteres ofrece posibilidades para la mejora genética (selección o cruce). En las gallinas locales, el plumaje presentaba una elevada variación y distintas tonalidades.

Palabras clave: *gallina local, caracterización, rendimientos productivos, diversidad genética, morfobiometría, Mauritania*

Soumis: Le 21 août 2014; admis: Le 26 août 2015

1. Introduction

Les poules locales jouent un rôle important dans la vie des familles rurales et présentent les caractères adaptatifs nécessaires à la réussite d'élevage dans les conditions rurales surtout en Afrique. Suite à l'usage accru et la priorité accordée aux races commerciales (Bessadok *et al.*, 2003), les races locales sont aujourd'hui en grande partie marginalisées, menacées et souvent décriées. La disparition continuelle de ces races, constitue une menace pour les ressources génétiques locales par la perte irrémédiable de caractères ignorés aujourd'hui et potentiellement utiles demain (Commission nationale AnGR, 2003).

La connaissance de ces races locales en vue de l'amélioration de leur gestion rationnelle en tant qu'animaux de production représente donc un axe stratégique. C'est en ce sens que de nombreuses études ont caractérisé la poule locale en Afrique : Sénégal (Missohou *et al.*, 1998), en Tunisie (Bessadok *et al.*, 2003), au Congo Brazza ville (Akouango *et al.*, 2004), au Cameroun (Keambou *et al.*, 2007; Fotsa *et al.*, 2010), au Bénin (Youssao *et al.*, 2010), en Ethiopie (Nigussie *et al.*, 2010) et en Centrafrique (Bembide *et al.*, 2013). Néanmoins, aucune littérature n'a été rapportée sur la caractérisation de la poule locale en Mauritanie. Dans ce cadre, nous avons initié un travail de caractérisation dans un contexte de développement durable de l'aviculture familiale. L'étude présentée ici vise principalement à contribuer à la connaissance de la poule locale en vue de sa meilleure valorisation. D'une manière spécifique, il s'agit :

- de caractériser les pratiques de l'élevage et les performances de la poule locale;
- d'apprécier l'importance socio-économique de l'aviculture familiale dans la vie des ménages;
- d'évaluer la variabilité des caractéristiques morpho-biométriques de la poule locale.

2. Matériel et méthodes

2.1 Sites d'étude

L'enquête a été menée pendant les mois de mai et juin 2014, dans les trois villages de *Garak* (16°32´48,2″N 15°45´52″O), *Tounguen* (16°31´07,2″N 15°46´16,3″O) et *Jedida* (16°31´19,2″N 15°46´35,3″O) de la région de Trarza qui jouit d'un climat de type tropical, caractérisé par une saison pluvieuse variable s'étendant de juillet à septembre. Les précipitations moyennes sont à l'ordre de 223 mm. La température oscille entre 15 °C au mois de janvier et 39,2 °C au mois de juin avec une moyenne annuelle de 27,9 °C. L'agriculture et l'élevage sont fortement pratiqués par la quasi-totalité des populations de ces villages, situés sur le fleuve Sénégal et plus particulièrement sur le bras de Garak. Ils sont proches de l'Institut Supérieur d'Enseignement Technologique de Rosso. En absence de toute forme de financement pour ce travail, ces villages ont été choisis à raison de leur proximité de cette institution supérieure d'enseignement et de recherche pour la caractérisation de l'aviculture familiale.

2.2 Collecte des données

A l'aide d'une fiche d'enquête réalisée à cet effet, des informations ont été collectées auprès des éleveurs et mesurées sur leurs poules. Au total 56 familles, détenant 500 poules locales, ont été enquêtées et des observations directes ont été faites sur les élevages en plus des entretiens. L'objectif de l'enquête était de mieux comprendre les pratiques de gestion de l'aviculture familiale dans leurs systèmes d'élevage et d'identifier les contraintes majeures de cet élevage dans le milieu rural. Le questionnaire élaboré couvre des aspects socio-économiques (utilisation de l'aviculture, prix de vente), la conduite des troupeaux (alimentation, habitat, santé), les performances (production et reproduction) et des informations sur la diversité génétique avicole (couleur de plumage, paramètres morpho-biométriques). La connaissance de ces aspects aidera à orienter l'établissement d'un schéma ou d'un scénario d'amélioration et d'utilisation rationnelle des ressources avicoles en Mauritanie.

2.2.1 Données socio-économiques

Les entretiens avec les éleveurs étaient de type semi-ouvert. Le questionnaire s'est focalisé sur les points suivants:

- sexe de l'éleveur
- importance de l'aviculture comme activité économique
- utilisations de l'aviculture
- prix de vente des poules adultes
- effectif du troupeau
- conduite zootechnique et sanitaire
- infrastructures d'élevage disponibles

2.2.2 Données de paramètres de performances

Certains paramètres concernant les performances productives et reproductives ont été enregistrés tels que:

- le poids de l'œuf
- le poids du poussin d'un jour
- le poids vif des poules et coqs adultes
- l'âge à l'entrée en ponte
- le nombre d'œufs pondus par couvaison
- le nombre de couvaisons par an
- le nombre d'œufs éclos après la couvaison
- le nombre de poussins sevrés

2.3.3 Données morpho-biométriques

Les observations morpho-biométriques ont été faites sur 260 individus (69 coqs adultes et 191 poules adultes ayant pondu au moins une fois). Les caractères quantitatifs ont été mesurés à l'aide d'une balance électronique et d'un mètre ruban. Les caractères qualitatifs ont été décrits par observation visuelle.

Les données ont porté sur le sexe et le poids de l'animal, la couleur de plumage, la crête (hauteur, longueur et couleur), la couleur du barbillon, les caractéristiques des pattes (couleur, longueur). Pour chaque animal, nous avons également mesuré la longueur du corps et l'envergure des ailes et le périmètre thoracique.

Les différentes mesures corporelles individuelles (figure 1) ont été effectuées suivant les recommandations de la (FAO, 2013):

- longueur corporelle: distance entre le bout de la mandibule supérieure et celui de la queue (sans plume);
- périmètre thoracique: circonférence de la poitrine prise en dessous des ailes et au niveau de la région saillante du bréchet;
- longueur de l'aile: longueur de l'aile étendue depuis la jonction de l'humérus à la colonne vertébrale jusqu'au bout de l'aile (sans plume);
- longueur du tarse: distance entre le calcanéum et la cheville.

2.3 Analyses statistiques

Les données collectées ont été saisies et soumises aux analyses statistiques descriptives à l'aide du logiciel SPSS version 17.0. Des distributions de fréquence, des moyennes arithmétiques, des écarts types ont été calculés pour les différentes variables. Une analyse de la variance (ANOVA) a été effectuée pour tester l'effet du sexe sur les différentes variables biométriques.

3 Résultats et discussion

3.1 Contexte socio-économique des aviculteurs

Cette étude montre la prédominance des femmes (60%) dans l'aviculture familiale. Cette tendance est comparable aux résultats rapportés par d'autres études dans des pays en développement (Kitalyi, 1998).

Les résultats de l'enquête montrent que le prix de vente des poulets adultes varie de 1250 à 3000 ouguiyas (3,13 à 7,5 €) avec un prix moyen égal à 1650 ouguiyas (4,13 €). L'argent de la vente des coqs et/ou des poules constitue une source de revenu et permet à la famille de s'approvisionner en denrées de base (riz, huile, sucre, thé, etc.). En effet, l'élevage de poules locales peut avoir plusieurs et multiples utilisations sans spécialisation bien différenciée (Tableau 1).

L'aviculture familiale engendre donc un revenu notable et malgré son importance, l'élevage de la poule locale est considéré comme une activité secondaire du ménage chez 85% des éleveurs. Elle est souvent associée à des activités agricoles, qui sont principalement l'élevage des ruminants et d'autres oiseaux (canards, pintades, dindes) et les cultures vivrières et maraichères, activités qui répondent aux besoins alimentaires quotidiens de la famille et génèrent également des revenus monétaires considérables.

D'après les déclarations des éleveurs, les motivations pour l'élevage des poules locales sont attachées à des considérations socio-économiques qui reflètent le niveau de pauvreté des populations rurales. Du fait de leur rusticité, les poules locales sont élevées en divagation avec de légers investissements, ce qui traduit l'incapacité de ces familles à investir de l'argent pour améliorer un système d'élevage souvent fragile. Il est important de prendre en considération ces contraintes, avant d'initier toute politique ou scénario d'amélioration des systèmes d'élevage traditionnel.

3.2 Mode de conduite des élevages avicoles

3.2.1 Alimentation des poules

Les résultats de l'enquête ont montré que 79% des éleveurs laissent les poules en mode de divagation pure. Donc, le système d'élevage est quasi-exclusivement extensif, caractérisé par une complémentation alimentaire chez 98% des éleveurs. Les familles élèvent quelques individus en moyenne avec 9,43 ± 7,43 poules/famille et une gamme de variation de 1 à 35 individus. Pour l'alimentation, les éleveurs utilisent très peu d'aliments composés mais valorisent toutefois des déchets ménagers (restes de la cuisine) et agricoles (mil, riz, repasse, etc.). Les éleveurs fournissent généralement l'aliment et l'eau dans du matériel de récupération utilisé comme abreuvoirs et mangeoires (figures 2 et 3).

3.2.2 Habitat des poules

Les poules sont abritées la nuit afin de limiter l'impact des prédateurs et du vol. Les abris de nuit, observés chez les éleveurs, sont très divers, construits à base de matériaux localement disponibles. Les habitats traditionnels ont l'inconvénient majeur d'être peu spacieux, moins aérés et pas assez hauts et le nettoyage est un peu difficile. Le

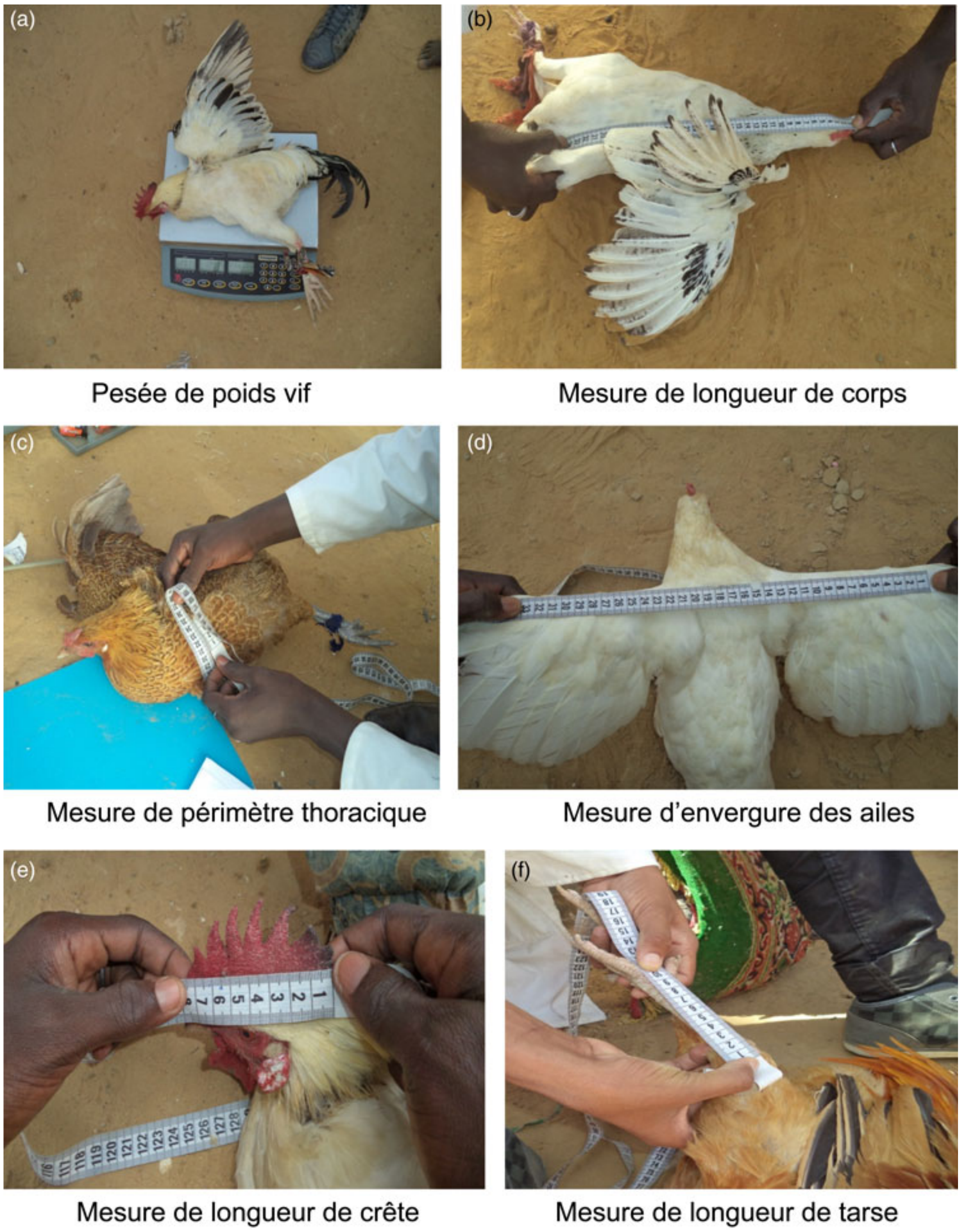

Figure 1. Prise des mensurations corporelles des poules locales adultes.

poulailler peut être construit en banco, en ciment ou en d'autres matériaux et couvert de paille ou de zinc selon les moyens du paysan et la disponibilité des matériaux (figure 4).

3.2.3 Santé de volailles

La santé des poules des élevages enquêtés est globalement très précaire avec un taux de mortalité (entre éclosion et sevrage) de poussin estimé en moyenne à 25%. Les problèmes de santé les plus fréquemment cités sont les mortalités massives (correspondant la maladie de Newcastle) presque toujours en saison chaude. Les résultats montrent que seulement 65% des éleveurs ont déclaré l'utilisation occasionnelle de médicaments et de soins vétérinaires. Egalement, une dizaine d'éleveurs ont rapporté connaître une épidémie qui a ravagé tous leurs troupeaux (la maladie de Newcastle) pendant la période de notre enquête.

Tableau 1. Utilisations de la poule locale en Mauritanie

Utilisation	Effectif	%
Autoconsommation	9	16,4
Vente et autoconsommation	9	16,4
Autoconsommation et don	22	40,0
Vente, autoconsommation et don	15	27,3
Total	55	100

3.3 Performances de reproduction et de production

L'abattage et la vente des poulets sont conditionnés par le degré d'urgence du besoin de l'éleveur ne dépendent

Figure 2. Troupeau se nourrissant de grains épandus sur terre.

Figure 3. Matériel utilisé comme abreuvoir et mangeoire.

généralement ni de l'âge ni du poids des poulets. L'âge moyen des poules à l'entrée en ponte est de 6 mois. De 3 à 4 couvaisons par poule et par an sont rapportées par les éleveurs. Le nombre d'œufs pondus par couvaison varie de 8 à 20 œufs par couvaison avec une moyenne de 12,96 ± 2,715 œufs par couvaison, ce qui peut rapporter 40 à 50 œufs par an. Le taux d'éclosion moyen calculé est de 70%. Cependant, seuls 75% des poussins éclos atteignent le sevrage. Le poids de l'œuf varie de 20 à 41 g avec une moyenne de 31 ± 4,81 g, alors que le poids de poussin d'un jour oscille entre 17 et 40 g avec une moyenne de 26 ± 6,03 g.

3.4 Etude morpho-biométrique des poules locales

3.4.1 Mesures quantitatives

Les résultats (Tableau 2) indiquent que les valeurs moyennes des mâles différent significativement ($p < 0{,}05$) des valeurs moyennes chez les femelles pour toutes les variables étudiées. Le poids vif moyen des individus étudiés s'élève à 1107 ± 268 g. Alors que le poids varie de 900 g à 2000 g chez les mâles avec une moyenne de 1324 ± 249 g, tandis que les femelles présentent un poids inférieur allant de 585 à 2000 g avec une moyenne de 1028 ± 229 g. Ces résultats sont comparables avec ceux mentionnés par plusieurs auteurs (Missohou *et al.*, 1998; Keambou *et al.*, 2007; Hako *et al.*, 2009; Fotsa *et al.*, 2010; Nigussie *et al.*, 2010 ; Bembide *et al.*, 2013). Le dimorphisme sexuel est en faveur des mâles pour tous les caractères étudiés. Les valeurs obtenues dans cette étude sont en général inférieures à celles observées par Bembide *et al.*, (2013) mais supérieures à celles de Moula *et al.*, (2012). Ces différences des résultats peuvent s'expliquer par les conditions d'élevage des animaux étudiés. Ainsi des facteurs intrinsèques tels que le phénotype, l'âge de l'animal et son état physiologique (particulièrement chez la femelle) pourraient également influencer les résultats. La comparaison de trois variables communes (poids vif, périmètre thoracique et longueur de tarse) entre notre étude et quatre études (Keambou et *al.*, 2007) au Cameroun, (Moula et *al.*, 2012) au Congo (RDC), (Bembide *et al.*, 2013) en Centrafrique et (Hassaballah et *al.*, 2015) au Tchad montrent que les moyennes des variables restent dans la gammes de variation de la poule africaine d'une manière générale (Figures 5, 6 et 7).

3.4.2 Mesures qualitatives

Les phénotypes observés au cours de notre enquête se caractérisent par une extraordinaire diversité de coloration du plumage issue du hasard des croisements. Les plumes des poules étaient soit unicolores soit multicolores

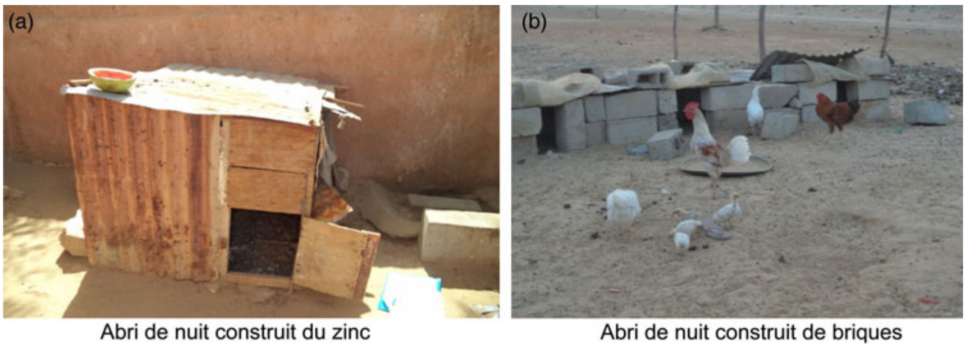

Figure 4. Modèles d'habitat des poules locales.

Tableau 2. Caractéristiques morpho-biométriques des poules locales selon le sexe

Sexe		PV	LCr	HC	LT	PT	LCo	LA
Femelles	Moyenne	1028	29,17	11,22	6,71	26,58	33,48	35,47
	Observation	191	191	191	191	191	191	191
	Ecart-Type	229	7,29	7,06	1,12	2,56	3,21	3,76
	CV (%)	22,26	24,99	62,92	16,69	9,63	9,58	10,60
Mâles	Moyenne	1324	73,27	36,53	7,95	28,37	36,91	39,81
	Observation	69	69	69	69	69	69	69
	Ecart-Type	249	17,71	10,56	0,96	2,46	2,89	3,42
	CV (%)	18,81	24,17	28,90	12,07	8,67	7,82	8,59
Total	Moyenne	1107	40,87	17,94	7,04	27,05	34,39	36,62
	Observation	260	260	260	260	260	260	260
	Ecart-Type	268	22,40	13,83	1,21	2,65	3,47	4,14
	CV (%)	24,22	54,80	77,09	17,18	9,79	10,09	11,30

PV : Poids vif (g), LCr : Longueur de crête (mm), HC : Hauteur de crête (mm), LT : Longueur de tarse (cm), PT : Périmètre thoracique (cm) LCo : Longueur du corps (cm), LA : Longueur des ailes (cm). CV : Coefficient de variation.

montrant des motifs très irréguliers ou pouvant aussi former des dessins parfaitement réguliers (plumage barré). A l'instar de la poule locale africaine dans les autres pays, plusieurs couleurs différentes ont été observées dans les populations étudiées (figures 8, 9, 10, 11, 12, 13, 14). Il s'agit des plumages blanc, blanc sale, blanc herminé, coucou doré, coucou argenté, fauve, fauve à queue noire, rouge, rouge à queue noire, saumon doré, saumon argenté, noire, mille fleurs, froment, caillouté, tout en passant par un panel des couleurs parfois difficile à identifier. La distribution des fréquences selon la couleur de plumage est consignée dans le Tableau 3. Cette multicoloration observée dans nos élevages avicoles traditionnel concorde avec les résultats obtenus par Moula *et al.*, (2012); Bembide *et al.*, (2013) au Congo et en Centrafrique et pour la poule africaine d'une manière générale. La structure du plumage était essentiellement lisse et de rares cas de plumage frisé (figure 15) ou de phénotype cou nu (figure 16) ont été observés. La crête des individus étudiés est principalement de type simple et de coloration essentiellement rouge, mais parfois pigmentée noire. Les barbillons suivent généralement la coloration de la crête. Diverses couleurs se retrouvent au niveau des pattes, qui sont majoritairement blanches et grises, avec l'existence d'autres couleurs minoritaires jaune, verte, rose. Les pattes sont rarement emplumées. La présence de cette multitude de couleurs de plumage et des pattes témoigne de l'existence probable d'une grande variabilité génétique de la poule locale dans la région de Trarza.

4 Conclusion

Cette étude a été menée dans le but de décrire l'élevage de la poule locale dans la région de Trarza. La description a

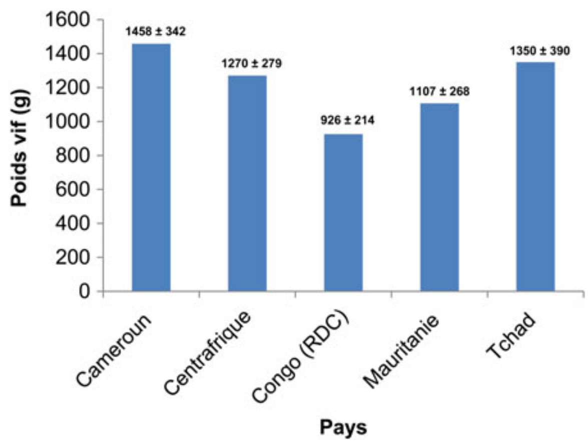

Figure 5. Variation du poids vif moyen par pays.

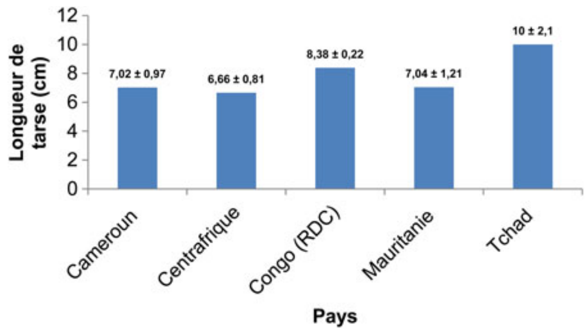

Figure 6. Variation de longueur de tarse moyenne par pays.

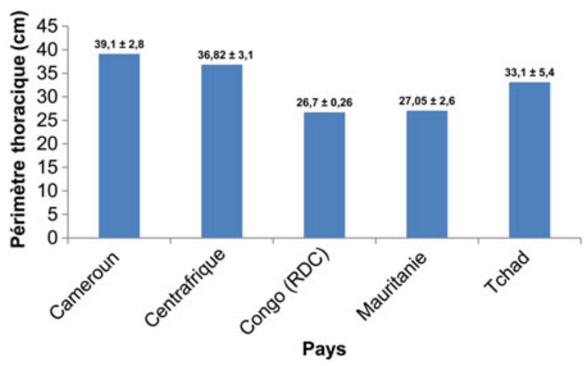

Figure 7. Variation du périmètre thoracique moyen par pays.

Figure 8. Plumage blanc.

Figure 9. Plumage noir.

Figure 10. Plumage fauve.

Figure 11. Plumage coucou.

Figure 12. Plumage rouge.

Figure 13. Plumage saumon.

concerné les techniques d'élevage, les aspects socio-économiques et la variabilité morpho-biométrique. Malgré la faible productivité et les conditions environnementales difficiles dans lesquelles elles produisent, les poules locales jouent un rôle socio-économique incontournable. L'élevage garde encore fortement son aspect traditionnel. Pour développer cette activité et améliorer davantage le profil socio-économique des éleveurs, des actions d'accompagnement (formation, sensibilisation,

Figure 14. Variantes phénotypiques dans un troupeau.

Figure 16. Type cou nu.

Tableau 3. Distribution des fréquences selon la couleur de plumage des poules

Couleur de plumage	Effectif	%
Blanche	59	22,7
Fauve	50	19,2
Coucou	35	13,5
Rouge	32	12,3
Saumon	30	11,5
Noire	22	8,5
Froment	5	3,5
Mille fleurs	9	2,7
Cailloutée	7	1,9
Autres	11	4,2

structuration, incitations financières) en direction des éleveurs sont nécessaires.

La poule présente une grande variabilité, tant dans sa morphologie que dans ses caractéristiques biométriques. Cette diversité génétique des poules locales n'est pas gérée. Cette richesse devrait néanmoins représenter un réservoir génétique pour identifier les gènes d'intérêt économique et adaptatif pour la constitution de types génétiques plus performants et rustiques, par le biais des croisements et de sélection en répondant aux objectifs des éleveurs. Une amélioration simultanée des conditions d'élevage devrait permettre d'accroître significativement la productivité de la poule locale pour en faire, particulièrement en milieu rural, une source sûre de protéines animales de qualité.

Pour la fiabilité et la robustesse des prochaines études de caractérisation de la poule locale en Mauritanie nous suggérons:

– que l'étude de la caractérisation soit élargie sur d'autres zones agro-écologiques de la Mauritanie;
– qu'une étude des performances soit entreprise en milieu contrôlé, afin de quantifier le réel potentiel productif de la poule locale en Mauritanie.
– qu'une analyse moléculaire avec des marqueurs moléculaires soit entreprise pour mieux évaluer la diversité au niveau du génome des populations locales de poules en Mauritanie.

Remerciements

Nous adressons nos vifs remerciements aux éleveurs qui ont été un moment donné une partie prenante de ce travail et ont eu le courage et la bonne volonté de répondre au questionnaire. Nous espérons que ce modeste travail contribue à améliorer la productivité de leurs élevages et surtout améliorer leur niveau de vie.

Figure 15. Type frisé.

Nous remercions infiniment les référés anonymes pour leurs améliorations constructives et pertinentes qu’ils ont apportées à ce travail.

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Estimation of genetic and phenotypic parameters of some important economic traits in Khazak native hen in Iran

Ahmad Ebrahimzadeh-Allahabad[1], Zhila Mahmodian[2], Zahra Pezeshkian[3] and A. Mollaei[2]

[1]*Animal Research Center of Zabol University, Zabol, Iran;* [2]*Graduate Student of Animal Science, Zabol University, Zabol, Iran;* [3]*Department of Animal Science, University of Guilan, Rasht, Iran*

Summary

The purpose of this study was the estimation of genetic and phenotypic parameters of important economic traits in Khazak native hens in Iran. The registered records of 7 434 Khazak native chickens containing 5 238 hens and 2 196 cocks in the research centre of Zabol University from 2007 to 2011 were used. The results of this study were compared with the results of studies on other native chickens breeding in Iran (Yazd: 4198, Mazandaran: 49 536, Esfahan: 23 108, West Azarbaijan: 24 890 and Fars: 30 279). Genotypic and phenotypic correlations between traits and heritability of traits were evaluated by univariate and bivariate animal models using ASREML software. The quantity of some traits such as the average egg production, weight of eggs produced, fertility, hatchability, age of sexual maturity and broodiness were a month 120, 45.15 g, 65.25 percent, 74.83 percent, 5.54 and 1.90, respectively. The heritability of sexual maturity age, the number of eggs produced and egg weight were 0.22 ± 0.41, 0.16 ± 0.13 and 0.50, respectively. The genetic correlation between the age of sexual maturity and the number of eggs produced were 0.95 ± 0.02 and 0.29 ± 0.07, respectively. The results of the study showed that decreasing the sexual age of maturity will lead to an increase in the number of eggs produced. The results of variance analysis showed that some factors such as hen age, broodiness ($P < 0.01$) and the weight of hens have a significant effect on hatchability.

Keywords: *Khazak hen, heritability, genetic correlation, sexual maturity age, egg production*

Résumé

Le but de cette étude a été d'estimer les paramètres génétiques et phénotypiques de certains caractères importants à intérêt économique des poules autochtones Khazak en Iran. Les données prélevées entre 2007 et 2011 sur 7 434 volailles autochtones Khazak (5 238 poules et 2 196 coqs) du centre de recherche de l'Université de Zabol ont été utilisées. Les résultats de cette étude ont été comparés à ceux d'études menées avec d'autres poules autochtones élevées en Iran (Yazd: 4 198, Mazandéran: 49 536, Ispahan: 23 108, Azerbaïdjan Occidental: 24 890 et Fars: 30 279). Les corrélations génotypiques et phénotypiques entre les caractères et l'héritabilité des caractères ont été évaluées avec des modèles animaux univariés et bivariés en utilisant le software ASREML. Les valeurs de certains caractères tels que la production moyenne d'œufs, le poids des œufs produits, la fertilité, le taux d'éclosion, l'âge à la maturité sexuelle et la couvaison ont été un mois de 120, 45.15 g, 65.25 pour cent, 74.83 pour cent, 5.54 et 1.90, respectivement. L'héritabilité de l'âge à la maturité sexuelle, du nombre d'œufs produits et du poids des œufs ont été de 0.22 ± 0.41, 0.16 ± 0.13 et 0.50, respectivement. Les corrélations génétiques entre l'âge à la maturité sexuelle et le nombre d'œufs produits ont été de 0.95 ± 0.02 et 0.29 ± 0.07, respectivement. Les résultats de l'étude ont montré qu'atteindre la maturité sexuelle à un âge plus précoce entraîne une augmentation du nombre d'œufs produits. Les résultats de l'analyse de la variance ont montré que certains facteurs tels que l'âge de la poule, la couvaison ($P < 0.01$) et le poids des poules ont un effet significatif sur le taux d'éclosion.

Mots-clés: *poule Khazak, héritabilité, corrélation génétique, âge à la maturité sexuelle, production d'œufs*

Resumen

El propósito de este estudio fue la estimación de los parámetros genéticos y fenotípicos de algunos caracteres importantes de interés económico en gallinas autóctonas Khazak de Irán. Se emplearon los datos tomados, entre 2007 y 2011, en 7 434 aves autóctonas Khazak (5 238 gallinas y 2 196 gallos) del centro de investigación de la Universidad de Zabol. Se compararon los resultados de este estudio con los resultados de estudios realizados con otras gallinas autóctonas criadas en Irán (Yazd: 4 198, Mazandarán: 49 536, Isfahán: 23 108, Azerbaiyán Occidental: 24 890 y Fars: 30 279). Las correlaciones genotípicas y fenotípicas entre los caracteres y la heredabilidad de los caracteres fueron evaluadas con modelos animales univariados y bivariados usando el software ASREML. Algunos caracteres tales como la producción media de huevos, el peso de los huevos producidos, la fertilidad, la incubabilidad, la edad a la madurez sexual y la cloquez ascendieron un mes a 120, 45.15 g, 65.25 por ciento, 74.83 por ciento, 5.54 y 1.90, respectivamente. La heredabilidad de la edad a la madurez sexual, del número de huevos producidos y del peso de los huevos fue de 0.22 ± 0.41, 0.16 ± 0.13 y 0.50, respectivamente. Las correlaciones genéticas entre la edad a la madurez sexual y el número de huevos

Correspondence to: Z. Pezeshkian, Department of Animal Science, University of Guilan, Rasht, Guilan, P. O. Box 416351314, Iran. email: zahra_pezeshkian@yahoo.com

producidos fueron de 0.95 ± 0.02 y 0.29 ± 0.07, respectivamente. Los resultados del estudio mostraron que alcanzar la madurez sexual a una edad más temprana conlleva un aumento en el número de huevos producidos. Los resultados del análisis de la varianza mostraron que algunos factores tales como la edad de la gallina, la cloquez ($P < 0.01$) y el peso de las gallinas tienen un efecto significativo sobre la incubabilidad.

Palabras clave: *gallina Khazak, heredabilidad, correlación genética, edad a la madurez sexual, producción de huevos*

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The Khazak hen is one of the native chicken species in the Sistan region of Iran and is small in size with short legs (Khash, 2006). Native hens are the most important genetic resource in every country because of their resistance to unsuitable environmental conditions. The genetic reservoir of native hens establishes the basis for the breeding of birds in many developing countries and there is additional evidence to support the productive and reproductive capacities and characteristics in native hens (Hoofman, 2005). The breeding of native hens for economic traits such as growth rate and level of egg production will result in an increase in the productivity levels of hens and will encourage traditional producers to choose native hens. The estimation of genetic parameters will help to determine the current position of native hen flocks and will help specialists to devise strategies for the future. Body weight during 8 and 12 weeks, age and weight at sexual maturity, the rate and weight of eggs produced based on the economic value are known as the most important economic traits in native hens (Kianimanesh, 2000). The evaluation of genetic parameters of economic traits is essential for the breeding of hens (Sapp *et al*., 2004) and different studies have been conducted in order to find the genetic parameters and the process of changes for some traits such as growth, number and weight of eggs produced, age of sexual maturity in native hens in Mazandaran (Kianimanesh, 2000), West Azerbaijan (Jilani *et al*., 2007), Isfahan (Nejati Javaremi, Kianimanesh and Kamali, 2002) and Fars (Kamali *et al*., 2007). But no comprehensive work on genetic and phenotypic parameters estimation and correlation between these traits in Khazak native hens has been published. The purpose of this study is to evaluate the level of genetic parameters and estimate the genetic and phenotypic processes in economic traits in Khazak native hens in the Sistan region.

Material and methods

The data used in this study were collected from the research station in the centre of Zahak, a town having a geographical length of 61°32′0E and geographical width of 31°12′0N and being around 30 km in distance from Zabol. A total of 80 hens and 8 roosters were used to analyse some of the important economic traits. Some traits such as the number of eggs produced, egg weight, fertility, hatchability, age of sexual maturity and broodiness and also the heritability of each trait and the genetic correlation between sexual maturity age and the number of eggs produced and between sexual maturity age and the egg weight have been evaluated in this study. The eggs were pulled from a special pasteboard and immediately transferred to the laboratory where they were cleaned, weighed and measured using a digital scale with accuracy of about ±0.01. The data were then transferred to the computer and the statistical files were established which were then used during this study. The data set consisted of the hen number, sire number, dam number, cage number, age of hen, hatchability, fertility, the level of egg production, weight of eggs produced and additional information on the quality traits of the eggs. The variance (covariance) components were evaluated using the REML and multiple trait animal models. Variances were evaluated using the DMU software (Madsen and Jensen, 2007) and the genetic parameters were estimated using the following bivariate model:

$$Y_i = X_i b_i + Z_i \alpha_i + e_i$$

where Y_i is the observation vector for the i^{th} trait, b_i is the fixed effect vector for the i^{th} trait and is connected to the X_i matrix (including the effect of egg numbers, the age of hen and rooster, broodiness, sexual maturity age, cage number and the weight of bird). α_i is the random effect vector for i^{th} traits and is connected to Z_i, and e is the residual effect vector. X_i and Z_i are the incidence matrixes for the i^{th} trait.

Discussion and results

The rate of egg production, fertility and hatchability

The heritability and average number of eggs produced by Khazak hens during the first 3 months were compared with other native breeds and are shown in Table 1. The average number of eggs produced per year by Khazak native hens is 120; whereas for other native breeds such as Marandi, Zardeh Kerk, Naked neck, it was 80, 65, 35, 130, 102 and 108 (Etemad Zadeh, 1988). The quantity for Rhode Island Red, White Leghorn and Barred Plymouth Rock breeds was equal to 234, 277 and 215 (Kiyani and Sanei, 2001). In general, the Khazak native hen had a higher rate of egg production per year compared with the other native breeds, but it was lower than industrial hens. The rate of egg production can be increased by conducting selected breeding programmes and as the fertility of Khazak is lower than other Iranian native

Table 1. The hatchability, fertility rate, average and heritability of the number of produced eggs during the first 3 months in Iranian native hens.

Native hen breed	The number of each breeds	Hatchability (%)	Fertility (%)	Average number of eggs	Heritability of the number of produced eggs during the first 3 months
Khazak	7 434	74.38	65.25	38.92	0.16 ± 0.13
Yazd	4 198	79.28	69.28	39.74	0.18 ± 0.01
Mazandaran	4 9536	80.23	70.14	38.54	0.158 ± 0.009
Fars	30 279	81.73	71.36	41.50	0.322 ± 0.012
Isfahan	23 108	82.19	72.30	37.82	0.185 ± 0.019
Azerbaijan	24 890	78.92	68.95	42.78	0.099 ± 0.018

($P < 0.01$).

hens there is a need to improve fertility using selected breeding programmes.

The average fertility for Khazak hens was about 65.25 percent and this is shown in Table 2. Some researchers reported that the average fertility was about 76.24 percent for dominant roosters and Fulani-ecotype chicken (Fayeye, Adeshiyan and Olugbami, 2005), whereas it was about 85 percent for Indian hens (Kamble *et al*., 1996). The fertility of hens increased along with an increase in the age of the hen, but fertility decreased when they reach 28 months. Increasing the weight of hens can lead to an increase in the rate of fertility, but this increase has included a fluctuation. The results also show that fertility can also be increased in brooding-hens too, but increasing the level of broodiness in hens more than once will cause a decrease to overall fertility (Hunt, Voisey and Thompson, 1977). The hatchability of Khazak hens where compared with other native Iranian hens and the results are shown in Table 1. The rate of hatchability in Khazak hens is lower than other breeds, with the average hatchability at about 74.83 percent for Khazak hens, while the rate of hatchability reported for industrial breeds about 86–93 percent and the range for Leghorn and for other breeds such as Cornish near to 93 and 86 percent, respectively (Kiyani and Sanei, 2001). The results of a similar study showed that the hatchability rate for Fulani-ecotype chickens in Nigeria was 48 percent (Fayeye, Adeshiyan and Olugbami, 2005). The level of hatchability in Khazak hens is as low as other native breeds, but this parameter will increase by selecting hens with higher levels of hatchability and by improving the nutrition and management status.

The results of analysis of variance indicated that the age of hens, broodiness ($P < 0.01$) and the weight of the hen ($P < 0.05$) had a significant effect on the hatchability rate. The hatchability increased along with the increase in the age of the hen. The weight of hen also had a distinctive influence on hatchability so that increasing the weight of the hens led to increase in hatchability, while increasing the level of broodiness led to a decrease in hatchability.

Table 2. Heritability of sexual maturity age in Iranian native hen.

Type of native hen	Sexual maturity age (days)	Heritability
Khazak	175	0.22
Yazd	172	0.21
Mazandaran	160	0.25
Fars	166	0.35
Isfahan	178	0.28
Azerbaijan	184	0.20

Sexual maturity age, broodiness and weight of eggs

The average age of sexual maturity for native hens in Khorasan, Yazd, Mazandaran, Fars, Isfahan and Azerbaijan basis on reports was about 5.63, 5.76, 5.36, 5.5, 5.96 and 6.616 months, respectively. The average age of sexual maturity of Khazak hens was 5.54 months with the average number of broodiness for Khazak hens at 1.90. The occurrence of broodiness is not an unnatural phenomenon and occurrences of more than one instance of broodiness for some breeds have been reported in other studies. The frequency of broodiness in native hens is more than industrial breeds as industrial breeds have been selected for least amount of broodiness and are reared in artificial environments with controls on the length of daylight. Selection against broodiness is more important in Khazak hens. The average weight of eggs in Khazak hens were 45.15 g, with the weight of an egg less in native hens. For example, during the study on Kedaknat native hens in India, the weight of the eggs was about 42.67 g in the Jobat region, while the weight of eggs in Meganegr was 41.99 and 41 g for the eggs produced from Acil hens (Singh *et al*., 2009). The mean weight of eggs produced by native hens was reported at about 42.87, 47.27, 43.87, 47.88 and 51.16 g in Yazd, Mazandaran, Fars, Isfahan and West Azerbaijan (Ghazikhani Shad, Nejati Javaremi and Mehrabani Yeganeh, 2007). The results of a study on three layers suggested that the weight of the egg was about 66.86, 64.44 and 52.45 for commercial strains with white shell, strains with brown shell and brown native Leghorn (Silversids, Korver and Budgell, 2006) and the weight of eggs for dwarf hens with brown shells about 53.85 g (Zhang *et al*., 2005). The egg weight was reported about 33.04 g for cross-breed hens (dominant rooster, Fulani hen) (Fayeye, Adeshiyan and Olugbami, 2005). The average egg weight in Khazak hens was better than other native hens, but the egg weight can be affected by additional factors such as the age of the hen, sexual maturity age, weight of the hen, broodiness and the number of cages. The results of analysis of variance showed that increasing the weight of a hen will cause an increase in the weight of eggs. The age of sexual maturity also had a significant effect on the egg weight ($P < 0.01$), by increasing the sexual maturity age to a certain level resulted in a decrease in the weight of eggs, but the weight of eggs increased as the hen reached puberty at 6 months. The weight of eggs increased along with the increasing weight of the hen, but a large increase in the weight of the hen led to a decrease in the weight of eggs. The weight of eggs decreased first and then increased along with an increase in the frequency of broodiness. The number of cages also had a significant effect on the weight of eggs due to the slight differences in nutrients in the diets. The Khazak hens had the higher heritability for egg weight compared with other Iranian native hens and the weight of eggs produced by them remained normal (Table 3).

Evaluating the genetic and phenotypic parameters

The bivariate models were used for evaluating the genetic and phenotypic parameters. The evaluated heritability for sexual maturity weight was about 0.35 using the animal model. Evaluating of heritability using different models for sexual maturity weight, coordination of body weight in the 12th week was similar to the estimated heritability using sib animal model. The coefficient of heritability for body weight during the 12th week was higher than the maturity weight. These differences can be attributed to maternal genetic and environmental factors or both. The estimated heritability for the number of produced eggs was relatively low and it was calculated at about 0.19 using the animal model. This estimated value was consistent with different studies which showed that values were low with a range between 0.33 and 0.67. The evaluated heritability for this trait was similar to the heritability of eggs produced using the hen–nest method (0.14) which was reported by other researchers using the animal model (Johnson, 1956). The estimated heritability using the sib animal model was more similar to the evaluated quantity, found using an animal model. The effect of maturity age and sexual maturity weight as connected variants on quantity of eggs produced shows that by increasing the sexual maturity age caused a decrease in egg production and increasing the sexual age weight will cause an increase in egg production. The total average for egg production was about 54.29.

Table 3. Heritability of weight of egg in Iranian native hen.

Type of native hen	Average of first egg weight (g)	Heritability of egg weight (g)	Average of egg weight (g)
Khazak	27.74	0.5	45.15
Yazd	30.22	0.24	42.87
Mazandaran	35.60	0.4	47.27
Fars	33.25	0.38	43.87
Isfahan	34.62	0.29	47.88
Azerbaijan	37.16	0.16	51.16

Evaluating the correlation between traits

The correlation between traits showed that a change in one trait would have an influence on the results of other traits. The genetic correlation between sexual maturity age and number of eggs produced and between sexual maturity age and the weight of eggs was about -0.95 ± 0.02 and 0.29 ± 0.07, while the averages showed the negative genetic correlation between these traits (in the range between 0.5 and 0.11) (Schwartz *et al.*, 1980). Genetic correlations between the body weight in the 12th week and the weight of eggs during the 28th and 32nd weeks were positive and the range of these correlations was from medium to small, with the quantities for them about 0.241, 0.229 and 0.289. The greatest genetic correlation has been seen between the body weight in the 12th week and the weight of eggs produced during the 32nd week. Positive and middle genetic correlations between the pre-mature body weight and the weight of eggs produced have been shown by other studies (Siegle, Van Middelkoop and Reddy, 1978). The quantity of evaluation of these traits was about 0.26 and is the same as the quantity of evaluation of these traits for native hens in Fars province. The genetic, phenotypic and environmental correlations are negative and high and the quantity of them was about −0.625, 0.555 and 0.543. The genetic correlation between sexual maturity age and the number of eggs produced was negative in most of the studies (Siegle, Van Middelkoop and Reddy, 1978). There was a negative and a medium genetic correlation between the number of eggs produced and the weight of eggs from 28th to 30th weeks and 32nd weeks, which was found in the range of −0.20 to 0.44 (Silversids, Korver and Budgell, 2006).

The quantity of some heritability traits such as egg weight, shell weight, shell index, colour of shell, egg width, egg length, the weight of yolk, albumen weight, albumen height, the colour of the yolk, yolk ratio, HU and albumen ratio were estimated at about 0.5, 0.54, 0.30, 0.15, 0.49, 0.36, 0.32, 0.61, 0.42, 0.19, 0.66, 0.46, 0.65, respectively, using bivariate models. The phenotypic and genetic correlations were evaluated among these traits, with the highest phenotypic and genetic correlations seen between the egg width and weight of egg among the external traits which were evaluated at about 0.91 and 0.96. The greatest phenotypic and genetic correlation has been determined between the HU and albumen height, which was calculated at about 0.97 and 0.99.

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Assessing the risk status of livestock breeds: a multi-indicator method applied to 178 French local breeds belonging to ten species

E. Verrier[1,2], A. Audiot[3], C. Bertrand[4], H. Chapuis[5], E. Charvolin[1,6], C. Danchin-Burge[7], S. Danvy[8], J.L. Gourdine[9], P. Gaultier[5], D. Guémené[5], D. Laloë[1], H. Lenoir[10], G. Leroy[1,2], M. Naves[9], S. Patin[11] and M. Sabbagh[8]

[1]INRA, UMR1313 Génétique animale et biologie intégrative, Jouy-en-Josas, France; [2]AgroParisTech, UMR1313 Génétique animale et biologie intégrative, Paris, France; [3]INRA, UE0057 DESLP, Saint-Laurent-de-la-Prée, France; [4]INRA, US0310 CTIG, Jouy-en-Josas, France; [5]SYSAAF, Centre INRA Val de Loire, 37380 Nouzilly, France; [6]Fondation pour la Recherche sur la Biodiversité, Paris, France; [7]Institut de l'Elevage, Paris, France; [8]IFCE, Le Pin-au-Haras, France; [9]INRA, UR0143 Unité de Recherches Zootechniques, Petit-Bourg, Guadeloupe-FWI, France; [10]Institut du Porc, Le Rheu, France; [11]Races de France, Paris, France

Summary

Breed risk status assessment methods are key components of country-based early warning and response systems. In this study, a multi-indicator method was developed to assess the risk status of livestock populations. Six indicators were used: (i) the current number of breeding females; (ii) the change in the number of breeding females over the last 5 years or generations (depending on the species); (iii) percentage of cross-breeding; (iv) effective population size; (v) breeders organization and technical support; and (vi) socio-economic context. To make these indicators comparable, observed values were converted into scores on a six-point scale (from 0 = no threat to 5 = maximum threat); a specific conversion method was used for each indicator. For each breed, the different scores were analysed graphically and an overall score was calculated by averaging the six separate indicator scores. This approach was applied to 178 French local breeds, belonging to ten different species: horse, donkey, goat, pig, chicken, turkey, goose and Pekin duck. A large percentage of local breeds were found to be at risk to be lost for farming, although the results were species dependent. All local equine and pig breeds, as well as almost all local poultry breeds appeared to be endangered. About 80 percent of local goat and cattle breeds, and half local sheep breeds were also found to be at risk. The usefulness of this method with regards to conservation strategies and public policy is discussed.

Keywords: *breeds, endangerment, indicators*

Résumé

La classification des races animales selon leur statut vis-à-vis d'un risque de disparition est un élément-clef d'un système national d'alerte et de suivi des ressources génétiques. Une approche multi-indicateurs a été développée pour établir le degré de menace d'une population animale domestique. Au total, six indicateurs ont été retenus : (i) le nombre total de femelles reproductrices, (ii) l'évolution de ce nombre dans les cinq dernières années, ou générations, selon l'espèce ; (iii) la proportion de croisement ; (iv) la taille efficace de la population ; (v) l'organisation des éleveurs et l'appui technique ; (vi) le contexte socio-économique. Afin de faciliter la combinaison de ces indicateurs de nature différente, les valeurs observées sont converties sur une échelle de 0 (absence de menace) à 5 (menace maximale), la correspondance entre valeurs observées et notes étant spécifique de chaque indicateur. Pour chaque race, les notes sont représentées de façon graphique et une note de synthèse est attribuée en calculant la simple moyenne des six notes. Cette méthode a été appliquée à 178 races locales françaises appartenant à dix espèces différentes : cheval, âne, bovins, ovins, caprins, porc, poule, dinde, oie, canard commun. Il a été ainsi montré que la plupart des races locales françaises peuvent être considérées comme menacées : toutes les races locales d'équidés et de porc, la quasi-totalité des races locales de volailles, environ 80% des races locales bovines ou caprines, et la moitié des races locales ovines. L'intérêt de cette méthode pour la définition de stratégies de conservation et l'élaboration de politiques publiques est discuté.

Mots-clés: *races, risque de disparition, indicateurs*

Resumen

La clasificación de las razas animales según su nivel de peligro en cuanto a su desaparición es un elemento de base para un sistema nacional de alerta y de monitoreo de los recursos genéticos. Un enfoque multicriterio ha sido desarrollado para establecer el nivel de peligro de una población animal doméstica. En total, se mantuvieron seis criterios: (i) el número total de hembras reproductoras, (ii) la evolución de este número en los cincos últimos anos, o las cincos generaciones, según la especie; (iii) la proporción de cruzamientos; (iv) el tamaño efectivo de la población, (v) la organización de los criadores y el apoyo técnico; (vi) el contexto socio-económico. Con el propósito de facilitar la combinación de estos criterios de tipo diferente, los valores observados fueron convertidos en una escala de 0 (ausencia de amenaza) a 5 (amenaza máxima), la correspondencia entre valores observados y notas siendo especifica por cada criterio.

Correspondence to: E. Verrier, AgroParisTech, 16 rue Claude Bernard, 75231 Paris 05, France. email: etienne.verrier@agroparistech.fr

Para cada raza, las notas están presentadas de forma gráfica y una nota de síntesis está calculada como la media de las seis notas. Este método ha sido aplicado a 178 razas locales francesas perteneciendo a diez diferentes especies: ganado, ovino, caprino, cerdo, caballo, asno, gallina, pavo, oca, pato común. Así se demostró que la mayoría de las razas locales francesas se pueden considerar como en peligro: todas las razas locales de équido y de cerdo, casi la totalidad de las razas locales de aves de corral, alrededor de 80% de las razas locales de ganado o caprinos y la mitad de razas locales de ovinos. Se discute el interés de este método para la definición de estrategias de conservación et la elaboración de políticas públicas.

Palabras clave: *razas, puesta en peligro, indicadores*

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Introduction

Livestock local breeds represent unique animal genetic resources. Their preservation and development are important to respond to major challenges such as consumer demand, climate change and production systems evolution. Assessing the risk status of livestock breeds is a key part of country-based early warning and response systems and should be performed before the implementation of any conservation actions or programs, *in situ, ex situ* or both. This recommendation is one part of the first strategic priority in the Global Plan of Action for Animal Genetic Resources (Interlaken International Technical Conference, FAO, 2007). The European Union provides support for endangered breeds, which is proffered based on a threshold number of breeding females established at the national level (CE Regulation Nr 1974/2006). The Food and Agriculture Organization (FAO) also classifies breeds as endangered mainly based on the number of breeding females (Loftus and Scherf, 1993; Scherf, 2000). However, breeds are disappearing not only because of demographic factors, but also because of genetic and socio-economic factors (Audiot, 1995; FAO, 2004); indeed, the sustainability of conservation programs depends on multiple issues (Lauvie *et al.*, 2011). As a consequence, several researchers have suggested using more elaborate risk assessment methods. For instance, Gandini *et al.* (2004) have proposed utilizing a method that combines demographic and genetic criteria (population growth rate based on the number of breeding females, and effective population size based on the numbers of breeding males and females), while Alderson (2003, 2010) has recommended identifying at-risk breeds using numerical scarcity, geographical concentration, genetic erosion (effective population size) and introgression rate. The present study presents a new risk assessment method that incorporates six indicators of demographic, genetic and socio-economic status. This method was checked on 178 French breeds belonging to ten domesticated species. The results are discussed in the context of breed conservation.

Materials and methods

General principle of the method

A multi-indicator approach was chosen that attempted to reconcile methodological simplicity with the need to account for the multiple factors that place breeds at risk. Indicators had to fulfill three conditions. First, they had to be unambiguously tied to breed risk status (i.e. they could not simultaneously represent a risk and contribute to conservation efforts). Second, they should show on what factors breeders could act to improve the status of a given breed. Finally, the information used to calculate them had to be fairly accurate and easy to collect.

Six indicators meeting these requirements were used to assess breed status. They were the following: (i) the current number of breeding females; (ii) the change in the number of breeding females over the last 5 years (mammals) or generations (poultry); (iii) the percentage of crossbreeding; (iv) effective population size; (v) breeder organization and technical support; and (vi) socio-economic context. The first two indicators reflect breed demography, the third and fourth reflect breed genetics and the last two reflect social and economic conditions. In contrast to the suggestion made by Alderson (2010), geographical concentration was not included because it was considered to be too ambiguous. For instance, if a breed is concentrated within a very small area (e.g., on farms in close proximity to each other), there is an increased risk in case of epidemics; however, exchanges among breeders are facilitated, potentially enhancing breed management and thus conservation.

In order to make the indicators comparable, observed scores were converted to fit a six-point scale, which ranged from 0 (no risk) to 5 (maximum risk). The conversion method used for each indicator is described in detail below (see section Converting indicator scores to fit a six-point scale).

Breeds under study

This multi-indicator approach was used to assess the risk status of 178 French "local breeds" belonging to ten domesticated species: horses, donkeys, cattle, sheep, goats, pigs, chickens, turkeys, geese and Pekin ducks. Here, the term "local breed" is defined as per French regulations (*Code Rural*, Article D-653-9) as "*a breed mainly linked to a specific territory by its origins, its location, or its use*", where "territory" means a small subsection of the country. Within this general definition, local breeds of mammals and poultry are defined differently.

Mammalian breeds are officially recognized by the government, namely the French Ministry of Agriculture. For each species, the list of officially recognized breeds and the sub-list of local breeds therein are defined by the government. In this study, all the officially recognized French local breeds belonging to six domesticated mammal species were assessed (Table 1). This amounted to a total of 114 breeds (i.e. about three-fourth of the 158 recognized breeds belonging to these species). In France, sheep is the only domesticated mammal whose stock is primarily composed of local breeds. In other species, local breeds are in the minority (1–30 percent depending on the species; results not shown here).

For poultry, because of the way in which breeding is carried out, the concept of the breed differs. Partly for this reason, French poultry breeds are, as yet, not officially recognized. However, they do exist and are referred to as "breeds" by breeders. The French Ministry of Agriculture is working to institute a poultry-breed recognition process. All French poultry breeds are local (as per the above definition), tend to be rare and are kept by both fancy breeders and farmers wanting to develop an original and/or high-quality line of poultry production. Consequently, in this study, local poultry breeds were the breeds for which the information required for the recognition process has been well established. In total, 63 local poultry breeds, mainly chicken breeds, were examined (Table 1).

Data collection and analysis

Three main sources of information were used: (i) available zootechnical databases; (ii) interviews or written exchanges with the staff of breeders' associations; and (iii) surveys by experts from technical or research institutes. For mammals, national public databases were used. For poultry, private databases were used and may have differed somewhat in their content across breeds. In all cases, when information on a given breed was inconsistent, it was cross-validated.

For each breed, the converted scores for the six indicators were plotted using a radar chart. An overall score (X) was calculated by taking the simple mean of the six separate indicator scores (X_i):

$$X = \frac{1}{6}\sum_{i=1}^{6} X_i$$

In theory, it would have been possible to weight the indicator scores differently. However, because there is currently no reason for granting more weight to one indicator vs another, the simple mean was used instead. Basic statistics (i.e. mean, variance and Pearson correlation coefficients) were obtained, and a principal component analysis using the different breeds' indicator scores was performed.

The method was adapted to provide us with a non-or-all status of the breeds, i.e. "Endangered" vs "Not endangered", required to apply a public policy to support rare breeds. In addition, the FAO system for risk assessment (Loftus and Scherf, 1993) was applied to all breeds under study. To allow the comparison with the proposed method, a score was allocated to each of the possible status in the FAO system, the highest score meaning the higher risk (Table 2). Note that, by nature, the status "extinct" also considered by FAO did not apply to our set of breeds. Also note that the FAO system is based on thresholds on the number of breeding females (*Nf*) and the number of breeding males (*Nm*) that do not depend on the species. The distribution of our overall scores and the status "Endangered" vs "Not engendered" deduced from our method were analysed according to the status in the FAO system.

Table 1. Number of breeds studied categorized by species group and species.

Species group	Species	No of local breeds	Total No of officially recognized breeds
Mammals	Horse	16	21
	Donkey	7	7
	Cattle	28	47
	Sheep	47	57
	Goat	10	14
	Pig	7	12
	Total	115	158
Poultry	Chicken	47	–
	Turkey	3	–
	Goose	9	–
	Pekin duck	4	–
	Total	63	–
Total		178	158

Note that, in France, no poultry breed is officially recognized (the recognition process is underway).

Converting indicator scores to fit a six-point scale

Number of breeding females

The basic principle is to define thresholds of number of breeding females that depend on the capacity to increase a breed actual population size, according to the preproduction abilities of the species. The lower this capacity, the higher is the risk for the breed to be lost. In other words, for a given number of breeding females, breeds from species with a small capacity (e.g. horse) are considered to be more endangered than breeds from species with a higher capacity (e.g. chicken).

Capacity to maintain population size is quantified by calculating the minimum time required to double a breed's actual population size. The term "minimum" means that we consider the most favourable conditions from a demographical point of view. Then, we assume that all suckled (mammals) or live-born (poultry) young females are kept

Table 2. Basic principles of the FAO system to assess the risk status of livestock breeds and arbitrary scores assigned to the different status.

Status	Assigned score	Conditions on the numbers of breeding males (Nm) and females (Nf)	Other condition
Not at risk	0	$Nm > 20$ and $Nf > 1\,000$	
Endangered-maintained	1	$5 < Nm \leq 20$ or $100 \leq Nf \leq 1\,000$	The breed is maintained by an active public conservation program or within a commercial or research facility
Endangered	2	$5 < Nm \leq 20$ or $100 \leq Nf \leq 1\,000$	
Critical-maintained	3	$Nm \leq 5$ or $Nf < 100$	The breed is maintained by an active public conservation program or within a commercial or research facility
Critical	4	$Nm \leq 5$ or $Nf < 100$	

When the number of breeding females is close to one of the two thresholds (100 or 1 000), other indicators such as the evolution of the actual population size or the proportion of cross-breeding may also be taken into account. From Loftus and Scherf, 1993.

for breeding (no selection of replacement females). However, to be realistic, we admit that a given proportion of old females are voluntary culled, for health or fertility problems, for instance.

Assuming a sex ratio equal to half, the number of young females available in any given year (Yf_t) is equal to:

$$Yf_t = \frac{1}{2}N \times Nf_t$$

where Nf_t is the number of breeding females in year t and N is the number of suckled or live-born offspring (mammals and poultry, respectively) per female per year.

After culling, the remaining number of old females (Of_t) is equal to:

$$Of_t = (1 - R)Nf_t$$

where R is the annual proportion of old females culled after breeding. Both N and R are assumed to be constant over time.

Under the hypothesis of no selection of replacement females, after a number of years, the equation describing the change in the number of breeding females from one year to the next is as follows:

$$Nf_{t+1} = \left(1 - R + \frac{1}{2}N\right)Nf_t$$

However, this equation may be not valid during the first few years because young females are not immediately available for breeding. Indeed, for species whose age of females at birth of their first offspring is higher than one year, extra females kept in year t do not have time to be bred and give offspring in year $t+1$. Then, this equation was considered immediately valid for poultry and pig but was applied with a delay of 2, 3 or 4 years, for small ruminants, cattle and equids, respectively. Finally, the minimum time required to double a species' population size, hereafter referred as "doubling time" (DT), and the parameters used to calculate this time, are provided in Table 3. Clearly, DT is longest for equines and shortest for poultry, with all the other species falling in-between.

Capacity to increase the actual population size decreases as DT increases. As a consequence, breed risk thresholds were initially assumed to be proportional to DT. Following a consensus reached by the scientific community and policy makers, it was decided that a cattle breed is considered to be endangered when its number of cows

Table 3. Means of the demographic and reproduction parameters used in this study for different species or species groups.

Species or species group	No. of offspring suckled (mammals) or born alive (poultry) per female per year	Culling rate of old breeding females (%)	Female age at birth of first offspring (years)	Minimum time required to double actual stock[a] (years)	Maximum percentage of cross-breeding that allows stock stability[b] (%)
Horse and donkey	0.6	15	4	8	40
Cattle	0.8	20	3	6	50
Sheep and goat	1.5	20	2	3	72
Pig	9–12	25	1	1	94
Poultry	40–150	100	0.5	0.5	95–99

It should be noted that the local and rather unspecialized breeds examined in this study have a lower productivity and a higher age at first birth of offspring than do mainstream breeds. Note also that a large variability in the productivity was observed between pig breeds or poultry species, this variability being much lower in ruminants and equids breeds.
[a]Assuming that all young females are kept for breeding (no selection of replacement females).
[b]Above this percentage, the annual number of young purebred females is lower than the annual number of old females culled after breeding.

falls below 7 500 (FAO, 2004; European Regulation CE Nr 1974/2006; Alderson, 2003, 2010). This value and the associated value of DT in cattle (equal to 6, see Table 3), were used as reference points for proportionally. Then, for a given species, the value of the threshold (T_{Nf}) was first computed by applying a simple cross-multiplication:

$$T_{Nf} = 7\,500 \times \frac{\mathrm{DT}}{6}$$

At this step, thresholds ranged from 10 000 females for equines to 625 females for poultry.

Three adjustments were made to these initial values to obtain the final values. First, in France, sheep and goats are raised in large to very large flocks and losing a single flock may have strong negative consequences. For this reason, the thresholds for these species were increased. Second, the pyramidal breeding system used in poultry and pigs, even for local breeds, was considered to provide a degree of security. Consequently, thresholds for these species were slightly decreased. Third, all values were rounded for the sake of ease in communication. The result was that the risk threshold was set at 10 000 breeding females for horses and donkeys, 7 500 for cattle, 6 000 for sheep and goats, 1 000 for pigs and 500 for poultry.

By convention, the above thresholds were considered to correspond to the upper limit for a score of 3. The thresholds for the other scores were also defined by convention, with values that remained realistic: (i) the upper limit for a score of 5 (maximum risk) was the rounded threshold used by some authors when describing a breed's status as critical (FAO, 2004; Alderson, 2010); (ii) the lower limit for a score of 0 (no risk) was 10 times the risk threshold; and (iii) the thresholds for the other scores were intermediate between these upper and lower values and were defined in a multiplicative way. The grid used to convert the observed actual population sizes into scores is provided in Table 4.

Recent evolution of the number of breeding females

Demographic trends were assessed over 5 years in mammals and over five generations in poultry. The trends (T_5) were determined by simply comparing the current number of breeding females (Nf_t) to the number present 5 years or generations before (Nf_{t-5}):

$$T_5 = \frac{Nf_t - Nf_{t-5}}{Nf_{t-5}}$$

Breeds with stable or increasing population sizes were considered to be at no risk at all and were thus allocated a score of 0.

For breeds with decreasing population sizes, scores were assigned using the half-life (HL) concept. By convention, a breed was considered to be at maximum risk (score of 5) when the time required to halve its population size (its HL) was less than 25 years (for mammals) or 25 generations (for poultry). If Nf_0 is the initial number of breeding females and the demographic trend per year or per generation (Ta) is constant over time, then the number of breeding females at time t is:

$$Nf_t = Nf_0(1 + Ta)^t$$

A population's HL corresponds to the value of t when Nf_t equals to $(1/2)Nf_0$:

$$HL = \frac{\log(1/2)}{\log(1 + Ta)}$$

From this equation, it can be shown that a HL of 25 corresponds to an annual trend (Ta) of -0.027 (decrease of 2.7 percent per year or per generation). This value corresponds to a rate of decline of 12.9 percent over 5 years or generations (T_5). In order to make it easier to fit the values to a scale from 1 to 5 (recalling that the score of 0 was applied only to no-risk breeds), this value was rounded to -12 percent. Subsequently, the score increased by 1 point when the 5-year or five-generation rate decreased by 3 percentage points. The conversion grid, which was the same for all species, is provided in Table 5.

Percentage of cross-breeding

In this study, "cross-breeding" refers to the practice of cross-breeding (e.g. for commercial purposes) plus any other reasons for which offspring were excluded from

Table 4. Grid for converting the observed number of breeding females into scores, depending on species or species group.

Horse and donkey	150	1 250	10 000	30 000	100 000
Cattle	150	1 000	7 500	25 000	75 000
Sheep and goat	150	1 000	6 000	20 000	60 000
Pig	75	300	1 000	3 000	10 000
Poultry	75	200	500	1 500	5 000
5	4	3	2	1	0

Scores range from 0 (no risk) to 5 (maximum risk), and the numbers given are the bounds for a particular score. For example, for horse and donkey breeds, a score of 5 is given when the number of females is below 150, a score of 4 when the number of females is between 150 and 1 250, and so on.

Table 5. Grid for converting the observed change in the number of breeding females over the last 5 years (mammals) or generations (poultry) into scores.

All species		−12%		−9%		−6%		−3%		0%	
	5		4		3		2		1		0

Scores range from 0 (no risk) to 5 (maximum risk), and the numbers given are the bounds for a particular score; scoring is not species dependent. For example, a score of 0 is given when the trend is positive or null, a score of 1 when the trend is between −3 and 0% and so on.

the breed's stud book (e.g. unknown parentage). A direct consequence of cross-breeding is that fewer young animals are potentially available to replace old breeding animals that have been culled. Using the same notation system as above, if C is the proportion of offspring born from cross-breeding or excluded from the stud book for other reasons, then the number of young purebred females available for breeding (Yf) is described by the equation:

$$Yf = \frac{1}{2}N(1 - C) \times Nf$$

A null value of C means that a breed is not at risk and, therefore, corresponds to a score of 0.

At the other extreme, a score of 5 (maximum risk) was allocated when C was high enough that breeding animals could no longer be replaced (i.e. the number of young purebred females was lower than the number of culled old females). If C_{max} is the maximum value of C allowing replacement, then C_{max} is first determined by solving the following equation:

$$\frac{1}{2}N(1 - C) \times Nf_t = (1 - R) \times Nf$$

where R is the rate at which old females are culled (see section Number of breeding females). Then, C_{max} can be defined in the following way:

$$C_{max} = 1 - \frac{2R}{N}$$

This maximal value of cross-breeding was calculated using the same parameters employed to calculate the number of breeding females. The species-specific values of C_{max} are provided in Table 2 (last column). Indeed, because of their high level of fecundity, poultry and pigs have a very high rate of cross-breeding that allows replacement; in contrast, cross-breeding has to be restricted in low-fecundity species such as equines or cattle.

Having defined the thresholds for the scores of 0 and 5, the thresholds for the intermediate scores were then spaced at equal distances between these lower and upper values (Table 6). Note that, for simplicity's sake, the thresholds used to allocate a score of 5 were rounded for pigs and poultry.

Effective population size

Effective population size (Ne) is a parameter of paramount importance when monitoring both domesticated and wild animal populations. For instance, it allows changes in genetic variability within populations to be predicted (Wright, 1931). Because the availability of molecular data was very heterogeneous across local breeds, effective population sizes were estimated using exclusively genealogical data, by applying the procedure implemented by the French National Observatory of Genetic Variability of Ruminant and Equine Breeds (Danchin-Burge *et al.*, 2014).

For each breed, the sample population comprised animals born over the last 4 or 5 years or generations, depending on demographics (overlapping vs separate generations) and the amount of data available. In equines, a large number of both male and female young are registered yearly therefore the sample population comprised both males and females. In other species, only a few males are registered yearly and consequently the sample populations comprised females only. As recommended by Leroy *et al.* (2013), the method used to estimate Ne depended on pedigree depth as assessed by the equivalent number of known generations (EqG)

Table 6. Grid for converting the observed percentage of cross-breeding into scores, according to species or species group.

Horse and donkey		0		10		20		30		40	
Cattle		0		12.5		25		37.5		50	
Sheep and goat		0		18		36		54		72	
Pig		0		23		46		69		92	
Poultry		0		24		48		72		96	
	0		1		2		3		4		5

Scores range from 0 (no risk) to 5 (maximum risk), and the numbers given are the bounds for a particular score. For example, for all species, a score of 0 is given when the percentage of cross-breeding is 0 (no cross-breeding at all); for horse and donkey breeds, a score of 1 is given when the percentage of cross-breeding is between 0 and 10% and so on.

(Boichard Maignel and Verrier 1997). This parameter is estimated by counting the number of known ancestors of each animal and can be interpreted as follows: pedigree depth is equivalent to the depth in a population where all ancestors are known over a number of generations equal to *EqG*.

If pedigree depth was sufficiently great ($EqG \geq 2.5$), then the rate of kinship within the population ($\Delta\Phi$) was estimated as per Cervantes *et al.* (2011). *Ne* was then estimated using the following classic equation (Wright, 1931):

$$Ne = \frac{1}{2\Delta\Phi}$$

If pedigree depth was shallow ($EqG < 2.5$), then *Ne* was estimated as follows:

$$\frac{1}{Ne} = \frac{1}{4Nm} + \frac{1}{4Nf}$$

where *Nm* and *Nf* are the numbers of male and female breeding animals, respectively.

There are many possible ways of converting effective population size into an indicator of breed risk status (e.g. Frankham, Bradshow and Brook 2014). As in the case of the change in the number of breeding females, the time required for a given decrease in genetic variability was used. Because genetic variability changes asymptotically over time under pure drift, it is not useful to estimate its *HL* because it refers to a far too distant time point. For instance, when the effective size of a population is 40, the *HL* of its genetic variability is 55 generations (i.e. about five centuries of equine selection). We therefore used nine-tenth-of-life (*NTL*), i.e. the time required for genetic variability to decrease by 10percent under drift. The expected proportion of heterozygotes at an anonymous locus (*He*) was used as an estimate of genetic variability. According to Wright (1931), under pure drift, the value of this parameter at generation *t* (He_t) can be predicted if effective population size (*Ne*) is known:

$$He_t = He_0\left(1 - \frac{1}{2Ne}\right)^t$$

where He_0 is the initial value of *He*. By definition *NTL* of *He* corresponds to the value of *t* when He_t is equal to 0.9 He_0. Consequently,

$$NTL = \frac{\log(0.9)}{\log\left(1 - \{1/2Ne\}\right)}$$

By convention, we decided to allocate a score of 5 (maximum risk) to *NTL* values of less than ten generations. The threshold associated with this value was equal to 47.7, which was rounded down to 45. Also by convention, we decided to allocate a score of 0 (no risk) to *NTL* values of greater than 50 generations. The threshold associated with this value was equal to 237.5, which was rounded up to 245. These two extreme rounded values served as bounds to establish the thresholds for the intermediate scores: the score increased by 1 point when the estimated value of *Ne* decreased by 50 (Table 7).

Table 7. Grid for converting estimated effective size into scores.

All species		45		95		145		195		245	
	5	|	4	|	3	|	2	|	1	|	0

Scores range from 0 (no risk) to 5 (maximum risk), and the numbers given are the bounds for a particular score; scoring is not species dependent. For example, a score of 5 is given when effective population size is lower than 45, a score of 4 when it is between 45 and 95 and so on.

Breeder organization and technical support

This indicator clearly differs from the previously described indicators; the information required to define it was largely qualitative. The approach was to identify five different subindicators that described the degree to which breed management is organized and that express whether breeders benefit from support for the development of technical programs (Table 8). Subindicator scores were defined via risk presence vs absence: a score of 1 was allocated to situations in which breeds were most at risk, whereas a score of 0 was allocated to situations favouring good breed management. Note that, for some subindicators, it was possible to allocate intermediate scores (i.e. a score of 0.5). The total score for this indicator was the sum of the five subindicator scores.

Socio-economic context

The approach was the same as for the previous indicator. Five different subindicators were defined, which were

Table 8. Subindicators used to assess breeder organization and technical support.

Subindicator	**Score**
Breeders' association present	Yes = 0; no = 1
In situ management program	Yes = 0; no = 1
Stock in a cryobank	Yes, with more than ten donor animals = 0; yes with less than ten donor animals or no for a species for which cryobanking is technically impossible = 0.5; no for a species for which cryobanking is technically possible = 1
Technical support present	Yes, with local experts and national support = 0; yes, with either local experts or national support = 0.5; no = 1
Cohesion and collective dynamics of breeders	Yes = 0; intermediate = 0.5; no = 1.

The total score for the indicator is the sum of the scores of the five subindicators and thus ranges from 0 (no risk) to 5 (maximum risk).

Table 9. Subindicators used to describe the socio-economic context.

Subindicator	Score
Young livestock farmers start off raising the breed	Yes = 0; intermediate = 0.5; no = 1
Availability of the breed for sale	Yes = 0; no = 1
Markets for products and services	Yes, profitable and diversified = 0; yes, average = 0.5; no = 1
Labels used to distinguish products (PDO and so on)	Yes = 0; no = 1
Financial support given to territories	Yes = 0; no = 1

The total score for the indicator is the sum of the scores for the five subindicators and thus ranges from 0 (no risk) to 5 (maximum risk).

used to characterize the social and economic contexts farmers have to deal with (Table 9). As above, a score of 1 was allocated to situations in which breed value and development were adversely affected, whereas a score of 0 was allocated to situations in which breed value and development were most enhanced. Some subindicators could have intermediate scores. The total score for this indicator was the sum of the five subindicator scores.

Results

Examples of breed characterization

To illustrate the application of the risk assessment method, Figure 1 shows the radar charts obtained for three French local breeds: the Abondance cattle breed, the Boulonnais horse breed and the Rouen Pekin duck breed. These three breeds are in different situations.

The Abondance breed is a robust dairy cattle breed found in the northern French Alps, cows being moved between higher-elevation summer pastures and lower-elevation winter farms. The way the different scores were obtained can be described as follows:

(i) According to the national database for cattle breeding, 48 876 breeding females were present in 2013, which corresponds to a score of 1 (see Table 4).
(ii) According to the same database, there were 50 885 breeding females in 2008. Then, the evolution of *Nf* between 2013 and 2008 was equal to −3.9 percent, which corresponds to a score of 2 (see Table 5).
(iii) According to both *Institut de l'Elevage* (national technical institute for ruminants) and the Abondance breeders association, usually, about 10 percent of cows do not reproduce within the breed. This is mainly due to the practice of cross-breeding with bulls from beef breeds and, to a lower extent, to the lack of pedigree information of some female heifers because of the extensive farming system. Then, the score for the rate of "cross-breeding" was equal to 1 (see Table 6).
(iv) Based on the rate of kinship (pedigree depth was considered as being great enough), the effective size (*Ne*) of the breed was found to be equal to 51, which corresponds to a score of 4 (see Table 7).
(v) Dealing with organization and technical support (see Table 8), there is a well-established breeders'

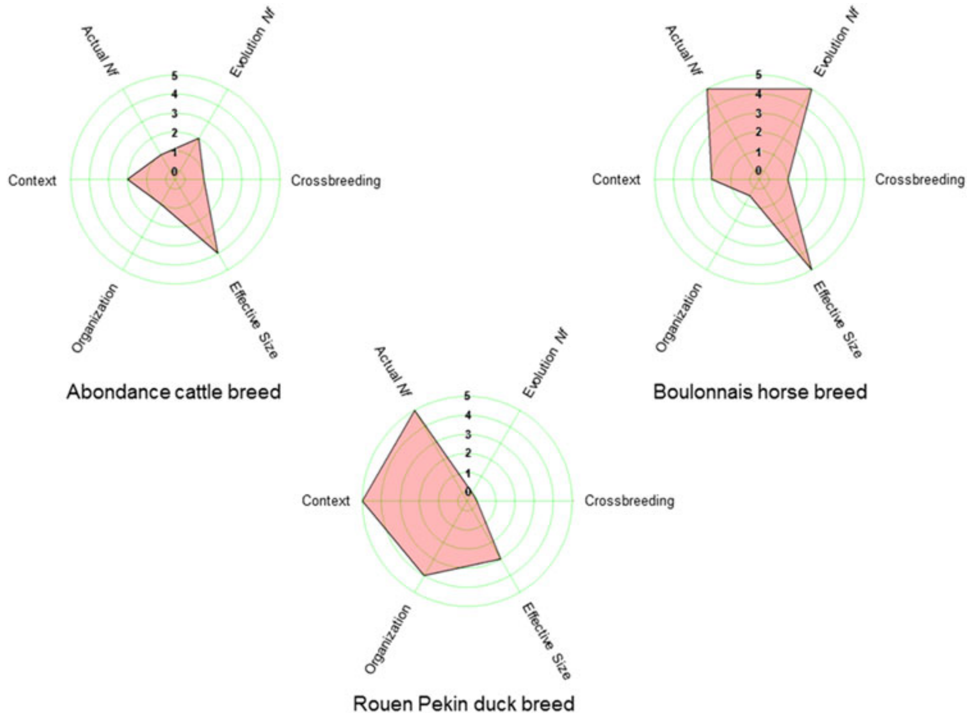

Figure 1. Example radar charts for three French local breeds. For each indicator, scores range from 0 (no risk) to 5 (maximum risk). Actual *Nf* = number of breeding females; evolution *Nf* = evolution of the number of breeding females during the last 5 years or generations; cross-breeding = percentage of crossbreeding; effective size = effective population size (*Ne*); organization = breeder organization and technical support; context = socio-economic context.

association (subscore = 0, i.e. no risk). A breeding company manages a breeding program that performed progeny testing of young AI bulls up until 2014 and that is now performing genomic selection (subscore = 0). In the national cryobank (http://www.cryobanque.org), there are 8 600 doses of semen originating from 66 different bulls (subscore = 0). Technical support is active, both at the national and local levels (subscore = 0). For a long time, there were controversies between breeders about the introgression of Red Holstein genes and, more generally, about the definition of breeding goals, with a clear opposition between breeders promoting a "true" mountain farming system and breeders from piedmont areas (Lambert-Derkimba, Lauvie and Verrier 2013) (subscore = 1). Finally, the score for "Organization" was equal to 1.

(vi) Dealing with the socio-economic context (see Table 9), according to the breeders' association, it is difficult for young farmers to start mainly because the access to land is highly competitive (subscore = 1, i.e. risk), and a few breeding females are available for sale (subscore = 1). The breed is mainly used to produce milk to make cheeses with a good diversity of products and high price paid to farmers for milk (Lambert-Derkimba, Lauvie and Verrier 2013) and also provides with services in the management of Mountain landscapes (Verrier *et al.*, 2005) (subscore = 0). In the area, there are four cheeses with a protected designation of origin (PDO) and a very short list of breeds allowed to produce milk for these cheeses, and it is estimated that 40 percent of the milk produced by all the Abondance cows is used for these PDO cheeses (Lambert-Derkimba, Casabianca and Verrier 2006) (subscore = 0). The breeders' association benefits from both local and national subsidies (subscore = 0). Finally, the score for "Context" was equal to 2.

Finally, the overall score for the Abondance breed was found to be equal to 1.83, signifying that this breed is facing a limited risk of extinction. The radar chart (Figure 1) provides with a valuable complementary information, clearly showing that the main concern about this breed is its low effective population size (note that such low values are commonly observed in dairy cattle populations subject to selection, e.g. Danchin-Burge *et al.*, 2012).

The other two breeds in Figure 1 are the draught horse Boulonnais breed and the local Rouen duck breed. Their overall scores were 3.08 and 2.83, respectively, meaning that these breeds are more endangered than the Abondance cattle breed. The Boulonnais breed received a high score because it received the maximum score for three indicators, namely the number of breeding females (in 2013, $Nf = 483$), the recent evolution of this number ($T_5 = -22.3$ percent) and the effective population size (on the basis of the rate of kinship, $Ne = 40$). In the case of the Rouen breed, the highest scores were found for the economic context (the breed is facing major economic difficulties), the number of breeding females (in 2013, $Nf = 100$) and the effective population size (based on the numbers of breeding parents only, $Ne = 53$).

Score distribution and correlations between indicators

The distribution of the overall scores (i.e. the simple means of the scores for the six indicators) for the 178 breeds examined is depicted in Figure 2. It is bimodal, with one peak between 1 and 1.5 and a second peak between 2.5 and 3.0. The distribution was skewed to the left (less risk): the lowest value was 0, for the Mouton Charollais sheep breed, and the highest value was 3.92, for the Bourbonnais donkey breed. The overall mean was 2.15 and the standard deviation was 0.90.

Certain indicators were correlated (Table 10). The largest positive correlations, ranging from +0.44 to +0.77, involved four indicators, namely the number of breeding females (Nf), the effective population size (Ne), the breeder organization and technical support (OTS) and the socio-economic context (SEC). The evolution of the number of breeding females (T_5) was more or less uncorrelated with the other indicators, whereas the percentage of cross-breeding was negatively correlated with the other indicators (−0.10 to −0.35). As a consequence, the overall score mainly depended on Nf, Ne, OTS and SEC, with correlations ranging from +0.71 to +0.81.

Differences in score distributions among species or groups of species are depicted in Figure 3. Clearly, poultry are distinct. First, the breeds belonging to the four poultry species form a cluster that is narrower than those formed by breeds of other species. This distribution pattern is probably a consequence of the fact that only poultry breeds undergoing official recognition were included in this study, and such breeds share many common characteristics. For instance, their actual population sizes are generally small, they experience no cross-breeding, they have an established breeders' association, the organisation of breeding is more or less pyramidal and they benefit from a technical support by the French federation of poultry breeding companies. Second,

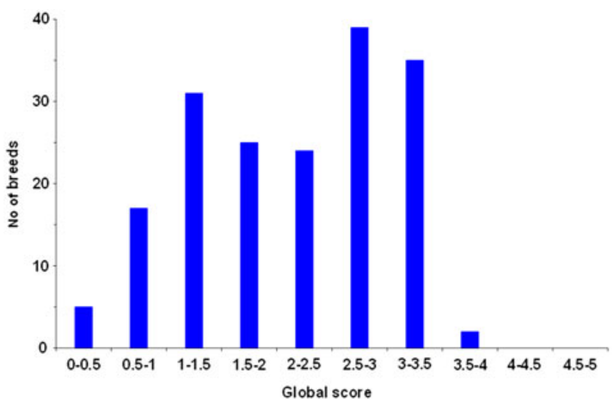

Figure 2. Distribution of overall risk assessment scores for the 178 local breeds examined. Scores range from 0 (no risk) to 5 (maximum risk).

Table 10. Pairwise correlations between the six indicators and the overall score on the 178 local breeds under study (based on the information collected in 2014).

Indicator	*Nf*	T_5	*C*	*Ne*	*OTS*	*SEC*	Overall score
Number of breeding females (*Nf*)	1.00	0.05	−0.35	0.73	0.59	0.65	0.81
Evolution of *Nf* in the last 5 years or generations (T_5)	0.05	1.00	0.20	0.08	−0.10	0.03	0.39
Percentage of crossbreeding (*C*)	−0.35	0.20	1.00	−0.29	−0.34	−0.35	−0.10
Effective population size (*Ne*)	0.73	0.08	−0.29	1.00	0.46	0.44	0.75
Breeder organization and technical support (*OTS*)	0.59	−0.10	−0.34	0.46	1.00	0.76	0.71
Socio-economic context (*SEC*)	0.65	0.03	−0.35	0.44	0.76	1.00	0.77
Overall score	0.81	0.39	−0.10	0.75	0.71	0.77	1.00

on the graph, there was minimal overlap among the poultry breeds and breeds belonging to other groups of species, mainly because the poultry breeds generally had smaller actual population sizes (results not shown).

Applying the multi-indicator method to help France implement European regulations aimed at saving endangered breeds

When applying the EU Council Regulation on support for rural development (RDR2), member countries can give subsidies to farmers who raise local breeds in danger of extinction (the agroenvironment measure). Among other rules, over the period from 2014 to 2020, each breed's number of breeding females and risk status must be assessed by a scientific institution. In France, the national research institute for agricultural research, namely INRA, coordinates such efforts, with the help of technical institutes and breeders' associations.

The multi-indicator method presented in this study was adopted. The purpose was to define clear and simple

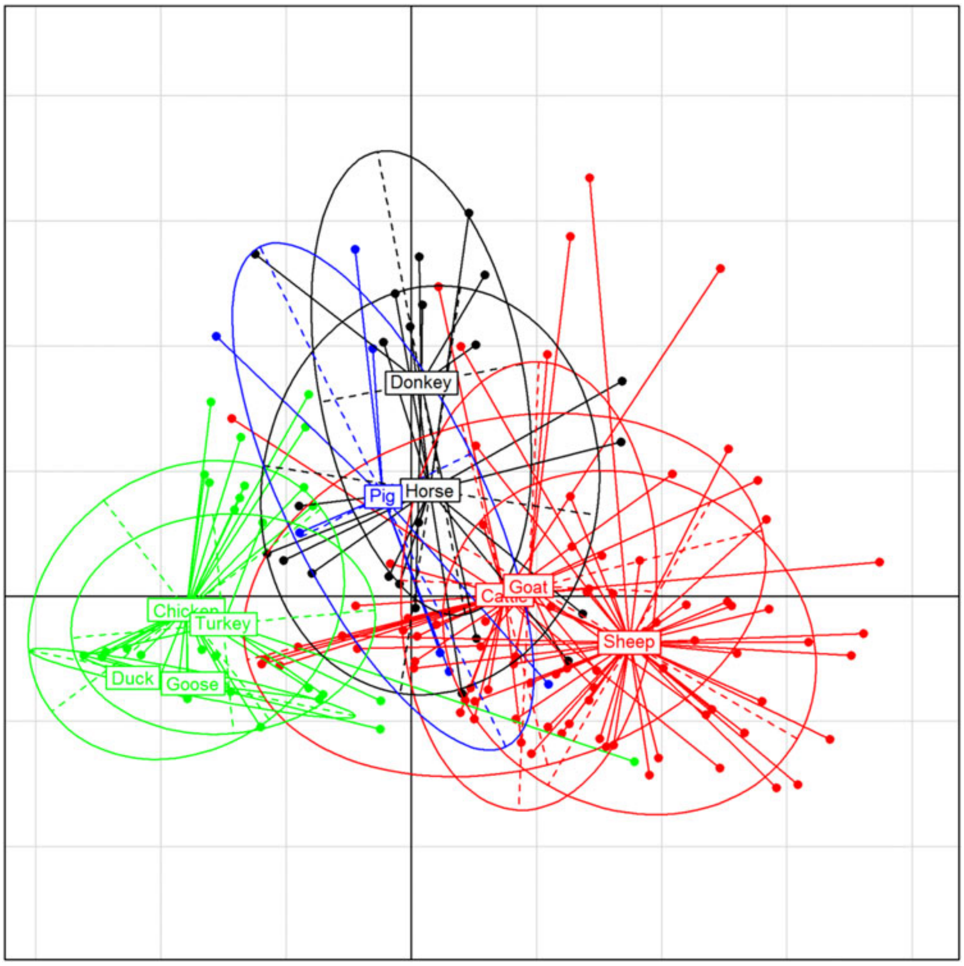

Figure 3. Principal component analysis of the scores of the 178 breeds examined (on the basis of the six separate indicator scores plus the overall score). Breeds were grouped by species clusters: black = equines (horse and donkey), red = ruminants (cattle, sheep and goat), blue = pig, green = poultry (chicken, turkey, goose and Pekin duck).

Table 11. Total number of French local breeds (according to French regulations) and the number of French local breeds considered to be endangered according to the proposed method (based on information collected in 2014).

Species	Total No of local breeds	Local breeds considered under adverse conditions		Local breeds considered endangered	
		Number	Percentage (%)	Number	Percentage (%)
Horse	16	7	44	16	100
Donkey	7	4	57	7	100
Cattle	28	16	55	21	75
Sheep	47	7	15	23	49
Goat	10	2	20	8	80
Pig	7	3	43	7	100
Chicken	47	39	83	45	96
Turkey	3	2	67	3	100
Goose	9	6	67	9	100
Pekin duck	4	4	100	4	100
Total	178	90	51	143	80

rules that could reveal whether or not breeds (and thus breeders) were eligible for subsidies under the agroenvironment measure. The multi-indicator method described above was adapted as follows:

(i) Species-specific thresholds for eligibility were defined based on numbers of breeding females (primary indicator).
(ii) The other five indicators were used to characterize other aspects of breed condition. Conditions were considered as being adverse if the mean of the five scores was greater than 2.5 or if two of the five scores were equal to or greater than 4.
(iii) If conditions were considered as being not adverse, the eligibility thresholds were the upper bounds associated with a score of 3 in the category "number of breeding females" (e.g. 10 000 mares, 7 500 cows, etc.; see Table 3). If conditions were considered adverse, threshold values were augmented by 20 percent.

Table 11 shows the results of applying this method to the 178 local breeds analysed in this study. Overall, about half the breeds under study were considered as being under adverse conditions (based on 5 indicators, actual number of females excluded). Overall too, the proportion of breeds considered endangered (based on the six indicators) is much higher (80 percent). This result shows that a number of breeds are endangered even if their conditions are not adverse, only because of their small actual population size. On the opposite, some breeds have a large actual population size but their conditions are considered adverse (results not shown here). Then, the value of the five other indicators is to provide us with a complementary view of the status of a given breed and to highlight the cases of breeds that could be endangered in the future due to current adverse conditions.

The different species showed different pictures. In the case of pigs, equines and poultry, all breeds or almost all breeds (96 percent of chickens) were considered endangered. For these species too, the proportion of breeds under adverse conditions was found to be the highest. These findings highlight that it is difficult to maintain local breeds of these species under current conditions in Europe. In contrast, only 50 percent of sheep breeds were found to be at risk. This result does not mean that sheep farmers find themselves in a better situation. It is a consequence of the fact that France's sheep stock mainly comprises local breeds, including many breeds with large to very large actual population sizes.

Comparison of the proposed method with the risk assessment system by FAO

Table 12 shows the distribution of the 178 breeds under study in the categories defined by the FAO system (see Table 2) and a comparison with the status of endangerment as assessed with our method (see above). All breeds are in three FAO categories only, i.e. no breed was considered as being "Endangered" or "Critical". This result is due to the nature of our set of breeds. For mammalian species, only the officially recognized breeds were considered. All

Table 12. Joint distribution of 178 French local breeds in the risk status defined by FAO (see Table 2) and in the status according to the proposed method.

Status according to FAO	Status according to the proposed method		Total	
	Not endangered	Endangered	Number	Percentage (%)
Not at risk	34	39	73	41
Endangered maintained	1	54	55	31
Critical maintained	0	50	50	28
Total	35	143	178	100

these breeds have a breeders' association and they are all managed within the framework of a selection program or a conservation program, conservation activities being coordinated at the national level species by species. Then, even if these breeds are considered as being "Endangered" or "Critical" because of their numbers of breeding animals, they are all considered as being "Maintained" according to the FAO criteria (see Table 2). For poultry, only the breeds for which a process of official recognition is ongoing were considered. All these poultry breeds have a breeder association (if not, the recognition process could not be started) and they all benefit of the technical support of the French federation of poultry breeding companies. Then, here again, all these breeds were considered as being "Maintained".

Results obtained with both systems were consistent for the worst situations (Table 12): all breeds considered as being "Critical maintained" and all breeds but one considered as being "Endangered maintained", according to the FAO system, were considered as being "Endangered" when using our method. The only exception was the case of a chicken breed, namely the Noirans-Marans breed, with a number of breeding females ($Nf = 753$) being below the FAO's endangerment threshold (1 000) but above that of our method (500). Conversely 53 percent (39/73) of the breeds considered as being "Not at risk" according to the FAO system, were considered as being "Endangered" according to our method: these 39 breeds belong to the sheep (19), cattle (10), horse (6) and goat (4) species (results not shown). These discrepancies were mainly due to differences in threshold for the number of breeding females (Nf). In the FAO system, thresholds are the same for all domesticated species, whereas, in our method, thresholds are species-dependent: for ruminants and equids species, our endangerment threshold is higher than that of the FAO system, whereas it is lower for poultry.

Figure 4 shows the distribution of the overall scores obtained with our method according to the status defined with the FAO system. Clearly, the higher the degree of threat according to FAO, the higher the median (wide horizontal line) and the lower the main range of variation (distance between the two whiskers) of the overall scores according to our method. The first result (median) illustrates some consistency between both methods. To be precise (results not shown), the Pearson correlation between the arbitrary scores assigned to the different FAO status (Not at risk = 0, Endangered maintained = 1, and so on, see Table 2) and our overall scores was found to be equal to +0.76 for all breeds from all species, ranging from +0.36 (goat) to +1.00 (duck). The second result (range of variation) illustrates the discrepancies evoked above: category "Not at risk" showed the wider range of variation because it comprised breeds considered as being "Not endangered" according to our method, and then with a low overall score, as well as breeds considered as being "Endangered" according to our method, and then with a high overall score.

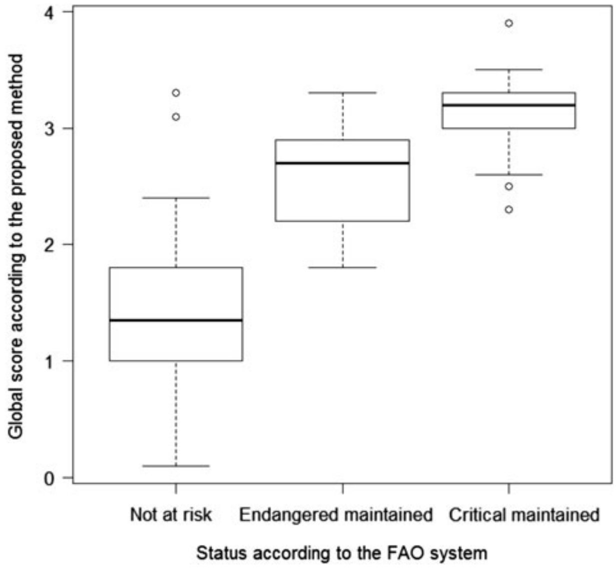

Figure 4. Boxplot of the global (overall) scores obtained with our method (ranging continuously from 0 to 5) according to the status of the breeds defined with the FAO risk assessment system (three categories represented only).

Discussion and conclusions

The aim of the method proposed here is to account for the various factors that place a given breed at risk of extinction. Some of the indicators employed, such as the current number of breeding females or its change over a 5-year period, are similar or equivalent to criteria used in other risk assessment methods (FAO, 2004; Gandini *et al.*, 2004). However, in contrast to other methods, which estimate effective population size (N_e) based on the number of breeding males and females, the method described here used pedigree information, because it can account for unbalanced progeny sizes and historical bottlenecks (Leroy *et al.*, 2013). Among the 178 breeds studied, 99 (56 percent) had enough pedigree information (EqG >2.5) to allow N_e to be estimated from the increase of kinship. It should be noted that, based on Leroy *et al.* (2013), the effective population sizes of the other breeds were probably overestimated.

Three indicators in the method proposed here, namely the percentage of cross-breeding, breeder organization and technical support and socio-economic context, have yet to be included in other methods, despite their very real impact on breed sustainability. In the case of the latter two indicators, many subindicators may be difficult to assess accurately and may require the opinions of experts. Some indicators included in other methods were not used here, either because they have an ambiguous relationship with risk status (as in the case of geographical concentration [Alderson, 2010], as discussed above) or because they were considered to have negligible effects on local-level risk status. For instance, except in a few controversial cases (e.g. Lauvie *et al.*, 2008), introgression rate is not currently considered to represent a threat for French local breeds. However, it should be noted that the cross-breeding practices examined here (i.e. production of cross-bred animals that will never breed) differ from introgression (i.e. production of cross-bred animals that will be the parents of future young).

Nevertheless, the multi-indicator method described in this study is probably more comprehensive than any other previously proposed methods (Gandini *et al.*, 2004; FAO, 2010; Alderson, 2010). To use a larger number of indicators and to average six different scores led to a more continuous view of the degree of risk. More specifically, we showed that our method and the FAO system were consistent for the breeds considered as being in the worst situations. However, because of using species-dependent thresholds for the number of breeding females and considering several other indicators, our method can lead to consider as being endangered for some breeds that are considered as being not at risk by FAO, as it was definitively the case for the set of breeds under study.

The information required to define the indicators is rather simple to obtain, and indicator values are easily calculated. Finally, the fact that the method uses a combination of several indicators should minimize the risk that its purpose will be subverted: the more indicators used to assess breed risk status, the harder will it be for breeders to voluntary maintain indicator values at levels that unlock subsidies.

As previously stated, the indicators and thresholds chosen in this study correspond to circumstances in France. While this method may be well suited to other European countries as well, it may not function adequately in countries where conditions are substantially different. For instance, in the second State of the World's Animal Genetic Resources for Food and Agriculture report (FAO, 2015), indiscriminate cross-breeding (i.e. introgression) was identified as the primary cause of genetic erosion in animal genetic resources in African countries, while it plays only a secondary role in Europe and the Caucasus. Similarly, the indicators or subindicators used should depend on the availability of the information required to calculate them. Risk assessment methods must therefore be adapted to local conditions and take into account specific threats, available information and potential incentives.

Finally, any method used must be able to evolve in response to feedback, technological advances (e.g. the use of genomic information) and changes in national and European legislation, which could either modify risk thresholds or prompt a change in indicators.

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Assessment of institutional capacities of the Gambia Indigenous Livestock Multipliers' Associations

O.F. Olaniyan[1], N.N. Fall-Diop[2], B. Faye[2], A. Secka[1], O.B. Smith[1] and M. Kebbeh[2]

[1]*International Trypanotolerance Centre, PMB 14, Banjul, The Gambia;* [2]*West African Rural Foundation, Sacré Cœur 3 VDN – Villa 10075 Dakar, Sénégal*

Summary

This exploratory study aims to understand and improve the performance of Gambia Indigenous Livestock Multipliers' Associations (GILMA – Fulladu and Saloum) as a way of enabling them to better respond to the challenges faced in fulfilling their institutional responsibilities. Using participatory institutional diagnosis, the GILMA members and experts were able to examine their associations and to stimulate collective reflection as a means of making the associations more efficient and effective. The findings of this diagnosis showed that functioning of both GILMAs was closely linked to the operations of their technical partners. This resulted to GILMAs which clearly lack defined vision and mission. Main issues to address include capacity development of GILMA's executive committee in terms of institutional management, group facilitation, participatory planning, effective strategies for partnership and ownership. Overall, this study developed pathways for revitalizing GILMAs into vibrant and self-sustaining indigenous ruminant livestock multipliers' associations that can effectively carry out specific roles and responsibilities within the three-tier Open Nucleus Breeding Scheme of the International Trypanotolerance Centre.

Keywords: *Association, breeding, GILMA, indigenous, multiplier*

Résumé

Cette étude exploratoire a été menée pour comprendre et améliorer la performance des Associations Gambiennes de Multiplicateurs de Bétail Autochtone (Gambia Indigenous Livestock Multipliers' Association/GILMA Fulladu and Saloum) et leur permettre ainsi de mieux relever les défis de l'accomplissement de leurs responsabilités institutionnelles. Grâce au diagnostic institutionnel participatif, les membres de GILMA et les experts ont pu examiner les bases fondamentales des associations et stimuler une réflexion collective pour les relancer et les rendre plus efficaces et efficientes. Les résultats de ce diagnostic ont montré que le fonctionnement de deux GILMAs était étroitement lié aux opérations des partenaires techniques avec des membres qui identifiaient leur mission et leur vision par rapport aux activités de leurs partenaires. En conséquence, les GILMAs ont manqué d'identité précise et indépendante. Les principaux problèmes à régler, à cet égard, incluront le développement des capacités du comité exécutif de chaque GILMA en gestion organisationnelle et planification participative ainsi que des stratégies efficaces de partenariat et d'appropriation. Dans l'ensemble, cette étudie a balisé les voies pour revitaliser les deux GILMAs en associations dynamiques et autonomes de multiplicateurs de bétail ruminant autochtone qui peuvent s'acquitter efficacement de rôles et responsabilités spécifiques dans le système d'amélioration génétique à noyau ouvert à trois-niveau du Centre International sur la Trypanotolérance.

Mots-clés: *multiplicateur, élevage, GILMA, association, autochtone*

Resumen

Con este estudio exploratorio, se pretende conocer y mejorar el trabajo de las Asociaciones de Criadores de Ganado Autóctono de Gambia (GILMA – Fulladu y Saloum), con el fin de permitirles dar una mejor respuesta a los desafíos a los que se enfrentan en el cumplimiento de sus responsabilidades institucionales. Al usar un diagnóstico institucional participativo, los miembros y expertos de GILMA fueron capaces de examinar sus asociaciones y de incentivar la reflexión colectiva, como modo de hacer las asociaciones más eficaces y eficientes. Los resultados de este diagnóstico mostraron que el funcionamiento de ambas GILMAs dependió estrechamente de las acciones de sus colaboradores técnicos. De ello se deduce que las GILMAs claramente carecen de una visión y una misión definidas. Entre las principales cuestiones a abordar se incluye el desarrollo de las capacidades del comité ejecutivo de las GILMAs en términos de gestión institucional, facilitación de grupos, planificación participativa y estrategias eficaces para la asociación y la propiedad. En términos generales, este estudio marcó vías para la revitalización de las GILMAs como asociaciones dinámicas y autosostenibles de criadores de rumiantes autóctonos, capaces de desempeñar eficazmente roles y responsabilidades específicos dentro del Esquema de Selección de Núcleo Abierto de tres niveles del Centro Internacional de Tripanotolerancia.

Palabras clave: *Criador, Selección, GILMA, Asociación, Autóctono*

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Correspondence to: O. F. Olaniyan, International Trypanotolerance Centre, PMB 14, Banjul, The Gambia. email: ofolaniyan@hotmail.com

Introduction

The roles of livestock farmers' institutions and their respective members in the management of animal genetic resources are becoming more important. In particular, the important roles which these resource-poor farmers can play in successful design and implementation of low-input breeding schemes was recognized by FAO (2007). Nevertheless, some farmers' associations become dysfunctional just a few years after their establishment due to technical, financial and institutional challenges (Rewe, 2009). Specifically, for some developing countries, such associations set up for the breeding and genetic improvements of indigenous animals have become redundant because their objectives were poorly understood by the members or they were inappropriately supported by the relevant stakeholders (Messer and Townsley, 2003). An appropriate assessment of livestock farmers' institutions in terms of formation, modes of operation and interaction is considered important in the context of sustainable animal breeding programme (Sun, 2007; Rewe, 2009).

The present study based on the three-tier Open Nucleus Breeding Scheme (ONBS) of the International Trypanotolerance Centre (ITC), examined the performance, participatory and institutional status of the Gambia Indigenous Livestock Multipliers Associations (GILMAs). The ONBS which was founded in 1995 has a primary objective to increase milk and meat production of three unique breeds of indigenous ruminant species (N'Dama cattle, West African Dwarf goat and Djallonke sheep) without losing their tolerance to trypanosomiasis and other endemic diseases. The GILMA (Figure 1) was established in 2002 in response to the need for effective multiplication and dissemination of superior breeding bulls, bucks and rams to other livestock farmers.

The major objectives of GILMA are to multiply and disseminate the genetically improved animals obtained from the ITC nucleus (first tier) to other farmers in the villages (third tier). ITC owns the nucleus animals and usually sells its selected elite/superior breeding males (bull, buck, ram) to GILMA at a subsidized price, while expecting these associations to in turn to sell the offspring of elite breeding males to the base famers at prices that will generate enough revenues for sustaining their operations. At its creation, both technical and financial supports for GILMA were offered by ITC and the Department of Livestock Services (DLS). In 2003, due to organizational and communication challenges, GILMA was divided along the River Gambia into two branches (GILMA Saloum and GILMA Fulladu). The membership of GILMA Saloum and GILMA Fulladu consisted of livestock farmers living in the north and south of the River Gambia, respectively. Meanwhile, the management of each branch was entrusted to the executive committee members who were elected during the general assemblies.

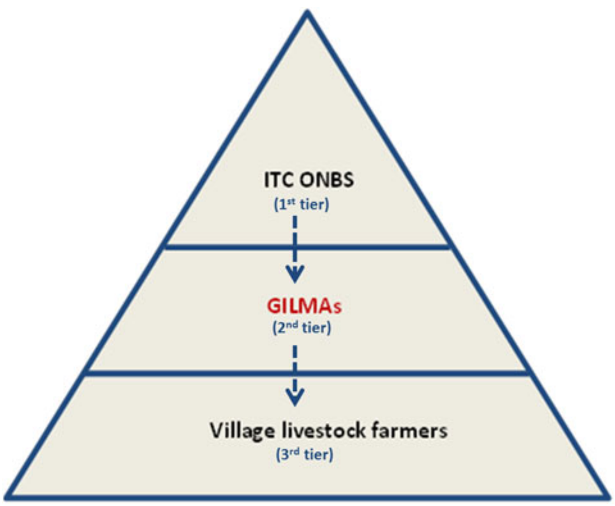

Figure 1. The position of GILMAs in relation to flow of superior male animals from the ONBS of ITC to village farmers.

Like many other farmers' organizations in sub-Saharan Africa, a preliminary assessment of the GILMAs (Fulladou and Saloum) done by ITC in 2012 showed that the two associations had continuously encountered institutional instability in terms of carrying out their set goals (ITC, 2012). This apparently resulted to functionally weak institutions that overly depended on major partners (ITC and DLS) for continuity and survival. To systematically address those challenges, proper assessment through institutional diagnosis and analysis of GILMAs is very important. Grimble (1998) emphasized the need for analysis of institutions in order to identify relationships among various actors and as well as clarify their roles and inherent trade-offs.

This exploratory investigation aims to understand the roles of local institutions involved in the breeding and genetic improvement of indigenous ruminant breeds by assessing how they are organized, what their challenges are, how they can be strengthened and made more sustainable concerning their roles and institutional mandates.

Materials and methods

In the planning phase which lasted for 2 days in February 2014, the experts reviewed and used content analysis to assess GILMAs' constitution, by-laws, registration certificate, bank statements and partners' report of the two associations. By regarding GILMA Saloum and Fulladu as the centre of diagnosis, an inception meeting for elaboration of action plans was held with the ITC staff. A list of materials, persons and organizations to be used for the Participatory Institutional Diagnosis (PID) was also compiled during this period. Meanwhile, PID as designed by the West Africa Rural Foundation (WARF) is a participatory diagnosis and learning tool for understanding an organization's strength and weaknesses. This tool was also used in this study to support identification of innovative changes in both internal and external environments of the GILMAs.

Table 1. Profile of the GILMAs.

	GILMA Fulladu	GILMA Saloum
Date of registration	31 March 2004	Not available
Status	Non-profit organization	Non-profit organization
Intervention areas	URR, LRR, WCR and CRR/South	NBR and CRR/North
Headquarters	Sololo	Kaur
Membership	Open to all aged 18 years and above. Each applicant is charged a registration fee and application for membership is made to the executive committee	Open to interested people subject to payment of registration fee and annual subscription. Membership application is made to the executive committee
Institutional arrangement	General assembly and executive committee	General assembly and executive committee
Affiliation to apex organization	National Farmers Platform of The Gambia since 2013	National Farmers Platform of The Gambia since 2005
Vision and mission	No statement	No statement
Objectives	To promote economic interest of members through the use of poverty alleviation strategies and collective income generating activities	To increase the purebred livestock of The Gambia by breeding pure indigenous cattle and small ruminants and give out the offspring to other farmers
Main activities	Multiplication of pure breeds of N'Dama cattle, West Africa Dwarf Goats and Djallonke sheep breeds	Multiplication of pure breeds of N'Dama cattle, West Africa Dwarf Goat and Djallonke sheep breeds

CRR, Central River Region; URR, Upper River Region; LRR, Lower River Region; NBR, North Bank Region; WCR, West Coast Region

The two PIDs in the form of a focus group discussion were conducted at Fulladu and Saloum and each lasted for three consecutive days. A semi-structured questionnaire was used and the participants consisted of nine and ten members of GILMA Fulladu and Saloum, respectively. They were purposefully selected based on their positions as executive members or as ordinary members with active participation in the affairs of GILMAs. Seven staff from ITC, DLS and PROGEBE (Regional Project on Sustainable Management of Endemic Ruminant Livestock) participated and provided support for the PID at each site of the GILMAs. The diagnosis of each association's institutional, technical and financial issues was done by allowing the participants to answer the questions written on the flip charts. The issues addressed during the PID included GILMAs' strategies for partnership, planning, decision making, reporting and communication. GILMAs' vision and mission statements were reappraised and the associations' strategies for resources mobilization and financial management were assessed by the experts. The diagnoses ended with feedback and briefing sessions on the outcomes of PID. Site visits were also made to GILMA Saloum and GILMA Fulladu members' livestock herds in order to gather more information about their livestock herds and flocks.

In addition to focus group discussions, the experts used individual interviews of participants to engage them in the process of participatory learning and analysis. At the end of field diagnosis, a general feedback and validation workshop was held in order to share the results of PID and to give the relevant stakeholders a general overview of the major constraints and challenges affecting GILMAs' overall functionality as the multipliers of indigenous ruminant breeds in The Gambia. The opportunities and potentials for strengthening the GILMAs were also presented during this workshop while various suggestions of the stakeholders' groups were incorporated into an agreed action plan for revitalizing the two groups.

Results

The desk reviews of relevant documents and the PID generated the following findings:

Institutional landscape of the GILMAs

Both GILMA Saloum and Fulladu were registered as non-profit organizations with clearly stated objectives. Each association (Table 1) has a constitution as well as by-laws, and the executive committees are responsible for an overall management.

With regard to constitution and by-laws, GILMA Fulladu has an appropriate legal document where its objectives and operations are explicitly stipulated, while the statutory bodies of the association are the general assembly and executive committee. In the by-laws, the association was meant to convene at least one annual general meeting, in addition to other special executive committee meetings. Statutorily, the executive committee which consists of the chairperson, vice chairperson, treasurer, secretary, auditor, organizer and adviser can occupy such positions for a 5-year term, while there is a possibility to be re-elected only once through elections of the general assembly. However, the GILMAs were operating outside their constitutional mandates with irregular annual general and executive meetings as well as non-compliance to terms of office by the executive members. Also, there were just a few youths in both the executive committee and in the overall membership.

Regarding membership, any interested person above 18 years of age can apply regardless of gender, ethnic, religious, political party or other affiliations. Applications for membership are made to the executive committee who has the authority to either grant or refuse admission. However, interviews during the diagnosis showed that roles and responsibilities were not clearly understood by many members and even by the leaders. In addition, there have been no annual general or executive committee meeting since 2005 due to lack of continuous support for such activities from ITC and DLS. Similar to GILMA Fulladu, statutory bodies of GILMA Saloum are the annual general assembly and the executive committee. However, there were some discrepancies between the written contents of the by-laws and the verbal assertion of interviewed members. Also the mistake concerning date on the registration certificate of the association was not realized by any of the members prior to the period of this study. GILMA Saloum convened three executive committee meetings between 2003 and 2004, but there was no annual general meeting. Only one out of its seven executive committee members could read and write in the English language and they were all older than 35 years of age. In addition, there were just a few women in leadership positions and the associations had no office building and facilities.

Assessment of GILMAs' performance

As a strategy for multiplication of the genetically selected male animals, the GILMA executive committee, on behalf of all members was expected to purchase elite bulls, bucks and rams from ITC ONBS flocks/herds at discounted price and utilize them only for breeding purpose. Oral interviews and assessment of current records (Table 2) indicates that only a few number of elite males were bought by the GILMA members. Also, activities such as marketing and facilitation of members' access to livestock production inputs were not documented.

The above table also shows that after 10 years of existence, very little progress was realized in terms of the expected GILMAs' roles and responsibilities. The reason for this poor achievement was attributed to the organizational and managerial weaknesses of the associations coupled with institutional instability of the GILMAs' supporting partners which are mainly ITC and DLS. Consequently, the inability of GILMAs to cope with various challenges made the two associations very redundant and institutionally fragile within the ONBS of ITC. Furthermore, there was loss of revenues from sale of elite male animals' offspring because the first breeding stock of bucks, rams and bulls purchased from ITC and retailed to members of GILMA were not recorded and monitored up to the time of this study.

Table 2. Assessment of GILMAs' activities since 2002 to date.

Activities	GILMA	
	Saloum	Fulladu
Purchase of ITC elite stock	Eight bucks, three rams	Five bulls
Facilitating members' access to livestock inputs[1]	No record	No record
Marketing and commercialization of offspring	Limited	Limited

[1]Livestock input refers to veterinary services, breeding facilities and relevant knowledge.

This participatory diagnosis also showed that the current partnership mechanisms between the GILMAs and stakeholders are either absent or not very strong. In addition, the capacities of both GILMAs in terms of strategic financial and technical partnership were very low. As a result, partners' goods and services including access to genetically improved animals, health care, supplementary feeds and marketing facilities were not harnessed by the associations. Even though ITC as one of the technical partners of GILMA used to provide breeding males and organize capacity building workshops, such activities had dwindled due to institutional and financial instability of this research Centre since 2006. DLS, on the other hand, also provided capacity building, monitoring, data recording, access to livestock shows, animal health and watering facilities. However, DLS also experienced institutional instability due to frequent changes in its organizational structure. As a result, its capacity to support the breeding programme especially at the levels of multipliers and livestock farmers was significantly undermined. Besides that, the GILMAs did not take full advantage of relevant livestock and development projects that were at their reach.

Weaknesses in communication and financial management

Poor information flow between members was one of the major constraints that hindered effectiveness and efficiency of the GILMAs. Additionally, the widespread locations of members' farms and houses resulted in poor communication and social interactions. Also, meetings were infrequently held and due to low literacy level of the executive committee members, it was difficult for them to record the number of elite animals purchased and retailed to their members.

Both GILMAs had financial challenges which consequently undermined overall discharge of their statutory roles and responsibilities. Although the first action plan and annual budget at the inception of GILMA was made in partnership with ITC and DLS, those documents were not subsequently reviewed for the strategic purpose of running the two associations in effective and progressive ways. Similarly, the procedures, management practices and accounting systems for normal transactions were neither formalized nor transparent due to inadequate knowledge in petty cash book keeping and financial management.

Although retailing of elite bulls' offspring was supposed to be an important source of income for each association, this was not realized due to lack of appropriate skills in small-scale entrepreneurship. The GILMAs also lacked the basic skills to properly develop proposals, manage the available financial resources and assets or reinforce existing partnerships. The executive committees of the two associations were also not aware of any external funding mechanism and did not demonstrate any initiative that could lead to securing financial opportunity with partners or similar organizations.

Neither GILMA had an annual budget, financial record or loan recovery system. Subsequently, the proceeds that would have accrued from the elite animals sold on credit to members were yet to be recovered, even after 10 years. Also, the few financial resources of the two associations were spent without receipts and records. The procurement of goods and services, as well as commercial transactions were arbitrarily conducted based on loose contracts and moral trust. Although each association has an auditor in the executive committee, there was no audit report and the resources supposedly saved in the bank accounts of the associations were not known by their treasurers. Even though the GILMAs were established to reduce unemployment and poverty rate of members, there was no record of how those goals have being achieved. Furthermore, only few instances of profiting from the animals sold at the individual level were reported, while members of the executive committees were not remunerated.

In this participatory diagnosis, we realized that the processes of decision making in both GILMAs were not transparent. Even though executive committee members asserted that decisions were taken unanimously, this was contradicted by lack of annual general assembly as this was the only entity authorized to take strategic decisions according to the by-laws. Decisions concerning overall management of the associations were not participatory and there was no follow-up on subsequent communication procedures which could have adequately informed the members.

Discussion

The PID used in this study follows the guidelines of Messer and Townsley (2003) and Akpo *et al*. (2012) in analysing the linkages between various actors and stakeholders of local institutions. Involvement of GILMA members and stakeholders in joint reflection and elaboration of a coherent action plan resulted in mutual interactions, improved communication, as well as identification of convergences and divergences at different institutional levels and scales. The discovery and diagnostic approaches embedded in this particular methodology enhanced better understanding of typical farmers group's challenges and opportunities in the context of developing countries. Being used as a stimulating tool for identifying causes and consequences of dysfunction in an association, the PID in the case of GILMAs critically examined both the formal and informal aspects of the two associations with focus on inclusiveness in decision making, financial management and communication strategies. The general approach and outputs of PID which are based on participatory learning, coaching and mentoring principles will strengthen the institutional capacity of GILMAs towards achieving a better management of endemic animal genetic resources in The Gambia. This type of activity, which focused on collective assessment of farmers groups' functionalities by the relevant stakeholders, was also considered very important for sustainable animal breeding programmes (FAO, 2007; Rewe, 2009).

The objectives of this assessment in line with Grimble (1998) and Sun (2007) emphasized the need for analysis of local institutions and community-based associations in order to identify relationships among various actors with respect to clarity of roles and inherent responsibilities. Specifically, an assessment of each GILMA's leadership pattern, resources mobilization, financial management, organizational procedures, partnership strategies and appreciation of external funding environment provided good platforms to explore the associations' history, vision, mission and incentives. The participatory diagnosis as carried out in this study strengthened the key outcomes and also supported strategic reflection on the revitalization plan for capacity development of the GILMAs.

The gender composition of GILMA membership was identified in this study. A higher number of male members can be linked to sociocultural setting in which livestock ownership pattern is differentiated along the gender line in some developing countries. According to Olaniyan and Hiemstra (2012), small ruminant production in the Gambia is associated with women compared with men, who are more involved in cattle production. This is an indication that GILMA membership is majorly composed of male cattle owners even though the groups are open to interested individuals regardless of gender, ethnic, religious, political party or other affiliations. Also, the leadership of GILMAs skewed toward the executive committee members who have little formal education and were all older than 35 years. This pattern of leadership which consisted of more old members was believed to have impacted negatively on the growth, operation and continuity of the GILMAs as youths are believed to be more innovative,

Table 3. Revitalization plan for the GILMAs.

Themes	Actions	Implementation Strategies	Expected outcomes	Responsible agents
Strategic reflection and planning	• Strategic reflection involving all members and elected executive members of GILMAs • Participatory elaboration of annual programmes and identification of partners	Plenary and parallel sessions on the statement of vision, mission and strategic orientations Working groups and plenary sessions for the elaboration of annual programmes	A shared vision, mission and strategic plan	GILMA members, ITC staff, DLS staff and the WARF's experts
Capacity Building	• Organizational management and group facilitation • Communication & information management • Resources mobilization • Financial management • Rural and small-scale entrepreneurship • Livestock management	Training workshop to strengthen the capacity of GILMAs on key issues that are relevant for improving their institutional performance. This workshop aims to benefit various participants drawn from the executive committees, members and key partners	Executive Committee members have the required capacities to perform operations adequately with limited external support	GILMA executive committee members, ITC staff, DLS Staff, and National Farmers' Platform of the Gambia
Coaching and follow-up support	Field visits to GILMAs for *in-situ* assessments of progress in the implementation of revitalization plan, and to provide coaching/ mentoring support to address newly emerged issues	Regular *in-situ* coaching and follow-up support for GILMAs. These visits will seek to address specific problems and challenges associated with the implementation of revitalization plan	Specific problems and challenges are identified and addressed during implementation	ITC staff, DLS staff, and other local partners of GILMA

dynamic and adventurous. However, Jackson, Joshi and Erhardt (2003) states that although relation-oriented diversity expressed in terms of age or gender differences may have tendency to influence relationship among members of a group, it nonetheless does not have direct effect on the group's performance.

The mission and vision of either GILMA Fulladu or Saloum was not explicitly described. This observation undermines adequate understanding of GILMAs' roles and responsibilities as multipliers of endemic ruminant breeds within the ONBS of ITC. Another implication was the incapability of members to adequately describe the formation, evolution and historical progression of their associations. This culminates in their inabilities to precisely draw lessons from past initiatives and strategic interventions of partners. Meanwhile, a structured livestock breeding programme requires clearly defined goals and breeding objectives, consents and wilful participation of farmers in order to be successful (Sölkner, Nakimbugwe and Valle Zárate, 1998; Dekkers *et al.*, 2004). Furthermore, clearly defined visions and missions of a breeder society can enhance optimization of livestock breeding programmes, dissemination of genetic progress and sustainable management of animal genetic resources.

The unavailability of genetically improved animals from the ONBS of ITC as a result of institutional and financial instability illustrates the situation of a few breeding programmes in the developing countries. As an illustration, the National Beef Research Centre (NBRC) in Kenya, which operates a breeding scheme similar to ONBS of ITC, experienced stagnation due to a decentralized production and marketing of animals (Rewe, 2004), while inconsistencies in data collection and analysis by NBRC led to the withdrawal of some livestock farmers (Kahi, Wasike and Rewe, 2006). Meanwhile, a structured breeding and selection programme for producing genetically improved animals on a regular basis can be achieved through breeding activities such as animal recording, genetic evaluation, selection and mating (Hazel, Dickerson and Freeman, 1994).

The GILMAs' overdependence on ITC in addition to the inadequate knowledge of the associations' role and responsibilities can be addressed by considering the Boran Cattle Breeders Society (BRBS) which was responsible for its own administration, maintenance of stud book and marketing of elite animals (Rewe, 2009). Also, the mode of GILMAs' dependence on partners such as ITC and DLS can be minimized through self-organized livestock genetic improvement scheme in which the roles of professional and educated GILMA members will include data recording, maintenance of stud books and coordination of similar activities that are relevant for maintaining the indigenous breed in pure forms. This will give GILMAs the institutional status and sense of ownership over the endemic ruminant species in the Gambia. In order to analyse and interpret the data for selection and mating purposes, and to disseminate the improved genetic material of such a scheme through reproductive techniques, strategic partnership with ITC and DLS then becomes expedient and this needs to be explored accordingly.

Apart from ITC and DLS, there was no recorded action aimed at fostering GILMA's partnership with other relevant key stakeholders in the recent years. This type of isolation of GILMAs from potential partners is a manifestation of weak leadership. While GILMA Saloum and GILMA Fulladu are working on similar livestock breeding objectives, there was however no formal link between the two associations. As a result, the associations were unable to collaboratively draw any benefit from the developmental opportunities that exist in the livestock sector of the Gambia. This institutional weakness also hindered GILMAs' ability to benefit from strategic consultation with the relevant government agencies and community-based organizations. Such incongruence with the potential partners and sponsors is significant for the GILMAs and could partly explain the low performance of the two associations.

However, a collaborative breeding programme in which livestock breeders' association can strategically partner with researchers were described by Bosso (2006) and Kahi, Rewe and Kosgey (2005). At the sub-regional levels of sub-Saharan Africa, Rewe (2009) suggested a genetic improvement programme comprising the breeders' associations, government and national agricultural research institutions while Madalena *et al.* (2002) attributed the success of breeding programmes in Brazil to collaborations between breed societies, private firms, universities and research institutions. For the GILMAs, these associations' organizational skills and management needs to be improved in order to enhance better performance and strategic partnerships with research institutions and other relevant agencies in the Gambia. Although the idea of merging the two GILMAs into a single apex association that could facilitate clearly defined and better partnership may be a good approach, however such process should not be driven from outside the two associations as it may result in lack of ownership and commitment of members.

Conclusions

It can be concluded from this study that the GILMAs were not efficient at multiplying and disseminating the improved male breeding animals from the nucleus to livestock farmers in the villages. Their constraints and challenges were linked to internal factors and also, the institutional and financial challenges of partners such as ITC and DLS. To revive the GILMAs, various opportunities and potentials for strengthening the two associations were highlighted and agreed upon by the relevant stakeholders. Main issues to address will include capacity development of GILMA's executive committees in terms of institutional and financial management, group facilitation, participatory planning and improved strategies for partnership.

Recommendations

The plans presented here represent the necessary and realizable actions for developing self-reliant GILMAs. They are based on the principle of members' inclusiveness although with facilitation and capacity building supports from the partners of GILMA. Consequently, all actions aiming at reinforcing GILMAs must take into account the following issues:

- Draft of constitution and by-laws with the assistance of a legal adviser to ensure conformity with the members' aspirations and decisions;
- Clearly stated membership and registration fees;
- Clearly defined duties and rights of members;
- Restructuring and re-election of the executive committee members including new position for a deputy treasurer in the executive committee to enhance ease and transparency in cash management;
- Clear definition and documentation of roles and responsibilities of executive committee members in the local languages;
- Required minimum literacy level for any aspiring member of the executive committee;
- Development of strategic framework (vision, mission and strategic plan) for each GILMA;
- Reinforcement of GILMAs' strategic partnerships in order to benefit from the apparent opportunities that this may present.
- Implement the key capacity development themes, actions, and implementation strategies presented in Table 3.

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Recent Publications

The Governance of rangelands: collective action for sustainable pastoralism

Edited by P. M. Herrera, J. Davies and P. Manzano Routleddge, London Published in 2014, pp. 320 ISBN 978-1138785144

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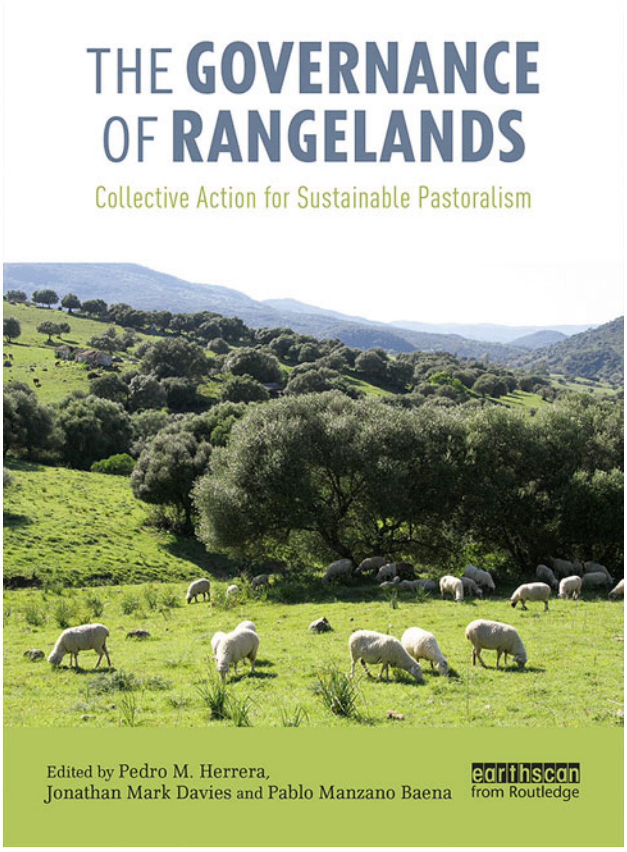

Governance is recognized to be a key factor in achieving the sustainable use of rangelands. Among the pillars having sustained pastoralist livelihoods for millenia (environment, economy and society), social control is fundamental in preventing misuse of resources or breakage of usage regulations. A fundamental adaptation component of pastoralists to the harsh landscapes they inhabit, in drylands, mountains or cold areas, is the risk-spreading strategy of communal land use and management, so collective use regulations of the land have been inevitable in all pastoralist systems on Earth. Respecting such rules guarantees the provision of ecosystem services and maintenance of ecosystem function – evidence of extensive livestock in providing such services is increasingly growing in the last decades. The long-term economic sustainability of livestock keeping is also only guaranteed by such a sound ecosystem management.

The right of users to manage rangelands is however a contentious issue. Attributing local communities the capacity to make decisions on the lands they use implies a delegation of power by the State that many governments regard suspiciously. In addition, rangelands are often owned either by the State or by private owners that may or may not practice complementary activities on such lands, thus further deepening potential conflict over such lands. The issue is further deepened by the disregard on communal ownership that modern economic theory poses, with troubles to e.g. get credits for livestock kept and therefore exacerbating the need for livestock keepers to own land, or by making it impossible to implement soil carbon fixation payment schemes.

In this context, it is therefore fundamental to understand the main challenge for pastoralists around land. The ownership of land becomes a secondary issue, tenure and access rights being much more important to guarantee livelihoods. In order to guarantee food security, sound environmental management and the maintenance of a basic economic activity in otherwise sparsely populated landscapes, the access to rangelands at the right times of the year is the most fundamental element.

Previous publications have already dealt with the issue on how rangeland users can secure their land access. Also at International Union for Conservation of Nature (IUCN), "The land we graze" (IUCN, 2011) was published in 2011 as a compendium of examples worldwide where pastoralist organizations and collectives secured their access to land. A further fundamental piece of information is "Restoring community connections to the land "(Fernández-Giménez *et al*., 2012), centred on China and Mongolia, a scenario particularly challenging because of the widespread land degradation problems as well as because of the troubles in overcoming the language barriers."

"The Governance of Rangelands" completes these views by presenting a compendium of experiences across different projects to enable local pastoralist communities in securing their user's rights. Case studies from fully industrialized countries such as the USA or Spain are combined with others from Morocco, Lebanon, Jordan, Mongolia, Niger, Cameroon, Kenya and Botswana to bring a global picture of the latest developments in the field – unfortunately, a case study in Bolivia had to be finally left out. The information is put in the context of rangeland use and governance to illustrate the full meaning of achieving sound community-controlled land tenure and use.

The book ultimately shows, through multiple examples and a thorough analysis, the importance of setting up governance schemes that are acceptable for the local communities in order to have them fully on board to work for the future of rangelands. Such a piece of information needs to be urgently taken into account for the policy formulation in rangelands by governments and for the intervention of development agencies and non-governmental organizations in these settings.

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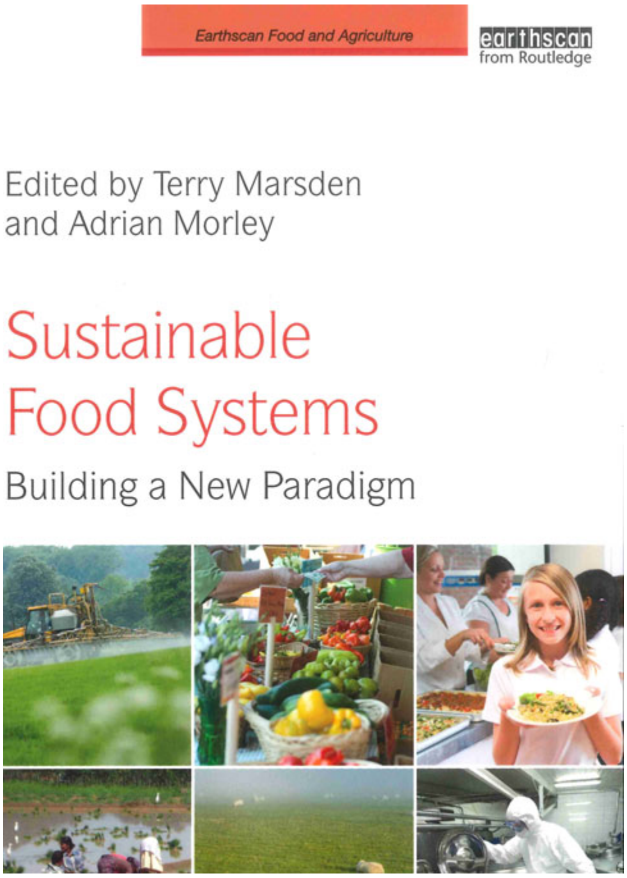

Sustainable food systems: building a new paradigm

Edited by T. Marsden and A. Morley Routleddge, London and New York Published in 2014, pp. 240 ISBN 978-0-415-63955-2

doi:10.1017/S2078633615000351

In response to the challenges of a growing population and food security, there is an urgent need to construct a new agri-food sustainability paradigm. This book brings together an integrated range of key social science insights exploring the contributions and interventions necessary to build this framework. Building on over 10 years of Economic and Social Research Council funded theoretical and empirical research centred at Business relationships, Accountability, Sustainability and Society (BRASS), it focuses upon the key social, economic and political drivers for creating a more sustainable food system.

Themes include:

- regulation and governance
- sustainable supply chains
- public procurement
- sustainable spatial strategies associated with rural restructuring and re-calibrated urbanized food systems
- minimizing bio-security risk and animal welfare burdens.

The book critically explores the linkages between social science research and the evolving food security problems facing the world at a critical juncture in the debates associated with not only food quality, but also its provenance, vulnerability and the inherent unsustainability of current systems of production and consumption. Each chapter examines how the links between research, practice and policy can begin to contribute to more sustainable, resilient and justly distributive food systems which would be better equipped to "feed the world" by 2050.

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Sustainable food systems: building a new paradigm

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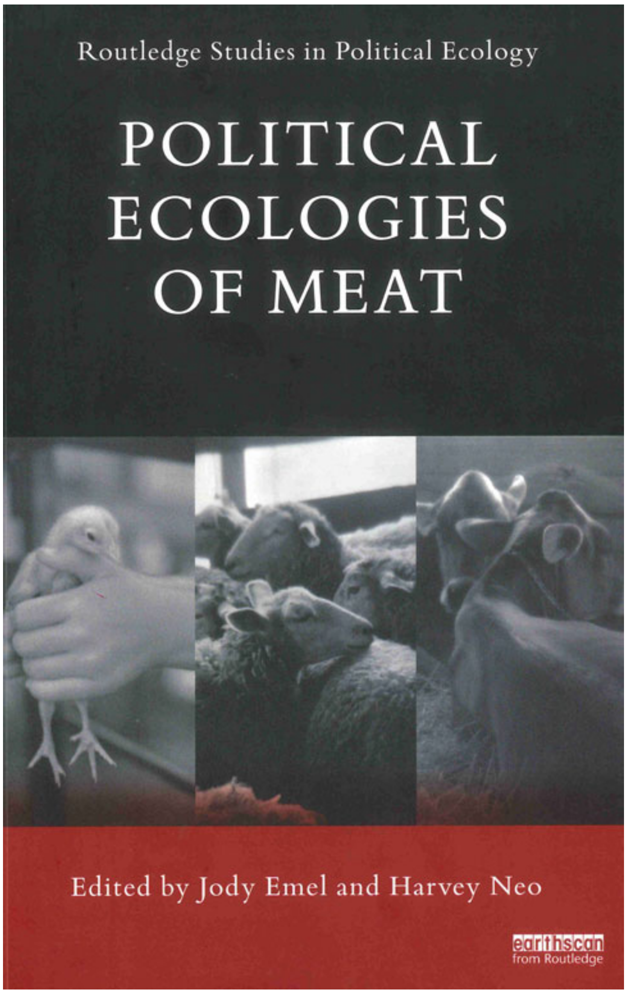
Livestock production worldwide is increasing rapidly, in part due to economic growth and demand for meat in industrializing countries. Yet there are many concerns about the sustainability of increased meat production and consumption from perspectives including human health, animal welfare, climate change and environmental pollution.

This book tackles the key issues of contemporary meat production and consumption through a lens of political ecology, which emphasizes the power relations producing particular social, economic and cultural interactions with non-human nature. Three main topics are addressed: the political ecology of global livestock production trends; changes in production systems around the world and their implications for environmental justice; and existing and emerging governance strategies for meat production and consumption systems and their implications.

Case studies of different systems at varying scales are included, drawn from Asia, Africa, the Americas and Europe. The book includes an editorial introduction to set the context and synthesize key messages.



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