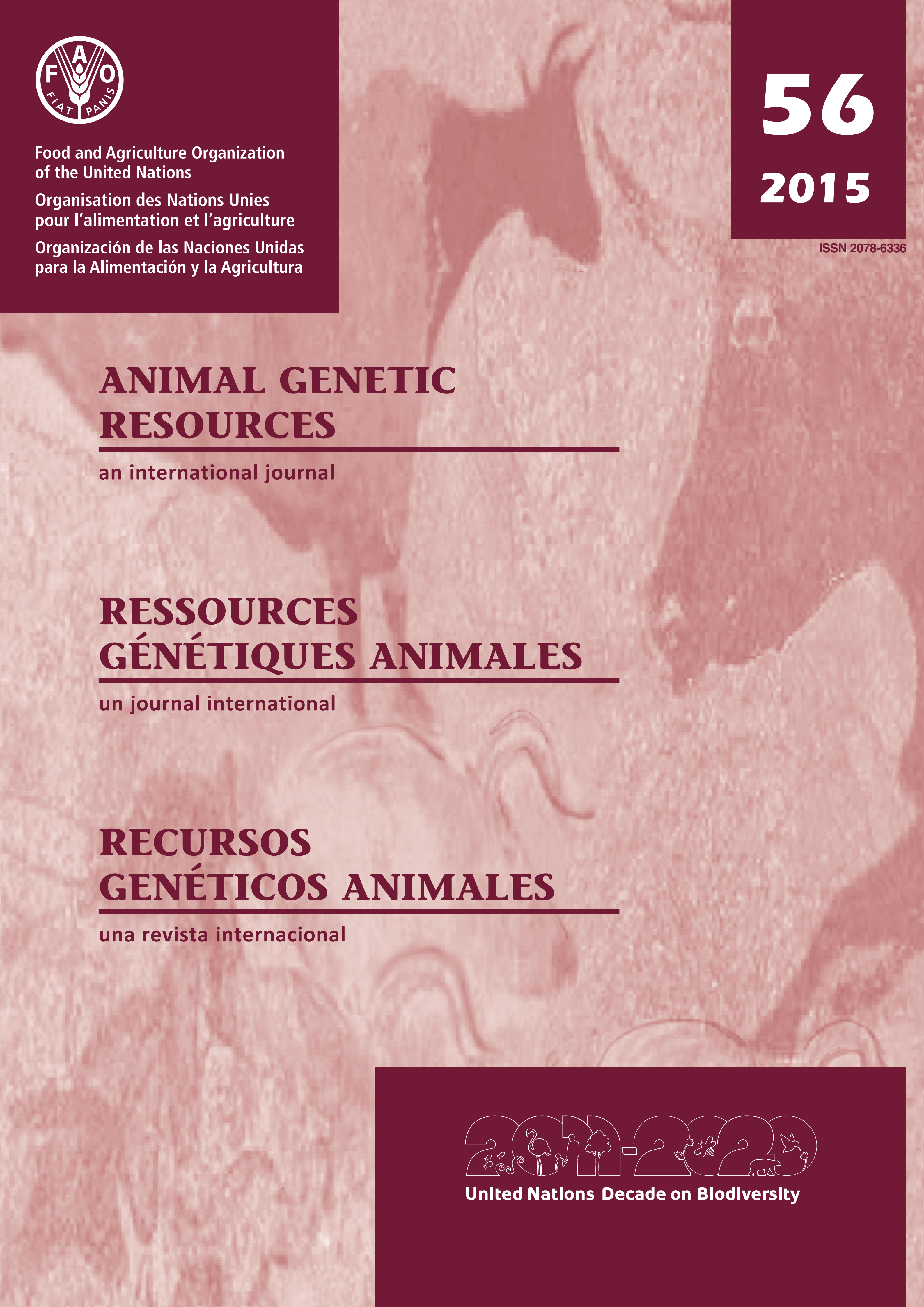

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Édition en ligne: Plateforme virtuelle de «Cambridge University Press» accessible sur www.journals.cambridge.org/agr. Veuillez consulter la page d'accueil pour accéder aux textes qui contiennent des liens de référence et dont tout le contenu peut être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

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ANIMAL GENETIC
RESOURCES

RESSOURCES
GÉNÉTIQUES ANIMALES

RECURSOS
GENÉTICOS ANIMALES

56
2015

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FOOD AND AGRICULTURE ORGANIZATION OF THE UNITED NATIONS
ORGANISATION DES NATIONS UNIES POUR L'ALIMENTATION ET L'AGRICULTURE
ORGANIZACIÓN DE LAS NACIONES UNIDAS PARA LA ALIMENTACIÓN Y LA AGRICULTURA

Animal Genetic Resources, 2015, 56, ii. © Food and Agriculture Organization of the United Nations, 2015
doi:10.1017/S2078633615000144

Editorial

Dear reader,

This issue of the journal provides you with 15 articles, ranging from classical characterization studies to the description of the institutional framework in the field of research with a specific focus on sub-Saharan African countries. Such studies contribute to the implementation of the *Global Plan of Action for Animal Genetic Resources*[1].

The Commission on Genetic Resources for Food and Agriculture oversees monitors and evaluates the implementation of the *Global Plan of Action for Animal Genetic Resources*. The 15th Regular Session of the Commission took place in Rome in January 2015. The meeting represented again an opportunity for its 178 member countries to review progress made in the implementation of the *Global Plan of Action*. The report of the session is now available on the Commission's Web[2] site dealing with many issues relevant to the readership of our journal.

The Commission welcomed the draft *Second Report on the State of the World's Animal Genetic Resources for Food and Agriculture*[3] as a comprehensive, timely and high-quality document. It requested the Food and Agriculture Organization of the United Nations (FAO) to finalize the Second Report. Furthermore the Commission called upon governments and donors to make available the financial resources necessary to translate, publish, print and distribute the Second Report and its in-brief version.

On another note, the Commission endorsed guidelines for the *Development of Integrated Multipurpose Animal Recording Systems*[4] being part in a series of publications prepared by FAO to support countries in the implementation of the *Global Plan of Action*. These have been prepared with the objective of helping countries to design and implement such systems and to maximize the chances that they will be sustained. They aim to put performance recording in a more general context, and hence to complement rather than replace the previous FAO guidelines.

In the editorial of the last issue I reported on the Global Databank for Animal Genetic Resources DAD-IS[5] which currently contains data from 182 countries and 38 species, and that based on DAD-IS data, trends in genetic erosion of breeds can be observed. Unfortunately the number of breeds where no risk status can be calculated is high with almost 60 percent. This is a result of either complete lack of information on population sizes or lack of updating of population data for a period of more than 10 years. With regard to this fact the Commission stressed the need for countries to regularly update their official national breed data in DAD-IS, or any other information system that automatically shares data with DAD-IS. The Commission stressed the importance of DAD-IS as the international clearing house mechanism for information on animal genetic resources, urged FAO to ensure long-term support for DAD-IS maintenance and invited donors to provide *ad hoc* support to enable the development of DAD-IS, as necessary.

As editor of a journal dealing specifically with animal genetic resources, please allow me to invite all authors and readers of our journal to assist the National Coordinators for the Management of Animal Genetic Resources[6] in improving data quality and quantity of DAD-IS, as such type of information is not only the basis for reviewing the impact of the *Global Plan of Action* but also for any meaningful decision for the management of national breed populations.

Yours sincerely,
Roswitha Baumung

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

[2] http://www.fao.org/nr/cgrfa/cgrfa-meetings/cgrfa-comm/en/

[3] http://www.fao.org/3/a-mm313e.pdf; http://www.fao.org/3/a-mm310e.pdf; http://www.fao.org/3/a-mm312e.pdf

[4] http://www.fao.org/3/a-mm379e.pdf

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

[6] http://dad.fao.org/cgi-bin/EfabisWeb.cgi?sid=-1,contacts

Animal Genetic Resources, 2015, 56, iii. © Food and Agriculture Organization of the United Nations, 2015
doi:10.1017/S2078633615000119

Editorial

Cher lecteur,

Ce volume du journal vous offre 15 articles, comprenant aussi bien des études classiques de caractérisation que des descriptions de cadres institutionnels dans le domaine de la recherche, avec un accent particulier sur les pays d'Afrique Subsaharienne. De telles études sont utiles pour la mise en œuvre du *Plan d'Action Mondial pour les Ressources Zoogénétiques*[1].

La Commission des Ressources Génétiques pour l'Alimentation et l'Agriculture surveille et évalue la mise en application du *Plan d'Action Mondial pour les Ressources Zoogénétiques*. La Quinzième Session Ordinaire de la Commission s'est tenue à Rome en janvier 2015. La réunion a marqué à nouveau l'occasion pour ses 178 pays membres d'examiner les progrès accomplis dans la mise en œuvre du *Plan d'Action Mondial*. Le rapport de cette session est déjà disponible sur le site web de la Commission[2]; de nombreux sujets d'intérêt pour les lecteurs de notre journal y sont traités.

La Commission a accueilli favorablement la version préliminaire du *Deuxième Rapport sur L'État des Ressources Zoogénétiques pour l'Alimentation et l'Agriculture dans le Monde*[3] en tant que document exhaustif, opportun et d'une grande qualité. La Commission a demandé à l'Organisation des Nations Unies pour l'Alimentation et l'Agriculture (FAO) d'achever le Deuxième Rapport. En outre, la Commission invite les gouvernements et les donateurs à fournir les ressources financières nécessaires à la traduction, la publication, l'impression et la distribution du Deuxième Rapport et de sa version abrégée.

Par ailleurs, la Commission a approuvé les Directives pour la *Mise en Place de Systèmes Intégrés et Polyvalents d'Enregistrement des Performances des Animaux*[4], dans le cadre d'une série de publications préparées par la FAO pour soutenir les pays dans la mise en œuvre du *Plan d'Action Mondial*. Ces directives ont été élaborées dans le but d'aider les pays à la conception et mise en place de tels systèmes et cherchant à maximiser les chances que ces systèmes perdurent. Les directives visent à placer le contrôle des performances dans un contexte plus général et ainsi compléter, plutôt que remplacer, les directives précédentes de la FAO.

Dans l'éditorial du volume dernier, je faisais référence à la Base Mondiale de Données pour les Ressources Zoogénétiques DAD-IS[5], qui contient actuellement des données de 182 pays et 38 espèces, et je signalais qu'à partir des données saisies sur DAD-IS il est possible de connaître l'évolution suivie par l'érosion génétique des races. Malheureusement le nombre de races pour lesquelles il n'est pas possible de déterminer l'état de risque est élevé (ces races représentent près du 60 pour cent). Ceci est dû soit à un manque complet d'information sur la taille des populations soit au fait que les données populationnelles n'ont pas été mises à jour pendant plus de dix ans. À ce sujet, la Commission a souligné qu'il est nécessaire que les pays mettent régulièrement à jour les données officielles sur leurs races animales dans le système DAD-IS ou dans tout autre système d'information assurant la mise en commun automatique de ces données avec celui-ci. La Commission a souligné l'importance du système DAD-IS en tant que centre d'échange international pour les ressources zoogénétiques, a demandé à la FAO d'assurer un soutien durable au système DAD-IS et a invité les donateurs à verser des contributions supplémentaires ponctuelles pour en financer le développement, si nécessaire.

En tant que rédactrice d'un journal consacré spécifiquement aux ressources zoogénétiques, veuillez me permettre d'inviter tous les auteurs et lecteurs de notre journal à aider les Coordonnateurs Nationaux pour la Gestion des Ressources Zoogénétiques[6] afin d'améliorer la qualité et la quantité des données publiées sur DAD-IS, puisque ces données servent non seulement à évaluer l'impact du *Plan d'Action Mondial* mais aussi à prendre des décisions importantes dans la gestion des populations raciales des pays.

Cordialement,

Roswitha Baumung

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

[2] http://www.fao.org/nr/cgrfa/cgrfa-meetings/cgrfa-comm/fr/

[3] http://www.fao.org/3/a-mm313e.pdf; http://www.fao.org/3/a-mm310e.pdf; http://www.fao.org/3/a-mm312e.pdf

[4] http://www.fao.org/3/a-mm379e.pdf

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

[6] http://dad.fao.org/cgi-bin/EfabisWeb.cgi?sid=-1,contacts

Animal Genetic Resources, 2015, 56, iv.
doi:10.1017/S2078633615000120

Editorial

Estimado lector,

Este volumen de la revista le ofrece 15 artículos, que abarcan desde los clásicos estudios de caracterización hasta la descripción de marcos institucionales en el ámbito de la investigación, con un enfoque específico hacia los países de África Subsahariana. Dichos estudios son de utilidad para la aplicación del *Plan de Acción Mundial sobre los Recursos Zoogenéticos*[1].

La Comisión de Recursos Genéticos para la Alimentación y la Agricultura supervisa y evalúa la aplicación del *Plan de Acción Mundial sobre los Recursos Zoogenéticos*. La Decimoquinta Reunión Ordinaria de la Comisión tuvo lugar en Roma en enero de 2015. El encuentro supuso una vez más una oportunidad para sus 178 países miembro de revisar los progresos realizados en la puesta en práctica del *Plan de Acción Mundial*. El informe de esta reunión está ya disponible en la página web de la Comisión[2]; en él se abordan muchas cuestiones de interés para los lectores de nuestra revista.

La Comisión acogió favorablemente el borrador del *Segundo Informe sobre la Situación de los Recursos Zoogenéticos Mundiales para la Alimentación y la Agricultura*[3] por considerarlo un documento exhaustivo, oportuno y de gran calidad. La Comisión solicitó a la Organización de las Naciones Unidas para la Alimentación y la Agricultura (FAO) la finalización del Segundo Informe. Asimismo, la Comisión hizo un llamamiento a los gobiernos y a los donantes para que faciliten los recursos financieros necesarios para traducir, publicar, imprimir y distribuir el Segundo Informe y su versión resumida.

Por otro lado, la Comisión aprobó las directrices para el *Desarrollo de Sistemas Polivalentes Integrados de Registro de Animales*[4], como parte de una serie de publicaciones preparadas por la FAO para ayudar a los países en la aplicación del *Plan de Acción Mundial*. Estas directrices han sido elaboradas con el objetivo de ayudar a los países en el diseño e implementación de tales sistemas y con el fin de maximizar las posibilidades de que éstos perduren. Las directrices pretenden situar el control de rendimientos en un contexto más general y así, complementan, más que sustituyen, directrices previas de la FAO.

En el editorial del pasado volumen, hice mención a la Base Mundial de Datos para los Recursos Zoogenéticos DAD-IS[5], que actualmente contiene datos de 182 países y 38 especies, y apunté que, de acuerdo con los datos introducidos en DAD-IS, es posible conocer la evolución de la erosión genética de las razas. Lamentablemente, el número de razas para las cuales no es posible determinar su situación de riesgo es elevado, representando éstas prácticamente el 60 por ciento. Esto se debe ya sea a una completa falta de información sobre los tamaños de población o a una falta de actualización de los censos por un periodo de más de diez años. En relación a este hecho, la Comisión insistió en la necesidad de que los países actualicen regularmente los datos oficiales sobre las razas de su país en DAD-IS o en cualquier otro sistema de información que automáticamente comparta los datos con DAD-IS. La Comisión subrayó la importancia de DAD-IS como repositorio internacional de información sobre los recursos zoogenéticos, instó a la FAO a garantizar un apoyo a largo plazo para el mantenimiento de DAD-IS e invitó a los donantes a prestar un apoyo específico adicional para el perfeccionamiento de DAD-IS, si fuera necesario.

Como editora de una revista dedicada específicamente a los recursos zoogenéticos, permítanme por favor que invite a todos los autores y lectores de nuestra revista a apoyar a los Coordinadores Nacionales para la Gestión de los Recursos Zoogenéticos[6] con el fin de mejorar la calidad y cantidad de la información publicada en DAD-IS, puesto que dicha información sirve no sólo para evaluar el alcance del *Plan de Acción Mundial* sino también para la toma de decisiones trascendentales en la gestión de las poblaciones raciales de cada país.

Atentamente,

Roswitha Baumung

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

[2] http://www.fao.org/nr/cgrfa/cgrfa-meetings/cgrfa-comm/es/

[3] http://www.fao.org/3/a-mm313e.pdf; http://www.fao.org/3/a-mm310e.pdf; http://www.fao.org/3/a-mm312e.pdf

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[6] http://dad.fao.org/cgi-bin/EfabisWeb.cgi?sid=-1,contacts

Animal Genetic Resources, 2015, 56, 1–7. © Food and Agriculture Organization of the United Nations, 2014
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Genetic diversity of different indigenous chicken ecotypes using highly polymorphic MHC-linked and non-MHC microsatellite markers

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Summary

The study investigated the genetic make-up of different ecotypes of indigenous chickens (ICs) in Kenya based on major histocompatibility complex (MHC)-linked and non-MHC microsatellite markers. Blood samples were collected from eight regions (48 birds per region) of Kenya: Kakamega (KK), Siaya (BN), West Pokot (WP), Turkana (TK), Bomet (BM), Narok (NR), Lamu (LM) and Taita-Taveta (TT) and genotyped using two MHC-linked and ten non-MHC markers. All MHC-linked and non-MHC markers were polymorphic with a total of 140 alleles, of which 56 were identified in MHC-linked markers. Mean number of alleles (Na and Ne), private alleles, heterozygosity and genetic distances were higher for MHC-linked markers compared with non-MHC markers. The *ad hoc* statistic ΔK detected the true numbers of clusters to be three for MHC-linked markers and two in non-MHC markers. In conclusion, Kenyan ICs belong into two to three genetically distinct groups. Different markers systems have different clustering system. MHC-linked markers divided ICs into three mixed clusters, composing of individuals from the different ecotypes whereas non-MHC markers grouped ICs into two groups. These IC ecotypes host many and highly diverse MHC-linked alleles. Higher allelic diversity indicated a huge amount of genetic variation in the MHC region of ICs and supported their reputation of being hardy and resistant to diseases.

Keywords: *ecotype, genetic diversity, indigenous chicken, MHC, population structure*

Résumé

Cette étude a cherché à connaître la configuration génétique de différents écotypes de poules autochtones du Kenya, sur la base de marqueurs microsatellites associés ou non au Complexe Majeur d'Histocompatibilité (CMH). Des échantillons sanguins ont été prélevés dans huit régions du Kenya (48 volailles par région): Kakamega (KK), Siaya (BN), Pokot Occidental (PO), Turkana (TK), Bomet (BM), Narok (NR), Lamu (LM) et Taita-Taveta (TT). Les échantillons ont été génotypés en utilisant deux marqueurs associés au CMH et 10 marqueurs non associés. Tous les marqueurs, aussi bien ceux associés au CMH que ceux non associés à celui-ci, ont été polymorphes avec un total de 140 allèles, dont 56 ont été identifiés avec des marqueurs associés au CMH. Le nombre moyen d'allèles (Na et Ne) et celui d'allèles privés, l'hétérozygotie et les distances génétiques ont été plus élevés pour les marqueurs associés au CMH que pour ceux non associés. La mesure statistique *ad hoc* ΔK a révélé que le vrai nombre de groupes est de trois pour les marqueurs associés au CMH et de deux pour les marqueurs non associés. En conclusion, les poules autochtones kényanes appartiennent à 2–3 groupes génétiques différents. Des systèmes différents de marqueurs présentent des méthodes différentes de groupement. Les marqueurs associés au CMH ont divisé les populations de poules autochtones en trois groupes mixtes, constitués d'individus provenant des différents écotypes, alors que les marqueurs non associés au CMH ont rassemblé les poules autochtones en deux groupes. Ces écotypes de poules autochtones abritent de nombreux et très divers allèles associés au CMH. Une plus grande diversité allélique est le reflet d'une grande quantité de variation génétique dans la région du CMH des poules autochtones, ce qui confirme leur renommée de volailles rustiques et résistantes aux maladies.

Mots-clés: *poule autochtone, écotype, CMH, structure populationnelle, diversité génétique*

Resumen

Este estudio investigó la configuración genética de diferentes ecotipos de gallinas autóctonas de Kenia, basándose en marcadores microsatélites asociados y no asociados al Complejo Mayor de Histocompatibilidad (CMH). Se tomaron muestras de sangre en ocho regiones de Kenia (48 aves por región): Kakamega (KK), Siaya (BN), Pokot Occidental (PO), Turkana (TK), Bomet (BM), Narok (NR), Lamu (LM) y Taita-Taveta (TT). Las muestras sanguíneas fueron genotipadas usando dos marcadores asociados al CMH y 10 marcadores no asociados. Todos los marcadores, tanto asociados como no asociados al CMH, fueron polimórficos con un total de 140 alelos, de los cuales 56 fueron identificados en marcadores asociados al CMH. El número medio de alelos (Na y Ne) y de alelos privados, la heterocigosis y las distancias genéticas fueron mayores para los marcadores asociados al CMH que

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para los marcadores no asociados. El estadístico *ad hoc* ΔK detectó que el número real de conglomerados era de tres para los marcadores asociados al CMH y de dos para los marcadores no asociados. En conclusión, las gallinas autóctonas keniatas pertenecen a 2–3 grupos genéticos distintos. Sistemas de marcadores distintos presentan diferentes modos de agrupación. Los marcadores asociados al CMH dividieron las poblaciones de gallinas autóctonas en tres conglomerados mixtos, formados por individuos de los diferentes ecotipos, mientras que los marcadores no asociados al CMH agruparon las gallinas autóctonas en dos grupos. Estos ecotipos de gallinas autóctonas albergan muchos y muy diversos alelos asociados al CMH. Una mayor diversidad alélica fue reflejo de una gran cantidad de variación genética en la región del CMH de las gallinas autóctonas, lo cual confirma la fama de estas aves de ser rústicas y resistentes a enfermedades.

Palabras clave: *gallina autóctona, ecotipo, CMH, estructura poblacional, diversidad genética*

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Introduction

Indigenous chickens (ICs) (*Gallus gallus domesticus*) are widely distributed throughout Africa under diversified geographical and agro-ecological conditions. Geographically isolated IC populations are subjected to local climatic conditions and each region is thought to host some unique types of chickens, hereafter called ecotypes. Such ecotypes are anticipated to possess' unique combinations of alleles on genes that may confer adaptation to local environment (Mwacharo *et al.*, 2007). These ecotypes may have evolved independently and genetically diverged as a result of natural selection. Some insight into Kenyan IC ecotypes (Kilifi, Taita, Muranga, Kisii, Kitui, Marsabit, Nandi, Meru, Homa Bay and Kakamega) have been achieved using microsatellite markers (Mwacharo *et al.*, 2007, 2013b). However, several ecotypes remain unknown. Furthermore, none of the studies described above did study the major histocompatibility complex (MHC) of ICs in different ecosystems.

IC populations are raised under scavenging conditions characterized by a high parasite and infectious disease agent load. In order to survive, these chickens have to display a large plasticity in their immune-related genes. The MHC is associated with immune response (Parmentier *et al.*, 2004; Fulton *et al.*, 2006; Nikbakht, Atefeh and Neda, 2013) and disease resistance (Lamont, 1989). MHC can be used to study evolutionary process (Nikbakht, Atefeh and Neda, 2013). Microsatellite marker LEI0258 located within the MHC region has been used successfully in genetic diversity studies (Izadi, Ritland and Cheng, 2011; Chang *et al.*, 2012).

The objective of this study was to investigate the genetic make-up of different ecotypes of ICs in Kenya using both MHC-linked and non-MHC autosomal microsatellite markers.

Materials and methods

Sampling

Blood samples were collected from different regions (counties) of Kenya following FAO guidelines (2011). The covered counties included: Kakamega (KK) and Siaya (BN) in the Western region; West Pokot (WP) and Turkana (TK) in North Rift; Bomet (BM) and Narok (NR) in South Rift; Lamu (LM) and Taita-Taveta (TT) in Coastal region (Supplementary Figure S1). Each county represents an ecotype. Two mature chickens per household located more than 0.5 km away from its neighbours were sampled, resulting in a total of 768 birds (i.e. 96 samples per ecotype). One bird per household was genotyped to reduce the probability of sampling genetically related birds (i.e. 48 per ecotype). All samples were collected from free ranging IC populations. Blood samples (~2 ml in EDTA) were drawn from the wing vein of each bird.

DNA isolation, polymerase chain reaction (PCR) amplification and genotyping

Genomic DNA was obtained by standard phenol–chloroform extraction method. Individuals were genotyped with 12 microsatellite markers located on eight chromosomes (Supplementary Table S1). Two of these markers were MHC-linked markers (LEI0258 and MCW0371). The other 10 are non-MHC and are part of the 30 microsatellite markers recommended by ISAG/FAO (FAO, 2011) for chicken genetic diversity assessment. LEI0258 and MCW0371 were determined using PCR as described by McConnell *et al.* (1999) and Fulton *et al.* (2006).

Statistical analysis

MHC-linked markers LEI0258 and MCW0371 were examined together whereas ten non-MHC markers were analysed separately. Genetic diversity was assessed by calculating the number of alleles per marker and population (ecotype), observed (Ho) and expected (He) heterozygosity as well as fixation index (Fst) as a measure of genetic differentiation between populations. GenAlex software version 6.5b5 (Peakall and Smouse, 2012) was used to estimate observed mean (Na) and effective (Ne) number of alleles, Ho and He per population. Population software version 1.2.32 (Langella, 1999) was used for allele frequency and private allele identification. Population differentiation was estimated using Fst for each marker across ecotypes according to the variance-based method of Weir and Cockerham (1984) using FSTAT software Version 2.9.3.2 (Goudet, 2002). The significance of all the pair-wise Fst values was tested after permutations of multi-marker genotypes among samples and significance levels were reported after strict Bonferroni corrections to account for multiple comparisons (Rice, 1989). Genetic distances were calculated according to the Nei's standard genetic distance, Ds (Nei, 1972) and Dc (Cavalli-Sforza and Edwards, 1967) using Populations software version 1.2.32 (Langella, 1999). Analysis of molecular variance was performed to assess the percentage contribution of within and between population variations because of the geographic regions using the Arlequin 3.5 software (Excoffier and Lischer, 2011). The significance of the variance components was tested with 10 000 permutations. A Mantel test was used to investigate association between genetic differentiation (Rousset, 1997) and geographic distances (kilometres) between IC ecotypes using Isolation by Distance Web Service (IBDWS) version 3.23 (Jensen, Bohonak and Kelley, 2005). The significance level was calculated from 30 000 randomizations.

Structure software version 2.3.4 (Pritchard, Stephens and Donnerly, 2000) with the Bayesian model-based clustering method for inferring population structure using multi-locus genotypes was executed. The program was run 50 times for each assumed genetic cluster (K) value using the admixture and correlated allele frequencies model because IC ecotypes are likely to be similar due to common ancestry and frequent gene flow among nearly all the ecotypes within the terrestrial land of Kenya. Models with a burn-in period of 20 000 followed by 50 000 of Markov chain Monte Carlo iterations were implemented. Individuals were grouped into a predefined number of K clusters (K ranging from 1 to 8). Prior information on sampling locations was provided. Structure Harvester software version 0.6.93 (Earl and Vonholdt, 2011) was used to analyse the output of Structure program, to identify the optimal of clusters from $K = 1$ to 8. The *ad hoc* statistic ΔK, based on the rate of change in the log probability between successive K values, was used to detect the optimal numbers of clusters (Evanno, Regnaut and Goudet, 2005). Distruct software version 1.1 (Rosenberg, 2004) was used for graphical display. GSView software version 5.0 (Lang, 2012) was used to view Distruct postscript output. GenAlex software version 6.5b5 (Peakall and Smouse, 2012) was used for principal coordinate analysis (PCoA). The PCoA axes 1 (PC1) and 2 (PC2) were used to plot graphs.

Results

Genetic variability

All MHC-linked and non-MHC markers typed were polymorphic with a total of 140 alleles, of which 56 (40 percent) were identified in MCH-linked markers (Supplementary Table S1). Out of 56 alleles in MHC region, 46 alleles (194–550 bp) were observed in LEI0258 (Figure 1) and 10 for MCW0371 (198–207 bp). Observed number of alleles per locus ranged from 6 (ADL0268) to 46 (LEI0258). Twenty private alleles (14.3 percent of the total 140 alleles) were observed across eight IC populations (Table 1), of which 12 were detected in LEI0258 and 8 for non-MHC markers. Lamu ecotype had a higher number of private alleles compared with other ecotypes.

The Na and Ne per population were higher for MHC-linked markers compared with non-MHC markers (Table 1). Na per ecotype at MHC-linked markers ranged from 15.00 to 18.00 compared with 6.20 to 7.21 for non-MHC markers. Na for LEI0258 was higher than all other markers, ranging between 20 and 27 (Figure 1).

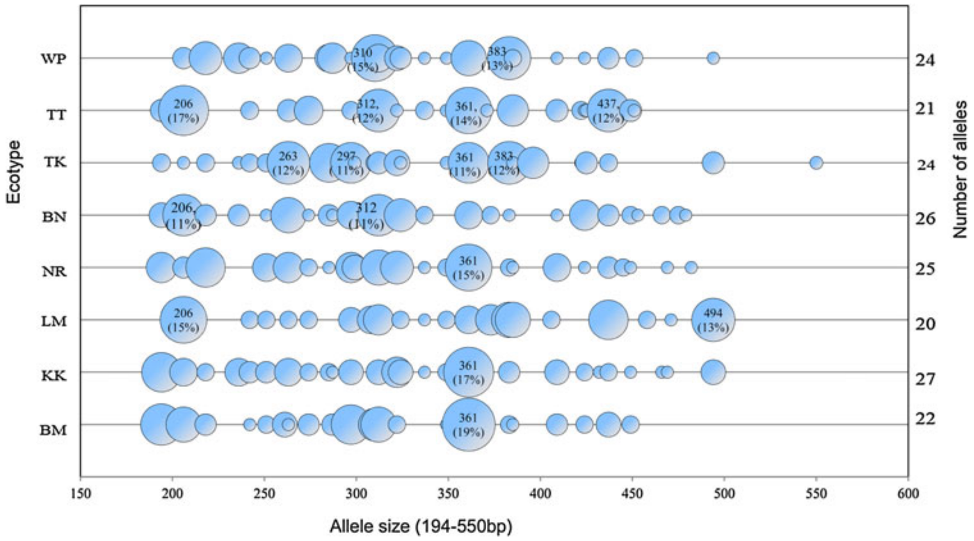


Figure 1. MHC-linked microsatellite marker LEI0258 allele frequencies in eight IC ecotypes. Alleles are identified by length in base pairs below and number of alleles per ecotype.

Table 1. Allelic patterns (Na, Ne, number of private alleles and He) in MHC-linked and non-MHC microsatellite markers across eight IC ecotypes in Kenya.

	Population	Na	Ne	Number of private alleles	Ho	He
MHC-linked microsatellite markers (LEI0258 and MCW0371)	BM	15.00	8.92	0	0.85	0.88
	KK	18.00	10.62	1	0.83	0.88
	LM	14.00	8.61	4	0.89	0.85
	NR	17.50	9.85	2	0.84	0.87
	BN	17.50	10.70	3	0.86	0.88
	TK	17.00	8.98	1	0.86	0.86
	TT	15.00	7.50	1	0.80	0.84
	WP	16.50	10.02	0	0.95	0.88
Non-MHC microsatellite markers	BM	6.30	3.47	1	0.69	0.70
	KK	6.70	3.72	1	0.71	0.72
	LM	5.70	3.24	0	0.67	0.68
	NR	6.50	3.42	1	0.69	0.70
	BN	7.10	3.82	1	0.70	0.73
	TK	6.40	3.23	2	0.67	0.68
	TT	6.20	3.06	1	0.67	0.66
	WP	6.70	2.72	1	0.68	0.71

Among the ecotypes, KK had the highest but LM the lowest Na. MHC-linked markers had slightly higher levels of heterozygosity compared with non-MHC markers. Ho values per population ranged from 0.80 to 0.95 and from 0.67 to 0.71 for MHC-linked and non-MHC markers, respectively. He was higher for MHC-linked markers (0.84–0.88) than non-MHC loci (0.66–0.73). Values for He were slightly less than Ho in LM and TT at MHC-linked and non-MHC markers, respectively.

Fst values varied between 0.01 and 0.03 for MHC-linked markers compared with 0.01–0.05 for non-MHC markers. Higher Fst values were observed for LM ecotype compared with the other populations. Ds and Dc between populations were higher in MHC-linked markers compared with non-MHC markers. Ds ranged from 0.02 to 0.33 and Dc from 0.13 to 0.46. Relatively long genetic distances were recorded between LM and the other ecotypes. Percentage of molecular variance for MHC-linked and non-MHC markers were high within individuals (>89 percent) compared among the ecotypes (<4 percent) and within individuals (<8 percent). A significant correlation between the genetic distances and geographic distances was observed. On average, MHC-linked markers produced a lower correlation coefficient (r) of 0.65 compared with 0.78 in non-MHC markers.

Population clustering

The *ad hoc* statistic *ΔK* detected the true numbers of clusters to be three for MHC-linked markers and two in non-MHC markers (Figure 2). PCoA-based principal coordinates 1 and 2 indicated three groups for MHC-linked markers and two in non-MHC markers (Figure 3). Although MHC-linked markers grouped ICs into three clusters, individuals from different ecotypes overlapped in principal coordinate space unlike distinct groups of LM (cluster one) and others (cluster two) for non-MHC markers.

Discussion

Genetic variability

All MHC-linked and non-MHC markers were highly polymorphic. Number of alleles including private alleles and their apparent difference in distribution across the ecotypes indicated the existence of genetic diversity between the

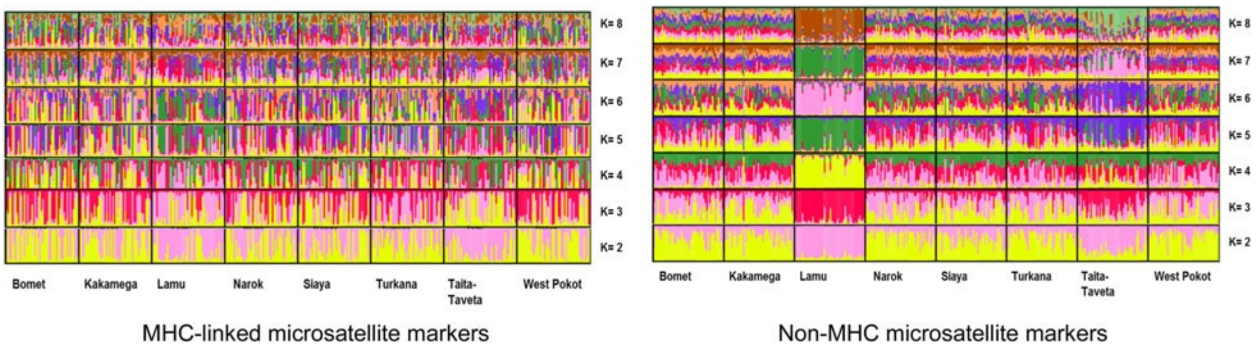
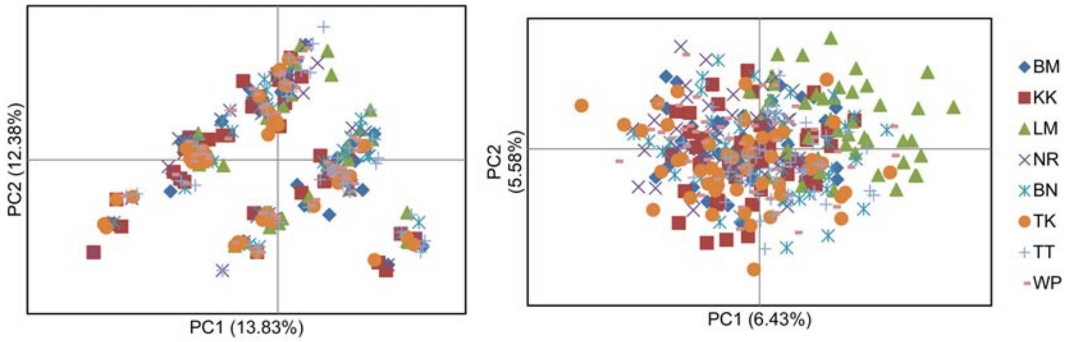


Figure 2. Proportions of admixtures observed in the eight IC ecotypes for MHC-linked and non-MHC microsatellite markers.



MHC-linked microsatellite markers

Non-MHC microsatellite markers

Figure 3. PCoA plot based on genetic distance for individuals for non-MHC and MHC-linked microsatellite markers.

populations. The genetic variations have been caused by differences in ancestral origin, migration routes, hybridization of origins, genetic drift, mutation and natural selection. ICs are anticipated to have multiple origins from wild ancestors in South Asia and Island Southeast Asia and have been introduced to Kenya through several entry points (Lyimo *et al.*, 2013; Mwacharo *et al.*, 2013a, 2013b). After introduction of ICs to Kenya, they spread separately via marine and multiple terrestrial routes (Mwacharo *et al.*, 2013a, 2013b) and their variations could be due to adaptation to the local environmental conditions provided by the specific route. Ancestors of LM ecotype are anticipated to have originated from Asia and distributed to Kenya and Tanzania through common water body of Indian Ocean. Lamu ecotype has a local name as “Kuchi” which is similar in name to Kuchi ecotype in Tanzania. Kuchi chicken in Tanzania is similar to Shamo game birds from “Kōchi” Prefecture of Shikoku Island in Japan and its thought to be its origin (Lyimo *et al.*, 2013). Genetic diversity of IC ecotypes might have been contributed by cross-breeding with chicken breeds from Asia and Europe. Cross-breeding started in 1950s in Kenya and was widely spread in the country through cockerel/pullet exchange programme initiated in 1976 (FAO, 2007).

Number of alleles for LEI0258 per ecotype varied from 20 to 27 in the present study are in the same range as reported for Kuchi (22) and Medium (23) ecotypes in Tanzania (Lwelamira *et al.*, 2008). Allelic diversity in MHC-linked markers is higher than non-MHC markers. The reason why the MHC region is so allele-rich and highly diversified is because survival is associated with additive allelic effects at the MHC locus (Eyto *et al.*, 2007) and pathogen-driven selection (Nielsen, 2005). Such polymorphism of MHC region in ICs is maintained by pathogen-driven balancing selection because of varying pathogen resistance over space and time (Hughes and Nei, 1989; Hedrick, Lee and Garrigan, 2002). ICs studied are kept under harsh scavenging tropical conditions of varying heat stress and frequent disease outbreaks. A higher allelic diversity in the MHC region boosts IC’s ability to tolerate disease challenges. However, this study did not prove the additive allelic effects of MHC locus.

Heterozygosity values for MHC-linked markers were higher than for non-MHC markers and in agreement with findings by Chazara *et al.* (2013) using wild species and unselected chicken populations. Ho were slightly lower than He in TT and LM ecotypes, suggesting selection against heterozygotes (Mogesse, 2007) and limited artificial selection (Dana, 2011) in these populations. Comparatively high Fst, Ds and Dc for LM population to the other ecotypes are as a result of restricted gene flow because of separation by Indian Ocean. Mantel test revealed positive correlation between genetic and geographic distances. Populations were sampled from eight different regions which are far apart (67–840 km) and the geographic distances had influence on the genetic structure of the farthest population (LM).

Population clustering

Studying the genetic variability of ICs would be important in establishing whether the whole population may be treated as a single gene pool or whether it should be subdivided. Cluster analysis using MHC-linked markers indicated three genetically mixed clusters (i.e. each cluster is composed of individuals from all the ecotypes). Such clustering suggested similar directional selection in the MHC region of chicken clustered together. However, this study did not prove if the MHC is under selection.

Non-MHC markers grouped ICs into two groups, LM (cluster one) and the other cluster composing of seven ecotypes (cluster two). Distinctness of LM from other IC populations indicated genetic uniqueness which could be as results of physical, geographical and socio-economic isolation of the populations. Main population barrier is Indian Ocean which isolated Lamu region from mainland. Population in cluster two are similar because of geographically proximity where, Western, North Rift valley and South Rift valley regions are very close, so it is easy for ICs to mix. Sharing of common routes from Nairobi to Turkana via Narok, Bomet, Siaya, Kakamega, and West Pokot might have made easier movement of ICs in these regions. Furthermore, residents of Western, North Rift valley and South Rift valley regions are sharing common working environment (huge tea plantations in Bomet, Kericho and Nandi counties). Interaction in such working place might have promoted the exchange of IC genetic material in form of gifts. Common cultures, living customs and intermarriages of tribes might have promoted frequent gene flow in the regions. Conversely, human interactions through trading between the studied regions as well as Kenya and other countries have led to mixing of chicken (Mwacharo *et al.*, 2013b).

Conclusion

Kenyan ICs belong to two to three genetically distinct groups (LM and others). Different markers systems have different clustering system. MHC-linked markers divided ICs into three mixed clusters, composing of individuals from the different ecotypes whereas non-MHC markers grouped ICs into two groups (LM and others). These IC ecotypes host many and highly diverse MHC-linked alleles. Higher allelic diversity indicated a huge amount of genetic variation in the MHC region of IC and supported their reputation of being hardy and resistant to diseases. Natural balanced selection driven by pathogen has enabled ICs to maintain genetic diversity which is crucial for adaptation to harsh scavenging conditions and local disease challenges.

Supplementary Materials

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

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Blood protein polymorphism and genetic diversity in locally adapted Muscovy duck (*Cairina moschata*) in Nigeria

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Summary

Characterization and genetic diversities among members of a species are fundamental to their improvement and conservation. This study was conducted to characterize and estimate genetic diversity in the ecotypes of the locally adapted Muscovy duck in Nigeria using blood proteins (haemoglobin, transferrin and albumin) and enzyme (carbonic anhydrase) markers. Blood samples collected from 20, 40 and 20 adult Muscovy ducks sampled randomly from the Rain Forest, Derived Savanna and Guinea Savanna ecotypes, respectively, were typed for blood proteins and enzyme polymorphism with cellulose acetate paper. Genetic variability in the studied population was accessed using heterozygosity (H), effective number of allele (n_e) and polymorphism (percent P). All the 13 allelic variants expressed at the four loci were expressed in the Derived Savanna ecotype but 12 each in the Rain Forest and Guinea Savanna ecotypes. Results showed that all the four loci were polymorphic (100 percent) and the estimated heterozygosity among them was similar (0.424–0.481). Similarity in the estimated genetic variability parameters among ecotypes indicate that the sub-populations understudy was under similar evolutionary forces and there were no appreciable differences among them.

Keywords: *blood protein, characterization, genetic diversity, heterozygosity, Muscovy ducks*

La polymorphisme de la protéin sanguine et la g énétique diversit é des carnards locaux moscovy (Cairina moschata) au Nigeria

Résumé

La caractérisation et les diversités génétiques parmi les members d'une spécie sont fondamentales pour leurs ameliorations afin de les conservation. Cet etude a ete sait pour pourvoir caracterises et estimer la diversite genetique dans les ecotypes des carnards locaux muscovys au Nigeria en utilisant le sang protein(Haemoglobine, le transferine et l'albumin) et l ' enzyme (L'anhydrase carbonique) marquers. Les echantillions saguines ramasses de 20, 40 et 20 adultes des carnards Muscovy ont ete pris respectivement par hazard des ecotypes de la foret, de la savvane derive, et de la savanne guinea. Ils ont ete tapes pour les proteins sanguine et l' enzymes polymorphism eaves les papierrs cellulose. La variable genetique de la population etudie a ete evalue en utilisant heterozygosite (H) les nombres des alleles (n_e) effectifs et la polymorphisme (%P0. Tous les treize variants alleliques montres dans les quatre locis sout aussi montres dans l'ecotype de la savanne derive mais les douze dans la foret et daus les ecotype de la guinea savanne. Les resultants montret que tous les quatre locis sont polymorphiques (100%0 et l'heterozygosite estimee parmi eux etait semblable (0.424–0.481). La similarite de la parameter variable de la genetique estmee parmie les ecotypes indique que les sousopopulations etudiees etaient similaires aux forces evolutionaire et il n' y avait pas de beaucoup difference parmi eux.

Mots-clés: *Protéin sanguine, caracterisation, la diversite genetique, l' heterozysite, le carnard muscovy*

Resumen

La caracterización y las diversidades genéticas entre miembros de una especie son fundamentales para su mejora y conservación. Este estudio fue llevado a cabo con el fin de caracterizar y estimar la diversidad genética en los ecotipos del pato mudo localmente adaptado en Nigeria, usando proteínas sanguíneas (hemoglobina, transferrina y albúmina) y marcadores enzimáticos (anhidrasa carbónica). Las muestras de sangre se tomaron en 20, 40 y 20 patos mudos adultos recogidos al azar de los ecotipos Selva, Sabana Derivada y Sabana de Guinea, respectivamente. En las muestras de sangre, se determinaron las proteínas sanguíneas y el polimorfismo enzimático con papel de acetato de celulosa. La variabilidad genética de la población estudiada fue evaluada en base a la heterocigosis (H), el número efectivo de alelos (n_e) y el polimorfismo (P, en tanto por ciento). Las trece variantes alélicas asociadas a los cuatro loci se expresaron en el ecotipo Sabana Derivada mientras que en los ecotipos Selva y Sabana de Guinea sólo se expresaron doce. Los resultados mostraron que los cuatro loci fueron polimórficos (100 por cien) y que la heterocigosis estimada fue similar entre ellos (0.424–0.481). La similitud entre ecotipos en las medidas de estimación de la variabilidad genética indica que las subpoblaciones objeto de estudio se hallaban bajo similares fuerzas evolutivas y que no existían diferencias apreciables entre ellas.

Palabras clave: *proteína sanguínea, caracterización, diversidad genética, heterocigosis, patos mudos*

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Introduction

Genetic diversities in the genome of indigenous livestock species in developing world are reservoirs of rare but valuable genes for production, adaptation and resistance to endemic diseases. Diversity is the product of interaction between environmental and genetic effects leading to the differentiation of the morphological, physiological and productive traits which are vital to all production systems, as it provides the raw materials for breed improvement, and for adaptation to changing circumstances (Ceriotti *et al.*, 2003).

DNA-based technologies are now the methods of choice for genetic characterization of livestock (Arora *et al.*, 2011); but its acceptance and applications in developing world are limited primarily due to the myriads of challenges such as its high cost, lack of infrastructural facilities and dearth of trained experts. Nevertheless, in the recent decades, advances in the field of biotechnology has opened up a completely new area at molecular levels with the method of techniques, such as routine electrophoresis employed for the detection of polymorphism at protein and enzyme loci as well as other serological and immunogenetic procedures for measurement of variation (Salako, Ijadunola and Aregbesola, 2007).

Protein/allozyme polymorphs remain tremendously useful, especially in developing countries, because of their utility, cost and amount of genetic information accessed or simplicity involved in data interpretation (Rege and Okeyo, 2006). A major plus for biochemical characterization is that biochemical markers do not depend on environmental factors, stable throughout ontogenesis and have a simple type of inheritance (Lee *et al.*, 1995). Though investigation on the genetic diversity of farm animals using microsatellite markers and other high technology procedures have been carried out in developing world; nevertheless, blood protein markers of farm animals have also been widely used for genetic structure and phylogenetic studies among breeds and types (Boujenane *et al.*, 2008; Zahrane *et al.*, 2011; Akinyemi and Salako, 2012), characterization and estimation of genetic diversity within and among breeds and species (Akinyemi and Salako, 2012; Yakubu and Aya, 2012).

Duck production is at the stage of infancy in Nigeria. Duck population was ranked third (9 553 911) after chicken (101 676 710) and guinea fowl (16 976 907) respectively (NBS, 2012) In Nigeria. Muscovy duck is the prevalent genus of duck reared in Nigeria (Duru *et al.*, 2006; Oguntunji, 2013) and is reared as a dual-purpose bird for meat and egg production but its meat output greatly outweighs its egg output in Nigeria (Oguntunji, 2013). At present, information on how Muscovy ducks were introduced to Nigeria in literatures are scanty. However, a report by Blench (1995) suggested that they were probably introduced on the sea-coast by the Portuguese and spread inland. Another undocumented version claimed that they were introduced by the Portuguese slave traders and explorers in the fifteenth century.

Studies on biochemical characterization and estimation of genetic diversity in Muscovy duck using blood protein polymorphism are scarce. Electrophoretic analysis of blood proteins and enzymes would be of immense contribution to the characterization of this locally adapted waterfowl and also provide insights into the genetic diversity existing among them. It has been documented that animal genetic resources in developing countries, in general, were being eroded through the rapid transformation of the agricultural systems, in which the main cause of the loss of indigenous animal genetic resources was the indiscriminate introduction of exotic genetic resources, before the proper characterization, utilization and conservation of indigenous genetic resources (FAO, 1999). Mariante and McManus (2004) corroborated this that studies were needed to characterize, identify and differentiate populations, while origin and history of breeds should be documented. In view of the foregoing, this study was undertaken to characterize and to investigate genetic diversity and similarity existing among ecotypes of Muscovy ducks found in Nigeria using blood protein markers.

Materials and methods

Animals

Blood samples were collected from unrelated 80 birds comprising 40 male and 40 female adults locally adapted Muscovy ducks in Nigeria. They comprise randomly sampled 20, 40 and 20 Muscovy ducks from the Rain Forest, Derived Savanna and Guinea Savanna agro-ecological zones which are herein referred to as ecotypes, respectively. These animals were extensively managed and owned by small scale holders. The climatic conditions of the study area have been earlier described by Oguntunji *et al.* (2008) and Yakubu (2011).

Laboratory analysis

About 3–5 ml of whole blood was collected from the wing vein of each apparently healthy bird into correspondingly labelled heparinized and unheparinized tubes. Heparin was added to act as anti-coagulant and blood contamination was prevented using separate syringes and needles for individual birds. These samples were kept refrigerated in ice packs and transported to the Animal Breeding and Genetics Laboratory of the Department of Animal Science, University of Ibadan, Ibadan, Oyo State, Nigeria for electrophoresis analysis.

The blood samples were centrifuged at 4 °C for 20 min at 3 000 rpm in order to separate plasma and erythrocyte. Erythrocytes were washed with 9 percent NaCl to free them from plasma proteins and were then lysed with fourfold cold distilled water in order to release the haemoglobin. Then plasma and haemolysates aliquots were stored at 4 °C prior to electrophoresis analysis.

The lysed red blood cells were used to determine haemoglobin (Hb) and carbonic anhydrase (CA) genotypes while plasma was used to detect transferrin (Tf) genotypes. Similarly, unheparinized blood samples were centrifuged at 4 °C for 20 min at 3 000 rpm in order to separate serum for electrophoresis analysis of albumin (Alb).

Electrophoresis polymorphisms were performed for the CA, Hb, Alb and Tf using cellulose acetate strips. The electrophoresis procedures for CA, Hb and Tf have been described by Akinyemi and Salako (2012) while Alb was electrophoresed with Tris Citrate pH 8. After electrophoresis, each strip was stained for few minutes and thereafter covered by destaining solution until the electrophoresis bands were visible, air-dried and scored.

Statistical analyses

All the investigated loci were co-dominant and gene frequencies were calculated by direct gene counting method. Genetic variability within the ecotype and sexes were estimated as follows.

Percentage of polymorphic loci (percent P): qualitatively, a marker is said to be polymorphic if it has two alleles and its most frequent allele in the population has a frequency of at most 99 percent (Sanjalj, Hemant and Robert, 2000; Nyamsamba *et al.*, 2003).

Heterozygosity (H): estimates of heterozygosity within ecotype was measured as the unbiased estimate of mean heterozygosity (Nei, 1978).

$$(H) = 1 - \sum X_i^2$$

where: X = the gene frequency of the ith allele in a locus, i = the number of loci.

$$\text{Effective number of alleles}\,(n_e): 1/1 - H$$

where: H = heterozygosity (Nyamsamba *et al.*, 2003).

Results

Genotypic distribution among locally adapted Muscovy ducks in Nigeria

The genotype frequencies of haemoglobin, carbonic anhydrase, transferrin and albumin are presented in Table 1. Besides, the electrophoretic patterns of the four blood protein markers are illustrated in Figure 1.

Haemoglobin

Three distinct genotypes of Hb (AA, BB and AB) were observed in the three ecotypes; however, Hb^{AA} genotype was prevalent (0.49) across the ecotypes.

Carbonic anhydrase

Electrophoretic analysis of CA locus revealed three distinct genotypes (CA^{FF}, CA^{FS} and CA^{MM}); nevertheless, genotype CA^{FF} was prevalent in the three ecotypes.

Table 1. Distribution of four blood protein genotypes in three ecotypes of locally adapted Muscovy ducks in Nigeria.

Loci	Genotype	RF[1] (20)	Ecotype DS[2] (40)	GS[3] (20)	Observed	Gene frequency
Hb	AA	5 (0.25)	30 (0.75)	4 (0.20)	39 (0.49)	A: 0.55
	AB	1 (0.05)	5 (0.125)	4 (0.20)	10 (0.13)	B: 0.45
	BB	14 (0.70)	5 (0.125)	12 (0.60)	31 (0.39)	
CA	FF	17 (0.85)	36 (0.90)	18 (0.90)	71 (0.89)	F: 0.913
	FS	1 (0.05)	2 (0.05)	1 (0.05)	4 (0.05)	S: 0.025
	MM	2 (0.10)	2 (0.05)	1 (0.05)	5 (0.06)	M: 0.063
Alb	AA	2 (0.10)	6 (0.15)	5 (0.25)	13 (0.16)	A: 0.231
	BB	–	14 (0.35)	6 (0.30)	20 (0.25)	B: 0.294
	CC	15 (0.75)	15 (0.375)	4 (0.20)	34 (0.43)	C: 0.438
	AB	3 (0.15)	1 (0.025)	2 (0.10)	6 (0.08)	D: 0.038
	AD	–	2 (0.05)	3 (0.15)	5 (0.06)	
	BC	–	1 (0.025)	–	1 (0.01)	
	CD	–	1 (0.025)	–	1 (0.01)	
Tf	AA	1 (0.05)	–	–	1 (0.01)	A: 0.019
	AD	–	1 (0.025)	–	1 (0.01)	B: 0.475
	BB	–	1 (0.025)	–	1 (0.01)	C: 0.419
	BC	15 0.75)	33 (0.825)	19 0.95)	67 (0.84)	D: 0.088
	BD	2 (0.10)	4 (0.10)	1 (0.05)	7 (0.09)	
	DD	2 (0.10)	1 (0.025)	–	3 (0.04)	
Total no. of genotypes	19	13	18	13		

(): Sample size analysed in parenthesis.

[1] RF, Rain Forest.

[2] DS, Derived Savanna.

[3] GS, Guinea Savanna.

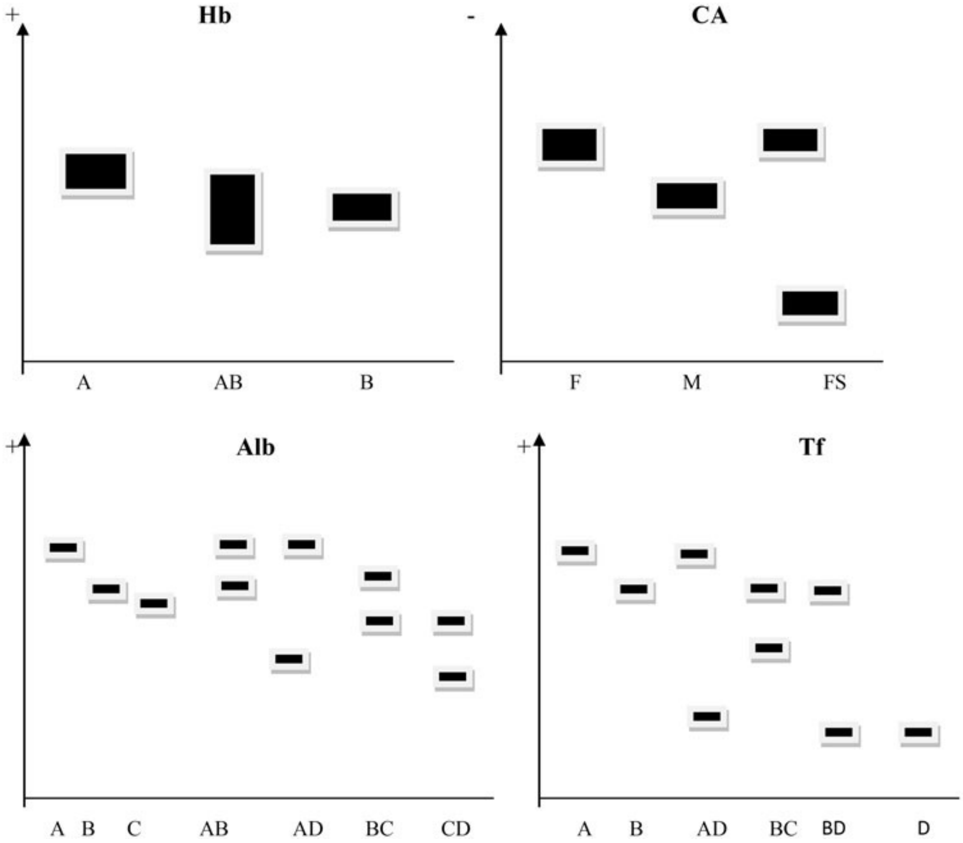

Figure 1. Diagram showing relative position of electrophoretic patterns of four protein loci in the locally adapted Muscovy duck in Nigeria using cellulose acetate paper strip.

Albumin

Seven distinct genotypes were observed at the albumin locus and incidence of Alb^{CC} was the highest.

Transferrin

Of the six genotypes typed for transferrin, genotype Tf^{BC} was the most frequent genotype in the sub-populations under study.

It is worthy of note that homozygous genotypes were prevalent at Hb (87.5 percent), CA (95 percent) and Alb (85 percent) loci of the studied population while heterozygous genotypes were prevalent (93.75 percent) at Tf locus.

Allelic frequencies distribution

The allelic frequencies of the four protein loci in the three ecotypes of Muscovy ducks are presented in Table 2.

Haemoglobin

Two alleles were expressed at the Hb locus of the three ecotypes. General analysis (Table 1) indicated prevalence of HbA (0.55).

Carbonic anhydrase

Alleles F, S and M were expressed at the CA locus of the studied populations. Combined data of the three ecotypes (Table 1) indicated further that allele CAF was prevalent (0.913).

Albumin

Four alleles (A, B, C and D) were identified at the Alb locus. General analysis (Table 1) indicated prevalence of allele C.

Table 2. Allelic frequencies at haemoglobin, carbonic anhydrase, albumin and transferrin loci in three ecotypes of the locally adapted Muscovy duck in Nigeria.

Locus	Allele	Rain forest (20)	Ecotype derived Savanna (40)	Guinea Savanna (20)
Hb	A	0.275	0.81	0.30
	B	0.725	0.19	0.70
CA	F	0.850	0.925	0.925
	S	0.025	0.025	0.025
	M	0.125	0.05	0.05
Alb	A	0.475	0.188	0.375
	B	0.375	0.375	0.350
	C	0.15	0.40	0.20
	D	–	0.038	0.075
Tf	A	0.05	0.013	–
	B	0.425	0.488	0.50
	C	0.375	0.413	0.475
	D	0.150	0.088	0.025
Total no. of alleles	13	12	13	12

(): Sample size analysed in parenthesis.

Table 3. Genetic variability at four loci in three ecotypes of locally adapted Muscovy duck in Nigeria.

System	Rain forest (20)	Ecotype derived Savanna (40)	Guinea Savanna (20)	Mean
		Heterozygosity		
Alb	0.611	0.663	0.691	0.655
CA	0.261	0.141	0.141	0.181
Hb	0.399	0.308	0.420	0.376
Tf	0.654	0.583	0.524	0.587
Mean H[1]	0.481	0.424	0.444	0.450
n_e[2]	1.927	1.736	1.799	1.821
P (percent)[3]	100	100	100	100

(): Sample size analysed in parenthesis.
[1] *H*, heterozygosity.
[2] n_e, effective number of alleles.
[3] P (percent), percentage of polymorphism.

Transferrin

Four allelic variants were detected at Tf locus. Alleles C (0.475) and B (0.419) predominated in three ecotypes (Table 1).

Genetic diversity among ecotypes

The results of the genetic variability among ecotypes are presented in Table 3.

Heterozygosity (H*)*

The heterozygosity value of the three ecotypes ranges between 0.424 and 0.480 while the average for the three ecotypes was 0.45.

Percentage of polymorphic loci (percent P)

All the protein-coding loci studied in the three ecotypes were 100 percent polymorphic.

Effective number of alleles (n_e)

The n_e ranges between 1.736 and 1.927; however, the average for the three ecotypes was 1.821.

Sex differences in gene and genotype frequencies distribution of blood proteins in the Muscovy ducks in Nigeria

The sex differences in gene and genotype frequencies of Hb, CA, Alb and Tf of male and female Muscovy ducks are presented in Table 4.

Haemoglobin

Three genotypes and two alleles were expressed at Hb locus in the two sexes. Genotype Hb^{AA} and allele A were the most frequent in both sexes.

Table 4. Gene and genotype frequencies (in parenthesis) of four blood protein markers in adult male and female Muscovy ducks in Nigeria.

Locus	Sex	Genotype	Observed	Gene frequency
Haemoglobin	Male	AA	20 (0.50)	A: 0.575
		AB	6 (0.15)	B: 0.425
		BB	14 (0.35)	
	Female	AA	19 (0.475)	A: 0.525
		AB	4 (0.10)	B: 0.475
		BB	17 (0.425)	
Carbonic anhydrase	Male	FF	37 (0.925)	F: 0.938
		FS	1 (0.025)	S: 0.013
		MM	2 (0.05)	M: 0.05
	Female	FF	34 (0.85)	F : 0.888
		FS	3 (0.075)	S: 0.038
		MM	3 (0.075)	M:0.075
Transferrin	Male	AA	1 (0.025)	A: 0.025
		BB	1 (0.025)	B: 0.475
		BC	33 (0.825)	C: 0.413
		BD	3 (0.075)	D:0.088
		DD	2 (0.05)	
	Female	BC	34 (0.85)	A: 0.013
		BD	4 (0.10)	B: 0.475
		AD	1 (0.025)	C: 0.425
		DD	1 (0.025)	D: 0.088
Albumin	Male	AA	5 (0.125)	A: 0.263
		BB	2 (0.05)	B: 0.125
		CC	21 (0.525)	C: 0.538
		AB	6 (0.15	D: 0.075
		AD	5 (0.125)	
		CD	1 (0.025)	
	Female	AA	8 (0.20)	A: 0.20
		BB	18 (0.45)	B: 0.463
		CC	13 (0.325)	C: 0.338
		BC	1 (0.025)	

Carbonic anhydrase

Three distinct genotypes were observed at the CA loci of both sexes. The CA^{FF} genotype and allele F were prevalent in both the male and female ducks Figure 2.

Transferrin

Five genotypes were observed in drakes while four were expressed in females. Comparative sex-associated

Figure 2. Scavenging adult female (left) and male (right) Muscovy ducks.

genotype expression of Tf revealed that genotypes Tf^{AA} and Tf^{BB} were only found in males while Tf^{AD} was only expressed in female ducks. Four alleles each were expressed in both sexes. Alleles B and C were the most frequent in the two sexes.

Albumin

Six of the seven genotypes expressed at the Alb locus were observed in male ducks except BC. Conversely, only four were observed in female ducks. Besides, allele C and B was prevalent in male and female Muscovy ducks, respectively.

Genetic diversity in male and female Muscovy ducks

Estimated genetic variability of male and female Nigerian Muscovy ducks are shown in Table 5.

Heterozygosity (H)

Result of the average heterozygosities of the sexes indicated that females had higher estimated value than males (0.485 vs. 0.455).

Effective number of alleles (n_e)

The n_e for male and female ducks was 1.835 and 1.923, respectively.

Percentage of polymorphism (percent P)

All loci investigated in both sexes were polymorphic (100 percent polymorphic).

Blood protein genotype frequencies distribution

Haemoglobin

Reports of empirical studies of blood protein polymorphism in Muscovy ducks and in relation to agro-ecological zones are scarce to compare with the results of the present study. However, results of the related studies in other poultry species such as chicken (Yakubu and Aya, 2012), chuckar (*Alectoris chuckar*) and pheasant (*Phasianus colchicus*) (Ugur *et al.*, 2006) are in agreement with the three genotypes reported for Muscovy ducks in this study.

The higher frequency of Hb^{AA} agrees with previous reports on Nigerian indigenous chickens (Salako and Ige, 2006; Yakubu and Aya, 2012) and in Chuckar and Pheasant (Ugur *et al.*, 2006). The prevalence of HbAA genotype among Nigerian Muscovy ducks may probably suggest adaptive roles for this genotype under harsh tropical environment.

Carbonic anhydrase

Scarcity of related studies in Muscovy ducks and other poultry species on carbonic anhydrase did not permit head-to-head contrast. It is worthy of note that a new variant was observed at this locus in five ducks and was temporarily designated as “MM”. The electrophoretic band of this new allele was just below the F and far from the S bands.

Albumin

Empirical studies on the electrophoretic analysis of Muscovy ducks and other duck breeds are scare to validate results obtained in the present study. It is noteworthy that all the seven genotypes observed across the ecotypes were present in Derived Savanna ducks. This may probably be attributed to the larger sample size than in the other two ecotypes.

Transferrin

The observed six Tf genotypes reported in the present study for Nigerian Muscovy ducks was higher than the three reported for Kerinci ducks in Indonesia (Nur, Yusrizal and Manin, 2012). While genotype Tf^{BC} was prevalent in the population understudy; genotype Tf^{AA} was prevalent in Kerinci ducks (Nur, Yusrizal and Manin, 2012).

Prevalence of homozygous genotypes at Hb, CA and Alb loci is consistent with a related study on waterfowl whereby deficiency of heterozygosity at five loci of Lesser Snow Geese (Kuznetsov, Baranyuk and Takekawa, 1998) was reported. Cooke, Parkin and Rockwell (1988) suggested that deficiency of heterozygotes may be explained by scoring errors, null alleles, selection against heterozygotes and inbreeding. To the best of the knowledge of the authors, the population understudy has not been subjected to selection in any form and the sampled population was random mating; thereby foreclosing possibility of selection and inbreeding influencing predominance of homozygote genotypes. Barring any error in scoring of the genotypes; a

Table 5. Estimated genetic variability of male and female Muscovy ducks in Nigeria.

Sex	Total no of allele	Heterozygosity				Mean H^1	n_e^2	P^3 (%)
		Hb	CA	Tf	Alb			
Male (40)	13	0.489	0.117	0.595	0.620	0.455	1.835	100
Female (40)	12	0.499	0.204	0.586	0.631	0.480	1.923	100

(): Sample size analysed in parenthesis.

[1] *H*, heterozygosity.

[2] n_e, effective number of alleles.

[3] P, percentage of polymorphism.

major possible underlying factor for the prevalence of the homozygotes in the present study was Wahlund effect.

Allelic frequencies distribution

Haemoglobin

The observed differences in prevalence of different alleles in different ecotypes "tempted" to suggest possible adaptive role of these alleles in different environments. Nevertheless, the predominance of HbA allele in the Nigerian Muscovy ducks is consistent with similar reports in other poultry species, such as Chuckars and Pheasant (Ugur *et al.*, 2006) and Nigerian local chickens (Salako and Ige, 2006; Yakubu and Aya, 2012).

Carbonic anhydrase

To the best of the knowledge of the authors, the reported new allele designated as "M" in this study has not been reported previously either in Muscovy duck or any other poultry species. Ordás and San Primitivo (1986) also reported a new allele (M) at CA locus of a Spanish dairy sheep and its estimated frequency was 0.01. Similarly, Ibeagha-Awemu and Erhardt (2004) reported low frequency of 0.063 for this rare variant allele in Black-faced Mutton sheep. The low frequency of this rare allele in Nigerian Muscovy duck could be adduced to typing error or alternatively possibly indicates its negligible contribution to adaptation of this waterfowl in the study area and possibly its non relevance with yet-to-be-identified economic traits.

Albumin

Four alleles expressed at the Alb locus of Muscovy ducks in the present study contradicts the three reported for dabbling ducks (Paulauskas *et al.*, 2009). It is noteworthy that allele B alone contributed about one-third (0.350–0.375) of the allelic composition of the three ecotypes. This probably points to the importance of this allele to the survival and yet-to-be-known physiological role it played in the population understudy. Conversely, alleles A and B predominated among dabbling ducks of Palaearctic region (Paulauskas *et al.*, 2009).

Transferrin

Four alleles at the Tf locus of the Nigerian Muscovy duck in this study was higher than the two reported for Kerinci duck (Nur, Yusrizal and Manin, 2012) but lower than five in dabbling ducks of Palaearctic region (Paulauskas *et al.*, 2009). Comparable allelic frequencies and prevalence of alleles B and C in the studied population probably suggest importance of these alleles to their survival and adaptation to the study area.

Genetic variability among ecotypes

Heterozygosity (H)

Though comparable study on heterozygosity at biochemical protein loci of Muscovy duck is scarce; however, the range of average heterozygosity in the present study (0.424–0.481) is comparable to 0.43 and 0.41 reported for Pekin and Muscovy duck in Iran using 13 microsatellite markers (Ahmadi *et al.*, 2007) but higher than the ranges 0.185–0.366 and 0.094–0.119 reported for dabbling ducks (Paulauskas *et al.*, 2009) and Lesser Snow Geese (*Chen c. caerulescens*) of Wrangel Island (Kuznetsov, Baranyuk and Takekawa, 1998), respectively using blood protein markers. Furthermore, the mean H obtained for Muscovy duck in this study (0.45) is lower compared to 0.514, 0.527, 0.8079 and 0.86 reported for Beijing and Cherry Valley duck lines (Wu *et al.*, 2009), Muscovy ducks in China (Wu *et al.*, 2008) and ten Chinese indigenous egg-type duck breeds, (Hui-Fang *et al.*, 2010) respectively, using microsatellite markers. Higher values obtained in those studies could be linked to higher number of alleles segregating at different loci. This corroborates the well-established fact that heterozygosity values obtained with microsatellite markers are generally higher, due to the higher level of polymorphism than those obtained with protein markers (Ibeagba-Awemu and Erhardt, 2004; Akinyemi and Salako, 2012).

A major possible underlying factor responsible for comparable and moderate heterozygosity values cum diversity in the present study among the ecotypes might be attributed to the unrestricted "gene flow" between ducks of different ecotypes through inter-regional trade and human movement; thus promoting intermingling and exchange of genetic materials among ducks of different ecotypes. Furthermore, since this locally adapted waterfowl has not been subjected to selection for genetic improvement or undergone directional selection for a particular blood protein genotype in the study area; therefore, the comparable estimated H values for the ecotypes are suggestive that these sub-populations are under the influence of similar evolutionary forces.

Furthermore, it is worthy of note that the average H of each ecotype (0.424–0.481) and the estimated mean value (0.450) for the three ecotypes using blood protein markers in this study were within the recommended range (0.3–0.8) for markers to be useful for measuring genetic variation in a population (Takezaki and Nei, 1996). Heterozygosity (H) is one of the indices used to assay genetic variation of each population and the value indicates the diversity level of the marker (Wu *et al.*, 2008).

The estimated average H within the recommended range indicates genetic variability in the studied ecotypes and suggests further the possibility of exploring this for genetic improvement of this waterfowl. Genetic diversity as observed in the studied population is an important attribute of a specie/population for adaptation to diverse environmental challenges. Besides, it is also a veritable tool for animal breeders in selection and genetic improvement of farm animals. The moderate heterozygosity value reported for the three ecotypes lends credence to the widely believed assumption that gene pools of the locally adapted animals are rich and are reservoirs of rare genes.

It is worthy of emphasis that in the three ecotypes, highest estimated mean *H* was obtained at Tf and Alb loci compared with CA and Hb. Higher mean *H* values at TF and Alb loci are attendant effects of higher number of genotypes (7 and 6, respectively for Alb and Tf; 3 each for Hb and CA) and alleles (4 each for TF and Alb; 3 each for CA and Hb). Various studies have shown that higher number of allele affects estimated heterozygosity values (Akinyemi and Salako, 2012).

Percentage of polymorphic loci (percent P)

Complete polymorphism at the protein-coding loci investigated in this study corroborated the report of Nur, Yusrizal and Manin (2012) on indigenous Kerinci duck in Indonesia where the three loci examined were polymorphic. Conversely, only 7 of the 15 loci examined in dabbling ducks were polymorphic (Paulauskas *et al.*, 2009). The observed polymorphism is an indication of absence of selection with respect to the investigated loci and reinforce the widely reported diversity in the genome of indigenous livestock species in developing countries.

Effective number of alleles (n_e)

Effective number of allele (n_e) is an index used to reveal the genetic diversity of the populations and also to assay the effect of alleles in each population (Wu *et al.*, 2008). Empirical reports on n_e in Muscovy duck using biochemical markers are sparse. Of recent, Wu *et al.* (2008) reported 5.7351 for Chinese Muscovy duck. This value is higher compared to the result of this study. The disparities observed in the two populations could be linked to the higher number of alleles (281) and 20 (microsatellite) loci examined by Wu *et al.* (2008). The higher values obtained for the ecotypes and the population under study in general suggested that the sub-populations have better abilities to keep the effective alleles when selection, mutation or genetic drift have occurred (Wu *et al.*, 2008).

Sex differences in blood protein polymorphism in locally adapted Muscovy duck in Nigeria

Related studies on association of sex with biochemical polymorphism of blood proteins in Muscovy duck are sparse to compare with results of the present study.

Haemoglobin

The higher frequencies of Hb^{AA} genotype in male and female Muscovy ducks in the present study were in agreement with the report of Yakubu and Aya (2012) on male and female Nigerian local chickens but contrasted with the report of Salako and Ige (2006) on Nigerian indigenous chickens where heterozygous males and females predominated. The prevalence of HbA gene in male and female Muscovy ducks is in tandem with reports on Nigerian local chickens (Salako and Ige, 2006; Yakubu and Aya, 2012). The high frequency of HbA in the two sexes of Nigerian Muscovy ducks is a pointer to the absence of sex-influence on its expression.

Carbonic anhydrase

Prevalence of higher frequency of CA^{FF} genotype and allele CAF in the two sexes indicate absence of sex-influence on its expression and also indicates the importance of gene F to the survival and adaptation of this water fowl to the study area.

Transferrin

Prevalence of genotype Tf^{BC} in the two sexes coupled with higher frequency of genes TfB and TfC is a clear indicator of the importance of the two genes in the population under study. Besides, similarities in the distribution of the genes of the two sexes also indicate that sex had no influence on the expression of the Transferrin genotypes and alleles.

Albumin

Since the sexes of the population under study have not been selected on the basis of a particular blood protein; discrepancies observed in relation to the genotype and gene frequencies of Alb in this study may possibly be attributed to sex effect. A related study on waterfowl also reported exclusive expression of some alleles at the five loci of male and female Lesser Snow Geese (Kuznetsov, Baranyuk and Takekawa, 1998). Predominance of genes A and B in males; B and C in females possibly indicate the possibility of unknown sex-specific or sex-related physiological advantages those genes confer on each sex. However, disparities observed in distribution of this protein marker are subject to confirmation with a large sample and or studies conducted in controlled environment.

Estimated genetic variability of male and female Muscovy ducks in Nigeria

Comparative studies of the association of sex with genetic diversity estimated from blood protein markers are lacking to validate the result of the present study.

Heterozygosity (H)

The average *H* for the two sexes were within the range (0.3–0.8) required for a species to qualify for genetic improvement (Takezaki and Nei, 1996) and also indicates further allelic richness and diversity of this population. Besides, the estimated *H* for the male and female Muscovy ducks in this study were higher than the values reported for male (0.094–0.130) and female (0.114–0.119) Lesser Snow Geese (Kuznetsov, Baranyuk and Takekawa, 1998).

Effective number of allele (n_e)

Higher values of n_e in females compared to males could probably be attributed to the attendent effect of higher H of females.

Percentage of polymorphic loci (percent P)

Polymorphicity at all loci of examined in this agrees with similar studies on both sexes of Nigerian local chickens (Salako and Ige, 2006; Yakubu and Aya, 2012).

Conclusion

Similarity in frequencies of biochemical protein genotypes and alleles in the three ecotypes and between the sexes is an indication that neither ecotype nor sex influence their distributions and that they are under similar evolutionary forces.

The values of the estimated genetic diversity parameters for the ducks in this study indicate that all ecotypes are variable in their genome and that there are chances for genetic improvement if crossed with exotic or Muscovy ducks from another population not covered in this study.

Besides, application of DNA technologies such as microsatellite markers would help a lot to elucidate further genetic diversity existing in this waterfowl as they have been shown to be more informative due to generation of many loci and alleles.

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Current status and phenotypic characteristics of Bulgarian poultry genetic resources

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Summary

Poultry biodiversity conservation is a great challenge for many countries. Within the last several years, the number of endangered local breeds has increased, leading to a considerable loss of genetic resources. A similar trend was observed among the poultry breeds, including chicken, local turkey and goose breeds/lines established in Bulgaria, part of which is definitely lost. Currently these breeds/lines are at risk and/or threatened with extinction. The information obtained by phenotypic characterization of these breeds is the first step for planning the management of poultry genetic resources through setting up improved selection schemes and conservation strategies. In this paper, we reviewed the current state of knowledge regarding the morphological and phenotypic diversity of local poultry breeds and some old productive poultry lines in Bulgaria.

Keywords: *Bulgarian poultry breeds, conservation, phenotypic characterization, production performance*

Résumé

La conservation de la biodiversité avicole s’avère un grand défi pour beaucoup de pays. Au cours des dernières années le nombre de races locales menacées a augmenté, ce qui a entraîné une perte considérable de ressources génétiques. Une tendance similaire a été observée parmi les races de volailles (races et lignées locales de poules, dindons et oies) établies en Bulgarie, dont certaines ont été perdues à jamais. De nos jours ces races ou lignées sont menacées et/ou en voie de disparition. Obtenir de l’information par le biais de la caractérisation phénotypique de ces races représente le premier pas pour planifier une gestion des ressources génétiques avicoles basée sur la mise en place de schémas de sélection et de stratégies de conservation. Cet article cherche à évaluer l’état actuel des connaissances sur la diversité morphologique et phénotypique des races avicoles locales et de certaines lignées anciennes en Bulgarie.

Mots-clés: *races avicoles bulgares, performances productives, caractérisation phénotypique, conservation*

Resumen

La conservación de la biodiversidad avícola supone un gran reto para muchos países. En los últimos años ha aumentado el número de razas locales amenazadas, lo cual ha traído aparejada una pérdida considerable de recursos genéticos. Se ha observado una tendencia similar entre las razas de aves de corral (razas y líneas locales de gallinas, pavos y gansos) establecidas en Bulgaria, parte de las cuales se han perdido ya definitivamente. Actualmente estas razas o líneas están amenazadas y/o en peligro de extinción. La obtención de información mediante la caracterización fenotípica de estas razas constituye el primer paso para la planificación de una gestión de los recursos genéticos avícolas basada en el establecimiento de esquemas de selección y estrategias de conservación. En este artículo se evalúan los conocimientos actuales en relación con la diversidad morfológica y fenotípica de razas avícolas locales y de algunas antiguas líneas productivas en Bulgaria.

Palabras clave: *razas avícolas búlgaras, rendimientos productivos, caracterización fenotípica, conservación*

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Introduction

Approximately 30 percent of total animal protein consumed by human on the planet originates from poultry (Permin and Pedersen, 2000). In 2010, poultry meat ranked the second after pork meat, contributing to 33.4 percent of the world’s meat production, mostly from commercial broiler chicken industry (USDA database and FAO database, cited in Trostle *et al*., 2011). Modern poultry farming worldwide is based on the use of a limited number of chicken breeds and lines. White Leghorn and Rhode Island Red are the leading breeds among commercial egg layers while Cornish and White Plymouth Rock are the

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major broiler breeds (Fulton, 2006). However, under intensive systems of rearing for high productivity, the hybrid chickens suffer from several problems, such as feather pecking, high mortality, cracked and stained eggs as well as diseases such as ascites syndrome, Cellulitis, sudden death syndrome, tibial dyshondroplasia, osteoporosis, etc. (Julian, 2005; Sørensen, 2005). In consequence of these negative repercussions, the welfare movements and organizations have great concern on modern poultry farming, especially with respect to the well being of birds under commercial farming conditions (Lukanov and Aleksieva, 2013). Intensification of poultry with the use of high-performance hybrids has led to the displacement of less competitive breeds and circumscription of genetic diversity (Gandini and Villa, 2003; Hillel *et al.*, 2003; Beaumont, Bihan-Le Duval and Magdelain, 2004). Over the past half-century, a considerable portion of avian genetic stocks has disappeared (Pisenti *et al.*, 1999; Fulton and Delany, 2003). The assessment of local breeds and lines is important for maintaining genetic variation. Many local breeds could be used in poultry breeding industry as carriers of valuable genes that determine important traits such as resistance to diseases, adaptation to ecological conditions, eggshell colour and hardness, body constitution, meat and egg traits. The characterization of animal genetic resources (AnGR) for food and agriculture requires three types of information of their phenotype, genetics and history (FAO, 2012a). Phenotypic characterization of AnGR is the process of identifying distinct populations/breeds and describing their external and production characteristics in a fixed environment and management, taking into consideration of the factors that influence them. Phenotypic and molecular genetic characterizations of AnGR are complementary to each other to measure genetic diversity for better understanding and sustainable utilization. The information provided by this characterization is essential for planning the management of AnGR at local, national, regional and global levels (FAO, 2012a).

In this context, the phenotypic characterization is fundamental and the first step for the evaluation of AnGR.

Poultry genetic diversity in Europe

The significance of AnGR and especially poultry genetic resources has been discussed in many forums (FAO, 1998, 2007, 2012b; Delany, 2003; Fulton and Delany, 2003). About 30 percent of all poultry breeds have been classified as at risk. Among avian species, chickens have by far the highest number of breeds at risk on a global scale (FAO, 2012a, 2012b).

Europe has the highest number of local avian breeds (851), followed by Asia (408), Africa (146) and Latin America regions (138). Near Middle East, North America and Southwest Pacific regions have the lowest number of reported local breeds (FAO, 2012b). Compared with other regions, Europe has also the highest number of transboundary chicken breeds, defined as breeds that occur in more than one country. A major role in preservation of the poultry breeds reared in Europe, North America and Australia is due to the long tradition in exhibition and ornamental poultry breeding dating back to middle nineteenth century. The existence of a significant number of regional transboundary breeds has implication for management and conservation of AnGR, and highlights the need for cooperation at regional or subregional levels (FAO, 2012b).

For local breeds or lines of chickens, there is paucity of knowledge at the production, pedigree and population structure at molecular levels (Blackburn, 2006).

Recently, an information system was installed in Bulgaria to monitor the diversity of farm animals – EFABIS (http://efabis-bg.iasrj.eu) which is part of the global network FABISnet. The information system will collect data on AnGR in the country, which will be shared with other members of the network and the global database – DAD-IS of the FAO.

This paper focuses on the status, phenotypic characterization and some productive traits of the Bulgarian local chicken breeds, which represent both a heritage and a reservoir of variability but under threat of extinction presently.

Bulgarian poultry genetic resources

The list of Bulgarian poultry breeds, old productive lines and their primary productive performances are summarized in Table 1.

The shares of Bulgarian domestic poultry breeds by species are shown in Figure 1.

Present status, morphology and production performance of Bulgarian chicken breeds

Local Bulgarian chickens include five breeds – Black Shumen chicken, Stara Zagora Red chicken, Katunitsa chicken, Bregovska dzhinka chicken (Bulgarian crested bantam) and Struma chicken (including bantam form). A total of 14 productive lines were developed for the first three breeds (Table 1). Currently all breeds are at risk and threatened with extinction, demonstrated by their drastic decline in number and their low consistency (Lalev *et al.*, 2011). In spite of their endangered status, these chicken breeds are well appreciated for their ability to adapt to extensive and organic rearing systems.

Black Shumen chicken was developed in Shumen region in Northeastern Bulgaria in the late 19th and early 20th centuries by folk breeding. The breed is distinguished by its black plumage, red earlobes, red iris and production

Table 1. Productive performances of Bulgarian avian breeds/lines.

Breed/line	Type	Body weight (male/female, kg)	Laying capacity (egg number)[1,2,3,4]
Domestic chicken (*Gallus gallus domesticus*)			
Black Shumen chicken	Egg	2.0–2.5/1.4–1.8	150–180[4]
Line B		2.0–2.2/1.6–1.7	280–290[4]
Line D		2.0–2.1/1.8–1.9	290–300[4]
Line T		2.1–2.2/1.4–1.5	106–107[1]
Line P		2.1–2.2/1.4–1.5	102–103[1]
Line N		2.2–2.3/1.4–1.5	104–105[1]
Line SZ-80M		2.2–2.3/1.6–1.7	200–220[4]
Line SZ-80B		2.0–2.2/1.6–1.7	260–265[4]
Stara Zagora Red	Dual-purpose	2.8–3.5/2.3–2.5	220–240[4]
Line E		3.0–3.2/2.2–2.4	220–240[4]
Line NG		3.0–3.2/2.2–2.4	240–260[4]
Line Ss		3.0–3.5/2.2–2.5	210–220[4]
Katunitsa chicken	Meat	4.6–6.5/4.0–5.5	120–150[4]
Line G		4.0–4.2/3.2–3.5	165–170[4]
Line M		4.7–4.8/3.6–3.7	63–64[2]
Line L		4.2–4.4/3.2–3.3	89–90[2]
Line K		4.1–4.2/3.3–3.4	96–97[2]
Bulgarian crested bantam	Ornamental	0.75–0.95/0.6–0.8	60–120[4]
Struma chicken		3.2–3.8/2.8–3.2	130–150[4]
Struma chicken bantam		0.75–0.95/0.6–0.8	60–80[4]
Domestic turkey (*Meleagris gallopavo domesticus*)			
Nova Zagora Bronze	Light	7.0–8.0/3.0–5.0	30–50[4]
Line NCB	Light	15.0–16.0/9.0–10.0	70–80[3]
Line LL	Light-heavy	14.0–15.0/8.0–9.0	115–120[3]
Line MH		25.0–27.0/12.0–13.0	50–60[3]
Domestic goose (*Anser anser domesticus*)			
Local geese	Medium	6.0–7.5/4–5.5	20–25[4]
Benkovska white goose		5.5–7.0/4–5.5	22–25[4]

[1] Laying capacity per 120 days.
[2] Laying capacity per 160 days.
[3] Laying capacity per 6 months.
[4] Laing capacity per year.

of white-shelled eggs with slightly creamy tinge. This breed thrives despite unfavourable conditions like poor feeding and breeding as well as presence of predators and disease outbreaks. The breed has the following characteristics: high vitality and stamina, excellent reproductive abilities, relatively good egg production and egg weight. Improvement of chicken in Shumen region began in the middle of the twentieth century through crossing local black hens with Black Minorca cocks for improved body weight, egg production and egg size. In the 1980s, the second stage of genetic improvement of this breed crossing with Rhode Island Red was carried out for consolidation of its body shape, leading the development of a new, large body-sized dual-purpose breed, called Black Large.

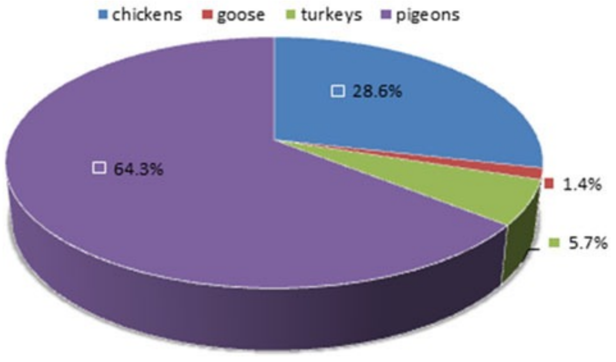

Figure 1. Shares of Bulgarian avian breeds by species.

By the end of the twentieth century, Black Shumen chicken was fairly well distributed, although not numerous. Presently, small flocks are reared in experimental stations, agricultural colleges and institutes, as well as in private yards. A conservation flock with 170 birds (150 ♀ and 20 ♂), which are insufficient for a sustainable conservation program of this breed, was established in 2010 and is managed by the Agricultural Institute, Stara Zagora (Lalev *et al.*, 2011). Agricultural University – Plovdiv supported another small flock (20–30 birds) for educational purpose (Petrov, Lukanov and Gerzilov, 2011). Approximately 200 breeding birds of this breed in black and blue plumage colours are kept by hobbyist breeders in the country. Birds of this breed are also kept by several breeders in Serbia, Turkey, Romania, Russia, Netherland, France and Germany.

The Black Shumen breed has black plumage with green tinge (Petrov, Lukanov and Gerzilov, 2011) (Figure 2). In recent years, blue colour plumage has been introduced

Figure 2. Black Shumen chicken breed: cockerel (left) and hen (right) (orig.).

from blue Australorps (Figure 3). The breed is characterized by moderately wide head (Lukanov, 2013) and medium size beak which is black and slightly curved. The eyes are large, bright and orange-red. The face is red and covered with some short black feathers. In some females (Figure 4), a facial fibromelanosis can be seen, a condition of dermal hyperpigmentation (melanization) due to a mutation in domestic chicken that is supposed to have originated in South East Asia (Lukanov and Genchev, 2013). The comb is straight, single and relatively large with 5–7 points in males. In the hens, the comb is a straight or slightly slumped to one side. Wattles are relatively large, rounded. The neck is of medium length and well feathered. The body is elegant, harmonious, robust, cylindrical and slightly upright. Shoulders are relatively broad, rounded, partly covered by the hackle plumage. The back of the rooster is moderately wide and long, slightly sloping back towards the tail while it is horizontal for the hens. Saddle area is well feathered, medium length with a sharp transition to the tail. In the roosters, breasts are round with relatively high position. The abdomen is moderately wide and well developedin hens, while in the roosters it is retracted. The tail is relatively large, open, carried on about 40–45° to the horizontal line in both sexes, while the roosters has well-developed, broad sickle feathers. The wings are relatively long, close fitting to the body, parallel to the topline, without departing from the outline of the body. Thighs are well feathered and medium in length. Shanks are grey-black coloured, in medium length, strong and unfeathered. The body weight of the cock is about 2.0–2.5 and 1.4–1.8 kg for hens. Egg production is 150–180 eggs per year depending on the use of illumination. The eggs have white shell with a creamy shade and weigh about 50–55 g.

Wide variations in body size exist while the colours of the plumage varied in white or red feathers or strong violet hue. Targeted and in-depth studies on the productivity of the Black Shumen chicken and its crossbreds with *dw* barred hens in Bulgaria were carried out by Mincheva (2006). The author found that the birds from the Black Shumen breed reached sexual maturity at 184 days of

Figure 3. Blue Shumen cockerel (left) and hen (right) (orig.).

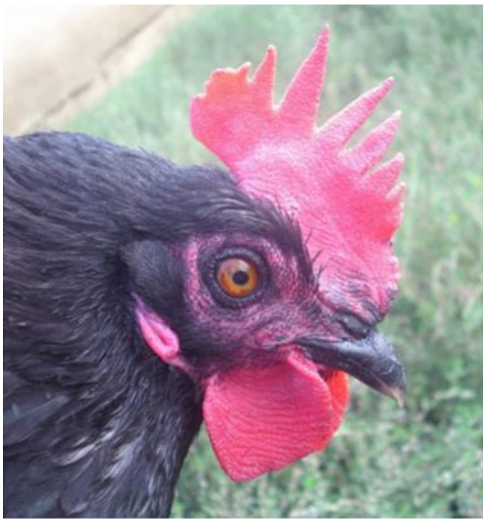

Figure 4. Head of Black Shumen hen with facial fibromelanosis (orig.).

age, with an average egg production of 58.29 and 60.59 percent in the first and second productive years, respectively. The mean egg weight was 47.58 g. The averaged live weights of pullets at sexual maturity and of hens at 48 weeks of age were 1 505 and 1 544 g, respectively (Table 2).

Petrov, Lukanov and Gerzilov (2011) studied the production performance of Black Shumen chicken under extensive rearing system. The average egg production for the 23-week period from the onset of lay was 45.4 percent. The egg weight increased with increasing age of birds and ranged from 40.40 to 53.60 g.

Stara Zagora Red chicken is native to Stara Zagora region and distributed mainly in Central Southern Bulgaria. Establishment of the breed was started in the middle of the twentieth century through crossing local red hens with Rhode Island Red roosters for the improvement of growth rate, body weight, egg production and egg mass. The breed has very good adaptatability to local conditions and good egg production. The colour of the plumage is red-brown with mahogany tint and the tail is black with a green sheen.

The breed was developed with the objective of producing highly productive birds with good body weight and laying capacity suitable for extensive and semi-intensive poultry farming. However, the breed began declining in the late 1980s to be ultimately replaced by commercial hybrids. The breed is currently critical. The only flock in Bulgaria is maintained by the Agricultural Institute in Stara Zagora with a population of about 300 hens and 60 roosters. These birds are considered as part of national gene pool with the name StR line maintained under controlled breeding conditions.

Table 2. Study in three consecutive years of live weight in Black Shumen chicken breed (Mincheva, 2006).

Year of the study	Live weight at start laying eggs (g)	Live weight at 48 weeks old (g)
2003	1 535.14 ± 21.48	1 591.86 ± 32.35
2004	1 550.73 ± 17.95	1 541.18 ± 21.00
2005	1 430.56 ± 17.12	1 515.91 ± 22.49
Average	1 505.47 ± 11.53	1 544.06 ± 14.13

Stara Zagora Red chicken has a medium body size, wide head, single-comb and well-developed wattles (Figure 5). The comb and earlobes are red and eyes are in orange-red colour. The beak is short, strong, well curved and in slight yellowish colour. The neck is in medium length and good feathered. The back is broad and relatively long. The breasts are round, long and well muscled. The shanks are not very long, vertically placed and yellow coloured. The tail is in medium size, well spread, and carried at a relatively high position above the horizontal line. The plumage colour is red-brown and the tail is black (Nozhchev and Tsonkov, 1969). Hens are characterized by calm temperament, tolerant to various weather conditions and unpretentiousness to the feed and rearing. These birds are one of the good dual-purpose breeds with intensive growth in males and good laying capacity in hens. The live weights are 2.3–2.5 and 2.8–3.5 kg for hens and cocks, respectively (Lalev *et al.*, 2011; Lukanov, 2011). The egg production is 220–240 eggs per year with an egg weight about 58 g.

The main reproductive and egg productive performances in this breed are shown in Table 3.

Ornamental chickens

Three ornamental breed groups of chickens are commonly reared in Bulgaria: Bregovska dzhinka chicken, Struma chicken and Struma bantam chicken.

Bregovska dzhinka chicken (Bulgarian crested bantam)

This is a breed group of true bantams in Northwestern Bulgaria, especially in the region of Vidin and Bregovo. “Dzhinka” is the Bulgarian folk word for true bantams. Due to unintentional selection and different vision of each breeder, these birds still have a great variability in their morphological characteristics.

Bregovska dzhinka breed group is characterized by the presence of well-developed crest (small in roosters and well developed in hens), single or rose comb, white or red earlobes and well-manifested feathered legs with vulture hocks (Figure 6). The colour of the plumage varied in three major colours (black–red–white) and black–white mottled variations. The pullets start laying at about 5.5–6 months of age and the egg production is low, in a range of 60–120 eggs per year and weighing 30–35 g each. These birds are suitable for ornamental

Figure 5. Stara Zagora Red chicken (orig.).

purpose, resistant to some parasite and infectious diseases, unpretentious and excellent brooders. The body weight is 0.75–0.95 kg for the roosters and 0.6–0.8 kg for the hens.

Struma chicken standard and bantam

There was report for the presence of hens with a beard, crest and feathered legs at the end of the nineteenth century in Bulgaria (Figure 7). This breed group was established in the region around the Struma River by local breeders. The creation of miniature version of the Struma chicken (Struma bantam) began in the last decade by introducing the Bregovska dzhinka chicken. It is difficult to determine the actual number of breeding birds on the ground because these birds are bred from amateur poultry breeders, mainly in Western Bulgaria.

The plumage colour varies widely, the most stable ones are black–white mottled, red–white mottled, barred and white. These birds were part of several major exhibitions in Bulgaria and their popularity has grown steadily because of their extravagant appearance. They are excellent brooders. The roosters weigh about 3.2–3.8 kg and the hens 2.8–3.2 kg. The laying capacity is not very good – one hen can lay 130–150 eggs per year with an averaged egg weight about 50 g. The bantam version has appearance of the Bregovska dzhinka chicken, but they do have a well-developed beard (Figure 8).

Table 3. Reproductive performance and egg production in Stara Zagora Red chicken.

Parameters	
Body weight in day-old chicks (g)	41.20
Body weight of laying hens in 5-months of age (g)	2 400
Mortality at 90-days of age (%)	2.80
Start of egg-laying, age in days	165
Egg production (laid eggs) for 200 days	129.57
Average egg weight from layers (g)	57.43
Fertilized eggs (%)	89.23
Hatch of eggs set (%)	71.79
Hatch of fertile eggs (%)	80.75

Katunitsa chicken (line AN)

This breed group is of meat type and developed by Alexandar Nikolov in his poultry farm in the village of Katunitsa near Plovdiv in the late 1990s in collaboration with Agricultural University of Plovdiv (Nikolov and Gerzilov, 2011).

Katunitsa chicken (line AN) was developed by a strict selection by mass and plumage colour in a population of dual-purpose chickens in the area of Katunitca village. The nucleus flock of Katunitsa chicken is about 400 breeding birds and they are extremely popular in the Plovdiv region and gaining greater popularity in Bulgaria. The body is large, massive, deep, wide and well muscled. The plumage is soft with greyish-copper red colour in the hens and black–red in the roosters. The legs are pale yellow and the beak is dark with a yellow tip. The comb is medium sized and single. The earlobes are red (Figure 9).

Both males and females are characterized by rapid growth performance and excellent meat-qualities. The live weight at 12 weeks of age is 1.75–1.85 kg for females and 2.45–2.55 kg for males, at the beginning of egg laying (20–21 weeks old) above 3.00 kg for pullets and 4.40 kg for cockerels, and at 52 weeks old 4.0–4.2 kg for hens and 4.6–4.7 kg for cocks (Gerzilov *et al.*, 2013). Egg production is 120–150 eggs with weight of 60–62 g. These breeds are suitable for organic production of chicken meat.

Figure 6. Bregovska dzhinka breed group (orig.).

Figure 7. Struma hen at the Bulgarian National show 2013 (orig.).

Present status of other Bulgarian poultry breeds

Local turkey (Nova Zagora Bronze turkey)

These are small local turkeys, spread in the area around Nova Zagora, Stara Zagora, Yambol, Pazardzhik, Pavlikeni and Gorna Oryahovitsa (Figure 10). During the second half of the twentieth century, many high productive breeds were imported and there was a sporadically cross-breeding with local birds. During this period, the Ministry of Agriculture of Bulgaria approved local bronze turkeys from Nova Zagora region as a breed named as Nova Zagora Bronze turkey (Lukanov, 2011).

Figure 8. Struma bantam hen at the Bulgarian National exhibition 2013 (orig.).

Figure 9. A flock of Katunitsa chicken (line AN) at Alexandar Nikolov poultry farm (orig.).

This turkey breed is characterized by low body weight, low egg production, highly resistant to some parasite diseases (like Histomonosis) and undemanding with excellent adaptability and good reproductive capabilities. These turkeys have a strong brooding instinct. Local people use them to brood chicken eggs. Plumage is mainly bronze coloured but there are also white, blue, bourbon, etc. (Ivanov and Shishkov, 1968). The body weight of the males is 7–8 kg and of the females 3–5 kg. Laying capacity is about 30–50 eggs per year with weight around 80 g (Donchev *et al.*, 1997).

Nova Zagora bronze turkeys use pastures very well and are easy to breed, but are not convenient for industrial production of meat due to their low productive capacity. The birds can be used for organic turkey meat production.

Local geese

Different geese are widespread in the areas around the river valleys in Bulgaria and they have a predominantly grey–white plumage (wild). They were created by the folk selection. Birds with small crests and also curly feathered geese could be seen in different parts in Bulgaria. Local geese are characterized with quick maturity, relatively good meat productivity and adaptive capabilities. During the second half of the twentieth century, breeding for improvement of the liver size was conducted by crossing local geese with Emden goose, Toulouse goose and Hungary goose and the new birds were called Benkovska White goose (Rangelov and Ivanov, 1987). Due to the global trend to reduce the production of foie gras from geese at the expense of those from mule ducks, pure Benkovska White geese have become limited in number.

The body of this breed goose breed is relatively large and deep. Its neck is of medium length and in black colour.

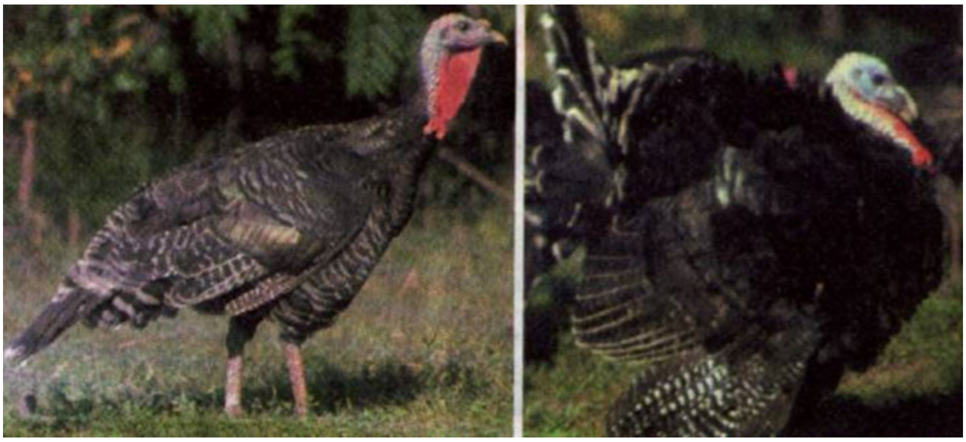

Figure 10. Bulgarian local turkeys (Donchev *et al*., 1997).

Its back is wide, long and in grey to grey-white. These geese have a broad and deep chest. Their heads are medium-sized. Their peaks are orange and there are orange circles around their eyes. Their abdomen and tail are white. Benkovska White goose has one or two abdominal skin folds. The legs are of medium length, well muscled, wide set and orange (Figure 11). The body weight of females is 4.0–5.5 kg and of males 6–7.5 kg. Egg production is low, about 20–25 eggs per year. Eggs weigh about 180–190 g. Benkovska White goose achieves a mass of 4.2–5 kg at 70 days old and 9–11 kg for fatten mature birds. Their livers reach 450–500 g and a maximum of 1 100 g can be achieved after overfeeding (Lukanov, 2011).

Conclusions

The information on the genetic and phenotypic characteristics of Bulgarian local poultry breeds and lines is very limited. Today, the main Bulgarian poultry breeds and old productive lines are only kept in closed flocks in Agricultural Institute in Stara Zagora and Agricultural University in Plovdiv. This type of conservation is very risky since the whole flocks can be lost if there is an epidemic. This implies the need for segmentation of breeds into small flocks in different regions. The hobby poultry breeders could play a major role to preserve some of the breeds and lines. Through the encouragement of organic poultry production or special products, these breeds can find their place in modern poultry farming.

There is an urgent need to document the genetic diversity of local poultry resources and design strategies for their sustainable conservation. Molecular characterization of local poultry breeds in the near future will aid considerably in the maintenance of existing genetic stocks in Bulgaria.

Figure 11. Benkovska White goose (orig.).

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Phenotypic characterization of local Ghanaian chickens: egg-laying performance under improved management conditions

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Summary

Egg production performance of 571 local Ghanaian chickens and 107 SASSO T44 chickens kept under improved management conditions were analysed. Average egg weight, hen-day egg production and feed conversion ratio (FCR) were determined for the three experimental chicken ecotypes. Hen-day production was significantly ($P < 0.05$) higher in the savannah local chicken ecotype than the forest ecotype and SASSO T44 chickens. Egg weights of local Ghanaian chickens compared favourably with values reported for local chickens in Africa. On the average, SASSO T44 had significantly ($P < 0.05$) higher egg weights and feed intake compared with the local chicken ecotypes. The local chicken ecotypes on the other hand, had significantly ($P < 0.05$) better feed conversion ratios than SASSO T44 chicken. Local Ghanaian chicken ecotypes have a more efficient FCR per every unit of egg produced compared with the control population. Low feed intake, good feed conversion ratios and adaptation to the environment are traits local chicken harbour which can be exploited in future breeding programmes to improve on chicken meat and egg production in Ghana. Ghanaian local chickens could thus be a valuable genetic resource for the development of an efficient egg production chicken breed adaptable to the humid tropical climates.

Keywords: *egg number, egg weight, feed conversion ratio, feed intake, local chickens*

Résumé

Des paramètres en rapport avec la production d'œufs ont été analysés chez 571 poules locales ghanéennes et chez 107 poules SASSO T44 soumises à des pratiques d'élevage perfectionnées. Le poids moyen des œufs, la production d'œufs par poule et jour et la conversion alimentaire ont été évalués chez trois écotypes de poule. La production quotidienne d'œufs par poule a été significativement ($P < 0.05$) plus élevée chez l'écotype local de poule de la savane que chez l'écotype de la forêt et que chez les poules SASSO T44. Compte tenu des valeurs de référence pour les poules locales africaines, les œufs des poules locales ghanéennes ont atteint un poids plutôt élevé. En moyenne, le poids des œufs et la consommation d'aliment ont été significativement ($P < 0.05$) plus élevés chez les poules SASSO T44 que chez les écotypes locaux de poule. Cependant, les écotypes locaux de poule ont présenté un taux de conversion alimentaire significativement ($P < 0.05$) meilleur que celui des poules SASSO T44. Les écotypes locaux de poule ghanéenne ont présenté une conversion alimentaire par unité d'œuf produite plus efficiente que celle de la population contrôle. Une moindre consommation d'aliment, un bon taux de conversion alimentaire et l'adaptation à l'environnement sont des traits caractéristiques des poules locales qui peuvent être exploités dans des futurs programmes de sélection afin d'améliorer les productions de viande de poulet et d'œufs au Ghana. Ainsi, les poules locales ghanéennes pourraient constituer une ressource génétique précieuse pour le développement d'une race de poule efficiente dans la production d'œufs et capable de s'adapter à des climats tropicaux humides.

Mots-clés: *poids des œufs, nombre d'œufs, consommation d'aliment, taux de conversion alimentaire, poules locales*

Resumen

Se analizaron parámetros de producción de huevos en 571 gallinas locales ghanesas y en 107 gallinas SASSO T44 explotadas bajo condiciones de manejo mejoradas. Se evaluaron el peso medio de los huevos, la producción de huevos por gallina y día y la conversión del alimento para tres ecotipos de gallina. La producción de huevos por gallina y día fue significativamente ($P < 0.05$) mayor en el ecotipo local de gallinas de la sabana que en el ecotipo de la selva o que en las gallinas SASSO T44. Teniendo en cuenta los valores de referencia para las gallinas locales de África, los huevos de las gallinas locales ghanesas alcanzaron un peso más bien alto. De media, el peso de los huevos y el consumo de alimento fueron significativamente ($P < 0.05$) mayores en las gallinas SASSO T44 que en los ecotipos locales de gallina. Sin embargo, los ecotipos locales de gallina presentaron un índice de conversión del alimento significativamente ($P < 0.05$) mejor que el de las gallinas SASSO T44. Los ecotipos locales de gallina ghanesa mostraron una conversión del alimento por unidad de huevo producida más eficiente que la de la población control. Un bajo consumo de alimento, un buen índice de conversión del pienso y la adaptación al entorno son rasgos característicos de las gallinas locales que pueden ser explotados en futuros programas de selección con el fin de mejorar las producciones de carne de pollo y de huevos en Ghana. Así, las gallinas locales ghanesas podrían representar un valioso recurso genético para el desarrollo de una raza de gallina eficiente en la producción de huevos y con capacidad de adaptación a climas tropicales húmedos.

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Palabras clave: *peso del huevo, número de huevos, consumo de alimento, índice de conversión del alimento, gallinas locales*

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Introduction

Poultry production has important economic, social, nutritional and cultural benefits in developing countries (Tadesse *et al.*, 2013) providing animal protein of high biological value in terms of eggs and meat (Penderson, 2002; Ahmad *et al.*, 2010; Moula *et al.*, 2013). In most developing countries today, poultry production is still based on the scavenging local chicken flocks (Kitalyi, 1998; Dana, 2009; Osei-Amponsah, Kayang and Naazie, 2013). Free ranging chickens comprise about 80 percent of the continent's poultry flock in Africa, producing about 1 695 620 metric tonnes of eggs and 2 096 000 metric tonnes of meat annually, almost exclusively from scavenging in the backyards with little or no extra input, management or health care (Guèye, 1998; Dana, 2009). These chickens contribute to food security, protein nutrition and empowerment of rural women whilst alleviating poverty (Guèye, 1998; Branckaert *et al.*, 2000; Etim *et al.*, 2013; Adomako *et al.*, 2014; Ayim-Akonor and Akonor, 2014). Local chickens therefore play a crucial role in breaking the vicious cycle of poverty, malnutrition and disease (Roberts, 1992; Osei-Amponsah, Kayang and Naazie, 2012; Afolabi *et al.*, 2013).

In Ghana, poultry production is based on the traditional free range local chickens in the country-side, peri-urban and urban centres as well as a commercial sector based on intensive systems of rearing around the principal towns and cities. Egg production in Ghana has seen a steady increase (GAIN, 2013) with nearly 15 000 metric tonnes recorded between 2004 and 2012 (FAOSTAT, 2013). Similar to other countries in Africa, rural poultry production accounts for 60–80 percent of the national poultry population (Okantah *et al.*, 2003; Gyening, 2006). At the beginning of the 21st century, the rural poultry population was estimated at 12 million (Amakye-Anim, 2000), increasing to 20 million by 2005 (Aning, 2006). Currently, it is estimated that there are about 25 million free-roaming village poultry in Ghana. The poultry subsector is practised by about 66 percent of the 3.7 million households in Ghana, especially on the Guinea Savannah agro-ecological zone (Aning, 2006). Ghanaian local chickens therefore represent a huge genetic resource of immense value to the livelihoods of many families and households.

Table 1. Composition of ration fed to experimental chickens.

	Chick starter	Grower ration	Layer ration
Maize (%)	50	55	55
Wheat bran (%)	25	20	20
Concentrate (%)	25	20	20
Shell grits (%)	–	–	5
CP (%)	19	15.5	17.5
ME (kcal/kg)	2 770	2 640	2 620

CP, crude protein; ME, metabolizable energy.
Source of concentrate – Agricare Feed Products, Ltd, Ghana.

Egg production is a crucial aspect of poultry production and therefore the number of eggs produced by a hen in a production cycle, daily hen-housed egg production, low mortality rate and efficient feed conversion rate are important traits in the success of a poultry enterprise (Grobbelaar, Sutherland and Molalakgotla, 2010). In Ghana, income from the sale of eggs from local chickens contributes significantly to the family budget (Okantah *et al.*, 2003; Aboe *et al.*, 2006; Osei-Amponsah, Kayang and Naazie, 2012). Therefore, local chicken farmers need to know the number of eggs that can be produced by a hen in a production cycle to enable them make informed decisions about efficient production. Hardly any research has been done on this local genetic resource to characterize them either at the phenotypic or the genetic level and the potential of local chickens for egg production is unknown. Lack of data on the productive performance of chickens makes it difficult to develop sustainable egg production programmes.

A project to characterize Ghanaian local chicken was undertaken with funding from the French Government through the DURAS project. This paper presents results of the egg production potential and feed conversion efficiency for egg production of Ghanaian local chickens raised under improved management as compared with that of SASSO T44 chickens, a French *Label Rouge* free range chicken, raised under the same management in Ghana.

Materials and methods

Local chickens from the forest and savannah zones of Ghana used in this study were hatched at the Livestock and Poultry Research Centre (LIPREC), University of Ghana. LIPREC is located on latitude 05°40′N and Longitude 00°16′W on the Accra Plains which forms part of the Coastal Savannah. Annual rainfall of the ARC is 785 mm with a range of 128–1 709 mm distributed bi-modally. The long rainy season usually occurs between March and July with a peak in June and the short rainy season occurs between August and November with a peak in October. Mean monthly temperatures range from 24.8 °C in August to 28.3 °C in February with a mean of 26.9 °C. Relative humidity at 1 500 h ranges between 58 and 83.7 percent and is slightly lower at 0 9:00 h.

Two hundred Chicks of SASSO T44 day-old chicks were imported from France to coincide with the hatch of the local chicks. Chicks of each ecotype were managed similarly in three replicates in one deep litter house. In all, 227, 224 and 107 females of the savannah, forest and SASSO T44 chickens survived to produce egg records for analyses. Management of the experimental chickens has been described by Osei-Amponsah, Kayang and Naazie (2012). Briefly, chickens were given the same starter (0–4 weeks), grower (4–18 weeks) and finisher (after 18 weeks) rations, compositions of which are as indicated in Table 1. The feed consumption and eggs laid by each replicate were recorded daily. The number of eggs laid by local and SASSO T44 chickens between 22 and 49 weeks of age were evaluated against their feed consumption.

Average hen-day production, calculated as percentage of hens in lay and feed intake, were recorded on a daily basis. Feed conversion ratio (FCR) was then calculated as the ratio of feed consumed per gram of egg produced. Analysis-of-variance (ANOVA) procedures were used to measure the effect of breed (ecotype) on average feed intake, average egg weight and feed conversion. Test of difference of means on the data was performed by the Least Significant Difference (LSD) method using GenStat Release 10 (Payne *et al.*, 2007).

Results

Average feed intake and egg weight were significantly ($P < 0.05$) higher in SASSO T44 chickens than in the local chicken ecotypes (Table 2). SASSO T44 chickens consumed more feed for every unit of egg produced.

The age at first egg production was 22 weeks for all ecotypes, even with *ad libitum* feeding. Average percent egg production (hen-day production) and FCR were both significantly ($P < 0.05$) superior in the local chicken ecotypes. However, SASSO T44 chickens produced heavier eggs than local chickens throughout the study period (Figure 1). The forest chickens were on the average inferior to the savannah chickens in egg weight but consumed less feed per every unit of egg produced though this was not significant. Irrespective of the ecotype of chickens, egg weights increased during the study period (Figure 2).

Table 2. Egg production performance of local and SASSO T44 chickens.

Chicken ecotype	N	Average feed intake (g/bird/day)	Average egg weight (g)	Feed conversion ratio (FCR)
Savannah	227	71.9 ± 1.5^{c}	38.0 ± 0.4^{c}	1.93 ± 0.05^{b}
Forest	244	75.2 ± 2.0^{b}	40.1 ± 0.4^{b}	1.91 ± 0.06^{b}
SASSO T44	107	145.1 ± 7.7^{a}	48.9 ± 0.8^{a}	2.87 ± 0.15^{a}

^{a,b,c} within columns, means followed by different superscripts are significantly different.

The highest percent hen-day production recorded by the experimental chickens was between the period 24 and 34 weeks of age (Figure 2). Percent hen-day production in the savannah chicken ecotype was better compared with the forest chicken ecotype. In general, fluctuations in hen day production in SASSO T44 chickens were comparable with those of the local chicken ecotypes.

Discussion

In chickens egg production can start anytime from 18 weeks of age. The fact these chickens all began laying from week 22 implies that they are late starters. The late start of egg production is likely an adaptation for surviving under scavenging conditions. Egg production is very demanding of nutrients and so under free range it is likely that the bird must first build its reserves adequately before engaging in this nutrient demanding activity and hence adapted to starting later rather than earlier. The relatively higher egg weights obtained for SASSO T44 chickens compared with local chickens can be attributed to genetic differences. This is expected because heavy birds such as the SASSO T44, a strain of the French *Label Rouge* free range chickens, consume more feed and lay larger eggs (Leeson, Caston and Summers, 1997). The average egg weights of local Ghanaian chickens fall within the range reported for village chickens in Africa (Guèye, 1998; Adomako, Hagan, and Olympio, 2010). However, Adomako *et al.*, (2014) found higher egg weights in naked neck local-exotic crossbred chickens. Small egg size is a characteristic of indigenous tropical fowl breeds and this may be an adaptation to the tropical climate (Smith, 1974; Aganga, Tshwenyane and Molefhe, 2003). Egg production traits are quantitative in nature with a continuum between high and low-performing birds (Zaman, Sørensen and Howlider, 2004; Chatterjee *et al.*, 2008).

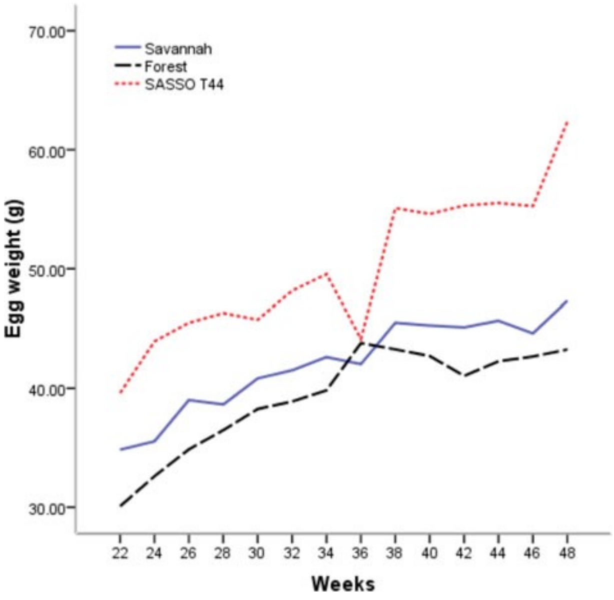

Figure 1. Variation in egg weight of experimental chicken

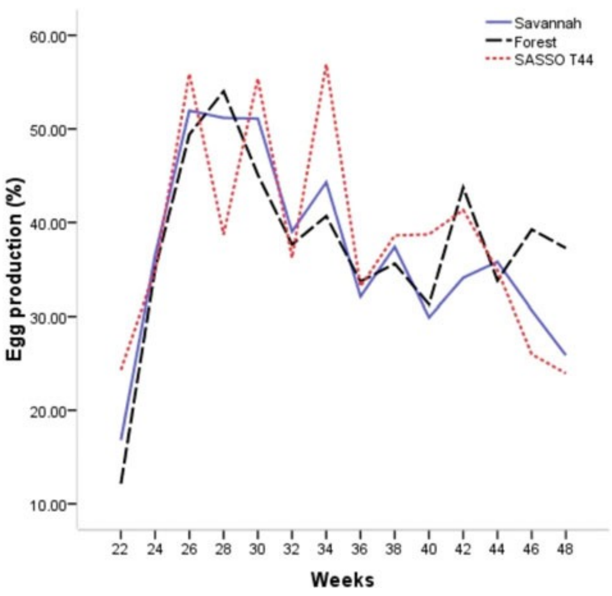

Figure 2. Egg production (%) of experimental chickens.

For instance, Nthimo (2004) found average egg weights ranging from 46.6 to 52 g in native Lesotho chickens which are higher than those of local Ghanaian chicken ecotypes, whilst Sazzad (1992) found the average egg weight for the exotic chicken breeds to be 72 percent higher than that of a local chicken breed. Addison *et al.* (2013) and Tadesse *et al.* (2013) reported average egg weights of between 49 and 60 g for exotic chickens raised in Ghana and Ethiopia, respectively.

Differences in egg production and quality exist between different strains of laying hens (Grobas *et al.*, 2001; Anderson, 2002). Results of average egg weights of local Ghanaian chicken ecotypes are lower than those reported for indigenous chickens of Iraq (Al-Rawi and Al-Athari, 2002) but superior to those reported for native chickens of South Africa (van Marle-Köster and Casey, 2001). Values of egg weights, laying percentage and FCR obtained in the present study were better than those obtained for local Bangladesh chickens but lower than Rhode Island Red (RIR) and White Leghorn (WLH) hens (Yeasmin, Howlider and Ahammad, 2003). Rahman, Baqui and Howlider (2004) reported average egg weights 49.4 and 48.7 g and feed consumption of 96 and 98.4 g/bird/day in a study on RIR × (Fayoumi) FAY and FAY × RIR crosses. The relatively lower egg weights observed in the present study compared with those observed by Rahman, Baqui and Howlider (2004) would be largely attributable to genotypic variations. Vij, Tantia and Vijh (2006) characterized the native Punjab Brown chicken of India and reported average egg weight of 46.01 g which is slightly higher than average egg weights obtained in the present study due to genetic and environmental effects.

Egg production curves describe the relation between number of eggs and time of the laying period and their shape is defined by sexual maturity (which marks the onset of production), followed by a stage of increasing production to a maximum or production peak followed by a steady decline in egg production or persistency of production (Wolc *et al.*, 2011).The egg production curves of the experimental chickens followed the typical egg production curve for a flock which increases during the first 8 or 9 weeks of production and decreases to the end of the production period (Grossman and Koops, 2001). The laying cycle of a chicken flock usually covers a span of about 12 months starting when the birds reach about 18–22 weeks of age, depending on the breed and season (Jacob, Miles and Mather, 2000). Flock production rises sharply and reaches a peak of about 90 percent between 6 and 8 weeks after which production gradually declines to about 65 percent after 12 months of lay (Jacob, Miles and Mather, 2000). In the present study, the highest hen-day (peak of) production for SASSO T44 chickens was observed at the same age as those of the local chicken ecotypes indicating an insignificant effect of genotype on this trait under the experimental conditions. Egg production of indigenous chickens of Ethiopia peaked between age 26 and 29 weeks (Mogesse, 2007) as obtained the current study. Rahman, Baqui and Howlider (2004) in a study on RIR × (Fayoumi) FAY and FAY × RIR crosses reported average percent egg production for the two crosses respectively as 48.2 and 52.8; The RIR × FAY and FAY × RIR crossbreeds reached peak egg production at 25 and 26 weeks of age, thereafter the egg production decreased as observed generally in the present study.

Results of egg-laying performance in the present study are lower than those reported by Anderson (2002) for brown and white hens and egg-type crosses of chickens based on Fayoumi, Leghorn, ISABROWN, Mandarah and R strains raised in Morocco. In comparison, eggs of the chicken ecotypes in the present study were lighter but the FCRs of local Ghanaian chicken ecotypes were better than the egg-type crosses (Benabdeljelil, Lahbabi and Bordas, 2003). Except for the RIR breed, egg production per cent for Ghanaian local chickens were higher than Bangladesh local chickens and their crosses with RIR and (Barred Plymouth Rock (BPR)) (Sazzad, 1992).

Birds considered to have better feed efficiency typically have a lower proportion of feed intake to body weight gain (Willems, Miller and Wood, 2013). FCR reported for native chickens of South Africa (van Marle-Köster and Casey, 2001) are inferior to those recorded for local Ghanaian chicken ecotypes. Galal *et al.* (2007) however reported lower feed conversion ratios for hens with the dwarf gene in Egypt compared with the three ecotypes in the present study. Mogesse (2007) found average feed intakes ranging from of 86.03 to 98.46 g/bird/day in various indigenous chickens of Ethiopia which are higher than those recorded for local Ghanaian chickens but lower than SASSO T44 chickens. Egg-laying percentage of chickens in the present study are lower than those of local Deshi Dwarf and Fayoumi chickens of Ethiopia and its crosses with WLH (Yeasmin, Howlider and Ahammad, 2003) but local Ghanaian chickens on the average consume less feed per gramme of egg produced.

Results of the present and other studies indicate substantial variations in egg production abilities of different chicken ecotypes. Egg production can be affected by such factors as feed consumption (quality and quantity), water intake, intensity and duration of light received, parasite infestation, disease, and numerous management and environmental factors (Jacob, Miles and Mather, 2000). Local chickens have low output expressed as low egg production, small egg size, slow growth rate and poor survival of chicks (Tadelle, 2003). Under village conditions the annual egg production per bird ranges from 20 to 100 eggs with an average weight ranging from about 30–50 g (Guèye, 1998). Such low productivity of indigenous chickens has been partly attributed to poor management practices, in particular lack of proper health care, poor nutrition and housing (Dutta, Islam and Kabir, 2013). South African indigenous chickens for instance performed much better in all egg production parameters under improved housing and management (Grobbelaar, Sutherland and Molalakgotla, 2010).

Improving the environment of chickens should thus contribute immensely towards improvement of their production qualities including egg production (Varguez-Montero *et al.*, 2012). The present study indicates that egg production of local chickens compares favourably with SASSO T44 chickens meaning that with proper management, more eggs can be obtained from local chickens than what obtains under free range. This is an opportunity to bridge the wide gap between demand and supply of animal protein. This should increase poultry production to provide required animal protein for human beings (Das *et al.*, 2007) whilst decreasing unemployment (Khawaja *et al.*, 2013) particularly among the youth.

Conclusions

Local chicken ecotypes had significantly ($P < 0.05$) lower average egg weight and feed intake per bird compared with SASSO T44. However, the local chicken ecotypes had comparable egg production performance and better feed conversion for every unit of egg produced. Local Ghanaian chickens can therefore be said to be relatively more efficient egg producers. Low feed intake, good feed conversion ratios and adaptation to the environment are traits local chicken harbour which can be exploited in a breeding programme to improve on chicken meat and egg production in Ghana.

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Statement of interest

The authors declare no conflict of interest.

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Phenotypic characterization of the Nigerian Muscovy Ducks (*Cairina moschata*)

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Summary

Phenotypic description helps in assessing the physical attributes of species and is also an indicator of the relevance and importance attached to such attributes in their natural environments. This study was conducted to describe patterns and distribution of phenotypic diversity in Nigerian Muscovy ducks. One thousand and twenty (1 020) adult male and female Muscovy ducks reared extensively were randomly drawn from the Rain Forest, Derived Savanna and Guinea Savanna agro-ecological zones/ecotypes and were visually appraised and scored for plumage, skin, shank, feet/web, bill, bean and caruncle colours. Data on qualitative traits were analysed with descriptive statistics (percentages) while fixed effect model was used to investigate relationship between plumage and skin colours and body weight. Results revealed variations in qualitative traits; however, across ecotypes, the predominant plumage, skin, shank, feet, bill, bean and caruncle colours were mottled (45 percent), white (88 percent), yellow (50 percent), yellow (60 percent), black (58 percent), black (69 percent) and red (84 percent), respectively. Besides, significant ($P < 0.05$) association was observed between plumage and skin colours and body weight. The reported variations in phenotypic traits of Nigerian Muscovy ducks indicate diversity in their genome, absence of selection and the need for their selection and improvement.

Keywords: *agro-ecological zone/ecotype, Muscovy ducks, phenotype, plumage*

Résumé

La description phenotypique donne l’evaluation rapide des attributs physiques des species; elle aussi est l’indicatrice de la pertinence et l’imprtance qu’on donnet a tells attributs dans les environs naturels. Cet ‘etude a ete fait pour decrier la modele et la distribution de la diversite phenotypique des canards Muscovy Nigerians. On a e’leve mille vingt (1 020) adultes canards muscovys (males et femelles extensivement et its ont ete pris par hazard des zones de la Foret, de la Savanne derive et de la Savanne guinea agro-ecologique et its out ete evalue a travers les ailes, la peau, la cuisse, la patte, le bec, le bejauna et la couleur caruncle. Les donnes sur les traits de la qualite ont ete analyse aves les statistiques descriptive (les pourcentages) tandis que la modele e ‘fix effect’ a ete employe pour determiner les effets de la plume et les couleurs de la peau sur le poids du corps. Les resultants nous revelent les variations dans les traits de la qualite. A travers les ecotypes, les plume predominantes, la peau, la cuisse la patte, le bec, le bejaune et les couleurs caruncle ont ete tachete (45%), le blanc (88%), le jaune (50%), le jaune (60%), le noir (58), le noir (69%) et la rouge (84%) respectivement. Neanmoins, la plume et la couler de peau a vraiment ($P < 0.05$) touché le poids du corps. La diversite phenotypique observe dans les canards Muscovy Nigerians montre l’absence de la selection et l’aiguillage pour l’ametioration de leur genetique.

Mots-clés: *La zone agro-ecologique/Ecotype, les canards muscovys, la phenotype, la plume*

Resumen

La descripción fenotípica sirve para definir las características físicas de las especies, siendo a la vez una indicación de la relevancia o importancia acordada a tales características en su entorno natural. Este estudio fue llevado a cabo para describir los patrones y la distribución de la diversidad fenotípica en patos mudos nigerianos. Mil veinte (1020) patos mudos adultos, machos y hembras, manejados de manera extensiva fueron tomados al azar de las zonas/ecotipos agroecológicos Selva, Sabana Derivada y Sabana de Guinea. Dichos patos fueron examinados de manera visual, anotándose para cada uno de ellos el color del plumaje, de la piel, de los tarsos, de los pies/membrana, del pico, del gancho de la punta del pico y de las carúnculas. Los datos de los rasgos cualitativos fueron analizados con estadísticos descriptivos (porcentajes) mientras que se usó un modelo de efectos fijos para investigar la relación entre el color del plumaje y el de la piel y el peso vivo. Los resultados sacaron a la luz la existencia de cierta variabilidad en los rasgos cualitativos. Sin embargo, el color predominante del plumaje, de la piel, de los tarsos, de los pies, del pico, del gancho de la punta del pico y de las carúnculas fue moteado (45 por ciento), blanco (88 por ciento), amarillo (50 por ciento), amarillo (60 por ciento), negro (58 por ciento), negro (69 por ciento) y rojo (84 por ciento), respectivamente, con independencia de los ecotipos. Asimismo, se detectó una relación significativa ($P < 0,05$) entre los colores del plumaje y la piel y el peso vivo. Las

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variaciones detectadas en los rasgos fenotípicos de los patos mudos nigerianos reflejan una diversidad en su genoma, la falta de selección y la necesidad de su selección y mejora.

Palabras clave: *zona/ecotipo agroecológico, patos mudos, fenotipo, plumaje*

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Introduction

Muscovy ducks are integral part of rural poultry production in Nigeria (Oguntunji and Ayorinde, 2014). Preponderance of this waterfowl, popularly known as local ducks are concentrated in the northern part of the country while majority of the few reared in southern part have been 'banished' to rural communities. In the recent years, the population of this waterfowl has been observed dwindling (Ogah and Ari, 2012). Taboos, myths, social bias and prejudice are the principal factors contributing to the remarkable fall in their numbers coupled with the lack of interest in their domestication and low patronage of their products.

Furthermore, the discrimination suffered by this water bird in Nigeria is exemplified further in the absence of its commercial production and dearth of researches on its comprehensive characterization; encompassing phenotypic, genetic, morphological, biochemical, immunological, among others.

Efficient utilization of a species or breed is premised on accurate knowledge of its unique characteristics differentiating it from other breeds or species. Most of such unique characteristics in farm animals are recognized primarily based on physical (outward) attributes such as body size, colour and shape of the horns (Khan, Khan and Mahmood, 2008). Phenotypic diversities observed in a population, breed or species are products of interaction of evolutionary forces such as selection, migration, mutation and various management and environmental challenges the animals have been exposed to over the years (Oguntunji, 2013). The observed phenotypic diversities in a population are pointers to the importance attached to certain phenotypic characteristics by the farmers and the end-users of animal and its products which could be of social, economic and religious relevance in a society (Oguntunji, 2013).

Documentation of the existing genetic resources, including the description of population phenotypic characteristics, cultural importance and genetic uniqueness is one of the main areas of the livestock conservation activities (Ruane, 1999; Duchev and Groeneveld, 2006). To make the conservation of indigenous breeds a reality and ensure sustainable use of their genetic diversity, it is particularly desirable that their phenotypic characteristics and performance be evaluated in their home tracts and under traditional management conditions (Zarate, 1996).

In view of the foregoing, it is evident that characterization and conservation of diverse genetic attributes inherent in the indigenous livestock species are imperative and long overdue in order to take inventory and maintain their genetic biodiversity, enhance food security of the teeming population and boost economic activities in the developing countries (Oguntunji, 2013).

Comprehensive phenotypic characterization of Nigerian Muscovy ducks describing and comparing qualitative traits of ducks in different agro-ecological zones (AEZs) are lacking; while the few available ones are restricted to some localities (Hassan and Mohammed, 2003; Raji, Igwebuike and Usman, 2009; Chia and Momoh, 2012). Against this background, the present study was conducted to provide comprehensive report on the patterns and distributions of qualitative traits in Muscovy ducks drawn from three agro-ecological zones in Nigeria.

Materials and methods

Study areas

Adult Muscovy ducks were randomly drawn from three AEZs in Nigeria: Rain Forest, Derived Savanna and Guinea Savanna. The climatic conditions of the study areas have been described by Yakubu (2011), Ogah, Momoh and Dim (2011) and Oguntunji (2013).

Experimental animals and sample sizes

For easy identification, Muscovy ducks sampled in Oyo and Osun States are herein after referred to as Derived Savanna ecotype, while those sampled in Lagos and Niger States are referred to as Rain Forest and Guinea Savanna ecotypes, respectively.

The 1020 Muscovy ducks (287 adult males and 733 adult females) used in this study were owned by small-scale farmers and were mostly traditionally managed with little or no supplementary feeding and medication. The ducks were provided with improvised housing made of low cost locally available materials such as bamboos, tree branches, mud, old iron sheets, palm fronds, dry grasses and leaves. Few duck farmers provided them with wooden cages. Only sexually matured birds were covered in this study. This is imperative because sexual maturation as influenced by sex hormones affects expression of the qualitative traits investigated. Besides, data were collected only on apparently healthy birds.

Data collection

Qualitative and quantitative data were taken on 203, 519 and 298 Muscovy ducks randomly sampled from the Rain Forest, Derived Savanna and Guinea Savanna AEZs, respectively.

Adult male and female Muscovy ducks sampled in each AEZ were individually assessed and scored for seven qualitative traits namely; plumage, skin, shank, feet/web, bill, bean and caruncle colours. All these were visually appraised and scored according to the sex and ecotype of the ducks as described by FAO guidelines on phenotypic characterization of chickens and ducks (Manuel, 2008).

Statistical analyses

Data on qualitative traits were analysed using descriptive statistics (percentages). Besides, fixed effect model was used to investigate association of plumage and skin colours with body weight of male and female ducks.

$$Y_{\imath jk} = \mu + P_{\imath} + S_j + e_{\imath jk}$$

$Y_{\imath jk}$ = individual body measurement; μ = overall mean; $P_{\imath}$ = fixed effect of plumage colour ($\imath$ = white, black, mottled, ash, blue); S_j = fixed effect of skin colour (j = white and yellow); $e_{\imath jk}$ = experimental error, assumed to be independently, identically and normally distributed, with zero mean and constant variance, i.e. $_{\imath}$ $_{\imath}$nd (0, r^2).

Significant differences in association between plumage colours and body weight were determined using Duncan's Multiple Range Test (DMRT) at 5 percent probability level.

All statistical analyses were performed using the SPSS (2001) version 16.

Results

The frequency distribution of the qualitative traits is presented in Table 1.

Plumage colour

The frequency distribution of plumage patterns across the AEZs showed that the predominant (45 percent) plumage colour was mottled while blue (0.55 percent) had the

Table 1. Qualitative characteristics of adult Muscovy ducks in Nigeria – absolute numbers of ducks analyzed, relative numbers in parenthesis

		Agro-ecological zone			**Sex**		**Overall**
Trait	**Class**	**Forest (203)**	**Derived Savanna (519)**	**Guinea Savanna (298)**	**Male (287)**	**Female (733)**	**(1 020)**
Plumage pattern	White	12 (5.91)	63 (12.14)	36 (12.08)	50 (17.42)	61 (8.22)	111 (10.88)
	Black	57 (28.08)	207 (39.38)	83 (27.85)	91 (31.71)	256 (34.92)	347 (34.02)
	Ash	15 (7.39)	49 (9.44)	35 (11.74)	13 (4.53)	86 (11.73)	99 (9.71)
	Blue	—	4 (0.77)	—	—	4 (0.55)	4 (0.39)
	Mottled	119 (58.62)	196 (37.76)	144 (48.32)	133 (46.34)	326 (44.47)	459 (45.00)
Skin colour	White	170 (83.74)	488 (94.03)	244 (81.88)	249 (86.76)	653 (89.09)	902 (88.43)
	Yellow	33 (16.26)	31 (5.97)	54 (18.12)	38 (13.24)	80 (10.91)	118 (11.57)
Shank colour	Yellow	80 (39.41)	285 (54.91)	145 (48.66)	116 (40.42)	394 (53.75)	510 (50.00)
	Black	75 (36.95)	147 (28.32)	112 (37.58)	146 (50.87)	188 (25.65)	334 (32.75)
	Slate	42 (20.69)	71 (13.68)	35 (11.74)	21 (7.32)	127 (17.33)	148 (14.51)
	Ash	6 (2.96)	16 (3.08)	6 (2.01)	4 (1.39)	24 (3.27)	28 (2.75)
Feet colour	Yellow	101 (49.75)	342 (65.90)	170 (57.05)	179 (62.37)	434 (59.21)	613 (60.40)
	Ash	6 (2.96)	16 (3.08)	18 (6.04)	4 (1.39)	36 (4.91)	40 (3.92)
	Black	54 (26.60)	105 (20.23)	75 (25.17)	87 (30.31)	147 (20.05)	234 (22.92)
	Slate	42 (20.69)	56 (10.79)	35 (11.74)	17 (5.92)	116 (15.38)	133 (13.04)
Bill colour	Red	18 (8.87)	106 (20.42)	66 (22.15)	69 (24.04)	121 (16.51)	190 (18.62)
	Black	119 (58.62)	290 (55.88)	183 (61.41)	190 (60.20)	402 (54.84)	592 (58.04)
	Ash	18 (8.87)	93 (17.92)	12 (4.03)	24 (8.36)	99 (13.51)	123 (12.06)
	Brown	3 (1.47)	18 (3.47)	18 (6.04)	—	39 (5.32)	39 (3.82)
	White	6 (2.96)	12 (2.31)	6 (2.01)	4 (1.39)	20 (2.73)	24 (2.35)
	Yellow	21 (10.34)	4 (0.77)	7 (2.35)	—	28 (3.82)	28 (2.75)
	Slate	18 (8.87)	—	6 (2.01)	—	24 (3.27)	24 (2.35)
Bean colour	Ash	42 (20.69)	128 (24.66)	18 (6.04)	32 (11.15)	156 (21.28)	118 (18.43)
	Black	161 (79.31)	326(62.81)	220 (73.83)	219 (76.31)	488 (66.58)	707 (69.31)
	Red	—	16 (3.08)	30 (10.07)	4 (1.39)	42 (5.73)	46 (4.51)
	Brown	—	29 (5.59)	18 (6.04)	4 (1.39)	43 (5.87)	47 (4.61)
	White	—	20 (3.85)	12 (4.03)	28 (9.76)	4 (0.55)	32 (3.14)
Caruncle colour	Red	179 (88.18)	438 (84.39)	235 (78.86)	211 (73.52)	641 (87.45)	852 (83.53)
	Red-black	12 (5.91)	73 (14.07)	57 (19.13)	69 (24.04)	73 (9.96)	142 (13.92)
	Light yellow	9 (4.43)	—	—	—	9 (1.23)	9 (0.88)
	Black	3 (1.48)	8 (1.54)	6 (2.01)	7 (2.44)	10 (1.36)	17 (2.44)

lowest frequency. It is noteworthy that the only four blue-plumaged Muscovy ducks found in this study were in the Derived Savanna AEZ.

Sexual dimorphism in plumage colour

The predominant plumage types in the two sexes were mottled (Male 46.34 percent; Female 44.47 percent) and black (Male 31.71 percent; Female 34.92 percent).

Skin colour

White and yellow skin colours were observed in Muscovy ducks of the three AEZs. However, preponderance of ducks in each AEZ had white skin; 83.74, 94.03 and 81.88 percent, respectively, for RF, DS and GS.

Sexual dimorphism in skin colour

The relative distribution of skin colours in the two sexes was comparable; majority of male and female Muscovy ducks had white skin representing 86.76 and 89.09 percent, respectively.

Shank colour

Table 1 shows that half (50 percent) of the sampled Muscovy ducks had yellow shanks. Other variants were black (32.75 percent), slate (14.51 percent) and ash (2.75 percent). In tandem with general analysis, yellow shank had the highest frequency in all the AEZs.

Sexual dimorphism in shank colour

The relative distribution of shank colours in the two sexes showed that yellow and black shanks constituted the highest proportions in female (53.75 percent) and male (50.87 percent) Muscovy ducks, respectively. Furthermore, the distribution of shank colouration indicated that frequency of certain colours were exceptionally higher in one sex than the other. For instance, about half (50.87 percent) of all drakes sampled had black shank compared to about one-quarter (25.65 percent) of the females. In addition, incidence of slate shank in females was higher than twice that observed in males (17.33 vs 7.32 percent).

Feet/web colour

Yellow feet had the highest frequency (60.10 percent) followed by black (22.94 percent), slate (13.04 percent) and ash (3.92 percent). The distribution and frequency of feet colour in each zone followed the same trend as observed in the general analysis.

Sex differences in feet/web colour

Table 1 showed that the frequency of occurrence of yellow (62.37 vs 59.21 percent) and black (30.31 vs 20.05 percent) feet were higher in males compared with females. Conversely, frequencies of ash (4.91 vs 1.39) and slate (15.83 vs 5.92) feet colours were higher in females than males.

Bill colour

Across the ecotypes, the predominant bill colour was black (58.04 percent). Similarly, black was the predominant bill colour in all the AEZs.

Sex differences in bill colour

Majority of male and female Muscovy ducks had black bills; 66.20 and 54.84 percent, respectively. It is worthy of note that three bill colours (brown, slate and yellow) were not observed in males.

Bean colour

Highest proportion (69.31 percent) of Muscovy ducks had black bean. Others were ash (18.43 percent), brown (4.61 percent), red (4.51 percent) and white (3.14 percent). The relative distribution of bean colours in each AEZ indicates prevalence of black bean.

Sex differences in bean colour

Majority of male (76.31 percent) and female (66.58 percent) Muscovy ducks had black beans while the frequencies of occurrence of other bean colours were higher in females than in males except white.

Caruncle colour

The relative distribution of caruncle colours indicates that red caruncle was predominant (83.53 percent). Others were red-black (13.92 percent), black (1.66 percent) and pale/light yellow (0.88 percent). In agreement with the result of the general analysis, separate analysis of each AEZ indicated that majority of ducks had red caruncles. Pale/light yellow caruncle was found only in Rain-Forest ducks representing 4.43 percent of the sampled ducks in the zone.

Sexual dimorphism in caruncle colour

Prevalence of red caruncle was observed in the two sexes. Though, both male and female ducks had red-black caruncle, sex differences were observed in its distribution. About one-quarter (24.04 percent) of male ducks were red-black caruncled in contrast to 9.96 percent of the females. Besides, all the four caruncle variants were observed in female ducks but only three in males. No male duck had pale/light yellow caruncle.

Association of plumage patterns with body weight

There was significant ($P < 0.05$) association between plumage colour and body weight: white-plumaged Muscovy ducks were heaviest (2.02 kg) and were significantly heavier than mottled (1.91 kg), black (1.83 kg), blue (1.65 kg) and Ash (1.61 kg) coloured counterparts (Table 2). Significant ($P < 0.05$) association of plumage colour with body weight was also observed on the body weight of adult male Nigerian Muscovy ducks but not ($P > 0.05$) in females.

Skin colours and body weight

Table 3 shows that skin colour significantly ($P < 0.05$) differed with regard to body weight in male but not ($P < 0.05$) in female Muscovy ducks. The yellow-skinned male ducks were heavier ($P < 0.05$) than their white-skinned counterparts (2.82 vs 2.61 kg). Besides, analysis of pooled data indicated that yellow-skinned Muscovy ducks were significantly ($P < 0.05$) heavier than their white-skinned counterparts.

DISCUSSION

Plumage colour

The observed highest frequency of mottled plumage for Muscovy ducks in the present study agrees with the reports of Chia and Momoh (2012) and Barnejee (2013) on Muscovy ducks of North-central Nigeria and West Bengal, India, respectively. Conversely, Black and multi-coloured were the predominant plumage colours among North West (Hassan and Mohammed, 2003) and North Eastern (Raji, Igwebuike and Usman, 2009) Nigeria Muscovy ducks, respectively.

The relative distribution of the plumage patterns of Muscovy ducks across AEZs might be attributed to social preference. Solid black and white animals, most especially birds, are usually linked with *gods/spirits* and rituals in Nigeria; therefore, most duck farmers and consumers prefer mottled ducks because of their mixed plumage colour; hence, its highest proportion in the population understudy. Ikeobi *et al.* (2001) corroborated this assertion that social preference in addition to natural selection and adaptation are the major causes of the variation in plumage colour.

Table 2. Association of plumage colour with body weight of adult male and female Muscovy ducks

Plumage colour	Sex Male $N = 287$	 Female $N = 733$	Overall $N = 1\,020$
Ash	$2.48^{b} \pm 0.13$ (13)	1.48 ± 0.24 (86)	$1.61^{b} \pm 0.41$ (99)
Blue	—	1.65 ± 0.31 (4)	$1.65^{ab} \pm 0.31$ (4)
Black	$2.55^{ab} \pm 0.39$ (91)	1.58 ± 0.26 (256)	$1.83^{ab} \pm 0.52$ (347)
Mottled	$2.70^{a} \pm 0.34$ (133)	1.59 ± 0.24 (326)	$1.91^{ab} \pm 0.57$ (459)
White	$2.68^{a} \pm 0.44$ (50)	1.48 ± 0.27 (61)	$2.02^{a} \pm 0.69$ (111)

^{ab}Means within column with different superscripts are significantly different ($P < 0.05$).
() Number of ducks analysed in parenthesis.

Table 3. Association of skin colour with body weight of adult male and female Muscovy ducks

Skin colour	Sex Male $N = 287$	 Female $N = 733$	Overall $N = 1\,020$
White	$2.61^{b} \pm 0.36$ (249)	1.57 ± 0.26 (653)	$1.85^{b} \pm 0.55$ (902)
Yellow	$2.82^{a} \pm 0.37$ (38)	1.57 ± 0.25 (80)	$1.97^{a} \pm 0.65$ (118)

^{ab}Means within column with different superscripts are significantly different ($P < 0.05$).
() Number of ducks analysed in parenthesis.

The small proportion of white-plumaged Muscovy ducks in the present study agrees with the report of Hassan and Mohammed (2003) on northwest Muscovy ducks but contradicts other previous studies on plumage colour of Muscovy duck in Nigeria (Raji, Igwebuike and Usman 2009; Chia and Momoh, 2012) whereby white Muscovy ducks were approximately one-third of the populations. The low frequency of white Muscovy ducks in all the AEZs understudy could be attributed to the religious roles ducks with such plumage are used for. Probing of household owners revealed that white Muscovy ducks command higher price than others and are in high demand for rituals and religious purposes. This submission was also further substantiated by duck sellers in the study area. This observation agrees with the reports of Leulseged (1998) and Gueye (1998) that plumage and skin colours have cultural and religious functions. In addition, the postulated function of plumage colouration as mean of camouflage (Ayeni, 1980) might be another factor responsible for low frequency of white-plumage Muscovy ducks in the studied population. The exceptionally-low frequency of occurrence of blue plumage in Nigerian Muscovy ducks might probably be attributed to social preference and or may be that the segregating allele(s) for it is/are recessive(s).

Plumage colour and sexual dimorphism

Of recent Barnejee (2013) reported higher frequency of black and white (mottled) compared to Sepia for the two sexes of Muscovy ducks in India. Social preference for a particular plumage colour in a gender of Muscvy ducks has neither been observed nor reported in the study area, therefore; the observed skewed distribution of white and ash plumage colours could probably be attributed to the influence of sex hormones or sex-linked genes or combination of some or all the postulated factors. Coyne, Kay and

Pruett-Jones (2007) reported that in most groups of birds, plumage traits (e.g. feather colour or elongation, appearance of colour patches) appear to be oestrogen dependent, with male-specific traits expressed only in the absence of that hormone.

Skin colour

The prepoderance of white-skinned Muscovy ducks in this study corroborated results of FAO sponsored projects on ducks in Cambodia (FAO, 2009a) and Egypt (FAO, 2009b). The low frequency of yellow skin (11.54 percent) in this study is in contrast to the expected 25 percent for an autosomal recessive gene in a random mating population where the studied population was drawn, thus, suggesting possible effect of salient genetic and non-genetic factors.

Skin colouration is determined by xanthophyll and melanin and the combined effects of the duo resulted in varying phenotypes (Mancha, Mbap and Abdul, 2006a). It has been established that yellow skin is influenced by the amount of carotenoids, primarily xanthophylls in the feed (Hutt, 1949). Smyth (1990) buttressed this further that yellow skin is the result of the expression of carotenoid pigments in the skin of the birds; and the more the carotenoids, the more intense the yellow colour. In view of this, the observed low frequency of yellow skin pigmentation of Nigeria Muscovy ducks in this study might probably be a reflection of the nutritional status of the sampled birds. Since the population understudy were mostly reared on the extensive system with little or no attention paid to the dietary needs of the birds or modification of their feed.

The report of Mancha, Mbap and Abdul (2006a) lends credence to this assertion that relative abundance of white-skinned fowl could be higher even when genetically yellow-coloured skin was higher in a population due to nutrition. These researchers attributed such atypical observation to lack of special diets like yellow maize and alfalfa leaf meals. The lack of such ingredients results in pale colour in genetically yellow-skinned birds (Mwalusanya *et al.*, 2002; Lesson and Walsh, 2004). Against this background, it is highly probable that some genetically yellow-skinned ducks were inadvertently scored as white-skinned; hence, the low frequency of yellow-skinned Muscovy ducks in the population under study.

Furthermore, putting into consideration the relationship between plumage patterns and skin colour of Muscovy ducks in the present study, it is worth emphasizing that the reported skin colours were also possibly influenced by the pleiotropic actions of genes responsible for plumage colours. A general observation in this study was that all solid white and mottled Muscovy ducks (black and white ducks with more white plumage distribution) had yellow skin while all blacks and mottled ducks (with more of black plumage) had white skin. Besides, all deep ash-plumaged ducks had white skin except those with more of lighter pigmentation (ash-coloured with more of white distribution) had yellow skin.

Sexual dimorphism in skin colour

Reports of sexual dimorphism in skin colour of Muscovy duck are scarce to validate the result of the present study. The numerical higher frequency of yellow skin in males compared with females is consistent with previous studies on Nigerian (Mancha, Mbap and Abdul, 2006b) and Ethiopian (Dana *et al.,* 2010) indigenous chickens. Smyth (1990) attributed higher percentage of yellow-skinned male possibly to diversion of the yellow pigment to egg yolk formation in females. Furthermore, superior foraging behaviour of cocks, guaranteeing access to better feed resource base was posited as a possible reason for higher yellow skin among Ethiopian cocks than females (Dana *et al.,* 2010).

Shank colour

Comparison of shank pigmentation distribution in this study and other related studies in Nigeria revealed disparities. Contrary to the four shank colours reported in this study; Chia and Momoh (2012) reported three major classes for Muscovy ducks sampled in North-Central Nigeria. They reported further that majority of ducks had black-yellow shank representing 53.5 percent followed by all-black (36.5 percent) and all-yellow (10.0 percent). Diversities observed in variants of shank colour in this study could be adduced to absence of selection coupled with indiscriminate mating among the local ducks. Contrary to the widely observed white shank colour in domestic chickens, no Muscovy duck was found having white shank in the present study. This might probably be attributed to genetic differences in the inheritance of shank colour in the two species.

Putting into consideration the trend of plumage patterns and shank pigmentation of Muscovy ducks in this study, it seems that expression of shank colour is not exclusively genetically controlled but probably influenced also by the plumage colour. A general observation in the sampled ducks across the ecotypes was that no white Muscovy duck had slate/grey, ash or black shank but yellow; likewise no black duck had yellow shank but black and slate/grey. Furthermore, among the mottled and ash-plumaged ducks, patches of yellow pigment distribution and intensity were in the same direction and depended on the relative distribution of white feather; the more the white plumage the more the yellow pigment distribution and intensity on the shank. It is therefore hypothesized that gene (s) responsible for light pigmentations (white and ash plumage patterns) influence(s) expression of yellow shank while the gene(s) responsible for black plumage pattern influence(s) expression of black and slate/grey shank colours.

A previous study by Nordskog (1970) on shank pigmentation of Fayoumi breed of chicken lends credence to the observation reported in this study. His report showed that not only shank colouration genes are responsible for shank colour but also the plumage genotype. He stated further that almost invariably, shank colour of birds with dark plumage is slate or green (melanin) and of birds with light plumage is yellow or white (non melanin).

Sexual dimorphism in shank colour

The observed trend of shank pigmentation in the two sexes suggests likelihood of certain modifying genes that are sex-linked/influenced which are influencing shank pigmentation of male and female Muscovy ducks in addition to the segregating alleles controlling the expression of shank colour. Alternatively, an underlying factor that may be due to the effect of sex hormones may also contribute to the observed disparities in both sexes. Previous studies by Owens and Short (1995) and Kimball (2006) buttressed this assertion that in most avian species, testosterone is involved in inducing non-plumage traits such as bill and leg colour, presence of wattles, spurs and combs, as well as behavioural traits such as aggression and male-specific sex displays.

Feet/Web colour

It is noteworthy that distribution pattern of feet colour is similar to what was observed for shank colour; this is suggestive that possibly their inheritances are controlled by the same genes but different modifying genes and are also influenced by the same non-genetic factors.

Similarly to what was observed for shank and skin pigmentations, relationships were also observed between plumage patterns and feet/web colors. All solid white ducks had yellow feet while all blacks had black or slate/grey feet. Majority of mottled ducks had yellow feet or yellow-black. Among few with yellow-black feet, the more the white plumage distribution, the more intense the yellow colour of the feet and vice-versa. In addition, no ash-plumaged duck had black shank.

In general, it seems white and ash plumage genes are responsible for the expression of yellow feet/web while gene(s) coding for black plumage colour is/are connected with the expression of black and slate/grey feet colours.

Sex differences in feet/web Colour

The distribution pattern of web colours of the two sexes probably suggests sex influence. The frequency of occurrence of black web in males was about 50 percent higher than observed in females (30.31 vs 20.00 percent); thus corroborating higher frequency of black shank in males in this study. Conversely, though at low frequency, the frequency of slate (15.38 vs 5.92 percent) and ash feet/web (4.91 vs 1.39 percent) colours were higher in females compared with males.

Furthermore, on shank and feet colour frequency distribution, there is likelihood that their pigmentation is under the influence of the same genes; putting into consideration the same number of colour types and predominance of yellow and black colour in the two sexes and in the pooled data.

Bill colour

Comparison of the number of classes of bill and frequency of the bill colours in this study with the previous studies in Nigeria revealed disparities. In contrast to seven classes reported in this study, Chia and Momoh (2012) classified North-central Nigeria Muscovy duck bills to three (all black, black-yellow and black pink) while Hassan and Mohammed (2003) classified those of Northwest Nigeria to four (black, white, black-white and ash-white). Furthermore, discrepancies were observed in the proportion of bill colours. Black-yellow was the predominant bill colour among North-central Nigeria ducks (Chia and Momoh, 2012) while majority of ducks in North-west Nigeria had black-white bill (Hassan and Mohammed, 2003).

Sex differences in bill colour

Scarcity of related study on sex differences on bill colour of Muscovy ducks did not permit head-to-head comparison of the result of the present study. The absence of certain variants in males and skewed distribution of those expressed in the two sexes is a pointer to possible sex-influence on the diverse colours of the bill which might have been influenced through the action of sex-linked genes, sex-influenced genes, sex-limited genes or sex hormones.

Bean colour

Results on related studies on bean colours of Muscovy ducks are scare to compare the result of the present study. However, it should be noted that all the major classes of bill were represented in the Derived Savanna and Guinea Savanna while only two (ash and black) were found in Rain-Forest ducks. Since the population understudy has not undergone selection for any qualitative traits, the immediate and remote causes of absence of red, brown and white bean colours in Rain-Forest Muscovy ducks are not understood.

Sex differences in bean colour

Comparison of classes of colour scored for bill and bean in the two sexes indicate a common trend whereby black colour was higher in males whereas ash and brown were prevalent in females, thus suggesting possible sex-influence on the expression of bean colour in Muscovy ducks.

Caruncle colour

In tandem with the results of this study, red caruncle was reported for three-quarters of Cambodian Muscovy ducks (FAO, 2009a). However, only two variants; red and red-black colours were reported for Cambodian Muscovy ducks (FAO, 2009a) contrary to four in the present study.

Higher frequency of black caruncle corroborates observation of relationship between plumage and skin, shank, feet colours in this study. Irrespective of the sex, no white Muscovy duck had black or red-black caruncle but red.

Sex differences in caruncle colour

Though, both male and female ducks had red-black caruncles, sex differences were observed in its distribution. About one-quarter (24.04 percent) of male ducks were red-black caruncled in contrast to 9.96 percent of the females. Higher frequency of red-black caruncle in males than in females is consistent with earlier report in this study that frequency of black colour was higher in shank, feet, bill and bean of male compared with female Muscovy ducks. Besides, only females had pale yellow caruncles. Since preferential selection of caruncle colour has not been observed or reported in the studied population and the population from which the samples were drawn were random mating ones; therefore, the asymmetrical distribution of red-black and pale yellow caruncle colours in the two sexes may be ascribed to the effect of sex hormone.

A general observation on caruncles of the two sexes was that caruncle of males was more prominent and brighter (having shining appearance) compared with females that were smaller and dull. Dimorphism in caruncle size and appearance may be attributed to the fact that this secondary sexual characteristic is influenced by sex hormone.

Association of plumage colour with body weight

In agreement with the result of this study, Raji, Igwebuike and Usman (2009) reported significant effect of plumage colour on live weight of adult Muscovy ducks studied in the North-east Nigeria where multicoloured Muscovy ducks were reported to have highest live weight. Similarly, mottled Muscovy ducks were significantly heavier than their sepia counterparts in West Bengal, India (Barnejee, 2013). Conversely, no significant effect of plumage colour on body weight was reported on northwest Nigeria Muscovy ducks by Hassan and Mohammed (2003).

The higher mean body weight of lighter pigmented-plumaged ducks (white and mottled) in this study may be related to their superior physiological adaptation to heat stress, associated with elevated ambient temperatures in tropical environments. It is well known that lighter surfaces reflect heat better than darker surfaces. Animals with lighter coats reflect more light (Silva, La Scala Junior and Tonhati, 2003) and absorbs between 40 and 50 percent less radiation than those with dark coats (McManus *et al.*, 2011); resulting in lower thermal absorption and lower body thermal load, thereby conferring physiological advantage on them compared to others with coloured/dark surfaces. Asserting on possible reasons for highest body weight of white West African Dwarf (WAD) sheep, Ozoje and Kadri (2001) stated that the effect of white coat on body weight of extensively-reared WAD sheep may be influenced through its role in temperature-regulation and body metabolism under conditions of high ambient temperatures prevalent in the study area.

Besides, another possible underlying factor for the superior body weight of white and mottled Muscovy ducks may be the pleiotropic action of genes controlling inheritances of those plumage colours. It is also possible that the highest mean live weight of white Muscovy ducks may be another contributory factor responsible for its low frequency in this study. Their superior live weight probably makes them a prime target for sale in order to meet pressing financial needs, for the entertainment of august visitors, and as a source of meat for the family during festival periods, thus representing a form of negative selection against white ducks.

Association of skin colour with body weight

Literatures on relationship between skin colour and live weight of Muscovy ducks are lacking for comparison with the results of the present study. The observed superior mean body weight of yellow-skinned ducks may be attributed to pleiotropic effect of the gene(s) responsible for its expression. Alternatively, there is likelihood that superior live weight of yellow skinned ducks could be linked to pleiotropic action of plumage (white and mottled) colour genes. Preliminary investigation on relationship between plumage colour and skin colour of Muscovy duck in the present study revealed that majority of white and mottled ducks had yellow skin; and ducks with such plumage colours had higher mean live weight compared with black, ash and blue-plumaged counterparts.

Conclusion

Phenotypic diversities observed in the expression of the traits under study are indicative of absence of selection and abundant diversity in the gene pool of locally adapted Muscovy ducks in Nigeria awaiting selection and improvement for breed identification and classification. Higher frequencies of black shank, feet, bill, bean and caruncle colours in males are suggestive of likelihood of the influence of sex hormones in their expressions. The reported relationships between plumage colours and expression of skin, shank, feet and caruncle colours attests to the possible pleiotropic effect of plumage-coding genes. Further investigations under controlled experiments with large sample sizes are needed for validation of the reported association of plumage and skin colours with body weight.

Supplementary material

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

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Molecular typing of the major histocompatibility complex B microsatellite haplotypes in Cameroon chicken

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Summary

The chicken major histocompatibility complex B (MHC-B) – a cluster of genes associated with natural disease resistance or susceptibility – has been investigated in experimental and inbred lines by serological typing. However, that method showed some weaknesses for its use on out breeds. This study aims to explore the genetic diversity of the MHC-B of Cameroon indigenous chicken through molecular typing with LEI0258 and MCW0371 microsatellite markers. MHC-B haplotypes of 290 chickens from four agro-ecological zones were identified and compared with published haplotypes. Alleles were analysed for genetic diversity and relationship among Cameroon chicken populations. Hypothetically new LEI0258 alleles and haplotypes were detected. Overall, polymorphism parameters were relatively high in the Cameroon western highlands. The analysis of molecular variance revealed great variability (80.00 percent) between individuals than among and within ecotypes. The inbreeding coefficients of overall populations (F_{IT}), among population (F_{ST}) and within population (F_{IS}) were 0.26, 0.04 and 0.22, respectively, and all were highly significant ($P < 0.001$). A UPGMA tree based on Nei's D_A genetic distances showed a clear distinction between Cameroon and out-groups and a structuring of within-country populations into three clusters. There is a great genetic diversity of the MHC-B in Cameroon native chicken and also a need of sequencing of the identified alleles for an accurate identification prior to their assessment for natural disease resistance and responsiveness to vaccination.

Keywords: *Cameroon indigenous chicken, genetic diversity, immunity, major histocompatibility complex B (MHC-B)*

Résumé

Le complexemajeur d'histocompatibilite B (CMH-B) de poule est un groupe de gènes impliquésdans la résistance aux maladies. Il a été typé chez les lignées consanguines de poule par la méthode sérologique. Cependant, l'application de cette méthode a montré des limites chez les populations naturelles non sélectionnées. Le but de cette étude est d'évaluer la diversité génétique du CMH-B de la poule locale du Cameroun à l'aide des marqueurs microsatellites LEI0258 et MCW0371. Les haplotypes B de 290 poulets échantillonnés dans 4 zones agroécologiques du Cameroun ont été identifiés et comparés aux haplotypes publiés. 42 allèles et des haplotypes hypothétiquement nouveaux du marqueur LEI0258 ont été détectés. En général, les paramètres du polymorphisme ont été plus élevés dans la zone des Hauts plateaux de l'Ouest. L'analyse de la variance moléculaire a révélé une plus grande variabilité (80.00 percent) entre les individus qu'à l'intérieur et entre les zones agroécologiques. Les coefficients de consanguinité dans la population (F_{IT}), entre les sous-populations (F_{ST}) et dans les sous- populations (F_{IS}) ont été faibles et tous significatifs ($P < 0.001$). L'arbre phylogénétique base de des distances génétiques D_A de Nei a mis en évidence une distinction claire entre les populations de poules du Cameroun et les exotique sainsi qu'une structuration des populations locales en 3 groupes. Cette étude a révélée une grande diversité génétique du CMH-B de la poule locale du Cameroun ainsi que la nécessité de séquencer les nouveaux haplotypes pour leur identification plus précise relative à leur évaluation pour la détermination de leurs fonctions immunitaires.

Mots-clés: *Complexe majeur d'histocompatibilité B, diversité génétique, (CMH-B), immunité, Poule locale du Cameroun*

Resumen

El complejo mayor de histocompatibilidad B de pollo (CMH-B) está vinculado a la respuesta inmunitaria. Ha sido bien estudiado en las líneas consanguíneas de pollo por el método de tipaje serológico. Sin embargo, la aplicación de este método a las poblaciones no seleccionadas de pollos ha demostrado serosos límites. El objetivo de este estudio ha sido de analizar el del CMH-B de la gallina local de Camerún por génotypage de 290 sujetos de 4 zonas agroecológicas del país, gracias a los marcadores micro-satélites LEI0258 y MCW0371. Alelos hipotéticamente nuevos han sido identificados, dentro de los cuales 4 recientemente puesto en evidencia en los altos bandejas del oeste Camerún para sus efectos sobre una producción elevada de anticuerpo contra la enfermedad de Newcastle. La variancia molecular de los efectos individuales ha sido superior (80.00 percent) a los efectos vinculados a la zona

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agro-ecológica. Los coeficientes de consanguinidad y de diferenciación han sido reducidos (débiles) pero significativos ($P < 0.001$) a los locus LEI0258 y MCW0371. El árbol filo genéticas basado sobre las distancias genéticas D_A de Nei ha puesto en evidencia una discriminación limpia entre las gallinas locales de Camerún y las gallinas exóticas asiquen estructuración de los primeros en 3 sobrepoblaciones. Los resultados han confirmados la existencia de una gran diversidad genética del CMH-B en el seno de las poblaciones de gallina locales de Camerún sin embargo, sería necesaria secuenciar los alelos hipotéticamente nuevos para su identificación más preciso en visto de las pruebas relativos a su función dentro de las respuestas inmunitarias especificas a diversos patógenos.

Palabras clave: *complejo mayor de histocompatibilidad, gallina local de Camerún, inmunidad, polimorfismo molecular*

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Introduction

The village or indigenous chickens (*Gallus gallus domestica*) of Cameroun are unselected populations kept under traditional management practices for millennia. They are mostly reared in a backyard system with low input. They provide better health and wealth to rural households thanks to their well appreciated high-grade proteins through meat and eggs (Moula *et al.*, 2012). They therefore contribute significantly to poverty alleviation and food security of more than 60 percent of families living in rural areas in Cameroon (HakoTouko *et al.*, 2013). However, the breeding stock is almost always renewed every year due to high mortalities. Bad management practices and disease outbreaks are the main causes with the Newcastle disease alone resulting more than 70 percent of avian mortalities in endemic areas (Buza and Mwamhehe, 2001; Mtileni *et al.*, 2012; HakoTouko *et al.*, 2013). Vaccination can be a good approach to solve the problem but its implementation in rural areas is not cost effective and most of the vaccines used are neither thermo-stable nor available, especially for remote areas. In such context, having the fittest and prolific genotypes which can resist or survive to disease outbreaks is a challenge and selection for disease resistance or tolerance is believed to be a long term strategy

Disease resistance is a poly-factorial trait with low to moderate heritability. It is controlled by environmental and genetic factors (Jie and Liu, 2011), including the major histocompatibility complex B (MHC-B) (Lamont, Bolin and Cheville, 1987; Taylor, 2004) and quantitative trait loci (QTL) scattered throughout the genome (Yonash *et al.*, 2001; Biscarini *et al.*, 2010). For these reasons, the expected genetic progress after selection for one or a few candidate genes might be low and time consuming. Besides, alleles or genes conferring resistance to a disease can express an opposite response against another disease or a different strain of the same pathogen (McBride *et al.*, 1981). The whole genome selection has been proposed (Fulton, 2012) but this approach is very expensive for developing countries. The selection for differential antibody responsiveness to vaccines or wild pathogen strains is an alternative (HakoTouko *et al.*, 2013) and exploration of the genetic diversity of genes or QTLs involved in the tolerance or resistance process is a prerequisite toward this step.

The chicken MHC-B is a cluster of immune function genes commonly identified by serological typing with polyclonal antisera produced by immunizations between birds having different haplotypes (Fulton *et al.*, 2006). It is located on the micro-chromosome 16. MHC region includes the BF, BG and BL genes as well as many other immune-related genes. It is the terminology used to distinguish between the MHC as originally identified as the B blood group locus from the MHC-Y which is a genetically unlinked separate cluster of MHC-like genes. The function of BF-encoded class I molecules is to present the antigen peptides resulting from the proteolysis of endogenous tumoural and viral proteins to T8 cytotoxic lymphocytes. BL-encoded class II molecules are responsible of presenting the antigen peptides resulting from the proteolysis of extracellular proteins to T4 lymphocytes (Chazara, 2010). The MHC-B is known for its implication to disease resistance or susceptibility to numerous pathogens. It is the case for fowl cholera (Jie and Liu, 2011), avian leucosis virus (Yoo and Sheldon, 1992), Marek's disease virus (Bacon, Hunt and Cheng, 2001), Rous sarcoma tumour virus (Taylor, 2004), *Salmonella* (Cotter, Taylor and Abplanalp, 1998) and Newcastle disease (Lwelamira *et al.*, 2008; HakoTouko *et al.*, 2013). Serological typing is applied on inbred lines for the development of serological reagents with the majority being derived from the White Leghorn breed (Fulton *et al.*, 2006). It is limited by cross-reactivity and not effective on outbred populations (Kroemer, Guillemot and Auffray, 1990; Fulton, Young and Bacon, 1995). Inbred lines contain limited combinations of BG, BF and BL genes. In outbred populations, novel alleles and combinations of alleles lead to difficulties of producing haplotype-specific antisera, resulting in inaccurate haplotype identification. An accurate typing of outbred chicken populations is important for the development of new serological reagents as well as for differential antibody responsiveness related studies. Studies have been done on the molecular typing of the MHC-B, also known as the core MHC, using the microsatellite markers LEI0258 andMCW0371, mapped to chromosome 16 (McConnell *et al.*, 1999; Buitenhuis *et al.*, 2003). These markers are closely located to genes of the MHC-B and successfully investigated as genetic markers for MHC haplotype using polyclonal allo-antisera (Fulton *et al.*, 2006; Chazara, 2010). The objective of this study was to identify existing and new MHC-B microsatellite haplotypes in Cameroon chicken populations prior to their evaluation for differential antibody responsiveness to vaccines or infections.

Materials and methods

Sample collection

Adult chickens were randomly sampled in four agro-ecological zones of Cameroon (Figure 1) according to their GPS coordinates and the importance of the family poultry production. The names of agro-ecological zones (ecotypes) are according to "Institut de la Recherche Agronomique pour le Développement (IRAD Cameroon)". The description of agro-ecological zones of Cameroon has been reported (Fotsa *et al.*, 2011). Table 1 shows the characteristics of agro-ecological zones and the number of chickens sampled per zone. Some local phenotypes of the native chickens of Cameroon in their natural environment are shown in Figure 2.

Blood samples were collected and stored on Whatman FTA filter cards (Whatman International Ltd). A total of 366 chickens of both sexes were sampled, of which 290 were native chickens, 32 were from commercial breeds comprising two broiler lines (21 chickens) and Lohmann brown layers (11 chickens) reared countrywide and suspected to be the main vector of genetic introgression of exotic strains within-country native chicken populations. An additional 54 samples from 13 Korean chicken populations were used as out-groups.

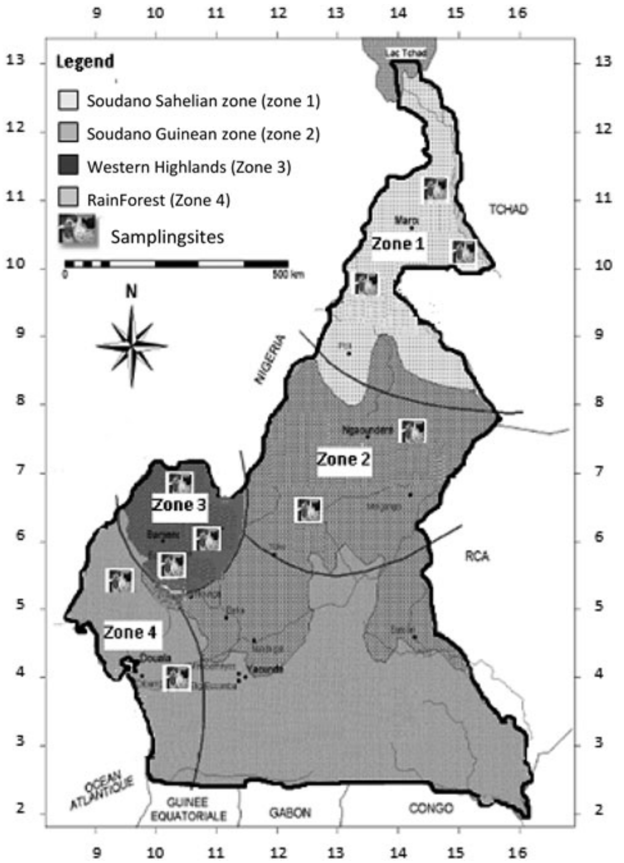

Figure 1. Cameroon map showing the four sampled agro-ecological zones and sampling sites. *Note:* Geographical point coordinates are shown on horizontal and vertical graduated axes.

PCR amplification and genotyping of MHC-B microsatellite markers

Two highly polymorphic MHC-B microsatellite markers, LEI0258 and MCW0371 (Fulton *et al.*, 2006), were used. The DNA was extracted by the boiling method and duplex PCR was done using 50 ng of genomic DNA with 10 pmol of each primer in a total PCR volume of 10 µl using 6 µl of ready to used Dream *Taq* PCR Master Mix (2X) (Fermentas) and 3.6 µl water of nuclease-free. The primer sequence were CACGCAGCAGAACTTGGTAAGG forward and AGCTGTGCTCAGTCCTCAGTGC reverse for LEI0258 and CTGCTCCGAGCTGTAATCCTG forward and TTTCATGGCATCCTAAGATG reverse for MCW0371. The optimal PCR conditions were determined by gradient PCR using aTECHNE TC-PLUS PCR machine. PCR using optimal conditions was performed with a9800 Fast Thermal Cycler (Applied Biosystems) using the following thermal cycling conditions: initial denaturation of 5 min at 95 °C followed by 30 cycles of 30 s denaturation at 94 °C, 45 s primer annealing at 60 °C and 1 min primer extension at 72 °C, and then a final extension step of 10 min at 72 °C. Allele sizes relative to an internal size standard (GENESCAN-500(LIZ)) were analysed on an automated DNA sequencer (ABI PRISM® 3730) and scored with Genemapper version 4.1.

Statistical analysis

Genetic diversity indices such as allele frequencies, mean number of alleles (Na), observed (Ho) and expected (He) heterozygosities, and polymorphism information contain (PIC) were calculated for each population using Microsatellite Toolkit (Park, 2001). Allelic richness (i.e. the corrected mean allele number in the standardized sample size, AR) was calculated using FSTAT 2.9.3 (Goudet, 2001). Analysis of molecular variance (AMOVA) was achieved using Arlequin 3.5.1.3 according to the procedure of Weir and Cockerham (1984). Wright's F-statistics (within population inbreeding [F_{IS}], total inbreeding [F_{IT}], and among population genetic differentiation [F_{ST}]) for each locus and overall population and pair wise F_{ST} values were obtained with STAT using the variance-based method of Weir and Cockerham (1984). Unbiased estimate of exact P-values were obtained using the Markov Chain Monte Carlo (MCMC) algorithm (Guo and Thompson, 1992). Genetic relationships among populations were estimated by constructing a dendrogram based Nei's D_A genetic distances

Table 1. Characteristics of agro-ecological zones and number of chickens sampled per zone.

Zone	Name	Vegetation	GPS	Elevation (m)	Temperature (°C)	Rainfall (mm/year) and hygrometry (%)^1	Number of native chicken sampled
1	Soudano sahelian	Steppe	10°20′48″N, 15°07′33″E to 10°53′58″N, 14°33′55″E	328–336	28–45	500 (35–65)^1	62
2	Soudano guinean	Savannah	07°03′35″N, 13°43′44″E, to 07°31′67″N, 13°50′33″E	1 209–1 251	20–26	1 500 (43–88)^1	22
3	Western highlands	Savannah	05°06′00″N, 10°25′04″E to 05°71′15″N, 10°99′00″E	1 081–1 403	11–27	2 000 (>80)^1	175
4	Rainforest	Forest	04°10′07″N, 09°18′02″E to 04°58′31″N, 09°58′00″E	547–911	22–29	3 000 (>85)^1	31

Hygrometry.

Figure 2. Various phenotypes of Cameroon native chickens.

Table 2. Allelic patterns and *F*-statistics for each loci across Cameroonian native chicken populations.

Locus	Chromosome	N_A	ASR	F_{IS}	F_{IT}	F_{ST}
LEI0258	16	42	166–494	0.146***	0.185***	0.046***
MCW0371	16	6	201–211	0.320***	0.343***	0.035***
All	16	48	–	0.223***	0.255***	0.041***

***$P < 0.0001$.

N_A, total number of allele; ASR, allele size range; F_{IS}, within population inbreeding; F_{IT}, total inbreeding; F_{ST}, among population genetic differentiation.

Nei, 1972) using UPGMA method implemented in PHYLIP version 3.5 with 1 000 bootstraps (Felsenstein, 2009).

Results

Genetic diversity

The two MHC-B markers amplified a total of 48 alleles, of which 6 alleles (201 to 211 bp) at MCW0371 and 42 alleles (166 to 494 bp) at LEI0258 (Table 2). LEI0258 and MCW0371 allele sizes amplified as well as their frequencies are presented in Tables 3 and 4. Genetic diversity indices for each native chicken ecotype and for the out-groups are presented in Table 5. The least values observed for Na, Ne and AR were 10.00, 7.00 and 8.06, respectively. The highest values for the same parameters were 21, 7.82 and 8.61, respectively. Overall, the lowest values were observed in the Soudano-Guinean ecotype while the highest were in the western highlands. The two microsatellite markers used were highly informative with a PIC greater than 0.70. Overall, genetic diversity indices were higher in Cameroon population compared to out-groups. The marker LEI0258 was the most polymorphic. The AMOVA (Table 6) revealed 5.70 percent of variation among Cameroon ecotypes and 11.29 percent variation among individuals within ecotypes. The greatest variability (83.00 percent) was among individuals.

Table 3. Sizes in base pair (bp), frequencies (%) and numbers of LEI0258 allele sizes observed in the local chicken population of Cameroon. Please make that the data of out-groups are not included!

LEI0258 allele size (bp)	Number of LEI0258 alleles	Frequency (%)	LEI0258 allele size (bp)	Number of LEI0258 alleles	Frequency (%)
166	1	0.17	324	15	2.60
182	2	0.35	336	6	1.04
188	2	0.35	348	2	0.35
194	34	5.88	350	30	5.19
200	1	0.17	360	105	18.17
206	5	0.87	364	3	0.52
218	20	3.46	372	9	1.56
226	1	0.17	382	1	0.17
236	2	0.35	384	16	2.77
238	2	0.35	394	8	1.38
242	7	1.21	396	2	0.35
250	15	2.60	408	2	0.35
260	38	6.57	420	4	0.69
262	9	1.56	422	4	0.69
272	2	0.35	424	6	1.04
284	12	2.08	448	18	3.11
286	21	3.63	454	2	0.35
296	49	8.48	464	1	0.17
310	58	10.03	478	1	0.17
312	59	10.21	488	1	0.17
322	9	1.56	494	1	0.17

Genetic differentiation and relationships among populations

The global inbreeding coefficients of overall populations, among population and within population (F_{IT}, F_{ST} and F_{IS}) were 0.26, 0.04 and 0.22, respectively (Table 2), leading to an overall F_{IS} of 0.26. All were highly significant ($P < 0.001$) for both LEI0258 and MCW0371 loci. For all native chicken ecotypes the F_{IS} showed a significant ($P < 0.001$) deficit in heterozygotes ranging from 0.11 in Soudano-Sahelian to 0.41 in Soudano-Guinean.

Nei's genetic distance (D_A) (Table 7) was lower between within-country ecotypes of chickens compared to out-groups. Within-country ecotypes, the smallest D_A (0.046) was observed between Rain forest and Western highlands while the largest (0.10) was between Rain forest and Soudano-Guinean. As it is expected (Figure 3), local chicken ecotypes are closely related to each other but distant to exotic strains (out-groups). Soudano-Sahelian ecotype is close to Western highlands and then to Rain forest than to Soudano-Guinean.

Table 4. Sizes in base pair (bp), frequencies (%) and numbers of MCW0371 allele sizes observed in the local chicken population of Cameroon.

MCW0371 Allele size (bp)	Number of MCW0371 alleles	Frequency (%)
201	2	0.35
203	65	11.25
205	91	15.74
207	243	42.04
209	110	19.03
211	62	10.73

Discussion

A total of 42 alleles ranging from 166 to 494 bp for LEI0258 were detected in this study while allele sizes of 181–552 bp (Fulton *et al.*, 2006) and182–539 bp (Chazara, 2010) have been reported.

The absolute number of alleles (42) is greater than 24 alleles reported by Lwelamira *et al.* (2008; for Tanzanian chickens) and 29 alleles by Fulton *et al.* (2006) but smaller than 52 alleles reported on 80 different populations or lines of Africa, Asia and Europe by Chazara (2013). The number of alleles can vary according to sample size, population or breed (HakoTouko *et al.*, 2013). In fact, very few or limited combination of alleles do exist in selected populations. This has been confirmed in inbred, experimental and commercial lines (Juul-Madsen *et al.*, 2006; Muir *et al.*, 2008) and in this study with 36 LEI0258 alleles in the Western highland chicken ecotype (unselected population). Chazara *et al.* (2013) reported a higher LEI0258 number of allele (18) in local chicken population of Benin as compared to Cameroon (15) but, lower allele number in local populations of Ghana (14), Ivory Coast (9) and Morocco (10). The same authors reported the lowest LEI0258 allele number in commercial and experimental chicken lines, namely INRA Immune Response 2 (4) and Brown egg layer B (6). The real number ofLEI0258 alleles detected in 290 Cameroon chicken samples might

Table 5. Diversity parameters in four Cameroonian native chicken ecotypes over the studied MHC-B markers.

Ecotypes	Allele	N_A	Ne	AR	He	Ho	G	PIC	F_{IS}
Soudano-Sahelian	LEI0258	24.00	11.01	11.35	0.917	0.838	0.917	0.902	0.086*
	MCW0371	05.00	3.15	4.78	0.688	0.597	0.689	0.645	0.133
Soudano-Guinean	LEI0258	15.00	10.08	11.56	0.922	0.682	0.927	0.892	0.265**
	MCW0371	05.00	3.92	4.92	0.762	0.318	0.773	0.706	0.588**
Western highlands	LEI0258	36.00	11.77	12.25	0.917	0.789	0.918	0.909	0.141**
	MCW0371	06.00	3.88	4.97	0.744	0.526	0.745	0.706	0.294**
Rain forest	LEI0258	20.00	11.37	12.13	0.927	0.774	0.930	0.906	0.167**
	MCW0371	5.00	3.92	4.93	0.757	0.419	0.763	0.709	0.450**
Overall (Cameroon)	LEI0258	23.75	11.06	11.82	0.921	0.771	0.923	0.902	0.165***
	MCW0371	05.25	3.72	4.90	0.738	0.465	0.743	0.692	0.366***
Korean	LEI0258	15.00	5.67	8.83	0.831	0.593	0.834	0.808	0.289**
	MCW0371	05.00	2.70	4.41	0.636	0.333	0.639	0.585	0.478**
Hybro	LEI0258	04.00	2.55	4.00	0.636	0.818	0.627	0.548	−0.304
	MCW0371	04.00	2.18	4.00	0.567	0.545	0.568	0.496	0.040
Lohmann Brown	LEI0258	07.00	4.57	7.00	0.818	0.909	0.814	0.753	−0.117
	MCW0371	03.00	1.58	3.00	0.385	0.273	0.391	0.326	0.302
Overall (Out groups)	LEI0258	08.67	4.26	6.61	0.762	0.773	0.758	0.703	−0.044
	MCW0371	04.00	2.15	3.80	0.529	0.384	0.533	0.469	0.273*

*,**,***$P < 0.5$, $P < 0.01$ and $P < 0.001$, respectively.

N_A, total number of alleles; Ne, number of effective alleles; AR, Allelic richness; He, expected heterozygosity; Ho, observed heterozygosity; G, gene diversity over loci; PIC, polymorphism information contain; F_{IS}, within population inbreeding.

Table 6. Analysis of molecular variance of MHC markers (LEI0258 and MCW0371) across Cameroon native chicken agro-ecological zones.

Source of variation	Degree of freedom	Sum of squares	Mean square	Variance component	Percentage of variation (%)
Among zones	3	12.16	4.050	0.049**	5.70
Among individuals within zones	285	323.3	1.134	0.097**	11.29
Between individuals	289	227.46	0.787	0.713**	83.00
Total	577	562.92			

**$P < 0.01$.

certainly be greater than the 42 observed. In this study, allele sizes relative to an internal size standard were analysed by genotyping. Therefore, same alleles identified in our study may carry different nucleotide sequences while different alleles with small size differences across separate studies may share same sequences.

In this study, the highest genetic diversity parameters observed among local chicken in the Western highlands (agro-ecological zone 3) are in conformity with those of Fotsa *et al.* (2011) and Keambou *et al.* (2014) using neutral markers. The highest genetic diversity in zone 3 can be tribute to a wide range of altitudes and climate variants (1–2 alternating dry and raining seasons) (Fotsa *et al.*, 2011). This zone exhibits the most diversified geographical and agro-ecological characteristics compare to other four zones (Keambou, 2013). Environmental factors are known to be significant on disease outbreaks and severity and then, may also affect the MHC haplotype distribution. The highest diversity of local chicken in the agro-ecological zone 3 is reinforced by the fact that it represents the most important zone as family poultry production is concerned with up to 56 percent of the national native chicken population(Teleu and Ngatchou, 2006; Keambou *et al.*, 2013). As expected, our results are consistent with the highest phenotypic diversity observed in Western highlands than in Rain forest (Fotsa *et al.*, 2008), In Western highlands (Keambou *et al.*, 2007) than in Soudano-Guinean and Soudano-Sahelian zones (Haoua, 2010). In theory, phenotypic characteristics are a combination of genotypic and environmental factors as well as interaction between both (Harlt, 1980). The lowest genetic diversity observed in this study in Soudano-Guinean populations confirms that of Keambou (2014, using neutral markers). It could be attributed to the production system and importance accorded in the area to other domestic animal species like cattle and small ruminants, to the detriment of local chickens kept as small close flocks by women (Haoua, 2010; Keambou *et al.*, 2014).

The clear segregation of within-country ecotypes and crossbreds (Lohmann Brown and Hybro) by the Nei's D_A distances can be explain either by a genetic originality or specificity of Cameroon chicken populations or by the

Table 7. Nei's D_A genetic identity (above diagonal) and genetic distance (below diagonal).

	1	2	3	4	5	6	7
SS (1)		0.9051	0.9469	0.9373	0.8590	0.7969	0.2580
SG (2)	0.0997		0.9105	0.9044	0.8418	0.7769	0.4232
WH (3)	0.0546	0.0938		0.9547	0.8023	0.7181	0.4128
RF (4)	0.0648	0.1004	0.0464		0.7864	0.7545	0.3854
Kor (5)	0.1519	0.1722	0.2203	0.2403		0.8604	0.2666
LB (6)	0.2271	0.2525	0.3312	0.2817	0.1504		0.1432
HY (7)	1.3550	0.8599	0.8849	0.9535	1.3219	1.9435	

SS, Soudano-Sahelian; SG, Soudano-Guinean; WH, Western highlands; RF, Rain forest; Kor, Korean; LB, Lohmann brown; HY, Hybro.

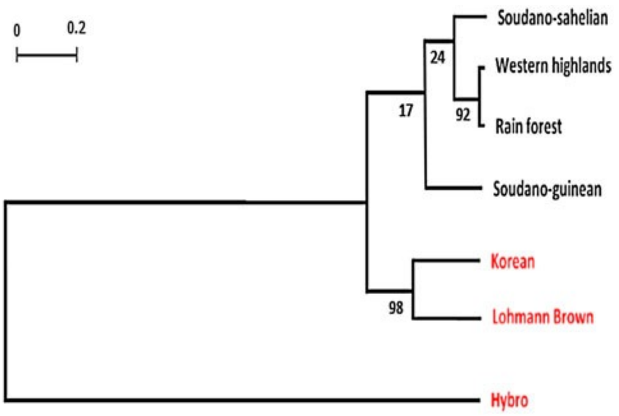

Figure 3. Dendrogram based Nei's D_A genetic distances using UPGMA method.

fact that Cameroon native chickens are outbred with more allelic combinations than the commercial ones with fewer allelic combinations.

Conclusion

The following findings can be concluded from the present study:

- The genetic diversity of Cameroon indigenous chicken as described by previous phenotypic characterization and genetic characterizations studies using neutral markers is confirmed with functional markers, namely LEI0258 and MCW0371 of the MHC-B.
- Cameroon native chicken population is clustered in three distinct groups according to agro-ecological zones (ecotypes) and their genetic make-up for LEI0258 and MCW0371 loci. The genetic diversity of the Cameroon native chicken MHC-B is very rich and potential resource for the development of new serological reagent adapted to chicken outbred populations.

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Statement of interest

The authors declare that they have no competing interests.

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Caracterización de ovinos en el litoral sur del Perú

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Resumen

En Perú la ovinocultura es una actividad tradicional para pequeños productores, que generalmente poseen animales criollos, los cuales son ignorados por políticas públicas y la comunidad científica, no estando reconocidos como raza, mostrando baja productividad y sufriendo cruzas con razas exóticas. Este estudio objetivó caracterizar fenotípicamente ovejas criollas y mestizas Hampshire Down, para uso en la conservación y mejoramiento del ovino criollo peruano. El año 2012, en el municipio rural de Ite, litoral sur del Perú, fueron evaluadas 200 ovejas adultas, clasificadas por posible genotipo (criollo o mestizo) y ambiente de crianza (humedales o chacras). Se analizaron medidas morfológicas y morfométricas; elaboraron índices, así como un análisis canónico y discriminante, utilizando el programa estadístico R. Los resultados mostraron ovejas mestizas con mayor aptitud cárnica que las criollas, ambas influenciadas por el ambiente, manejo, y mestizaje que amenazaría la conservación del ovino nativo. La adaptación de los rebaños fue vista en diferentes condiciones, pero algunas características deben mejorarse, requiriendo adecuada orientación técnica y servicios de extensión rural.

Palabras clave: *criollo, humedales, mestizaje, ovinocultura tradicional*

Summary

Sheep breeding is a traditional activity in Peru for small farmers, who generally possess Creole animals, which are frequently ignored in public policies as well as by the scientific community, not being recognized as a breed, showing poor productivity and having crosses with exotic breeds. This study aimed to characterize Creole and Hampshire Down crossbred ewes phenotypically, for using in the conservation and improvement of the Peruvian creole sheep. The year 2012, in the rural municipality of Ite, southern coast of Peru, 200 adult ewes were evaluated, classified by possible genotype (Creole or crossbred) and farm type (wetlands or ranches). Morphological and morphometric measurements were analysed; indices were drawn up and canonical and discriminant analysis were conducted, using the statistical program R. The results showed crossbred ewes with greater meat-producing capacity than the Creole, both influenced by the environment, management, and racial miscegenation that threatens the native sheep conservation. The adaptation of flocks was seen in different conditions, but some traits must be improved, requiring adequate technical orientation and rural extension services.

Keywords: *creole, miscegenation, traditional sheep breeding, wetlands*

Résumé

Au Pérou l'élevage des ovins est une activité traditionnelle pour les petits agriculteurs, qui généralement possèdent des animaux créoles, négligés par les politiques publiques et la communauté scientifique et n'ayant pas été reconnus en tant que race. Le bétail créole présente une faible productivité et fait l'objet de croisements avec des races exotiques. Cette étude visait à faire une caractérisation phénotypique de brebis créoles et croisées avec Hampshire Down, dans le but de conserver et améliorer le mouton créole péruvien. En 2012, dans la commune rurale d'Ite, dans le littoral méridional du Pérou, 200 brebis adultes ont été évaluées selon le génotype (créoles ou croisées) et l'environnement d'élevage (zones humides ou fermes). Des mesures morphologiques et morphométriques ont été analysées. Des indices ont été élaborés et des analyses canonique et discriminante ont été réalisées en utilisant le programme statistique R. Les résultats ont montré que l'aptitude bouchère des brebis croisées est plus affirmée que celle des créoles. Aussi bien les moutons créoles que ceux croisés sont influencés par l'environnement, les pratiques d'élevage et les croisements qui menacent la conservation des ovins indigènes. Suite à l'évaluation de l'adaptation des troupeaux dans des conditions différentes, il a été observé que certaines caractéristiques devaient être améliorées. Pour ce faire, une orientation technique appropriée et les services d'extension rurale s'avèrent nécessaires.

Mots-clés: *créole, croisement, production ovine traditionnelle, zones humides*

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Introducción

En Perú la ovinocultura es una actividad importante para los pequeños productores, que representan 75% de la

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población rural (Aliaga, 2009). INEI (2013) reportó 9 523 200 ovinos en el país, con un producto bruto interno de 157,25 millones de dólares estadounidenses. Esta especie se distribuye entre costa (5,1%), sierra (94,2%) y selva (0,7%), siendo la mayor población los criollos (81,0%), después Corriedale (11,4%), Hampshire Down (2,6%), Black Belly (0,9%) y otras (4,1%). La costa tiene poca precipitación pluvial, y por lo tanto requiere sistemas intensivos o semi-extensivos, que suelen utilizar residuos agrícolas como alimento. En la sierra y selva amazónica, los pastos naturales crecen producto de las lluvias, destacando los sistemas extensivos (FAO, 2004). El ovino proporciona carne, lana, cuero y estiércol, comercializándose un 70% (Flores *et al*., 2007), también es caja de ahorro en tiempo de necesidad, ya que puede ser vendido en cualquier época del año (Fulcrand, 2005).

Los ovinos descienden de troncos ancestrales Merino, Churro, Entrefino e Ibérico, traídos por colonizadores españoles a Perú en el siglo XVI (Alencastre & Gómez, 2005), y en más de 400 años de selección natural diferentes genotipos se combinaron, formando el ovino criollo o “chusco” (Flores, 2008). Las condiciones severas lo convirtieron en un animal rústico, pero con baja productividad, de tamaño pequeño y poca cobertura lanar (1,5 kg vellón), criado más por su carne, que puede registrar pesos de 27 kg en ovejas y 35 kg carneros (Alencastre & Gómez, 2005). Desde el siglo XX fueron sometidos a cruzas absorbentes con razas importadas en tentativa de “mejorarlos”, mas hubo poco éxito, ya que no están totalmente adaptadas a factores adversos de la ovinocultura peruana (Díaz, 2013), alterando lo avanzado en siglos naturalmente al introducir genes incompatibles con el medio, lo que fragiliza en ciertos aspectos a los nuevos individuos (Flores *et al*., 2007). El ovino criollo conquistó los sistemas de subsistencia, al soportar climas extremos, aprovechar pastos groseros, resistir enfermedades y tener buena reproducción (Fulcrand, 2005). Pero no es reconocido como raza por el Ministerio de Agricultura, que apenas introduce ovinos exóticos y forma compuestos genéticos. La asociación Arariwa y la Universidad Nacional del Altiplano trabajan con ovinos nativos, pero aún se necesitan más estudios que conduzcan a rebaños especializados y al uso adecuado de su rusticidad para cruza industrial, por lo que esta investigación objetivó caracterizar fenotípicamente ovejas criollas y mestizas, como subsidio en la conservación y mejoramiento zootécnico del ovino criollo peruano.

Material y métodos

Entre los meses de mayo y junio del año 2012, en el municipio rural de Ite, región Tacna, litoral sur del Perú, fueron evaluadas fenotípicamente 200 ovejas adultas, que al boqueo presentaron cuatro o más dientes incisivos inferiores permanentes. Fueron clasificadas según el relato de los propietarios y la interpretación zootécnica del investigador, en criollas y mestizas Hampshire Down (HD), agrupándolas por ambiente de crianza (Figura 1): 50 criollas de los humedales, 54 criollas de las chacras, 18 mestizas de los humedales y 78 mestizas de las chacras.

Vizcarra (2008) recopila datos sobre el clima de Ite, con temperaturas promedio de 16°C en julio y 28°C en febrero, escasas precipitaciones (<25 mm) durante invierno y humedad anual fluctuante (66–86%). En este lugar existen dos tipos marcados de ovinocultura; la primera es practicada por tradicionales ovicaprinocultores de los humedales, son alrededor de 19 familias de origen aymara, que pastorean rebaños en ese ecosistema de vegetación nativa, con 12 km de extensión y 2000 hectáreas de superficie, liberando sus animales durante el día y recogiéndolos al corral por la tarde. La otra crianza sería propia de agricultores de las chacras, que explotan ovinos bajo un sistema de estaca, pastoreándolos en asociación a bovinos en alfalfa y caprinos en grama o residuos de cultivos, tales como ají paprika (Montesinos *et al*., 2012; Montesinos *et al*., 2013). En el último censo, Robles (2009) registró 972 ovinos en los humedales y 1971 en las chacras. Generalmente la mano de obra es familiar, o se contrata un pastor (Aliaga, 2009). Para la colecta de datos se tuvo acceso a siete criaderos diferentes en los humedales y 51 pequeños productores en las chacras (Figura 2).

Las medidas morfométricas fueron registradas con balanza, cinta métrica y bastón zootécnico, en cuanto morfológicas visualmente, ambas adaptando la metodología de Oliveira *et al*. (2007). Variables morfológicas: perfil convexo y recto (PFCVX, PFRCT); ubre pequeña y grande (UBRPQ, UBRGR); condición corporal delgada, regular y gorda (CCDEL, CCREG, CCGOR). Morfométricas: peso vivo (PV), largo de oreja, cabeza, cuerpo y grupa (LOR, LCA, LCO, LAG), ancho de cabeza, grupa e isquión (ACA, ANG, AIS), altura a la cruz, esternón y grupa (ACR, AES, ALG), perímetro de tórax y caña (PTO, PCA), profundidad corporal (PCO), diámetro bicostal y

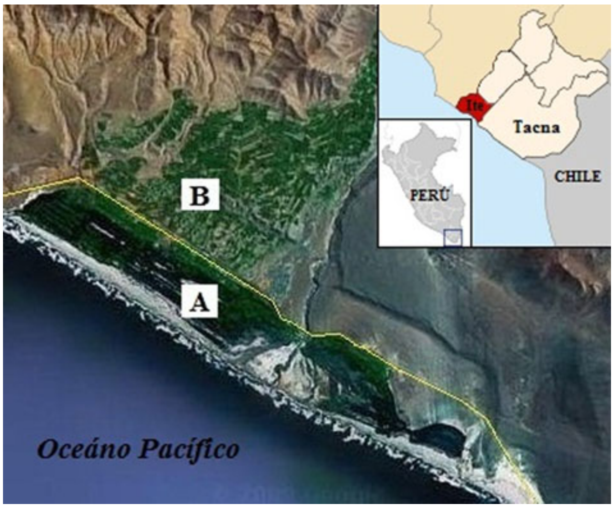

Figura 1. Mapa del municipio rural de Ite. (A) humedales, (B) chacras.

Figura 2. Sistema semi-extensivo en los humedales (a) y sistema bajo estaca en las chacras (b).

dorso-esternal (DBI, DDE). La caracterización fenotípica es base para la conservación animal, al identificar y clasificar razas (Dossa *et al.*, 2007). También se calcularon los siguientes índices zoométricos (Chacón *et al.*, 2011): cefálico ICE (ACA*100/LCA); corporal ICO (LCO*100/PTO); corporal relativo ICOR (LCO*100/ACR); proporción corporal IPRC (ACR/ALG); proporcional IPR (ACR*100/LCO); dáctilo-torácico IDAT (PCA/PTO); metacarpo-costal IMEC (PCA*100/DBI); pectoral IPEC ((ACR+ALG)/2)/AES; profundidad torácica IPRT (PCO*100/ACR); desarrollo torácico IDET (PTO/ACR); pélvico IPE (ANG*100/LAG); pélvico-transversal IPET (ANG*100/ALG); pélvico-longitudinal IPEL (LAG*100/ALG); balance INB (LAG*ANG)/(PCO*PCO). Estos índices clasifican al animal por tipo y función, combinando diferentes medidas corporales para encontrar su aptitud productiva (Salako, 2006).

Las medidas morfológicas y morfométricas obtenidas a campo fueron digitadas en planillas de Microsoft Excel, calculando así los índices zoométricos. Estos datos procedentes de cuatro grupos de ovejas fueron analizados, utilizando el programa computacional R (R Development Core Team, 2011). Primero se contabilizaron frecuencias de las variables morfológicas. Luego se realizó estadística descriptiva (promedio, desvío estándar y coeficiente de variación) de variables morfométricas e índices, para comparar los grupos mediante análisis de varianza y Test Scott-Knott, a nivel de significancia del 5%; todo esto a través del paquete EASYNOVA. Posteriormente se escogieron los parámetros morfométricos que tenían diferencia significativa, para elaboración de un análisis canónico y discriminante con los paquetes CANDISC y MASS.

Resultados y discusión

Análisis morfológico

Las ovejas criollas o “chuñas”, como las llamaban los pastores, tenían lana, cara y patas blancas, con pigmentación típica, parecida a la de sus ancestros Churros. Las mestizas eran de cara y patas negras, con lana algo amarillenta, similares a su línea parental Hampshire Down (HD), raza cárnica muy popular en la región, existiendo núcleos de animales puros en la sierra de Tacna. Se verificó que todas las hembras no tenían cuernos y la cola siempre estaba amputada (Figura 3).

Figura 3. Oveja criolla de los humedales (01) y mestiza Hampshire Down de las chacras (02).

Cuadro 1. Promedios de medidas morfológicas en cuatro grupos de ovejas, litoral sur del Perú.

Medidas morfológicas	**MECH**		**MEHU**		**CRICH**		**CRIHU**	
	N	**%**	**N**	**%**	**N**	**%**	**N**	**%**
Perfil convexo (PFCVX)	44	56,41	10	55,56	33	61,11	18	36,00
Perfil recto (PFRCT)	34	43,59	8	44,44	21	38,89	32	64,00
Total	78	100	18	100	54	100	50	100
Ubre pequeña (UBRPQ)	47	60,26	15	83,33	36	66,67	27	54,00
Ubre grande (UBRGR)	31	39,74	3	16,67	18	33,33	23	46,00
Total	78	100	18	100	54	100	50	100
Condición corporal delgada (CCDEL)	6	7,69	3	16,67	11	20,37	10	20,00
Condición corporal regular (CCREG)	54	69,23	6	33,33	40	74,07	36	72,00
Condición corporal gorda (CCGOR)	18	23,08	9	50,00	3	5,56	4	8,00
Total	78	100	18	100	54	100	50	100

MECH: mestizas chacras; MEHU: mestizas humedales; CRICH: criollas chacras; CRIHU: criollas humedales. N: número.

En el Cuadro 1, el PFCVX fue mayoritario en ovejas mestizas (chacras y humedales) así como en criollas de las chacras; estas últimas talvez por mestizaje con descendientes del HD, raza de marcado perfil convexo. En las criollas de los humedales superó el PFRCT, que puede indicar una etnia diferente. UBRPQ era mayoritaria en los grupos, sugiriendo que la producción láctea es exclusiva para la cría. CCREG fue superior para mestizas de las chacras y CCGOR en mestizas de los humedales. Se atribuiría al manejo de cada ambiente, ya que en las chacras los ovinos están confinados bajo estaca, a un espacio limitado de alimento; contrario al pastoreo de los humedales que es *ad libitum* casi todo el día. Animales de gran tamaño tienen mayores requerimientos alimenticios (Gomes *et al.*, 2013), por lo que la CCGOR de esas mestizas mostraría cierta adaptación, indicando posible uso de cruza industrial con razas especializadas, en pastoreo de vegetación nativa. La CCREG de las criollas confirmó su rusticidad y equilibrio en los dos sistemas de manejo, favoreciendo a la sanidad y reproducción del rebaño (Araújo Filho *et al.*, 2005).

Análisis morfométrico

Las ovejas mestizas de los agricultores fueron superiores en tamaño, seguidas por sus similares en los humedales y criollas de las chacras, en cuanto las criollas de los ovi-caprinocultores eran inferiores (Cuadro 2). Los grupos mostraron individualmente uniformidad morfométrica al obtener bajos coeficientes de variación (CV), menores a 5,62; importante para una futura categorización de las criollas a raza (Herrera, 2007).

Según Oteiza & Carmona (1993), el PV indica que todas las mestizas y criollas de las chacras son euméricas (40–60 kg); en cuanto criollas de los humedales más ligeras o hipométricas (<40 kg). Quizás por ser la alfalfa y los residuos de cultivos mejor oferta que la vegetación nativa, así

Cuadro 2. Promedios de medidas morfométricas (kg y cm) en cuatro grupos de ovejas, litoral sur del Perú.

Medidas morfométricas	**MECH**		**MEHU**		**CRICH**		**CRIHU**	
	PRMD	**DS**	**PRMD**	**DS**	**PRMD**	**DS**	**PRMD**	**DS**
Peso vivo (PV)	48,76^a	1,18	43,78^b	2,46	41,57^b	1,42	38,30^c	1,48
Largo de oreja (LOR)	12,26^a	0,19	11,44^b	0,41	12,28^a	0,23	11,50^b	0,24
Largo de cabeza (LCA)	26,28^a	0,23	24,06^c	0,47	24,87^b	0,27	23,72^c	0,28
Ancho de cabeza (ACA)	16,68^a	0,15	14,83^c	0,32	15,89^b	0,18	14,54^c	0,19
Altura a la cruz (ACR)	60,73^a	0,44	60,44^a	0,92	59,37^a	0,53	60,38^a	0,55
Altura de esternón (AES)	32,71^a	0,45	31,78^a	0,94	32,87^a	0,54	32,78^a	0,56
Altura de grupa (ALG)	63,42^a	0,39	63,94^a	0,82	62,33^a	0,47	62,78^a	0,49
Largo corporal (LCO)	83,01^a	0,65	82,06^a	1,35	79,52^b	0,78	80,02^b	0,81
Perímetro de tórax (PTO)	87,99^a	0,81	90,00^a	1,68	83,22^b	0,97	86,68^a	1,01
Profundidad corporal (PCO)	28,02^a	0,26	28,66^a	0,53	26,50^b	0,31	27,60^a	0,32
Diámetro (DBI)	23,23^b	0,34	25,67^a	0,71	22,43^b	0,41	23,38^b	0,43
Diámetro dorso-esternal (DDE)	28,27^b	0,29	30,00^a	0,61	27,69^b	0,35	27,98^b	0,37
Ancho de grupa (ANG)	25,06^a	0,33	21,39^c	0,69	23,70^b	0,39	21,82^c	0,41
Largo de grupa (LAG)	29,51^a	0,33	25,22^b	0,69	28,79^a	0,39	26,10^b	0,41
Ancho de isquión (AIS)	9,38^a	0,12	8,33^b	0,25	8,96^a	0,14	8,74^b	0,15
Perímetro de caña (PCA)	11,09^a	0,10	10,44^b	0,22	10,48^b	0,12	9,94^c	0,13

MECH: mestizas chacras; MEHU: mestizas humedales; CRICH: criollas chacras; CRIHU: criollas humedales. PRMD: promedio; DS: desvío estándar. Promedios con letra diferente (a, b, c) no son iguales por el Test Scott-Knott al 5%.

como expresión génica diferente al cruzar con HD (Montesinos *et al*., 2012). Las ovejas criollas superaron el PV promedio de 27 kg (Alencastre & Gómez, 2005) y fueron próximas a Criollas Colombianas (39,96 kg) estudiadas por Carneiro *et al*. (2010). LOR, LCA y ACA caracterizan poblaciones de acuerdo al origen étnico (Sañudo, 2009). En ovejas mestizas y criollas de las chacras destacó su dimensión craneana superior, seguidas por mestizas y criollas de los humedales, las cuales tenían valores similares, sugiriendo una posible cruza entre rebaños ya que pastorean en proximidad; caso diferente a ovinos de las chacras, que son estacados y los agricultores dirigen las montas, existiendo poca mixtura genética indeseada, salvo que ocurra contacto accidental con animales de otras propiedades. Las ACR, AES y ALG de todos los grupos fueron similares, mostrando nuevamente cierto mestizaje. ACR y ALG eran algo menores a las de ovejas nativas Makuie de Irán (Jafari, 2014). El LCO fue mayor en las mestizas, siendo característica dominante del tronco parental HD, independiente de ambiente y manejo, lo que indicaría un biotipo cárnico, superando en esa medida a todas las razas descritas por Carneiro *et al*. (2010). Según el PTO y PCO, las mestizas tienen buena apariencia cilíndrica, como el HD, por su gran volumen torácico. Las criollas de las chacras fueron las únicas con valores inferiores, quizás por su poco ejercicio físico al pastorear estacadas todo el día. Entre tanto las criollas de los humedales poseían mayor tórax, porque diariamente realizan caminatas en busca de alimento, lo que exige cierta capacidad respiratoria, algo también reportado en Criollas Lanadas brasileras (Silva *et al*., 2013). DDE excedió el DBI en todas las ovejas, por costillares menos arqueados al predominar profundidad sobre anchura, apuntando a un potencial lactogénico (Peña Blanco *et al*., 1990), especialmente en mestizas de los humedales. Las mestizas de las chacras poseen mayor caja pélvica (ANG, LAG y AIS), adecuada para reproducción; siguen las criollas de las chacras, y por último ovejas de los humedales. En criollas de las chacras podría deberse a cruzas absorbentes, ya que los agricultores prefieren animales anchos y cárnicos, tipo HD o “cara negra”. Las ovejas de los humedales tienen pelvis menor, con medida similar a criollas Chilote (Mella, 2010). Para mestizas de los humedales la causa podría ser un alto grado de sangre nativa, sabiendo que ese ambiente alberga más ovinos criollos, los cuales generalmente son de pequeño porte, por selección natural en condiciones adversas (Vargas *et al*., 2007). Para el PCA, mestizas de las chacras fueron superiores y criollas de los humedales inferiores, mostrando el hueso de la caña una diferencia entre animales pesados y más ligeros (Peña Blanco *et al*., 1990). Las extremidades finas favorecen al pastoreo en terrenos que dificultan el andar de grandes pezuñas (Herrera, 2007), confirmando PCA la adaptación de las criollas a los humedales.

La Figura 4 muestra mayor similitud morfométrica entre ovejas de las chacras, algo también reportado en la clasificación grupal del análisis discriminante (Cuadro 3).

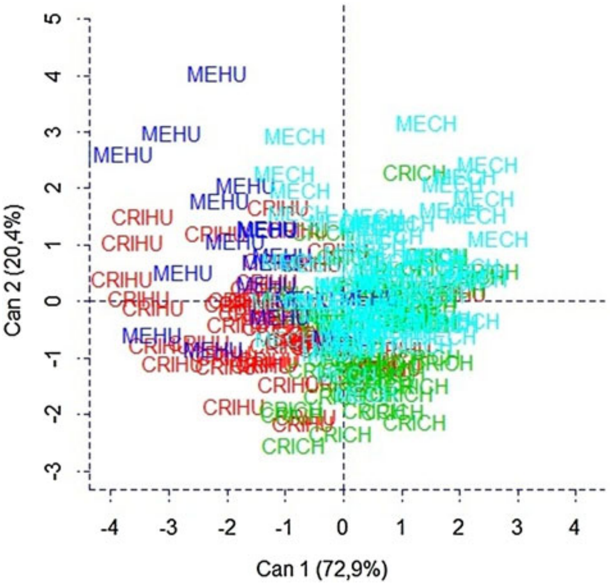

Figura 4. Análisis canónico para las medidas morfométricas.

Cuadro 3. Análisis discriminante en cuatro grupos de ovejas, litoral sur del Perú.

Grupo (N)	MECH	MEHU	CRICH	CRIHU	Tasa de acierto (%)
MECH (78)	44	0	26	8	56,4
MEHU (18)	1	7	2	8	38,8
CRICH (54)	25	0	23	6	42,6
CRIHU (50)	5	7	6	32	64,0

MECH: mestizas chacras; MEHU: mestizas humedales; CRICH: criollas chacras; CRIHU: criollas humedales. N: número.

Se observó que en cada ambiente predomina un fenotipo particular, siendo...

en las chacras el de ovejas mestizas HD, inclusive dentro del grupo de las criollas, ya que tienen medidas corporales parecidas. Esto debido a los agricultores, que realizan cruzas absorbentes con HD y/o mestizos, al desconocer lamentablemente el potencial del ovino criollo. En los humedales destacó morfométricamente el tipo nativo, que se encontró con alta incidencia entre las mestizas. Puede deberse al sistema tradicional, extrativista y de subsistencia que impera en ese ambiente, donde los criadores no tienen recursos económicos, ni tampoco costumbre de introducir desesperadamente animales exóticos (Montesinos *et al*., 2012). Las ovejas criollas de los humedales en la clasificación morfométrica obtuvieron tasa de acierto superior (64%), indicando mayor homogeneidad corporal, quizás porque esos rebaños están más sometidos a selección natural que artificial.

La conformación corporal es heredada e influenciada por el ambiente y las preferencias de los criadores hacia un tipo de animal (Miserani *et al*., 2002). Vale comentar que algunos pastores realizan tradicionalmente selección, castrando machos jóvenes con ligas de caucho (Figura 5), que asemejan la técnica del Elastrador (Rocha *et al*., 2010).

Figura 5. Método de castración practicado por ovicaprinocultores en los humedales de Ite.

Índices zoométricos

Las ovejas mostraron cierta uniformidad en los índices etnológicos por sus bajos CV (≤2,18). Algunos grupos obtuvieron valores similares (ICOR, IPR, IPRC e IPE), lo que podría indicar cruzamientos entre rebaños (Cuadro 4).

En el ICE fueron totalmente dolicocéfalas, debido al predominio del largo sobre ancho craneano (Parés, 2007); en este aspecto ovejas criadas en las chacras superaron a sus vecinas de los humedales, talvez por mayor mestizaje exótico y nativo en cada ambiente respectivamente. Todas son longilíneas (ICO > 86%) o de tronco alargado (Oteiza & Carmona, 1993). Los ICOR e IPR muestran mayor LCO que ACR, destacando las mestizas al heredar del HD la forma paralelepípeda, clásica en razas cárnicas (Salako, 2006). IPRC e IPE evidencian que todas las ovejas poseen grupa más alta que la cruz, según Herrera (2007), por escasa selección; y la grupa más larga que ancha, algo también reportado en Criollas Araucanas (Bravo & Sepúlveda, 2010). Estas características deben corregirse si se busca la especialización cárnica y facilidad de parto (Rodríguez *et al.*, 1990), ya que el ancho de grupa precisa ser más cuadrangular o concavilíneo, como registró Mernies *et al.* (2007) en ovejas Criollas Uruguayas.

En los índices funcionales (Cuadro 5), las mestizas de los humedales tienen mayores CV (≤4,55), quizás por ser producto de cruzas desordenadas entre rebaños. El IDAT sugiere que ovejas de las chacras tienden a ser cárnicas y las de los humedales más lecheras (Bravo & Sepúlveda, 2010), esto puede deberse al grado de mestizaje, alimento y manejo. Vale mencionar que los agricultores de las chacras destetan los corderos, amarrándolos a una estaca con temprana edad, dejando sus madres solas y a engorda. Diferente al destete en los humedales, que es de forma natural y tardío, por el sistema semi-extensivo practicado.

Cuadro 4. Índices etnológicos en cuatro grupos de ovejas, litoral sur del Perú.

Índices	**MECH**		**MEHU**		**CRICH**		**CRIHU**	
	PRMD	**DS**	**PRMD**	**DS**	**PRMD**	**DS**	**PRMD**	**DS**
Cefálico (ICE)	63,60^{a}	0,49	61,76^{b}	1,01	64,01^{a}	0,59	61,37^{b}	0,61
Corporal (ICO)	94,76^{a}	0,72	91,56^{b}	1,50	95,71^{a}	0,87	92,53^{b}	0,90
Corporal relativo (ICOR)	136,93^{a}	1,21	135,99^{a}	2,52	134,14^{a}	1,46	133,41^{a}	1,51
Proporcional (IPR)	73,36^{a}	0,77	73,74^{a}	1,61	74,97^{a}	0,93	75,97^{a}	0,96
Proporción corporal (IPRC)	0,96^{a}	0,004	0,95^{a}	0,010	0,95^{a}	0,006	0,96^{a}	0,006
Pélvico (IPE)	84,99^{a}	0,79	84,87^{a}	1,64	82,28^{a}	0,94	83,82^{a}	0,98

MECH: mestizas chacras; MEHU: mestizas humedales; CRICH: criollas chacras; CRIHU: criollas humedales. PRMD: promedio; DS: desvío estándar. Promedios con letra diferente (a, b) no son iguales por el Test Scott-Knott al 5%.

Cuadro 5. Índices funcionales en cuatro grupos de ovejas, litoral sur del Perú.

Índices	**MECH**		**MEHU**		**CRICH**		**CRIHU**	
	PRMD	**DS**	**PRMD**	**DS**	**PRMD**	**DS**	**PRMD**	**DS**
Dáctilo-torácico (IDAT)	0,13^{a}	0,001	0,12^{b}	0,003	0,13^{a}	0,002	0,12^{b}	0,002
Desarrollo torácico (IDET)	1,45^{b}	0,01	1,49^{a}	0,03	1,40^{b}	0,02	1,44^{b}	0,02
Pectoral (IPEC)	1,91^{b}	0,02	1,97^{a}	0,04	1,86^{b}	0,02	1,91^{b}	0,02
Profundidad torácica (IPRT)	46,20^{b}	0,46	47,49^{a}	0,95	44,73^{b}	0,55	45,98^{b}	0,57
Metacarpo-costal (IMEC)	48,15^{a}	0,63	41,28^{b}	1,31	47,08^{a}	0,76	43,37^{b}	0,79
Pélvico-transversal (IPET)	39,47^{a}	0,44	33,37^{b}	0,92	38,01^{a}	0,53	34,79^{b}	0,55
Pélvico-longitudinal (IPEL)	46,52^{a}	0,45	39,39^{c}	0,95	46,25^{a}	0,55	41,61^{b}	0,57
Balance (INB)	0,95^{a}	0,02	0,66^{c}	0,03	0,97^{a}	0,02	0,76^{b}	0,02

MECH: mestizas chacras; MEHU: mestizas humedales; CRICH: criollas chacras; CRIHU: criollas humedales. PRMD: promedio; DS: desvío estándar. Promedios con letra diferente (a, b, c), no son iguales por el Test Scott-Knott al 5%.

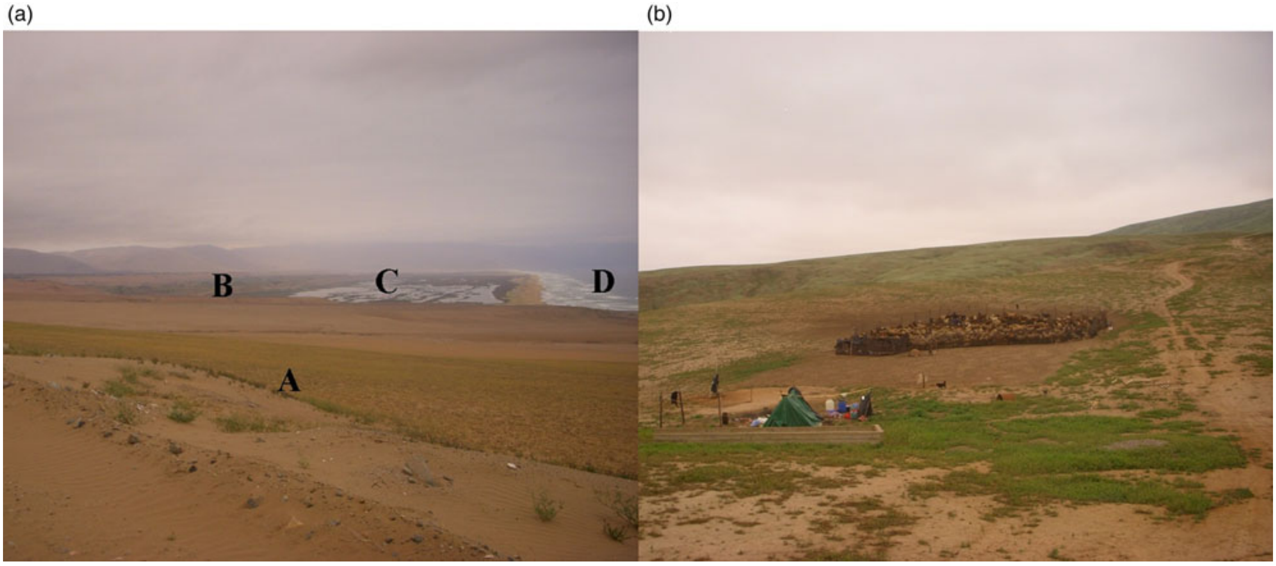

Figura 6. (a) Vista panorámica desde las 'lomas' (A), del municipio rural de Ite (B), los humedales (C) y el océano Pacífico (D). (b) Ovicaprinocultor trashumante con sus perros pastores y rebaño, lomas de Ite.

Según IDET, IPEC e IPRT, ovejas mestizas de los humedales aventajan a las demás por su profundidad torácica, que indicaría mayor capacidad respiratoria y lactogénica. En este aspecto son similares a ovejas de carne Aranesas, profundas de tórax y conocidas por la habilidad de criar corderos "a ubre" (Parés, 2007). Estas mestizas también son de piernas cortas, apropiadas en pastoreo al nivel del suelo. Los otros grupos tienen piernas más largas, así evitan la radiación calórica terrestre y obtienen velocidad (Álvarez *et al*., 2000), vital en ovinos de las chacras, pues permanecen estacados todo el día sin sombra, y en las criollas de los humedales para escapar de los depredadores (Montesinos *et al*., 2012). El IMEC revela potencia de las extremidades con relación a la masa corporal (Chacón *et al*., 2011), sobresaliendo las ovejas de los ovicaprinocultores por su adaptación para extensas caminatas de pastoreo y la subida de laderas cuando vuelven al corral. Se sabe que el fenómeno de "El Niño" trae lloviznas frecuentes, provocando brote temporal de vegetación nativa en los cerros áridos de la costa peruana que se llaman "lomas" (Dillon & Rundel, 1990). Éstas son aprovechadas por criadores de los humedales, que practican la trashumancia desde hace décadas, llevando sus rebaños hasta esos altos lugares, porque existe una mejora considerable en la producción animal (Figura 6).

IPET e IPEL mostraron ovejas de las chacras con mayor caja pélvica, que evidencia un desarrollo muscular en esa zona de cortes valiosos (Bravo & Sepúlveda, 2010). Las ovejas de los humedales son más estrechas, constatándose la falta de orientación técnica y extensión rural para los criadores. El INB fue mejor en ovejas de las chacras, quizás debido a la monta dirigida practicada por los agricultores, poseedores de algún saber zootécnico (Alves *et al*., 2010), y porque las ovejas son estacadas, lo que facilita su manejo reproductivo. Diferente a ovinos de los humedales que cruzan sin mayor control durante época reproductiva, la cual ocurre dos veces al año debido a fotoperiodo negativo de estos rebaños (Montesinos *et al*., 2013).

Conclusiones

Las ovejas mestizas tienen mayor aptitud cárnica que las criollas, ambas influenciadas por ambiente, manejo y mestizaje, lo que amenazaría al ovino nativo, el cual debe ser genotipado. Se detectó buena condición corporal y cierto potencial lactogénico en las mestizas de los humedales, sugiriendo el uso de cruza industrial con razas mejoradas, en esa vegetación nativa. Los rebaños se adaptaron a diferentes condiciones, pero aún existen características por mejorar, como altura de la cruz en relación a grupa y el ancho pélvico. Es urgente explorar más el ovino criollo y sus propietarios, para encontrar un nicho comercial atractivo, que genere buenos ingresos económicos, fomentando así la conservación *in situ* de este recurso genético animal.

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Caractérisation phénotypique du mouton de Vogan du Togo et relation avec le mouton Djallonké et le mouton sahélien

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Résumé

Le mouton de Vogan (MV) est une race ovine unique au Togo et serait issu de croisements entre la brebis Djallonké et le bélier sahélien. Il est très apprécié de par ses aptitudes zootechniques, mais son élevage est très localisé au sud-est du Togo. Ce travail vise l'étude des caractères phénotypiques de la race et la comparaison de ces caractères avec ceux des populations parentales (moutons Djallonké (MD) et moutons sahéliens (MS)). A cet effet, des données morphobiométriques ont été collectées en janvier 2013 sur 206 animaux dans les préfectures de Vô, de Kloto et d'Agou au Togo et sur 30 MS en mai 2013 autour de la ville de Bobo-Dioulasso au Burkina Faso. Les résultats obtenus ont montré que la couleur de la robe du MV est généralement bicolore (rousse, noire, chocolat), mais très variée. Les cornes, de forme variable, présentes chez tous les béliers, et fines ou en vestige chez les brebis, sont pour la plupart des cas prismatiques et orientées vers l'extérieur. Les caractères quantitatifs tels que la hauteur au garrot, la longueur du corps, la circonférence thoracique, la longueur de la queue, la longueur des oreilles, l'espace intercornes et la profondeur du thorax du MV sont inférieurs à ceux des MS, mais largement supérieurs à ceux des MD. La plupart des caractères du MV ont été influencés par le facteur canton ($p < 0,05$). Cette étude a confirmé la position «intermédiaire» du MV. L'exploitation de cette précieuse ressource ovine passera par sa caractérisation et sa diffusion.

Mots-clés: *mouton de Vogan, caractérisation phénotypique, Togo*

Abstract

The Vogan sheep (VS), a crossbreed between Djallonke sheep (DS) and sahelian sheep (SS), is a unique sheep breed in Togo. It is highly valued for its performances but its breeding is very localized in southeastern of Togo. The objective of this study was to update the breed's phenotypic characterization and to compare VS phenotypic features with those of parental populations (DS and SS). For this purpose, morphological data were collected in January 2013 from 206 animals in Vô, Kloto and Agou prefectures (Togo) and in May 2013 from 30 SS in Bobo-Dioulasso (Burkina Faso). Results showed that the coat colour was very variable. Horn shape was also variable but was generally prismatic and outward-oriented, present in all rams and fine or remains of them in ewes. Quantitative traits such as height at withers, body length, chest circumference, tail length, ear length, space between the horns and chest depth showed that VS traits are smaller than SS traits but are significantly superior when compared to DS traits. Most VS characters were influenced by geographic location ($p < 0,05$). This study confirmed the "intermediate" status of VS. The sustainable use of VS needs molecular characterization and a dissemination programme.

Keywords: *Vogan Sheep, phenotypic characterization, Togo*

Resumen

La oveja de Vogan (OV) es una raza ovina única de oveja en Togo y está producido por cruces de oveja Djallonké y el carnero Saheliano. Es muy apreciado por sus habilidades zootécnicas, pero su cría se encuentra al sureste de Togo. Este trabajo tiene como objetivo estudiar las características fenotípicas de la raza y la comparación de estas características con las de las poblaciones parentales (ovejas Djallonké (OD) y ovejas del Sahel (OS)). Para ello, los datos morfo biométrico se recogieron en enero de 2013 sobre 206 animales en las prefecturas de Vo, Kloto y Agou en Togo y sobre 30 OS en 2013 alrededor de la ciudad de Bobo-Dioulasso en Burkina Faso. Los resultados obtenidos mostraron que el color del vestido del OV es por lo general bicolor (rojizo, negro o chocolate), pero muy variada. Los cuernos de formas variables presentes en todos los carneros, finas o vestigio en las ovejas son en la mayoría de los casos prismática y orientada hacia el exterior. Los rasgos cuantitativos tales como la altura a la cruz, la longitud del cuerpo, la circunferencia de pecho, la longitud de la cola, la longitud de las orejas, el espacio intercuernos y la profundidad de pecho de OV son inferiores a los de la OS, pero en gran medida superior a los de OD. La mayoría de los rasgos de la OV se vieron influidos por el factor de cantón ($p < 0,05$). Este estudio confirma la posición "intermedia" de OV. La explotación de este valioso recurso ovino pasara por la caracterización y distribución.

Palabras clave: *Oveja de Vogan, caracterización fenotípica, Togo*

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Introduction

Parmi les ressources génétiques animales exploitées au Togo, les petits ruminants occupent une place importante et sont naturellement divisés entre les ovins qui prédominent au nord et les caprins qui dominent au sud du pays. Les races ovines rencontrées sont: le mouton Djallonké (MD) qui constitue l'essentiel du cheptel national ovin (environ 841 000 têtes en 1996) et le mouton de Vogan (MV) (190 000 têtes en 1983) (http://dad.fao.org). Le MV serait un produit de croisements entre la brebis Djallonké et le bélier sahélien (Amegee, 1983). Son nom local est *Sabalu*. Malgré les appréciations sur le MV, il n'existe aucun programme d'études et de valorisation de cette ressource. Les dernières études sur la connaissance de la race remontent aux années 80 (Amegee, 1978, Amegee, 1983; Amegee, 1984a; Amegee, 1984b) et sont limitées aux descriptions phénotypiques. Par ailleurs, jusqu'à présent, le MV est resté dans une zone qui peut être caractérisée comme «berceau de la race» à savoir le sud-est du Togo. Dans le contexte actuel des changements globaux notamment climatiques, de l'évolution des systèmes d'élevage et du marché, il est nécessaire d'actualiser les données phénotypiques sur le MV, de réaliser des études de caractérisation moléculaire de la race et surtout de proposer des stratégies pour sa diffusion. C'est dans cette optique que la présente étude a été menée pour, dans un premier temps, actualiser les données morphobiométriques du MV et établir une description comparative de ces caractères phénotypiques entre les MV et les populations parentales à savoir les MD et les MS. Cette étude cadre bien avec la stratégie prioritaire 1 du Plan d'actions mondial de la FAO pour les ressources zoo-génétiques (FAO, 2007).

1 Matériel et méthodes

1.1 Zone d'étude

L'étude a été menée dans la préfecture de Vô (pour les MV et les MD) dans la région de Maritime, les préfectures de Kloto et d'Agou (pour les MD) dans la région des Plateaux au Togo et dans la ville de Bobo-Dioulasso au Burkina Faso (pour les MS). La carte de la répartition des élevages échantillonnés au Togo est représentée sur la figure 1.

1.2 Matériel animal

L'étude a porté sur trois races ovines (Figure 2): le mouton Djallonké, le mouton sahélien et le mouton de Vogan. Les deux sexes (mâle et femelle) ont été inclus dans l'étude.

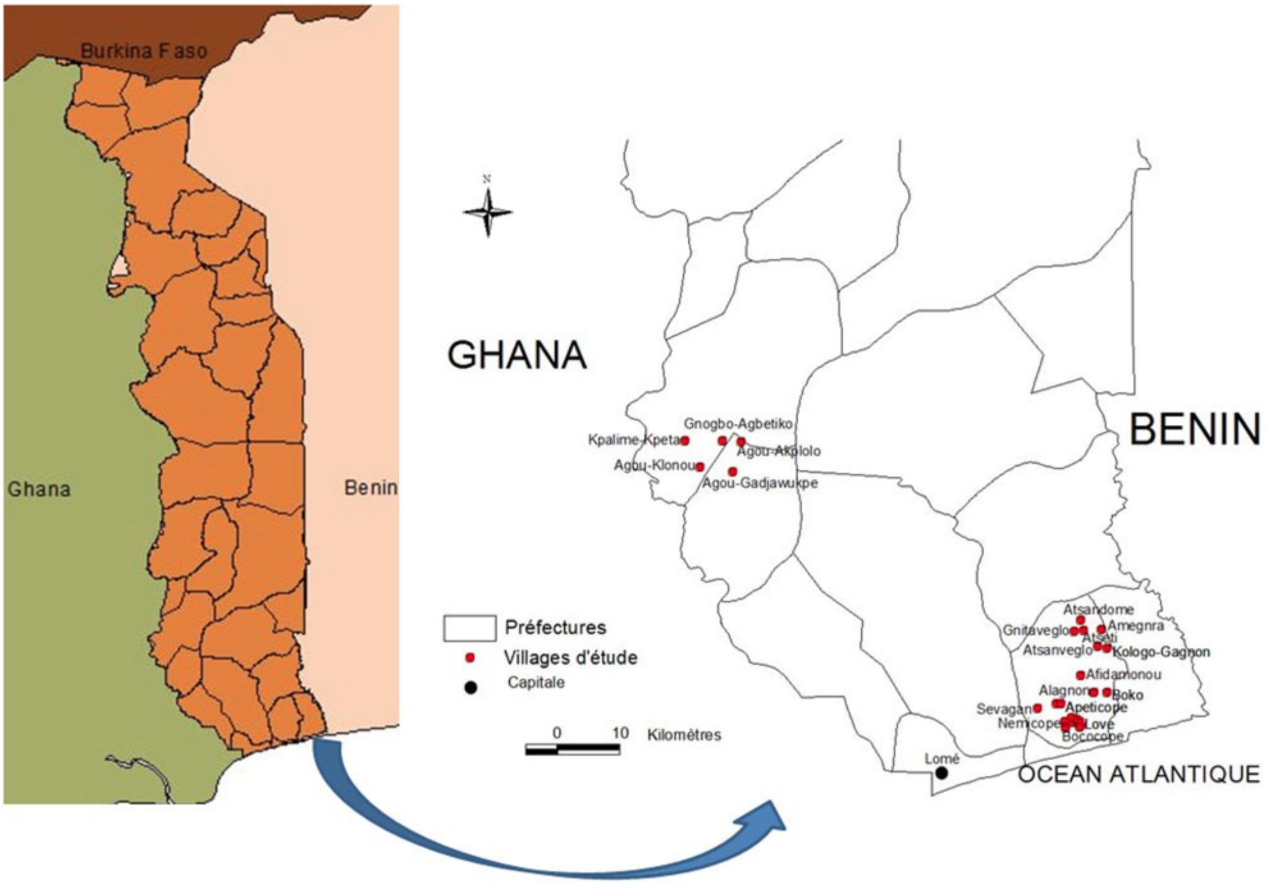

Figure 1. Zone d'étude.

Figure 2. Races ovines étudiées. (a) Brébis Djallonké avec des agneaux. (b) Troupeau de moutons de Vogan. (c) Troupeau de moutons sahéliens.

1.3 Méthodes

1.3.1 Echantillonnage des animaux

Les mesures morphobiométriques des animaux ont été menées du 16 au 21 janvier 2013 dans 7 cantons de la préfecture de Vô (Togoville, Wogba-Vogan, Sévagan, Koutimé, Vogan, Dzrékpo et Dagbati), 4 cantons de la préfecture d'Agou (Gadja, Klonou, Gnogbo-Agbétiko et Akplolo) et 1 canton de la préfecture de Kloto (Tové-Kpeta) et en mai 2013 dans la ville de Bobo-Dioulasso en ce qui concerne les moutons sahéliens. Les mesures morphobiométriques ont porté sur 236 moutons dont 104 MV et 50 MD dans la préfecture de Vô; 42 MD dans l'Agou, 10 MD dans le Kloto et 30 MS à Bobo-Dioulasso.

Les MD des préfectures de Kloto et d'Agou sont considérés dans cette étude comme des populations génétiquement conservées (témoins) car dans ces deux préfectures l'unique race ovine est la race Djallonké, ce qui limite les possibilités d'introgression de la race Djallonké par une autre race ovine.

Dans chaque troupeau, 1 à 10 individus les moins apparentés possibles ont été échantillonnés en fonction de la taille du troupeau pour avoir la plus grande variabilité possible.

1.3.2 Mesures morphobiométriques

Le guide établi par l'Organisation des Nations Unies pour l'alimentation et l'agriculture (FAO, 2012) a été utilisé pour décrire ou mesurer les caractères morphobiométriques. Au total, 23 caractères, dont 12 caractères qualitatifs et 11 caractères quantitatifs ont été enregistrés. Les données qualitatives (race (mouton djallonké, mouton de Vogan, mouton sahélien), sexe (mâle, femelle), type d'eumélanine, patron pigmentaire, présence ou absence d'étoile socquette, présence ou absence de frosting, présence ou absence de la barbiche et/ou des pampilles, structure des poils (court et dur, court et lisse, long et dur, long et lisse), port des oreilles (court et dressé, court et tombant, long et dressé, long et tombante), présence ou absence de la corne et description de la forme des cornes) ont été obtenues par simple observation des individus. Par contre, pour les données quantitatives (Figure 3), les mesures ont été effectuées après la contention (Figure 4a) de chaque animal. Les outils suivants ont été utilisés pour les mesures:

- Une canne-toise pour mesurer la hauteur au garrot, la profondeur du thorax et la longueur du corps;
- Un mètre ruban (Figure 4b) pour mesurer le cordonnet chanfrein, l'arc chanfrein, la longueur des oreilles, la longueur des cornes, l'espace intercornes, la circonférence thoracique et la longueur de la queue.

1.3.3 Analyses statistiques des données

Pour le traitement des données, une base de données a été constituée à l'aide du tableur Microsoft Excel 2007. Les analyses des données (qualitatives et quantitatives) ont été

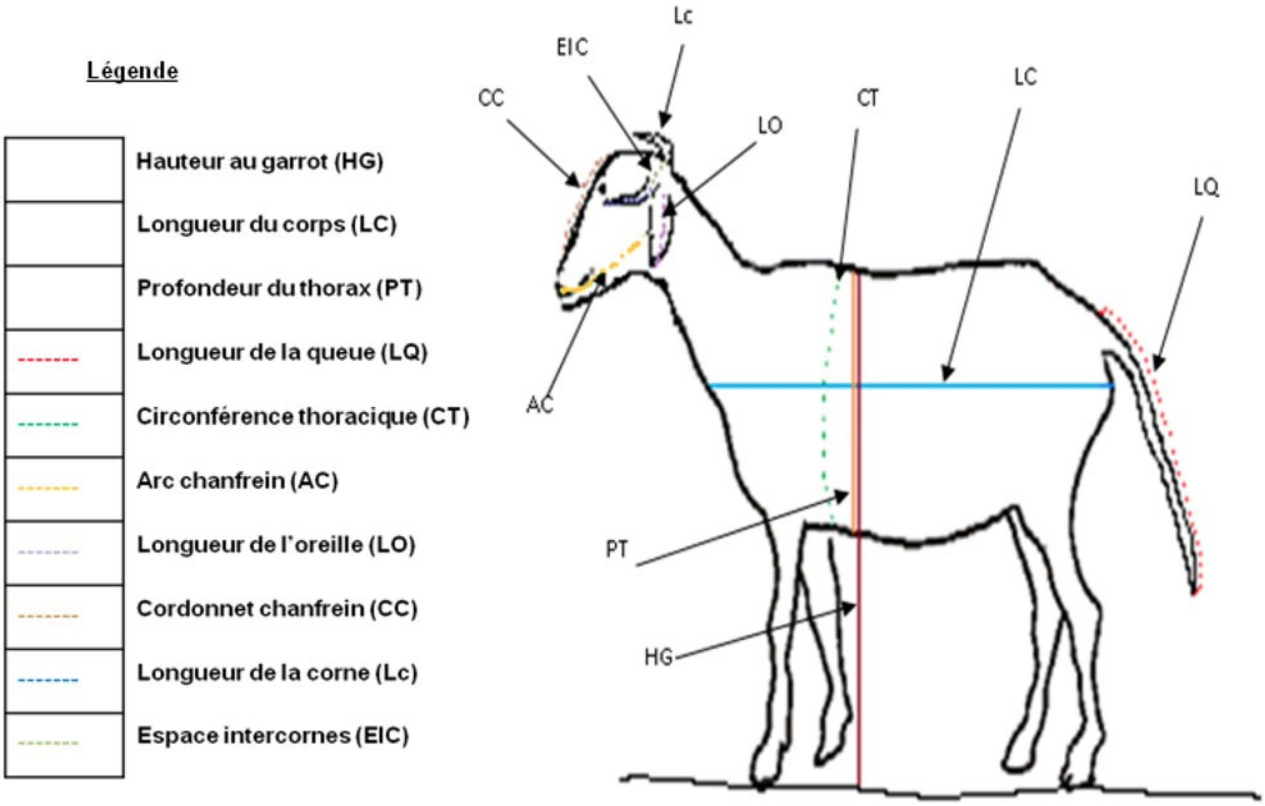

Figure 3. Modalités de mesures des variables quantitatives.

faites avec le logiciel R (R-Core-Team, 2012). Le seuil de significativité utilisé est de 5% pour l'interprétation des tests statistiques.

Les paramètres utilisés pour l'analyse des données qualitatives sont la fréquence et la proportion. Ces paramètres ont été calculés en fonction de la race, du sexe et de la localité.

Les variables quantitatives ont été exprimées sous forme de moyenne et l'écart-type, valeurs minimales et valeurs maximales. Ces variables quantitatives ont été évaluées en fonction des facteurs comme la race, le sexe, la localité et l'âge.

L'analyse en composantes principales (ACP) a permis d'établir la corrélation entre les variables quantitatives en utilisant le package FactoMineR implémenté dans le logiciel R (Husson *et al.*, 2014) tandis que l'analyse factorielle des correspondances a été utilisée pour identifier les variables qualitatives qui discriminent les trois populations.

Figure 4. Techniques de quelques mesures morphobiométriques. (a) Contention pour les prélèvements. (b) Mesure du périmètre thoracique avec le mètre ruban.

Des regroupements d'animaux ont été identifiés en supposant des clusters représentés par le paramètre k (k = 3 à 10). Les individus sont regroupés en fonction de la valeur de k supposée. Le package FactoMineR implementé dans le logiciel R a permis aussi de représenter les relations entre les variables quantitatives et les variables qualitatives utilisées.

2 Résultats

2.1 Structure des troupeaux de mouton de Vogan étudiés

L'âge moyen des moutons de Vogan inclus dans cette étude était de 2,7 ans (minimum = <1 an et maximum = plus de 4ans).

Les individus échantillonnés étaient majoritairement des femelles: 85% pour les MD (n = 87), 67% pour les MS (n = 20) et 70% pour les MV (n = 73). Dans tous les troupeaux, les femelles sont numériquement majoritaires.

2.2 Caractères qualitatifs

2.2.1 Patron pigmentaire et types d'eumélanine

Les fréquences des patrons pigmentaires observés chez les races ovines de cette étude sont présentées dans le tableau 1. On note une prédominance significative du patron pigmentaire illisible[1] chez les moutons Djallonké (64,71%, *p-value <0,001*) et les moutons sahéliens (50%, *p-value <0,001*). Cependant, chez les MV, les patrons pigmentaires illisible et bicolore (Figure 5) sont les plus rencontrés, respectivement dans les proportions de 42,31% (*p-value <0,001*) et 44,23% (*p-value <0,001*). L'absence de pigment (robe blanche uniforme) est plus rare chez les MV (1,92%) par rapport aux MS (30%) et MD (2,94%).

En ce qui concerne le type d'eumélanine, chez les MD, le type d'eumélanine est majoritairement le roux ou le noir et parfois le chocolat (test de Khi^2, *p-value <0,001*). Chez les MS, la robe est majoritairement blanche (test de Khi^2, *p-value <0,001*). Chez les MV, deux types d'eumélanine sont significativement distribués dans la population échantillonnée, le roux et le noir (ou du chocolat) (test de Khi^2, *p-value <0,001*).

2.2.2 Fréquence de l'étoile socquette et frosting par race ovine

Les étoiles socquettes (Figure 5a) sont plus fréquentes avec une différence significative au test de Khi^2 chez les MD (90,1%) que chez les MV (76,92%, *p-value = 0,01888*) et chez les MS (69,57%, *p-value = 0,02457*). Par contre, les frosting sont plus représentés avec une différence significative au test de Khi^2 chez les MS (69,23%, *p-value = 0,003029*) et les MV (42,31%, *p-value = 0,0131*) que chez les MD (24,74%). Il n'existe pas de différence significative au test de Khi^2 entre les MV et les MS pour les étoiles socquettes (*p-value = 0,6347*), et les frosting (*p-value = 0,1228*).

Tableau 1. Fréquences des caractères qualitatifs liés à la robe, aux oreilles et aux poils chez les moutons Djallonké, les moutons de Vogan et les moutons sahéliens.

Caractères	Mouton Djallonké (MD)	Mouton de Vogan (MV)	Moutons sahéliens (MS)
Patron pigmentaire (%)			
Bicolore [a]	20,59	44,23	10
Illisible [b]	64,71	42,31	50
Uniforme [c]	11,76	10,58	10
Non pigmentaire [d]	2,94	1,92	30
Tacheté [e]	0	0,96	0
Type d'eumélanine (%)			
Roux	40,2	56,73	0
Chocolat	10,78	14,42	10
Noir	40,2	19,23	3,33
Noir et roux	0,98	3,85	0
Blanc	5,88	2,88	86,67
Roux avec abdomen et pattes arrières blancs	1,96	2,88	0
Étoile socquette (%)			
Présence	90,1	76,92	69,57
Absence	9,9	23,08	30,43
Frosting (%)			
Présence	24,74	42,31	69,23
Absence	75,26	57,69	30,77
Structure de poils (%)			
Long et lisse	0	19,23	20
Court et lisse	16,67	79,81	80
Long et dur	7,84	0,96	0
Court et dur	75,49	0	0
Port de l'oreille (%)			
Dressé et court	86,27	0	0
Tombant et court	9,8	13,46	0
Tombant et long	3,92	86,54	100

[a] patron présentant deux zones bien distinctes de couleurs différentes; [b] non détermination des zones d'eumélanine et de phaeomélanine face aux extensions des zones blanches dans la robe; [c] patron présentant une seule couleur sur tout le corps de l'animal; [d] animal totalement de couleur blanche; [e] patron présentant des taches de couleurs différentes sur l'animal.

2.2.3 Structure des poils et port de l'oreille

Les poils des moutons de Vogan sont courts et lisses comme chez les moutons sahéliens contrairement aux moutons Djallonké qui possèdent des poils courts et durs. Les oreilles des moutons de Vogan et moutons sahéliens sont tombantes et longues (Figure 6) tandis que chez les moutons Djallonké les oreilles sont courtes et dressées. Tous ces résultats sont consignés dans le Tableau 1.

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[1] Illisible : lorsqu'il n'est pas possible de déterminer les zones d'eumélanine et de phaeomélanine face aux extensions des zones blanches dans la robe. Dans ce cas, la robe ne peut pas être déterminée à partir du patron pigmentaire.

Figure 5. Patron pigmentaire et type d'eumélanine avec étoile socquette chez les moutons de Vogan. (a) Etoile socquette sur le front. (b) Robe bicolore rousse.

2.2.4 Appréciation des cornes

La forme et la longueur des cornes sont variables selon le sexe. Les fréquences des femelles portant des cornes par race sont: 1,15% dans la race Djallonké, 9,59% chez les moutons de Vogan et 10% chez les brebis sahéliennes. Par contre, dans les trois races, tous les mâles portent des cornes. Par ailleurs, dans les trois races ovines, certaines femelles portent des vestiges de cornes semblables à de gros boutons dans les pourcentages de 16,44% chez les MV (12 femelles cornues sur 73 échantillons), 1,15% chez les MD (1 individu sur 87 échantillons) et 5% chez les MS (1 individu sur 20 échantillons). La fréquence du portage des cornes par sexe des races ovines est présentée dans le tableau 2.

Les formes des cornes varient également selon les races ovines (Tableau 2). Les MD portent tous les mêmes types de corne : forme «spiralée écartée vers l'extérieur puis en avant». Les MV présentent généralement le type «prismatique orientée vers l'extérieur» (Figure 7a) mais avec d'autres variantes de forme : forme «spiralée écartée vers l'extérieur puis en avant» pour les béliers (Figure 7b) et la forme «petite» pour les brebis (Figure 7c). Par contre, chez les MS, la forme générale des cornes est la forme «spiralée écartée vers l'extérieur puis en avant» avec diverses variantes chez les mâles que sont par ordre d'importance: la forme «spiralée orientée en avant mais souvent collée à la joue» (30% pour N = 10) et la forme «spiralée externe en avant et recourbée en arrière» (10% pour N = 10).

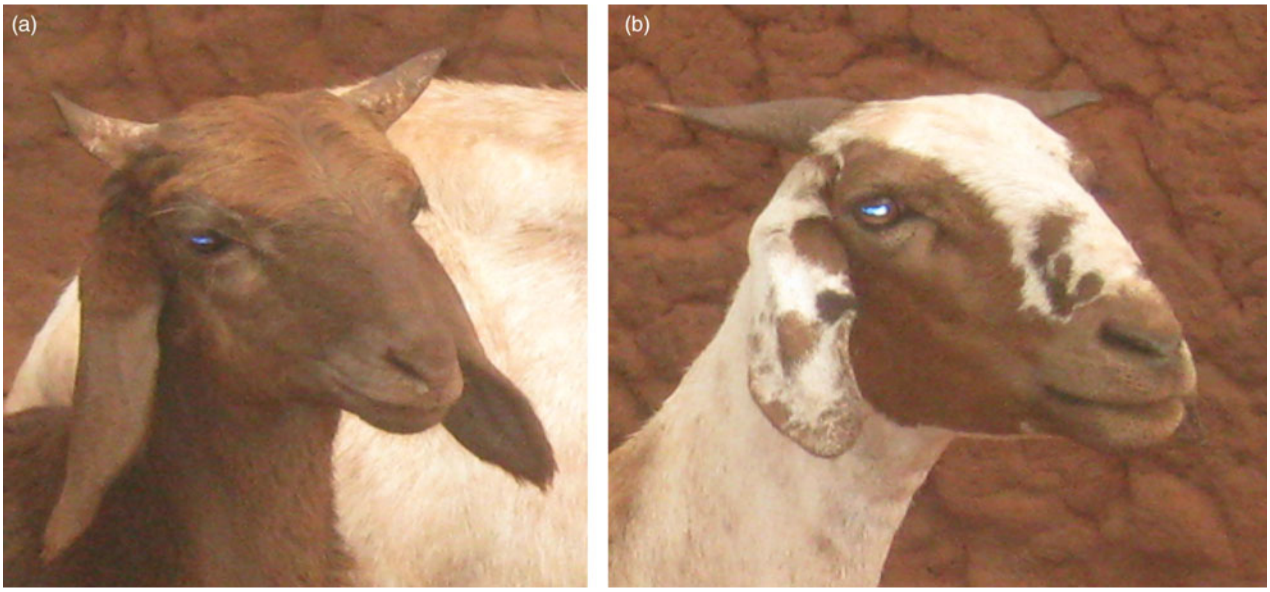

Figure 6. Port des oreilles des moutons de Vogan.6a. Oreille de type tombant long.6b. Oreille de type tombant court.

Tableau 2. Pourcentage des individus portant des cornes en fonction du sexe et de la forme de corne.

Caractères	Mouton Djallonké (MD)	Mouton de Vogan (MV)	Moutons sahéliens (MS)
Cornes (%)			
Femelles			
Absence	97,7	73,97	85
Vestige	1,15	16,44	5
Présence	1,15	9,59	10
Mâles			
Absence	0	0	0
Vestige	0	0	0
Présence	100	100	100
Formes de cornes (%)*			
M	0	0	30
H	100	13,79	60
H1	0	0	10
H2	0	3,45	0
G	0	82,76	0

*M: corne spiralée orientée en avant mais souvent collée à la joue; H: corne spiralée écartée vers l'extérieure puis en avant; H1: corne spiralée externe en avant et recourbée en arrière; H2: corne petite; G: corne prismatique orientée vers l'extérieur.

2.3 Données quantitatives

2.3.1 Caractères morphobiométriques par race ovine

Le tableau 3 décrit les moyennes ± écart-types et les valeurs extrêmes des caractères quantitatifs au niveau des races ovines étudiées.

Les caractères quantitatifs pour lesquels les moutons de Vogan présentent des valeurs moyennes significativement supérieures (t-test, *p-value <0,001*) à celles des MD sont : la hauteur au garrot (HG), la circonférence thoracique (CT), la profondeur du thorax (PT), le cordonnet chanfrein (CC), la longueur de la queue (LQ), la longueur des oreilles (LO) et la longueur du corps (LC). Par contre, ces performances moyennes des MV sont significativement inférieures (*p-value <0,01*) aux valeurs des MS. Aucune différence significative n'a été trouvée entre l'arc chanfrein des MV et celui des MS (*p-value = 0,65*) tandis que l'arc chanfrein (AC) des MV est significativement supérieur à celui des MD (*p-value <0,001)*. En ce qui concerne l'espace intercorne (EIC), aucune différence significative n'a été observée entre les MV et les MD (*p-value = 0,21*) tandis que la valeur de cet espace chez les MV est significativement inférieure à celle des MS (*p-value =*

Figure 7. Formes de cornes des moutons de Vogan. (a) Cornes prismatiques orientées vers l'extérieur (Forme G). (b) Cornes spiralées écartées vers l'extérieur puis en avant (Forme H). (c) Cornes petites (Forme H2).

Tableau 3. Caractères morphobiométriques par race ovine.

Caractères (cm)	Paramètres calculés	Mouton Djallonké	Mouton de Vogan	Moutons sahéliens
Hauteur au garrot (HG)	Extrêmes	38 – 78	57 – 83	61 – 87
	Moyenne ± Et	54,63^{3} ± 8,23	71,65^{2} ± 5,79	75,43^{1} ± 5,43
Circonférence thoracique (CT)	Extrêmes	59 – 102	72 – 109	77 – 111
	Moyenne ± Et	74,72^{3} ± 8,28	89,30^{2} ± 9,25	94,57^{1} ± 8,82
Longueur de corne (Lc)	Extrêmes	8 – 30	8 – 31	3 – 43
	Moyenne ± Et	17,00 ± 7,44	19,29 ± 6,04	26 ± 11,84
Espace intercornes (EIC)	Extrêmes	2 – 7	2 – 7	3 – 8
	Moyenne ± Et	3,94^{2} ± 1,48	4,50^{2} ± 1,39	5,67^{1} ± 1,61
Longueur d'oreille (LO)	Extrêmes	8 – 20	12 – 22	17 – 26
	Moyenne ± Et	11,61^{3} ± 2,61	18,45^{2} ± 2,08	21,63^{1} ± 2,48
Longueur de queue (LQ)	Extrêmes	15 – 52	26 – 55	37 – 57
	Moyenne ± Et	27,47^{3} ± 8,05	45,24^{2} ± 6,23	48,20^{1} ± 5,37
Arc chanfrein (AC)	Extrêmes	11 – 19	15 – 22	15 – 20
	Moyenne ± Et	14,67^{2} ± 1,57	17,44^{1} ± 1,55	17,56^{1} ± 1,22
Cordonnet chanfrein (CC)	Extrêmes	13 – 23	17 – 25	19 – 27
	Moyenne ± Et	16,44^{3} ± 1,87	20,74^{2} ± 1,87	22,90^{1} ± 2,07
Profondeur thoracique (PT)	Extrêmes	20 – 35	24 – 39	28 – 38
	Moyenne ± Et	25,24^{3} ± 3,25	31,50^{2} ± 3,09	33,17^{1} ± 2,74
Longueur du corps (LC)	Extrêmes	47 – 80	57 – 84	63 – 88
	Moyenne ± Et	58,47^{3} ± 6,30	71,02^{2} ± 6,03	74,83^{1} ± 5,55

^{1,2,3} sur la même ligne pour chaque paramètre, les valeurs affectées de même chiffre ne sont pas statistiquement différentes (p-value supérieure à 0,05; Et = Écart-type).

0,04). La race semble ne pas avoir d'effet sur la longueur de la corne (Lc) car aucune différence significative n'a été observée entre les MV et les MD (*p-value* = 0,29) et entre les MV et les MS (*p-value* = 0,08).

2.3.2 Influence du sexe sur les caractères morphobiométriques

Le facteur « sexe » a un effet significatif sur certains caractères quantitatifs (Lc, LC, CT) des races ovines comme le montre le tableau 4. Nos résultats montrent qu'il existe un dimorphisme sexuel chez les MD et les MS seulement pour la longueur de la corne tandis que chez les MV le dimorphisme sexuel a été observé aussi bien pour la longueur de la corne que pour la longueur du corps et la circonférence thoracique.

2.3.3 Influence de l'âge sur les caractères morphobiométriques

Les valeurs moyennes ± écart-types et les valeurs minimales et maximales des caractères quantitatifs des races ovines par rapport à l'âge ainsi que les résultats des

Tableau 4. Effet du sexe sur certains caractères morphobiométriques par race ovine.

Caractères	Race ovine	Echantillon		Moyenne ± Ecart-type		Significativité
		Femelle	Mâle	Femelle	Mâle	p-value
Hauteur au garrot: HG (cm)	Mouton Djallonké	87	15	54,32 ± 8,33	56,4 ± 7,65	0,3491
	Mouton de Vogan	73	31	71,59 ± 5,20	71,81 ± 7,07	0,878
	Moutons sahéliens	20	10	74,3 ± 4,87	77,7 ± 6,04	0,1426
Longueur de corne: Lc (cm)	Mouton Djallonké	87	15	10 *	17,47 ± 7,45	0,02691**
	Mouton de Vogan	73	31	9,86 ± 1,86	21,42 ± 4,34	<0,0001**
	Moutons sahéliens	20	10	4,5 ± 2,12	30,3 ± 6,9	<0,0001**
Longueur du corps: LC (cm)	Mouton Djallonké	87	15	58,45 ± 6,26	58,6 ± 6,75	0,9361
	Mouton de Vogan	73	31	72,12 ± 5,54	68,42 ± 6,45	0,007435**
	Moutons sahéliens	20	10	74,75 ± 5,14	75 ± 6,62	0,918
Circonférence thoracique: CT (cm)	Mouton Djallonké	87	15	74,89 ± 8,06	73,73 ± 9,68	0,6686
	Mouton de Vogan	73	31	91,06 ± 9,16	85,24 ± 8,24	0,003251**
	Moutons sahéliens	20	10	94,65 ± 8,70	94,4 ± 9,54	0,9453
Profondeur du thorax: PT (cm)	Mouton Djallonké	87	15	25,3 ± 3,13	24,93 ± 3,99	0,74
	Mouton de Vogan	73	31	31,82 ± 2,96	30,74 ± 3,32	0,1233
	Moutons sahéliens	20	10	33,05 ± 2,54	33,4 ± 3,24	0,7693

*Un seul individu; Et = Ecart-type. **Significativité au seuil de 5% au test de Student.

Tableau 5. Caractères morphobiométriques des races ovines par rapport à l'âge.

			Age					
Caractères (cm)			**<1 an**	**1 an**	**2 ans**	**3 ans**	**4 ans**	**5 ans**
Arc chanfrein (AC)	**MD****	Extrêmes	11 – 15	11 – 16	13 – 19	13 – 17	12 – 18	13*
		Moyenne ± Et	13,4 ± 1,24	14,24 ± 1,25	15,14 ± 1,88	14,62 ± 1,04	15,19 ± 1,58	13*
	MV**	Extrêmes	15 – 20	15 – 19	16 – 20	17 – 22	15 – 21	18 – 19
		Moyenne ± Et	16,17 ± 1,24	16,8 ± 1,2	17,64 ± 1,21	18,8 ± 1,32	18,03 ± 1,38	18,33 ± 0,58
	MS**	Extrêmes	15 – 17	16 – 17	18 – 19	17 – 18	17 – 20	17 – 19
		Moyenne ± Et	16 ± 1	16,33 ± 0,52	18,5 ± 0,71	17,5 ± 0,71	18,18 ± 0,98	18,17 ± 0,98
Cordonnet chanfrein (CC)	**MD****	Extrêmes	13 – 19	13 – 19	14 – 23	14 – 19	13 – 20	14*
		Moyenne ± Et	15,4 ± 1,92	16,06 ± 1,48	17,29 ± 2,52	16,15 ± 1,46	16,83 ± 1,7	14*
	MV**	Extrêmes	17 – 23	18 – 23	20 – 22	19 – 24	17 – 25	21 – 23
		Moyenne ± Et	19,75 ± 1,98	20,05 ± 1,73	21,27 ± 0,79	21,67 ± 1,35	21,19 ± 2,01	22 ± 1
	MS	Extrêmes	19 – 24	19 – 26	23 – 27	22 – 24	21 – 27	22 – 24
		Moyenne ± Et	21,33 ± 2,52	22,67 ± 2,8	25 ± 2,83	23 ± 1,41	23,09 ± 2,07	22,83 ± 0,75
Longueur de l'oreille (LO)	**MD**	Extrêmes	8 – 17	8 – 18	9 – 18	8 – 15	8 – 20	9*
		Moyenne ± Et	11,87 ± 2,72	11,71 ± 2,42	12,36 ± 3,25	10,62 ± 2,18	11,6 ± 2,56	9*
	MV	Extrêmes	14 – 21	15 – 21	19 – 21	16 – 21	12 – 22	19
		Moyenne ± Et	17,96 ± 2,33	18,15 ± 1,9	19,64 ± 067	18,2 ± 1,7	18,58 ± 2,42	20 ± 1
	MS	Extrêmes	19 – 21	18 – 26	17 – 26	23 – 24	17 – 25	17 – 23
		Moyenne ± Et	20,33 ± 1,15	22,17 ± 2,86	21,5 ± 6,36	23,5 ± 0,71	21,55 ± 2,34	21,33 ± 2,25
Longueur de la queue (LQ)	**MD**	Extrêmes	19 – 50	17 – 35	15 – 52	15 – 33	16 – 44	19*
		Moyenne ± Et	31,07 ± 9,4	26,76 ± 5,64	28,29 ± 11,17	23,77 ± 5,72	27,55 ± 7,54	19*
	MV**	Extrêmes	33 – 53	29 – 52	42 – 53	34 – 53	26 – 55	37 – 55
		Moyenne ± Et	45,17 ± 5,73	42 ± 7,28	48 ± 3,69	47,4 ± 5,88	45,16 ± 5,96	47,33 ± 9,29
	MS	Extrêmes	45 – 54	38 – 53	53 – 57	48 – 50	38 – 56	37 – 55
		Moyenne ± Et	49,33 ± 4,51	47 ± 5,62	55 ± 2,83	49 ± 1,41	48,36 ± 5,24	46 ± 6,6
Hauteur au garrot (HG)	**MD**	Extrêmes	45 – 67	40 – 69	44 – 78	43 – 62	38 – 73	45*
		Moyenne ± Et	54,47 ± 7,96	55 ± 6,77	55,93 ± 10,34	51,15 ± 5,26	55,40 ± 8,83	45*
	MV	Extrêmes	61 – 83	63 – 78	65 – 77	64 – 81	57 – 82	69 – 76
		Moyenne ± Et	71,38 ± 7,38	70,1 ± 4,81	71,82 ± 3,46	72,93 ± 4,45	72,03 ± 6,44	73,33 ± 3,79
	MS**	Extrêmes	61 – 73	68 – 81	78 – 85	72 – 76	68 – 87	72 – 82
		Moyenne ± Et	67,33 ± 6,03	75 ± 4,56	81,5 ± 4,95	74 ± 2,83	77,18 ± 5,08	75,17 ± 3,97
Longueur du corps (LC)	**MD****	Extrêmes	47 – 64	48 – 67	51 – 80	51 – 68	48 – 75	50*
		Moyenne ± Et	54,73 ± 4,88	57,24 ± 5,24	59,57 ± 8,18	57,38 ± 5,74	60,48 ± 5,96	50*
	MV**	Extrêmes	57 – 80	58 – 77	66 – 79	65 – 80	61 – 84	69 – 84
		Moyenne ± Et	67,92 ± 6,33	68,75 ± 5,14	72,18 ± 4,09	73,13 ± 4	72,94 ± 6,35	76,33 ± 7,51
	MS**	Extrêmes	63 – 71	66 – 75	83 – 83	74 – 74	72 – 88	72 – 77
		Moyenne ± Et	67,33 ± 4,04	71 ± 3,58	83 ± 0	74 ± 0	77,27 ± 5,64	75,5 ± 2,07
Profondeur du thorax (PT)	**MD****	Extrêmes	20 – 30	21 – 30	20 – 35	22 – 29	22 – 34	23*
		Moyenne ± Et	23 ± 3,18	24,35 ± 2,35	25,79 ± 4,1	24,85 ± 2,03	26,40 ± 3,14	23*
	MV**	Extrêmes	25 – 38	27 – 36	27 – 34	28 – 37	24 – 39	32 – 36
		Moyenne ± Et	30,13 ± 3,21	30,65 ± 2,58	31,73 ± 2,2	32,47 ± 2,97	32,32 ± 3,32	34 ± 2
	MS**	Extrêmes	28 – 33	30 – 34	34 – 38	32 – 34	30 – 38	30 – 37
		Moyenne ± Et	30 ± 2,65	31,5 ± 1,76	36 ± 2,83	33 ± 1,41	34,18 ± 2,64	33,67 ± 2,58
Circonférence du thorax (CT)	**MD****	Extrêmes	60 – 85	59 – 84	66 – 102	66 – 86	63 – 98	70*
		Moyenne ± Et	69,33 ± 7,16	72,12 ± 6,84	77,5 ± 9,98	73,38 ± 6,79	77,29 ± 8	70*

Continued

Tableau 5. Continued

Caractères (cm)			**Age**					
			<1 an	**1 an**	**2 ans**	**3 ans**	**4 ans**	**5 ans**
	MV**	Extrêmes	72 – 99	77 – 100	81 – 101	74 – 106	74 – 109	88 – 104
		Moyenne ± Et	83,14 ± 7,8	87 ± 7,71	89,89 ± 6,43	93 ± 9,78	92,26 ± 9,43	96,67 ± 8,08
	MS**	Extrêmes	77 – 92	84 – 92	103 – 106	95 – 98	89 – 110	86 – 111
		Moyenne ± Et	82,33 ± 8,39	88,17 ± 3,31	104,5 ± 2,12	96,5 ± 2,12	96,73 ± 7,88	99,17 ± 8,42
Longueur de corne (Lc)	**MD****	Extrêmes	8 – 25	24 – 24	0	27 – 30	10 – 27	0
		Moyenne ± Et	14 ± 5,14	24*	0	28,5 ± 2,12	18,5 ± 12,02	0
	MV**	Extrêmes	13 – 28	10 – 31	23 – 23	8 – 8	8 – 22	0
		Moyenne ± Et	20,73 ± 4,22	21,71 ± 7,16	23*	8 ± 0	14,33 ± 5,75	0
	MS	Extrêmes	22 – 22	27 – 30	33 – 33	31 – 31	3 – 43	6 – 6
		Moyenne ± Et	22 ± 0	28 ± 1,41	33*	31*	28,67 ± 22,28	6 ± 0
Espace intercornes (EIC)	**MD**	Extrêmes	3 – 7	2 – 2	0	2 – 3	3 – 6	0
		Moyenne ± Et	4,27 ± 1,35	2*	0	2,5 ± 0,71	4,5 ± 2,12	0
	MV**	Extrêmes	2 – 7	2 – 7	3*	6 – 6	4 – 7	0
		Moyenne ± Et	4,36 ± 1,18	3,71 ± 1,7	3*	6 ± 0	5,67 ± 1,03	0
	MS	Extrêmes	4 – 7	5 – 7	5*	5 – 5	3 – 8	8 – 10
		Moyenne ± Et	5,5 ± 2,12	6 ± 0,82	5*	5*	5 ± 2,65	9 ± 1,41

*Un seul individu dans la classe d'âge; Et = Ecart – type. **Le facteur « âge » a un effet significatif au seuil de 5% sur le caractère (ANOVA, *p – value <0,05*). MD: Mouton Djallonké; MV: Mouton de Vogan; MS: Moutons sahéliens.

comparaisons des différentes classes d'âges sont présentés dans le tableau 5.

2.3.4 Caractères morphobiométriques des moutons Djallonké par région

Le tableau 6 présente les moyennes ± écart-types, et les valeurs extrêmes des caractères morphobiométriques des MD dans la région Maritime (préfecture de Vô) et dans la région des Plateaux (préfecture de Kloto et préfecture d'Agou).

Les résultats montrent que les caractères morphobiométriques des MD de la région Maritime sont significativement supérieurs à ceux des MD de la région des Plateaux (*p-value <0,05*) sauf pour la longueur de la corne (*p-value = 0,34*).

2.3.5 Influence du canton sur les caractères morphobiométriques des moutons de Vogan

Le tableau 7 présente les moyennes ± écart-types et les valeurs extrêmes des caractères morphobiométriques des MV en fonction des cantons.

Le facteur «Canton» a un effet significatif sur tous les caractères morphobiométriques des MV présentés dans le tableau 7 (ANOVA, *p-value <0,05*). Deux types génétiques de MV avec des performances zootechniques significativement différentes (Test de Student, *p-value <0,05*) ressortent de cette analyse : un type de petit format dans les cantons de Koutimé et de Vogan et un autre de grand format dans les cantons de Togoville, Sévagan et Wogba-Vogan.

Les résultats de l'ACP présentent également cette tendance (Figure 8). En effet, à K = 3, les trois races se séparent avec les MV dans une position intermédiaire entre les MS et les MD mais avec quelques individus de moutons de Vogan dans le même groupe que les moutons sahéliens. A K = 5, la population de moutons de Vogan se divise en 2 sous-populations. A K = 6, quelques moutons sahéliens se séparent des moutons de Vogan. Les moutons Djallonké de la région Maritime ne s'isolent de ceux des Plateaux qu'à K = 8.

2.3.6 Assignation des moutons de Vogan selon les variables quantitatives

Les résultats de l'analyse principale des correspondances (à K = 3) ont assigné les moutons de Vogan à 45% comme un groupe à part (moutons de Vogan), à 54% comme les moutons sahéliens et à 1% dans le groupe des moutons Djallonké. La majorité des individus classés dans le groupe des moutons sahéliens proviennent des cantons de Wogba-Vogan, Togoville et Sévagan et seulement quelques uns du canton de Koutimé.

Tableau 6. Caractères morphobiométriques des moutons Djallonké dans la région Maritime et dans la région des Plateaux.

Caractères (cm)	Paramètres	Région Maritime	Région des Plateaux	Significativité (p – value)
Nombre d'animaux		50	52	
Hauteur au garrot	Extrêmes	46 – 78	38 – 62	
	Moyenne ± Et	60,42^1 ± 7,1	49,06^2 ± 4,61	4,95E – 15**
Arc chanfrein	Extrêmes	13 – 19	11 – 17	
	Moyenne ± Et	15,56^1 ± 1,46	13,81^2 ± 1,17	1,75E – 9**
Profondeur du thorax	Extrêmes	20 – 35	20 – 32	
	Moyenne ± Et	26,86^1 ± 3,34	23,69^2 ± 2,27	2,81E – 7**
Cordonnet chanfrein	Extrêmes	14 – 23	13 – 18	
	Moyenne ± Et	17,54^1 ± 1,81	15,38^2 ± 1,22	4,91E – 10**
Longueur de l'oreille	Extrêmes	9 – 20	8 – 15	
	Moyenne ± Et	13,5^1 ± 2,31	9,79^2 ± 1,22	1,48E – 15**
Longueur de la queue	Extrêmes	20 – 52	15 – 31	
	Moyenne ± Et	33,2^1 ± 7,05	21,96^2 ± 4,2	3,45E – 15**
Longueur du corps	Extrêmes	50 – 80	47 – 69	
	Moyenne ± Et	61,84^1 ± 6,16	55,23^2 ± 4,5	1,95E – 8**
Longueur de la corne	Extrêmes	8 – 25	12 – 30	
	Moyenne ± Et	15,33 ± 6,65	19,14 ± 8,36	0,3442
Espace inter corne	Extrêmes	2 – 7	2 – 5	
	Moyenne ± Et	4,56^1 ± 1,59	3,14^2 ± 0,9	0,04291**
Circonférence du thorax	Extrêmes	62 – 102	59 – 86	
	Moyenne ± Et	78,64^1 ± 8,48	70,94^2 ± 6,08	1,03E – 6**

^{1,2}Indication d'ordre au test de Student pour $p < 0,05$; Et = Ecart – type. **Significatif au test de Student.

2.3.7 Corrélation entre les variables quantitatives et qualitatives

Le cercle de corrélation entre les variables quantitatives et les variables qualitatives (Figure 9) a regroupé i) les variables liées à la coloration de la robe (patron pigmentaire, robe, type eumélanine, étoile soquette), ii) les variables liées à la corne (présence ou absence, forme, longueur et espace intercornes), iii) la structure des poils, iv) la localité (canton) qui est corrélée à la plupart des variables quantitatives et v) le sexe de l'animal qui est négativement corrélé aux variables liées à la corne.

Notons qu'il existe une relation linéaire entre les variables quantitatives suivantes : longueur du corps, profondeur thoracique, hauteur au garrot, longueur des oreilles, longueur de la queue, l'arc chanfrein et la circonférence thoracique (Figure 10).

3 Discussion

3.1 Caractères qualitatifs

Les patrons pigmentaires dominants observés chez les MV sont le patron bicolore et le patron illisible tandis que le type d'eumélanine est dominé par la couleur rousse. La grande variabilité présentée pour le patron pigmentaire, le type d'eumélanine et la couleur de la robe des MV avaient également été rapportée Amegee (1983) sur les MV du Togo. Cette variabilité pour ces caractères chez des animaux métis avait également été rapportée chez les agneaux issus du croisement entre moutons Djallonké et sahéliens en Côte d'Ivoire (Yapi-Gnaore, 1994). Les couleurs de la robe identifiées chez les MD dans notre zone d'étude (illisible roux ou noir) font partie de celles recensées par Hadzi (1996) au Togo et par Sangaré (2005) en Afrique de l'ouest de façon générale. Ces auteurs avaient en effet rapporté que la robe pie (noir ou roux) était majoritaire chez les MD. Par contre, les couleurs de la robe observées chez les MS (illisible) sont différentes de celles rapportées par Sangaré (2005) sur les moutons Peuls en Afrique de l'ouest (généralement bicolores) et cette différence peut se justifier par le type sahélien des individus échantillonnés et la taille de l'échantillon. En effet, dans le groupe des moutons sahéliens, il existe plusieurs races (ou type populationnel) avec des caractéristiques singulières (http://dad.fao.org).

La robe classique du mouton Bali-Bali est le blanc ou pie noir (http://dad.fao.org). Il apparaît ici que la couleur rousse des MV serait d'origine Djallonké tandis que la couleur noire d'origine sahélienne et les deux couleurs favoriseraient l'apparition de la robe brune (ou chocolat).

Les caractères qualitatifs qui rapprochent les moutons de Vogan des moutons sahéliens sont le port et la longueur des oreilles (longues et tombantes), la structure des poils (courts et lisses), les frosting (présents dans les proportions respectives de 42,31% et 69,23%) et les étoiles socquettes (présentes dans les proportions respectives 76,92% et 69,57%). Ces caractères chez les MV proviendraient des gènes hérités des moutons sahéliens car Sangaré (2005) a rapporté des résultats similaires en ce qui concerne le port des oreilles et la structure des poils sur les moutons Peuls en Afrique de l'ouest.

Le dimorphisme sexuel est bien marqué chez les MV pour le caractère « présence de la corne », car ce caractère est lié au sexe chez les ovins contrairement aux caprins chez

Tableau 7. Caractères morphobiométriques des moutons de Vogan par canton.

		Cantons					Significativité	
Caractères (cm)	**Paramètres**	**Koutime**	**Vogan**	**Togoville**	**Sévagan**	**Wogba – Vogan**	**Test ANOVA**	**Test de Student**
Profondeur du thorax	Extrêmes	27 – 34	25 – 32	24 – 38	26 – 39	32 – 36		
	Moyenne ± Et	29,69 ± 2,46	28,92 ± 2,19	31,69 ± 3,02	32,65 ± 3,31	33,7 ± 1,42	0,000158**	7,03E – 06**
cordonnet chanfrein	Extrêmes	17 – 22	17 – 22	17 – 25	18 – 24	21 – 24	–	–
	Moyenne ± Et	19,46 ± 1,61	19,42 ± 1,51	20,86 ± 1,80	21,2 ± 1,79	22,5 ± 1,08	6,92E – 05**	2,55 E-05**
Arc chanfrein	Extrêmes	15 – 19	15 – 18	15 – 22	15 – 20	16 – 21	–	–
	Moyenne ± Et	16,69 ± 1,32	16,08 ± 01	17,8 ± 1,54	17,5 ± 1,43	18,2 ± 1,55	0,00108**	2,09 E-05**
Longueur queue	Extrêmes	29 – 47	33 – 51	26 – 54	32 – 52	46 – 55	–	–
	Moyenne ± Et	39,69 ± 6,22	43,42 ± 5,53	46,45 ± 5,64	44,35 ± 6,38	50,5 ± 3,21	0,000163**	0,000933**
Longueur oreille	Extrêmes	15 – 22	12 – 21	12 – 22	14 – 21	19 – 21	–	–
	Moyenne ± Et	17,54 ± 2,22	17,25 ± 2,86	18,71 ± 1,94	18,45 ± 1,79	19,8 ± 0,92	0.0191**	0,01527**
Hauteur au garrot	Extrêmes	61 – 78	63 – 80	57 – 82	59 – 83	73 – 83	–	–
	Moyenne ± Et	67,38 ± 5,58	70,5 ± 0	71,92 ± 5,18	71,5 ± 6,11	77,6 ± 3,24	0,000635**	0,008454**
Longueur du corps	Extrêmes	57 – 78	59 – 75	63 – 82	61 – 84	73 – 84	–	–
	Moyenne ± Et	66,38 ± 6,34	66,17 ± 4,84	71,82 ± 5,01	72,05 ± 6,29	76,9 ± 3,28	6,06E – 06**	1,55E – 05**
Circonférence thoracique	Extrêmes	72 – 95	72 – 89	74 – 108	76 – 106	88 – 109	–	–
	Moyenne ± Et	83,62 ± 6,41	80,92 ± 5,78	90,85 ± 9,16	90,9 ± 8,61	97,2 ± 7,16	2,42 E-05**	2,29E – 07**
Longueur de corne	Extrêmes	16 – 21	17 – 24	8 – 27	17 – 31	8 – 24	–	–
	Moyenne ± Et	18,25 ± 2,63	20,1 ± 2,81	15,82 ± 7,26	24,86 ± 4,81	18,5 ± 6,75	0,0304**	0,7919
Espace intercornes	Extrêmes	3 – 5	2 – 7	3 – 7	2 – 5	4 – 6	–	–
	Moyenne ± Et	4 ± 0,82	4,5 ± 1,51	5,27 ± 1,35	3,29 ± 1,11	4,83 ± 0,98	0,0371**	0,6287

Et = Ecart – type. **Significatif au test.

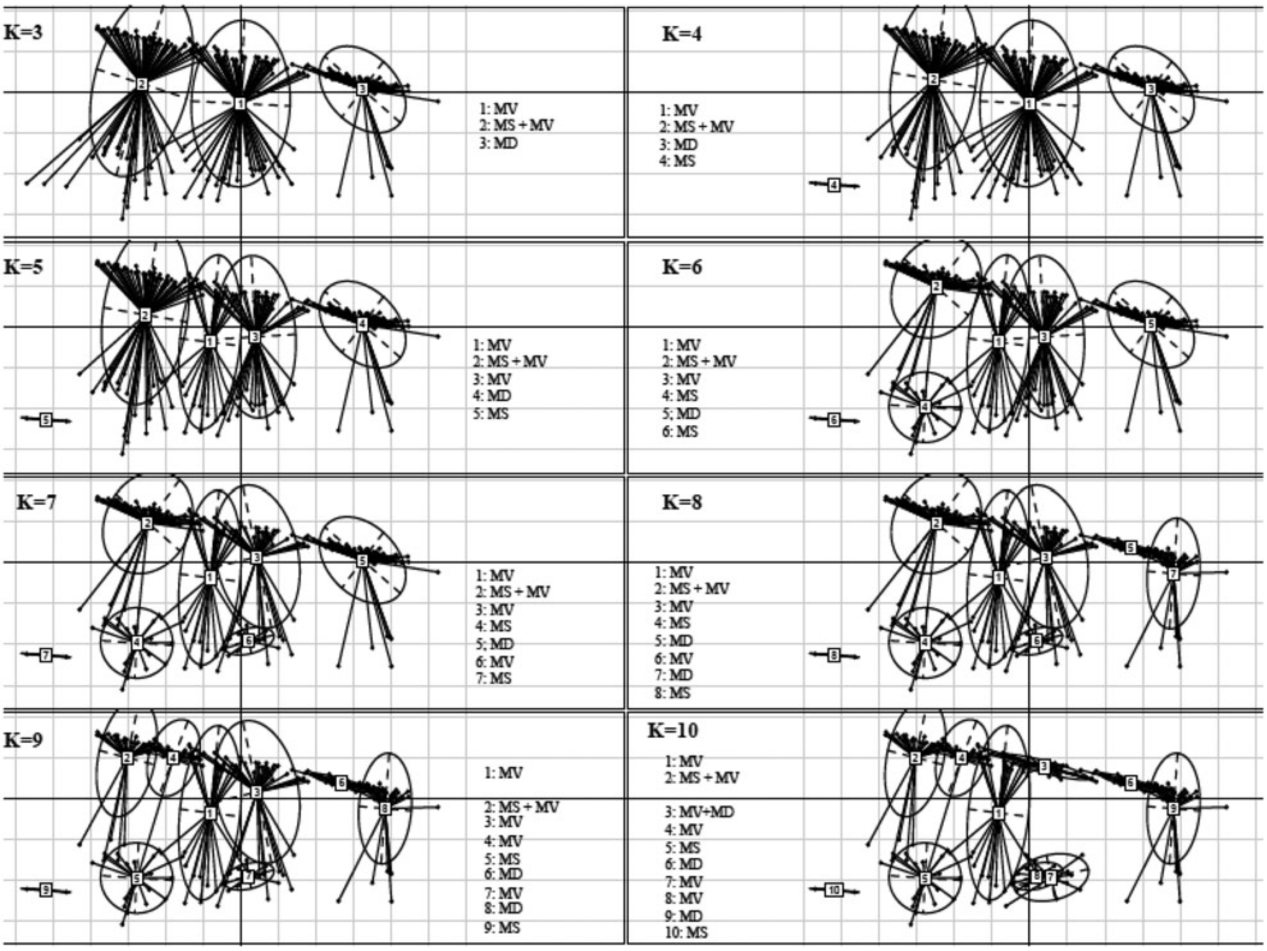

Figure 8. Analyses en composantes principales.

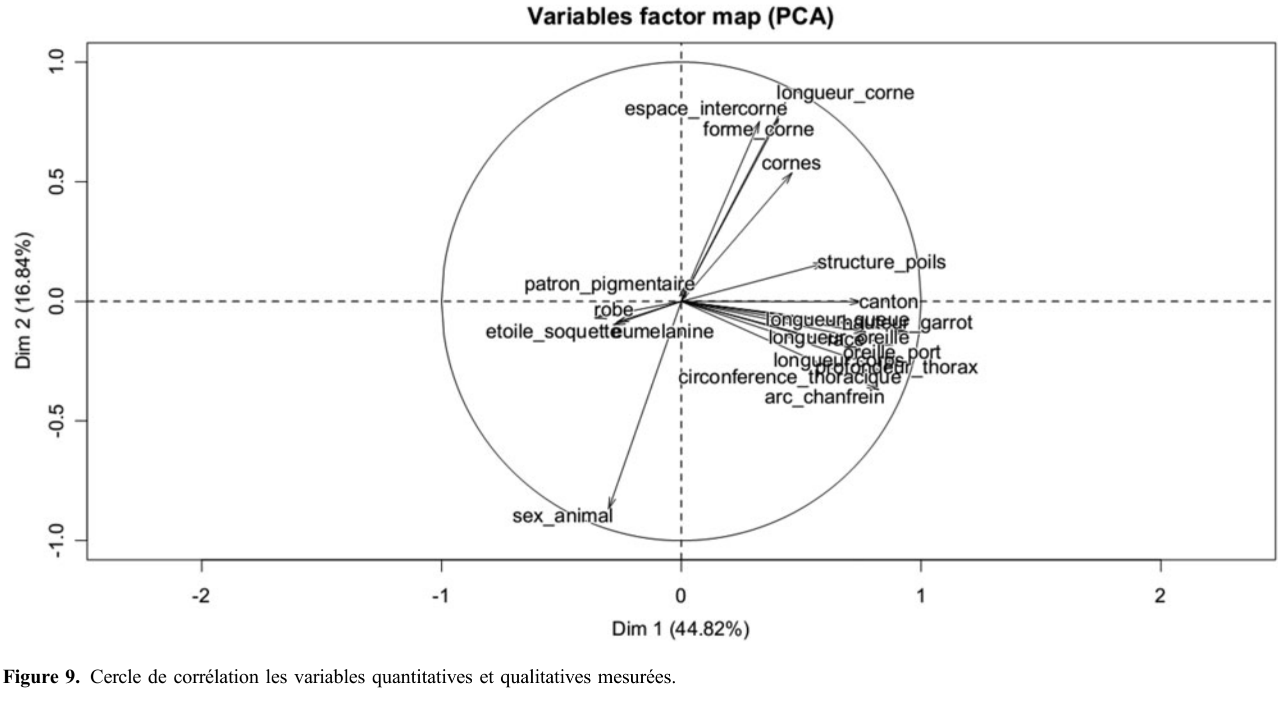

Figure 9. Cercle de corrélation les variables quantitatives et qualitatives mesurées.

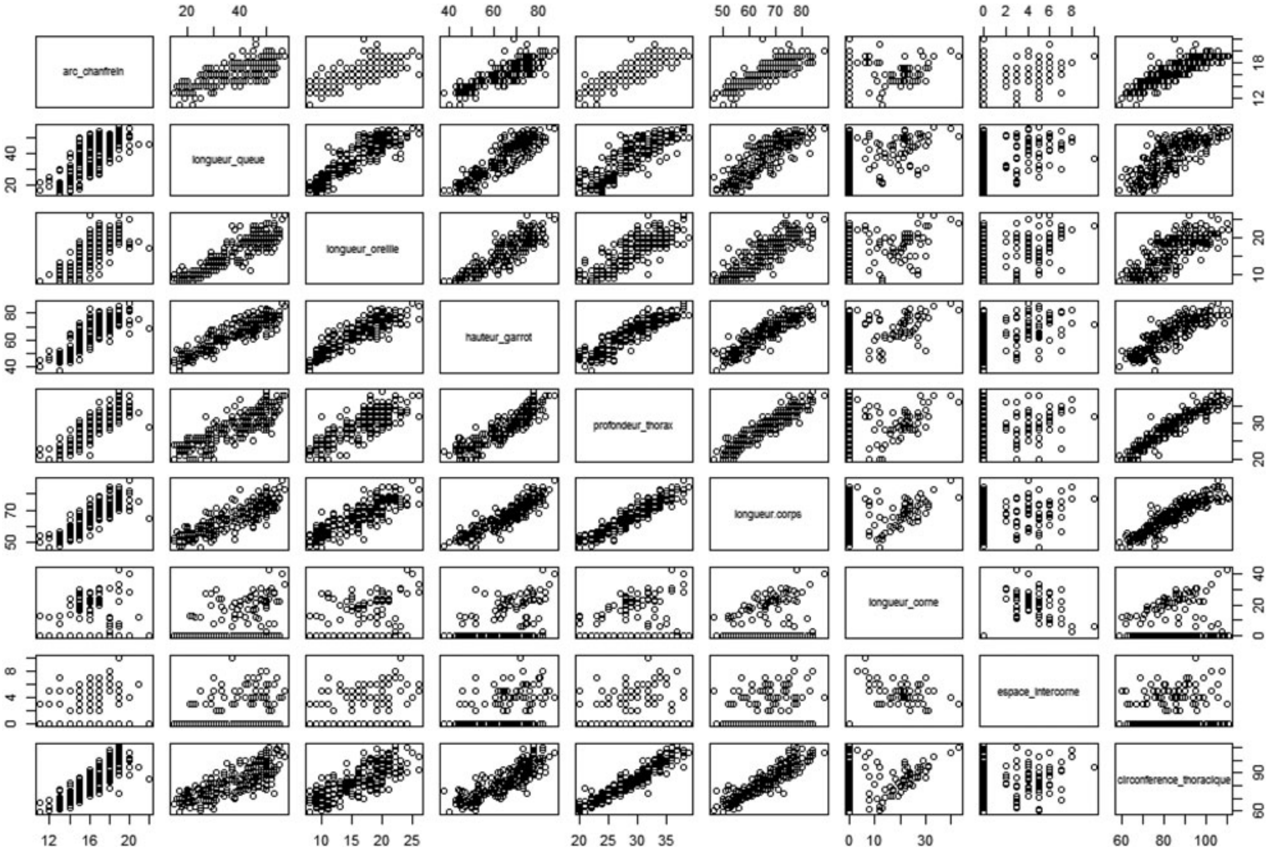

Figure 10. Corrélation entre paire de variables.

lesquels les deux sexes (chèvre et bouc) sont pourvus de cornes (Traoré *et al.*, 2006). Dans la présente étude, tous les béliers des trois races ovines étudiées sont pourvus d'une paire de cornes frontales tandis qu'une faible proportion de brebis en sont pourvues (1,15% chez les brebis Djallonké, 9,59% chez les brebis de Vogan et 10% chez les brebis sahéliennes). Lorsque les cornes existent chez les brebis, elles sont moins développées que celles des béliers. Amegee (1983) avait trouvé un pourcentage relativement supérieur (soit 5,58%) chez les brebis Vogan portant la corne. Cet écart pourrait être expliqué par le fait que cet auteur n'avait pas distingué les vestiges de cornes des vraies cornes comme nous l'avons fait dans la présente étude (16,44% des brebis avec des vestiges de corne).

Contrairement à ce qui avait été rapporté par Amegee (1983), dans notre étude, aucun mouton de Vogan ne portait d'appendices (ni pampilles ni pendeloques). Ce caractère qui est prédominant dans les populations ovines sahéliennes tend à disparaître chez les moutons de Vogan du Togo probablement dû au fait que, i) il n'y a plus de moutons sahéliens purs dans la zone d'étude ; ii) les croisements se font actuellement entre moutons de Vogan ou avec les moutons Djallonké ; iii) le climat du sud-est du Togo ne favoriserait pas l'expression de ces caractères. Ce qui rend encore plus singulière la race de Vogan comparativement aux moutons sahéliens.

3.2 Caractères quantitatifs

Les valeurs des caractères quantitatifs (HG, CT, PT, CC, LQ, LO, LC) des MV sont supérieures à celles des MD mais inférieures à celles des MS ce qui donne aux MV une position de race « hybride » entre les MD et les MS. Le dimorphisme sexuel n'a pas été observé dans la présente étude pour la HG, la CT et le PT contrairement aux travaux de Amegee (1983), probablement dû au fait qu'il y a eu plus de femelles que de mâles dans notre étude.

L'analyse des caractères quantitatifs laissent envisager pour la première fois qu'il y aurait deux types génétiques chez les MV dans la zone étudiée: les MV des cantons de Koutimé et Vogan (animaux de petit format) et les MV des cantons de Sévagan, Togoville et de Wogba-Vogan (animaux de grand format). La présence de ces deux types génétiques pourrait s'expliquer par les facteurs agro-écologiques mais aussi par l'ancienneté du début de l'élevage des moutons de Vogan dans les différentes localités. L'existence d'écotypes est bien connue chez les poules locales (Youssao *et al.*, 2010) et chez certaines races caprines (Fantahun *et al.*, 2013) mais pas encore observée chez les moutons de Vogan. Selon les déclarations de certains éleveurs du MV inclus dans la présente étude, le canton de Wogba-Vogan, serait l'origine et le point d'achat des MV actuellement répandus dans la préfecture de Vô. Les analyses de structuration génétique et de mesure du niveau d'introgression avec les marqueurs moléculaires (ADN) permettront de vérifier cette hypothèse (travaux en cours). Si cette hypothèse se vérifie, la constitution d'un noyau pourrait être envisagée à partir des animaux de ce canton.

La cohabitation des moutons Djallonké avec les MV dans cette zone a fortement influencé certains de leurs caractères morphobiométriques (HG, PT, CT, LC) par rapport aux moutons Djallonké de la région des Plateaux (préfectures de Kloto et d'Agou) où la seule race ovine est la race Djallonké. Ce résultat intéressant pourrait être exploité dans d'éventuels programmes d'embouche ovine utilisant des moutons issus de croisements entre MD et MV.

Les valeurs obtenues pour la hauteur au garrot (54,63 ± 8,23cm pour les MD et 75,43 ± 5,43cm pour les MS) sont semblables à celles présentées par Sangaré (2005) sur les MS (65-90cm) et les MD (40-60cm) d'une façon générale en Afrique de l'ouest. Cependant, ces valeurs sont supérieures à celles rapportées par Hadzi (1996) sur les MD au Togo (40-50cm). Ceci pourrait s'expliquer par i) les fortes valeurs obtenues chez les MD de la préfecture de Vogan ; ii) la cohabitation des MD de la préfecture de Vô avec les MV qui entrainerait des croisements entre ces 2 races ovines. Les valeurs de ce caractère chez les MD de la région des Plateaux sont similaires à celles rapportées par Hadzi (1996). Ces résultats montrent qu'il existe une possibilité de mieux valoriser les moutons de Vogan à travers i) leur diffusion dans d'autres régions du Togo, ii) leur utilisation dans les programmes d'amélioration génétique des ovins du pays, iii) la promotion de l'embouche ovine utilisant des produits de croisement entre MD et MV car ces produits présenteraient des caractères morphobiométriques meilleurs que ceux des MD. Toutes ces stratégies de valorisation ne pourront être évaluées que si la race est bien caractérisée.

L'une des limites à cette étude a été l'absence de la variable «Poids» dans les caractères quantitatifs. Néanmoins, selon les éleveurs et les observations faites sur le terrain, le gabarit de ces animaux est très apprécié. Une étude intégrant l'estimation du poids vif et le rendement carcasse pour établir une formule barymétrique de la race, une analyse socio-économique de l'élevage de la race sont nécessaires pour un plaidoyer en faveur de la mise en place d'une politique de valorisation de cette race au niveau national, régional et international. Amegee (1983) avait estimé le poids des moutons de Vogan entre 45 kg pour les béliers et 40 kg pour les brebis.

Conclusions

Le mouton de Vogan (MV) demeure une ressource génétique animale unique au Togo qui présente des performances phénotypiques appréciées par les éleveurs malgré le fait que les animaux soient élevés selon un système d'élevage traditionnel. Pour plusieurs caractéristiques morphobiométriques mesurées ou observées, les MV se positionnent comme une race intermédiaire entre les moutons Djallonké et les moutons sahéliens. Une amélioration du système d'élevage associée à une meilleure gestion des troupeaux pourrait permettre d'augmenter les performances de cette race ovine qui est déjà très appréciée. Des stratégies adéquates pour l'amélioration et une diffusion de la race sont nécessaires en vue d'une exploitation durable de ce patrimoine qui est jusqu'à présent resté très localisé au sud-est du Togo.

Une caractérisation fine de la race utilisant les marqueurs moléculaires (microsatellites) sont nécessaires pour compléter les caractères phénotypiques décrits dans la présente étude.

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Déclaration d'intérêts

Absence d'intérêts pertinents. [Note to editor : I have left the declaration in but we have deleted it from previous articles.]

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Annexe 1: Catégories de présentation

Catégorie 1: Espèces d'animaux d'élevage:

Petits ruminants (ovins)

Catégorie 2: Domaine technique

Caractérisation phénotypique

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Patterns of indigenous female cattle morphometric traits variations in Uganda: Evidence for farmers' selection to enhance agro-ecological fitness

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Summary

Globally, rural cattle keeping communities actively select and breed indigenous cattle to satisfy their interests and enhance adaptation to local landscapes. This study investigated how traditional systems in Uganda have shaped the morphometric population structure of indigenous cattle breeds. Ten linear morphometric traits were interrogated amongst 801 female cattle, comprising 46 Nganda (*Bos indicus*), 368 Ankole (*B. taurus indicus*) and 387 East African shorthorn zebu (EASZ, *B. indicus*). The study cattle were obtained evenly at random from 209 herds in their agro-ecological zones (AEZs) where they have been nurtured by traditional cattle keeping communities throughout Uganda. Age, AEZs and breed significantly influenced the variation of linear morphometric traits exhibiting a gradient of low, intermediate and high dimensions among the EASZ, Nganda and Ankole cattle, respectively. Likewise, the linear morphometric trait (Mahalanobis squared distance) diversity was significantly different exhibiting a gradient of low, intermediate and high variation between Nganda and EASZ, Ankole and Nganda, and Ankole and EASZ cattle, respectively. These findings demonstrate the role of agro-ecological fitness in the evolution of indigenous cattle morphometric population structure in Uganda. The study outcomes further provide a motivation to search for genes associated with the diverse morphometric features.

Keywords: *adaptation, agro-ecological fitness, female indigenous cattle, linear morphometric trait variation, Uganda*

Résumé

Globalement, le bétail rurales en gardant les communautés sélectionner activement et élèvent du bétail autochtones à satisfaire leurs intérêts et améliorer l'adaptation aux paysages locaux. Cette étude a examiné comment les systèmes traditionnels en Ouganda ont façonné la structure de la population morphométrique des races bovines autochtones. Dix traits morphométriques linéaires ont été interrogés entre 801 bovins femelles, comprenant 46 Nganda (Bos indicus), 368 Ankole (B. taurus indicus) et 387 East African Shorthorn Zébu (EASZ, B. indicus. Les bovins de l'étude ont été obtenus uniformément au hasard à partir de 209 troupeaux dans leurs zones agro-écologiques (ZAE) où ils ont été nourris par l'élevage traditionnel de maintien de communautés à travers l'Ouganda. Âge, ZAE et élever significativement influencé la variation de traits morphométriques linéaires présentant un gradient de dimensions faibles, intermédiaires et élevés chez les EASZ, Nganda et Ankole bétail respectivement. De même, le caractère linéaire morphométrique (Mahalanobis distance au carré) la diversité est significativement différente présentant un gradient de faible, moyenne et forte variation entre Nganda et EASZ, Ankole et Nganda, Ankole et bétail EASZ respectivement. Ces résultats démontrent le rôle de remise en forme agro- écologique dans l'évolution de la structure de la population des bovins morphométrique indigène en Ouganda . Les résultats fournissent en outre une motivation à rechercher des gènes liés aux caractéristiques morphométriques diverses.

Mots-clés: *L'adaptation, Remise en forme agro-écologique, Bovins indigènes des femmes, La variation des caractéristiques morphométriques, Ouganda*

Resumen

En todos los países del Mundo, las comunidades rurales de ganaderos seleccionan activamente y crían el ganado bovino autóctono con el fin de satisfacer sus intereses y de mejorar la adaptación al entorno local. Este estudio pretendió determinar de qué manera los sistemas tradicionales han conformado, en Uganda, la estructura morfométrica de la población de razas bovinas autóctonas. Se midieron diez rasgos morfométricos lineales en 801 hembras de ganado bovino, entre las cuales 46 de raza Nganda (*Bos indicus*), 368 de raza Ankole (*B. taurus indicus*) y 387 de Cebú de Cuernos Cortos del Este de África (EASZ por sus siglas en inglés, *B. indicus*). Los animales del estudio fueron tomados, por toda Uganda, equitativamente y al azar, de 209 rebaños, en las zonas agroecológicas en las que habían sido criados por comunidades tradicionales de ganaderos. La edad, la zona agroecológica y la raza influyeron significativamente sobre la variación de los rasgos morfométricos lineales, mostrando un gradiente de bajo, intermedio y alto en las medidas para el ganado EASZ, Nganda y Ankole, respectivamente. Asimismo, la diversidad en los rasgos morfométricos lineales (distancia cuadrática de Mahalanobis) difirió significativamente, mostrando un gradiente de bajo, intermedio y alto para la variación entre

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Nganda y EASZ, entre Ankole y Nganda y entre Ankole y EASZ, respectivamente. Estos resultados demuestran el papel de la adaptación a la zona agroecológica en la evolución de la estructura morfométrica de la población de ganado bovino autóctono en Uganda. Lo hallado en este estudio anima a buscar los genes asociados con las diversas características morfométricas.

Palabras clave: *Palabras clave, adaptación, encaje en la zona agroecológica, hembras de ganado bovino autóctono, variación en los rasgos morfométricos lineales, Uganda*

Submitted 29 August 2014; accepted 5 December 2014

Introduction

The Ministry of Agriculture, Animal Industry and Fisheries (MAAIF), and the Uganda Bureau of Statistics (UBOS, 2009) reported the population of indigenous cattle to be 10.64 million, spread throughout the country's agro-ecological zones (AEZs). The key indigenous cattle breeds comprise the Ankole (*Bos taurus indicus*) and EASZ (*Bos indicus*), although several variations of these two occur, named in respect of their keepers such as the Nganda, Nyoro, Karamojong and Nkedi breeds (Balikowa, 2011). The Ankole are present in the western and southwestern (Ndumu *et al.*, 2008b; Kugonza *et al.*, 2011), while the EASZ cattle are established in the eastern, northeastern, northern and west Nile regions of Uganda (MAAIF/UBOS, 2009; Balikowa, 2011). Several regions in central Uganda exhibit composite breeds between the Ankole, EASZ and Friesians giving rise to various grades of cross-bred cattle such as the Nganda, Nkedi, Serere, Nsoga and Kyoga (Bett *et al.*, 2013). They provide livelihoods to 26.1 percent of all households in Uganda through delivery of several goods and amenities as described by Kugonza *et al.* (2011); Hanotte, Dessie and Kemp (2010); Food and Agricultural Organisation of the United Nations (FAO, 2009). In addition, they facilitate sustainable utilization of marginal resources where no other type of agricultural investment is possible (Anderson, 2003; FAO, 2007). This is because indigenous cattle have become tolerant to endemic infections and have the ability to live on poor quality feed resources (Scarpa *et al.*, 2003; Taberlet *et al.*, 2008; Rege *et al.*, 2011). In this report, adaptation is used to refer to anatomical, physiological or behavioural traits that contribute to an individual's ability to survive and reproduce ("fitness") in an environment which it has evolved (Lamy *et al.*, 2012).

Local farmers exploit indigenous cattle adaptive traits to selectively breed for agro-ecological fitness and socio-cultural identity (Ndumu *et al.*, 2008a; FAO, 2009). Consequently, selective breeding has resulted into the evolution of undefined diverse indigenous cattle morphometric population structures (Ndumu *et al.*, 2008a, 2008b). These morphometric variations signify diversity and constitute appropriate genetic resources for future generations (Hoffmann, 2010) which deserve adequate conservation efforts. Present national policies favour the utilization of industrial cattle breeds for higher productivity to meet the increasing population food demands (MAAIF, 2012; Galukande *et al.*, 2013). But exotic breeds have inadequate adaptive agro-ecological fitness compared with indigenous cattle (Scarpa *et al.*, 2003) and therefore require more resource inputs to thrive under the local tropical conditions. Present policies aiming at higher productivity put local cattle genotypes at risk of obliteration (Taberlet *et al.*, 2008; Wilson, 2009). Knowledge of morphometric variation is useful for making inferences about farmers' roles in the evolution of indigenous livestock morphological diversity, landscape fitness and adaptation (Mwacharo *et al.*, 2006; Kugonza *et al.*, 2011). For example, smaller and stout body frames have evolved to enhance long-distance trekking and survival on scarce, less nutritive feed resources (Loquang and Köhler-Rollefson, 2005; FAO, 2007; Nalule, 2010; Herrero *et al.*, 2012).

Studies of indigenous cattle morphometric diversity in the different AEZs constitute an initial step in conservation of genetic resources and can be a basis for genetic improvement programmes. Additionally, body morphometric traits and adaptive features are useful for identification of breed qualities relevant to livestock farming community utility needs. The current advocacy for sustainable agricultural systems favours well-evolved local breed types as future candidates for conservation and utilization. Modern technics have now enabled the association of such traits with the genotypes enhancing the application of genetic marker-assisted selection with conservation of adaptive traits (Zhang and Li, 2011). Presently, Uganda's indigenous cattle morphometric population structure is partly described. The main objectives of this study were: (1) to establish nationwide indigenous cattle morphometric structure associated with AEZs and farmers' selective breeding practices; (2) to provide support to upcoming improvement and conservation schemes; and (3) to provide basic information for genome wide association studies (GWAS).

Materials and methods

Study area

This study covered the whole of Uganda due to the widespread distribution of indigenous cattle. The study area has been described in Kabi *et al.* (2014). Briefly, Uganda's total area is 241 550.7 square kilometres (sq. km), with open waters and land occupying 41 743.2 and 199 807.4 sq. km, respectively. The county's altitude ranges from 620 m (Albert Nile) to 5 111 m (Mt. Rwenzori peak) above sea level. The temperatures range from 16 to 26 ° C (April and November) and over 30 °C (December and

March) in most regions. Southern Uganda receives more rainfall (>2 100 mm), which decreases towards the north and northeast (<500 mm) turning into semi-arid conditions. These conditions influence the occurrence of well-vegetated savannah in western, southern and central regions, while dry plains occur in northern and northeastern regions of Uganda (UBOS, 2013). Several lakes and rivers occur, which influence the availability of natural pasture and water on which indigenous cattle systems entirely depend. Uganda's 10 AEZs have been described (Figure 1) as areas with homogeneous socio-economic, ecological and farming systems (MAAIF, 2004). They include the northeastern drylands (NED), northeastern savannah grasslands (NESG), northwestern savannah grasslands (NWSG), Kyoga Plains (KP), Lake Victoria Crescent (LVC), western savannah grasslands (WSG), western highland ranges (WHR), pastoral rangelands (PR), southwestern farmlands (SWF) and para savannahs (PS). Different indigenous cattle breeds are reared in all the AEZs, preferred for their tolerance to endemic tick-borne diseases and ability to survive on poor quality feeds (MAAIF/UBOS, 2009).

Data collection procedure

This study embraced a landscape sampling strategy defined by 50 grid cells, enabling an inclusive sampling across the 10 AEZs as previously explained in Kabi *et al.* (2014). Only female cattle were used in this study due to the low numbers of males available in the sampled herds. Ten linear morphological traits were measured from 801 randomly selected female cattle from 209 herds comprising 46 Nganda (*B. indicus*,), 368 Ankole (*B. taurus indicus*) and 387 EASZ (*B. indicus*). The Nganda sample size was quite low compared with other breed groups, however, they were considered due to the fact they are reared within crop–livestock localities and are regarded as *B. indicus* with unique attributes. An Etrex® global positioning system (GPS) handset device which employs satellite navigation system was used for recording the topographical positions of the different sample farms/herds. Locations (latitudes and longitudes) of the 209 were overlaid on the 10 AEZ using ArcGIS® version 10 to show the countrywide pattern of data collection as shown in Figure 1. Examples of indigenous cattle herds with unique but similar morphological feature and body colour patterns are shown in Figures 2 (a, b) and 3 observed during our field visits.

For each well-restrained female cattle positioned on a relatively even surface, sex, breed, age (months) based on dentition, 10 linear body measurements were recorded to the nearest centimetre (cm) using a flexible tape by the first author to minimize in between-individual variations as previously explained by Mwacharo *et al.* (2006) and Alderson (1999). The linear measurements taken on each animal were:

(a) horn length (HL) – the distance from the base of the horn to its tip,
(b) animal length (AL) – the distance from the top of the head to the base of the tail,
(c) fore arm length (FAL) – the distance from the elbow joint to the extreme end of hoof,
(d) fore arm circumference (FAC) – the perimeter distance of the metacarpal joint of the fore arm,
(e) face length (FL) – the distance from the muzzle to the top of the head,
(f) horn base circumference (HBC) – the perimeter distance at the base of the horn,
(g) length between the horn bases (LHB) – the distance between one horn base to the other,
(h) length between the horn tips (LHT) – the distance between one horn tip to the other,
(i) muzzle circumference (MC) – the perimeter distance of the muzzle
(j) tail length (TL) – the distance from the base of the tail to the end of tail switch.

The measurements were made before the cattle were grazed to avoid ascending biases of certain variables due to feed intake. Gestating females were excluded from this study. The age groups were estimated by dentition and clustered into four categories 7–24, 25–36, 37–72 and 73–192 based on minimal differences observed within the categories.

Statistical analysis

Data coding, cleaning and transformation were done in STATA® statistical package (2013). The analyses were performed using the linear regression model of STATA® (2013) and Statistical Package for Social Sciences (SPSS) version 21 (IBM® SPSS® 2012, New York, USA). Means alongside the standard errors (SE) and statistically significant differences between morphological traits based on the study cattle breeds, age groups and AEZs were calculated. Descriptive statistics of the morphometric traits and analysis of variance (ANOVA) were used to establish significant differences at $P \leq 0.05$.

Application of multivariate analysis to interrogate morphometric diversity and classifications of different cattle breeds has recently earned scientific credit (Yakubu, Salako and Imumorin, 2011). Linear statistical regression models to determine the trend of the 10 linear morphometric trait variations among age groups, AEZs and breeds were computed. The linear multiple regression models used took the format of

$$Y_{ijk} = \mu + B_i + \mathrm{AEZ}_j + \mathrm{A}k + (\mathrm{BAEZ})ij + (\mathrm{BA})jk + (\mathrm{BAAEZ})ijk + E_{ijk},$$

Y_{ijk} is the morphometric trait on the animal of the *i*th breed, sampled from the *j*th AEZ, categorized to the *k*th age group; μ the overall mean; B_i the effect of the *i*th breed (i = Ankole, Nganda, EASZ); AEZ_k the effects of the *k*th AEZ (k = NED, NESG, NWSG, KP, LVC, WSG, WHR, PR, SWF, PS); *Al* the effect of the *l*th age group (l = 7–24, 25–36, 37–72, 73–192 months); (BAEZ)*ik* the

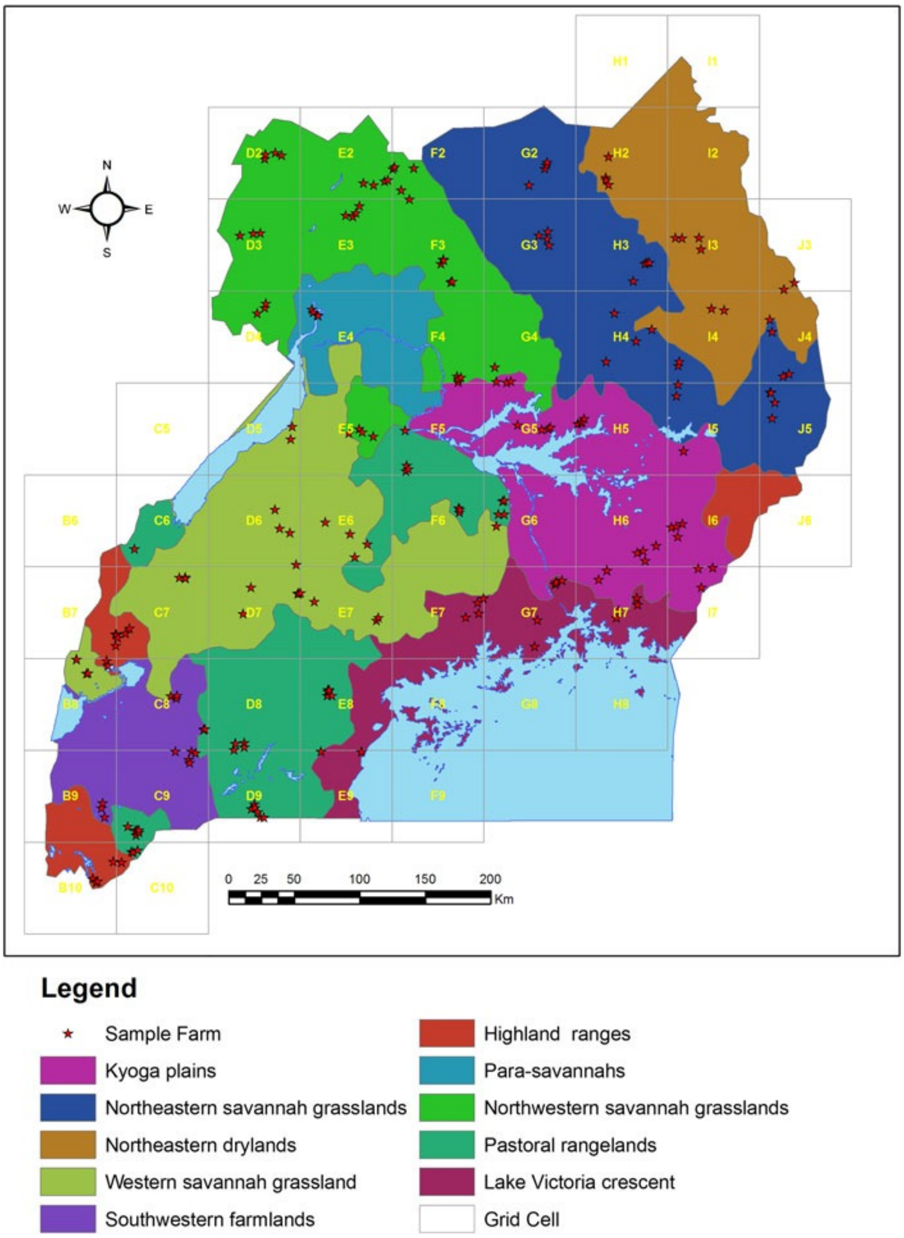

Figure 1. Agro-ecological zones (AEZs) of Uganda (adopted from MAAIF, 2004), grid cells and sampling sites.

interaction effect of the *i*th breed and *k*th AEZ; (BAEAZ) *ijk* the interaction effect of the breed, AEZ, age; and E_{ijk} the random error peculiar to each animal.

Linear regressions coefficients were used to predict the relationships of the 10 linear morphometric traits with the age groups and breed types. The estimated general linear model equation took the format of

$$Y_i = \beta_0 + \beta_1 X_1 + \beta_2 X_2 + \beta_3 X_3 + \beta_4 X_4 + \beta_5 X_5,$$

where Y_i is the morphometric variable; β_0 is the constant coefficient; β_1 to β_5 are the regression coefficients; X_1 and X_2 are the Nganda and EASZ cattle, respectively; X_3, X_4 and X_5 are the 25–36, 37–72 and 73–192 age groups, respectively.

Mahalanobis squared distances, morphometric classifications were computed in STATA® (2013). The stepwise discriminant analysis was performed to determine the most discriminating morphometric trait of the cattle breeds using the SPSS version 21 (IBM® SPSS® 2012, New York, USA).

Results

Age, breed and AEZs significantly influenced variation of linear morphometric traits of the female cattle studied. Age significantly influenced all traits except HBC, FAL and FAC, while AEZs and breed significantly influenced all the traits. Interactions of breed with AEZs influenced all traits except FAC, while interaction of breed with age, and AEZs with age significantly influenced FL and FAL, respectively. Interactions of age, breed and AEZs significantly influenced FL only. The summary of ANOVA for the variation of linear morphometric traits and levels of significance are shown in Table 1.

Generally, the study linear morphometric traits exhibited significant gradual increase from low, intermediate to high dimensions among the EASZ, Nganda and Ankole cattle breeds, respectively. All the study traits of Ankole cattle significantly differed among the age groups with exception of HBC. All the study traits of EASZ cattle exhibited significant differences among the age groups with exception of LHB, FAL and FAC. Among the Nganda cattle, the HL, FL, MC and AL exhibited significant differences within the different age groups. The traits generally increased along the age gradient, with older age groups exhibiting higher linear dimensions and providing a suitable source of breed differentiation as shown Table 2.

Linear morphometric traits from SWF, PR and WHR showed comparatively higher dimensions than traits from PS, NED, NESG and NWSG. The variations of morphometric traits within same cattle breeds sampled from different AEZs were observed. Similar traits of Ankole cattle from different AEZs were significantly different. Among the EASZ cattle similar traits exhibited significant differences with exception of LHB, while the LHB, HBC, FAL and MC of Nganda cattle exhibited significant differences as shown in Table 3.

Regression coefficients were used to exhibit the relationship of the 10 linear morphometric traits with breed and age groups. Coefficients of age and breed groups exhibited high levels of significance providing suitable prediction parameters of the linear morphometric traits. For example the HL may be estimated from the following general equation.

$$\mathrm{HL} = 44.3 - 26.9X_1 - 42.4X_2 + 4.5X_3 + 12.7X_4 + 20.4X_5,$$

where X_1 and X_2 are the Nganda and EASZ cattle, respectively; X_3, X_4 and X_5 are the 25–6, 37–72 and 73–192 age groups, respectively. The linear regression coefficients and their levels of significance are shown in Table 4.

Pairwise correlations among the various linear morphometric traits of the three cattle breeds are given in Table 5. Among the Ankole, all the study traits were significantly correlated except for MC versus LHB; whereas among the Nganda, significant correlation were observed in HL versus (LBT, LHT, HBC, FL), LHT versus (LHB, HBC, FL), HBC versus LHB, FL versus HBC, FAL versus (FAC, AL), FAL versus (TL, AL), FL versus (MC, AL), TL versus (MC, AL) and AL versus MC. The EASZ morphometric traits exhibited significant correlations except FAL versus LBT, FAC versus (LBT, LHB, HBC) and MC versus (LHB, HBC, FAL).

Table 1. Summary ANOVA for linear morphometric traits of indigenous female cattle.

		Mean squares and levels of significance for the various linear morphometric traits									
Sources of variation	**DF**	**HL**	**LHT**	**LHB**	**HBC**	**FAL**	**FAC**	**FL**	**MC**	**TL**	**AL**
Age	3	6559***	3 447**	242*	59^{NS}	69^{NS}	19^{NS}	271***	268***	1031***	9531***
Breed	2	162419***	124961***	5298***	8018***	1739***	741***	1617***	564***	3498***	40950***
AEZ	9	31702***	25609***	1354***	1112***	325***	208***	367***	231***	1193***	8377***
Breed × AEZ	7	5616***	3788***	199***	492***	41***	6^{NS}	63***	53***	480***	1170***
Breed × Age	6	975^{NS}	282^{NS}	73^{NS}	38^{NS}	12^{NS}	11^{NS}	25*	21	82	1108***
AEZ × Age	26	647^{NS}	707^{NS}	70^{NS}	99^{NS}	22**	9^{NS}	16^{NS}	7^{NS}	58^{NS}	475*
AEZ × age × breed	11	486^{NS}	518^{NS}	36^{NS}	78^{NS}	7^{NS}	8^{NS}	24**	10^{NS}	160^{NS}	169^{NS}
Residual	736	373	461	55	64	10	6	9	10	70	278

AEZ, agro-ecological zone; DF, degrees of freedom; EASZ, East African shorthorn zebu; HL, horn length; LHT, length between the horn tips; LHB, length between the horn bases; HBC, horn base circumference; FAL, fore arm length; FAC, fore arm circumference; FL, face length; MC, muzzle circumference; TL, tail length; AL, animal length.

$^{\mathrm{NS}}$, Not significant ($P > 0.05$); ***, very highly significant ($P < 0.001$); **, highly significant ($P < 0.01$); *, significant ($P \leq 0.05$).

Table 2. Variations of linear morphometric traits of indigenous female cattle breeds among the different age groups.

Breed	Age group	$n=801$	Morphometric traits (mean ± SE)									
			HL ± SE	LHT ± SE	LHB ± SE	HBC ± SE	FAL ± SE	FAC ± SE	FL ± SE	MC ± SE	TL ± SE	AL ± SE
Ankole ($n=368$)	7–24	17	35.7 ± 5.1^{a}	56.4 ± 5.8^{a}	17.8 ± 1.3^{c}	23.9 ± 2.2^{NS}	33.7 ± 0.7^{b}	21.1 ± 0.4^{b}	43.0 ± 1.0^{a}	35.8 ± 0.7^{a}	69.2 ± 2.1^{a}	193.5 ± 3.5^{a}
	25–36	34	44.0 ± 4.7^{a}	58.1 ± 4.8^{a}	22.1 ± 1.7^{c}	22.3 ± 1.6^{NS}	36.3 ± 0.7^{b}	22.4 ± 0.5^{b}	45.8 ± 0.7^{a}	37.2 ± 0.4^{a}	70.0 ± 1.4^{a}	203.8 ± 4.0^{a}
	37–72	147	56.8 ± 2.3^{a}	69.3 ± 2.3^{a}	21.8 ± 0.8^{c}	22.7 ± 0.8^{NS}	35.8 ± 0.3^{b}	22.3 ± 0.3^{b}	47.5 ± 0.3^{a}	39.0 ± 0.2^{a}	75.2 ± 0.7^{a}	216.7 ± 1.8^{a}
	73–192	170	66.8 ± 2.4^{a}	69.6 ± 2.4^{a}	19.9 ± 0.7^{c}	23.5 ± 0.8^{NS}	35.9 ± 0.3^{b}	22.8 ± 0.2^{b}	48.9 ± 0.3^{a}	40.4 ± 0.2^{a}	76.3 ± 0.7^{a}	225.3 ± 1.5^{a}
Nganda ($n=46$)	7–24	8	8.0 ± 5.0^{c}	27.0 ± 6.0^{NS}	16.5 ± 2.5^{NS}	12.0 ± 4.0^{NS}	34.5 ± 2.5^{NS}	19.0 ± 1.0^{NS}	42.5 ± 0.5^{c}	34.5 ± 3.5^{b}	70.0 ± 10^{NS}	186.5 ± 26.5^{b}
	25–36	11	25.8 ± 4.9^{c}	50.8 ± 7.0^{NS}	18.5 ± 2.0^{NS}	17.3 ± 2.7^{NS}	34.0 ± 0.8^{NS}	21.3 ± 0.6^{NS}	44.7 ± 1.0^{c}	35.5 ± 0.7^{b}	68.0 ± 4.8^{NS}	194.0 ± 4.0^{b}
	37–72	14	26.7 ± 4.3^{c}	43.5 ± 5.8^{NS}	15.0 ± 1.6^{NS}	17.6 ± 2.1^{NS}	34.3 ± 0.6^{NS}	23.3 ± 0.9^{NS}	46.4 ± 0.4^{c}	38.0 ± 0.4^{b}	76.9 ± 1.5^{NS}	208.2 ± 1.8^{b}
	73–192	13	39.2 ± 4.7^{c}	48.9 ± 5.1^{NS}	17.6 ± 1.6^{NS}	17.9 ± 1.3^{NS}	32.7 ± 0.6^{NS}	22.0 ± 0.3^{NS}	46.3 ± 0.4^{c}	37.7 ± 0.3^{b}	76.2 ± 1.3^{NS}	209.1 ± 2.6^{b}
EASZ ($n=387$)	7–24	23	8.9 ± 1.4^{a}	22.8 ± 2.4^{a}	11.9 ± 1.0^{NS}	11.4 ± 1.2^{b}	31.5 ± 0.5^{NS}	19.4 ± 0.6^{NS}	41.2 ± 0.6^{a}	34.7 ± 0.7^{a}	64.0 ± 2.3^{b}	180.7 ± 3.5^{a}
	25–36	25	12.1 ± 2.5^{a}	26.1 ± 3.7^{a}	11.6 ± 1.3^{NS}	12.0 ± 1.6^{b}	32.3 ± 0.6^{NS}	19.1 ± 0.2^{NS}	42.1 ± 0.5^{a}	34.6 ± 0.4^{a}	65.9 ± 1.6^{b}	193.3 ± 3.3^{a}
	37–72	110	15.3 ± 0.9^{a}	30.9 ± 1.4^{a}	13.3 ± 0.5^{NS}	13.4 ± 0.6^{b}	31.8 ± 0.3^{NS}	19.9 ± 0.2^{NS}	43.9 ± 0.2^{a}	37.5 ± 0.3^{a}	70.7 ± 0.8^{b}	199.3 ± 1.2^{a}
	73–192	229	20.6 ± 0.9^{a}	33.2 ± 1.0^{a}	13.7 ± 0.3^{NS}	14.6 ± 0.4^{b}	31.4 ± 0.2^{NS}	19.8 ± 0.1^{NS}	43.9 ± 0.2^{a}	37.2 ± 0.3^{a}	69.3 ± 0.6^{b}	199.0 ± 0.9^{a}

SE, standard error; HL, horn length; LHT, length between tips; LHB, length between the horn bases; HBC, horn base circumference; FAL, fore arm length; FAC, fore arm circumference; FL, face length; MC, muzzle circumference; TL, tail length; AL, animal length, age is measured in months, linear morphometric traits are measured in centimetres; EASZ, East African shorthorn zebu.

^{a,b,c}Refer to very highly significant ($P \le 0.000$) differences, highly significant ($P \le 0.00$) differences and significant ($P \le 0.05$) differences, respectively. ^{NS}, Not significantly difference. The linear morphometric traits for each breed were compared among the different AEZs in the same column indicated with the same superscript.

The Mahalanobis squared distances were calculated to estimate the levels of linear morphometric trait diversity for female cattle. The Mahalanobis squared distances were significantly different based on pairwise breed comparisons, exhibiting a gradient of low 1.61 (EASZ and Nganda), intermediate 2.09 (Nganda and Ankole) and high 4.15 (EASZ and Ankole) linear morphometric trait diversity as shown in Table 6.

Classification of the study cattle into breed groups using the linear morphometric traits was computed. The correct percentages of breed classification were Nganda (54.4), Ankole (70.1) and EASZ (79.3) as shown in Table 7. The occurrence of misclassification could be indicative of interbreeding between the different breed populations.

Stepwise selection of the five most discriminant linear morphometric traits were identified as HL, FAL, LBT, FL and FAC. These traits may be used to adequately discriminate the three indigenous female cattle breeds. Their levels of discriminating power are shown in Table 8.

Discussion

The present study has revealed that linear morphometric structures of indigenous cattle populations comprising the Ankole, Nganda and EASZ females vary with age, breed types and AEZs. This study utilized female cattle due to the fewer males within sampled herds since the later are kept mainly for breeding purposes. These variations are useful for cattle populations to adapt to different environments, and maybe utilized for livestock breed improvement initiatives and conservation of unique genotypes (Kugonza *et al.*, 2011). The aforementioned structures have been shaped through active selection of unique morphometric traits aimed at promotion of agro-ecological fitness and enrichment of socio-cultural identities among Uganda's cattle keeping communities. Consequently various indigenous cattle populations have evolved in specific AEZs, adopting the names of cattle keeping communities who breed them (Balikowa, 2011). This study reveals a significant upward trend of linear morphometric trait dimensions which may be described as low, intermediate and high for the EASZ, Nganda and Ankole cattle populations, respectively. These findings are in agreement with recent studies by Kugonza *et al.* (2011) who observed that the Ankole cattle have higher body linear measurements compared with the EASZ cattle. Studies in Tanzania (Mwambene *et al.*, 2012) and Kenya (Mwacharo *et al.*, 2006), on the Tanzanian Fipa, Kenyan Kamba and Masai zebu cattle linear morphometric traits revealed that HL, length between the horn tips, HBC measurements are similar to those of EASZ observed in this study although lower than those of Ankole cattle of Uganda. Since the HL and AL are directly correlated to body weights and cattle sizes (Kugonza *et al.*, 2011; Mwambene *et al.*, 2012), then Ankole cattle have evolved

Table 3. Variations of linear morphometric traits of indigenous female cattle breeds sampled from the different AEZs.

			Morphometric traits (mean ± SE)									
Breed	***n* = 801**	**AEZ**	**HL ± SE**	**LHT ± SE**	**LHB ± SE**	**HBC ± SE**	**FAL ± SE**	**FAC ± SE**	**FL ± SE**	**MC ± SE**	**TL ± SE**	**AL ± SE**
Ankole (*n* = 368)	12	NWSG	44.1 ± 6.0^{a}	61.0 ± 5.1^{a}	17.4 ± 1.7^{a}	24.5 ± 2.4^{a}	36.1 ± 0.8^{a}	21.5 ± 0.4^{a}	47.0 ± 1.2^{a}	39.3 ± 0.8^{a}	77.9 ± 2.3^{b}	220.4 ± 5.1^{a}
	47	KP	48.1 ± 4.7^{a}	49.6 ± 3.9^{a}	15.0 ± 0.6^{a}	24.0 ± 1.3^{a}	34.2 ± 0.4^{a}	21.2 ± 0.6^{a}	46.3 ± 0.7^{a}	39.4 ± 0.6^{a}	72.4 ± 1.5^{b}	211.6 ± 3.9^{a}
	28	LVC	28.0 ± 3.3^{a}	40.6 ± 2.9^{a}	17.9 ± 0.9^{a}	17.1 ± 0.5^{a}	32.5 ± 0.6^{a}	21.4 ± 0.4^{a}	44.8 ± 0.4^{a}	37.5 ± 0.4^{a}	73.4 ± 1.7^{b}	201.7 ± 2.7^{a}
	80	WSG	51.0 ± 3.5^{a}	61.3 ± 3.5^{a}	19.1 ± 1.0^{a}	20.9 ± 1.2^{a}	35.7 ± 0.4^{a}	21.8 ± 0.3^{a}	47.1 ± 0.5^{a}	39.4 ± 0.4^{a}	73.4 ± 1.0^{b}	214.6 ± 2.8^{a}
	58	WHR	52.0 ± 3.0^{a}	69.7 ± 3.0^{a}	21.6 ± 1.1^{a}	20.1 ± 1.1^{a}	36.5 ± 0.4^{a}	22.4 ± 0.2^{a}	47.1 ± 0.4^{a}	39.0 ± 0.3^{a}	76.2 ± 1.1^{b}	221.7 ± 2.2^{a}
	109	PR	76.9 ± 2.3^{a}	81.9 ± 2.5^{a}	22.9 ± 1.0^{a}	27.7 ± 1.0^{a}	36.7 ± 0.4^{a}	23.7 ± 0.2^{a}	49.7 ± 0.3^{a}	39.8 ± 0.3^{a}	75.1 ± 0.7^{b}	224.9 ± 2.0^{a}
	34	SWF	80.7 ± 3.9^{a}	85.0 ± 4.8^{a}	27.8 ± 1.9^{a}	21.4 ± 1.5^{a}	36.3 ± 0.4^{a}	23.4 ± 0.2^{a}	49.2 ± 0.6^{a}	39.7 ± 0.4^{a}	80.1 ± 1.8^{b}	223.7 ± 2.5^{a}
Nganda (*n* = 46)	11	NED	29.1 ± 8.2^{NS}	46.3 ± 8.9^{NS}	14.8 ± 1.0^{b}	20.5 ± 3.8^{c}	34.2 ± 0.7^{a}	22.5 ± 2.5^{NS}	45.3 ± 1.3^{NS}	35.1 ± 0.9^{c}	72.8 ± 6.0^{NS}	197.3 ± 6.0^{NS}
	18	LVC	29.4 ± 2.5^{NS}	44.9 ± 2.2^{NS}	15.4 ± 0.3^{b}	20.0 ± 1.0^{c}	31.7 ± 0.5^{a}	21.6 ± 0.3^{NS}	46.1 ± 0.3^{NS}	37.8 ± 0.3^{c}	76.8 ± 1.1^{NS}	204.7 ± 1.2^{NS}
	17	PR	33.8 ± 5.9^{NS}	47.9 ± 7.8^{NS}	18.2 ± 2.1^{b}	14.4 ± 2.0^{c}	35.0 ± 0.6^{a}	23.1 ± 0.6^{NS}	46.2 ± 0.5^{NS}	37.8 ± 0.5^{c}	75.5 ± 1.9^{NS}	210.5 ± 3.4^{NS}
EASZ (*n* = 387)	67	KP	23.3 ± 1.8^{a}	33.0 ± 1.8^{b}	13.7 ± 0.6^{NS}	15.2 ± 0.7^{a}	31.8 ± 0.4^{c}	20.4 ± 0.2^{c}	45.4 ± 0.4^{a}	38.4 ± 0.4^{a}	77.1 ± 1.0^{a}	204.1 ± 2.2^{c}
	12	LVC	20.0 ± 3.0^{a}	40.1 ± 4.0^{b}	20.0 ± 1.0^{NS}	14.5 ± 0.5^{a}	34.0 ± 1.0^{c}	21.5 ± 1.5^{c}	45.5 ± 4.5^{a}	41.5 ± 4.5^{a}	72.5 ± 2.5^{a}	210 ± 1.0^{c}
	45	NED	14.6 ± 1.6^{a}	26.6 ± 2.3^{b}	12.0 ± 1.0^{NS}	11.7 ± 1.0^{a}	31.8 ± 0.3^{c}	19.7 ± 0.4^{c}	43.8 ± 0.3^{a}	35.9 ± 0.3^{a}	66.5 ± 1.6^{a}	198.5 ± 1.3^{c}
	91	NESG	16.1 ± 1.0^{a}	29.3 ± 1.6^{b}	12.8 0.6^{NS}	13.4 ± 0.6^{a}	31.1 ± 0.3^{c}	19.2 ± 0.2^{c}	43.6 ± 0.3^{a}	36.8 ± 0.3^{a}	69.6 ± 0.8^{a}	195.1 ± 1.5^{c}
	107	NWSG	17.0 ± 0.9^{a}	32.5 ± 1.3^{b}	13.8 ± 0.4^{NS}	14.1 ± 0.5^{a}	31.4 ± 0.2^{c}	19.2 ± 0.2^{c}	42.8 ± 0.2^{a}	35.4 ± 0.4^{a}	66.4 ± 0.8^{a}	195.3 ± 1.2^{c}
	16	PS	13.5 ± 1.6^{a}	33.1 ± 2.5^{b}	15.0 ± 0.5^{NS}	14.1 ± 0.6^{a}	30.8 ± 0.3^{c}	19.5 ± 0.3^{c}	41.9 ± 0.4^{a}	35.0 ± 0.5^{a}	63.0 ± 1.0^{a}	193.8 ± 2.5^{c}
	29	PR	11.6 ± 1.3^{a}	29.8 ± 2.9^{b}	12.2 ± 1.1^{NS}	11.5 ± 1.1^{a}	30.6 ± 0.7^{c}	22.0 ± 0.5^{c}	44.1 ± 0.4^{a}	41.7 ± 0.8^{a}	66.6 ± 1.3^{a}	198.6 ± 2.4^{c}
	20	WSG	31.6 ± 5.4^{a}	41.9 ± 5.1^{b}	13.8 ± 0.9^{NS}	18.4 ± 2.0^{a}	33.7 ± 0.9^{c}	20.1 ± 0.4^{c}	44.2 ± 0.9^{a}	37.9 ± 0.8^{a}	70.8 ± 2.5^{a}	199.2 ± 5.1^{c}

AEZ, Agro-ecological zone; SE, standard error; HL, horn length; LHT, length between tips; LHB, length between the horn bases; HBC, horn base circumference; FAL, fore arm length; FAC, fore arm circumference; FL, face length; MC, muzzle circumference; TL, tail length; AL, animal length; EASZ, East African shorthorn zebu; NED, northeastern drylands; NESG, northeastern savannah grasslands; NWSG, northwestern savannah grasslands; KP, Kyoga Plains; LVC, Lake Victoria Crescent; WSG, western savannah grasslands; WHR, western Highland ranges; PR, pastoral rangelands, southwestern Farmlands; PS, para savannahs.

^{a,b,c}Refer to very highly significant ($P \leq 0.000$) differences, highly significant ($P \leq 0.00$) differences and significant ($P \leq 0.05$) differences, respectively. The linear morphometric traits for each breed were compared among the different AEZs in the same column indicated with the same superscript.

Table 4. Linear regression parameter estimates for prediction of the linear morphometric traits of female cattle based on the breeds and age groups.

	Morphometric trait (cm)									
	HL	**LHT**	**LHB**	**HBC**	**FAL**	**FAC**	**FL**	**MC**	**TL**	**AL**
	Coefficient ± SE									
Breed group										
Ankole	Reference									
Nganda	−26.9 ± 3.5***	−21.0 ± 3.6***	−3.9 ± 1.2**	−5.5 ± 1.3***	−2.4 ± 0.5***	−0.1 ± 0.4^{NS}	−1.7 ± 0.5*	−1.9 ± 0.5***	0.5 ± 1.3^{NS}	−12.1 ± 2.7***
EASZ	−42.4 ± 1.6***	−36.6 ± 1.7***	−7.3 ± 0.6***	−9.3 ± 0.6***	−4.2 ± 0.2***	−2.8 ± 0.2***	−4.2 ± 0.2***	−2.5 ± 0.2***	−5.9 ± 0.6***	−21.3 ± 1.2***
Age (months) group										
7–24	Reference									
25–36	4.5 ± 4.4^{NS}	3.4 ± 4.6^{NS}	2.2 ± 1.5^{NS}	0.06 ± 1.6^{NS}	1.4 ± 0.7*	0.5 ± 0.4^{NS}	1.7 ± 0.6**	0.8 ± 0.7^{NS}	1.1 ± 1.8^{NS}	10.4 ± 3.5***
37–72	12.7 ± 3.7***	10.6 ± 3.9**	2.5 ± 1.3*	0.9 ± 1.4^{NS}	0.9 ± 0.6^{NS}	0.8 ± 0.4^{NS}	3. 4 ± 0.5***	3.1 ± 0.6***	6.5 ± 1.4***	20.8 ± 2.9***
73–192	20.4 ± 3.6***	11.9 ± 3.8**	1.9 ± 1.2^{NS}	1.8 ± 1.4^{NS}	0.8 ± 0.5^{NS}	0.9 ± 0.4*	4.1 ± 0.5***	3.7 ± 0.6***	6.3 ± 1.5***	24.7 ± 2.9***
Constant	44.3 ± 3.6***	57.8 ± 3.8***	18.7 ± 1.2***	21.9 ± 1.3***	34.9 ± 0.5***	21.7 ± 0.4***	44.3 ± 0.5***	36.3 ± 0.6***	69.3 ± 1.4***	197.8 ± 3.8***
Adjusted R^2	0.5	0.36	0.18	0.21	0.27	0.21	0.32	0.16	0.13	0.31

EASZ, East African shorthorn zebu; SE, standard error; HL, horn length; LHT, length between the horn tips; LHB, length between the horn bases; HBC, horn base circumference; FAL, fore arm length; FAC, fore arm circumference; FL, face length; MC, muzzle circumference; TL, tail length; AL, animal length.

^{NS}, Not significant ($P > 0.05$); ***, very highly significant ($P < 0.001$); **, highly significant ($p < 0.01$); *, Significant ($P \leq 0.05$).

comparatively superior linear morphometric traits and body sizes compared with the EASZ.

The Mahalanobis squared distances computed among the three female cattle breeds were significantly different corresponding to high linear morphometric diversity among the study indigenous cattle breed types. This agrees with Ndumu *et al.* (2008b) who observed significant differences of morphometric distances between different clusters of Ankole cattle. The linear morphometric diversity was observed to be low between the EASZ and Nganda, intermediate between the Nganda and Ankole and high among the Ankole and the EASZ breeds. Recently, Bett *et al.* (2013) have reported that the Nganda group is a hybrid of the Ankole and EASZ, although more closely associated with the later. This explains the occurrence of low morphometric distances between Nganda and EASZ, and intermediate between the Nganda and Ankole. Similarly, the high morphometric distance between the Ankole and EASZ is strongly suggestive of high trait diversity between the two populations. These distances correspond to traditional farmers' dissimilarities of selective breeding criteria for desirable traits to enhance adaptation to contrasting AEZs.

The AEZ attributes support indigenous cattle through provision of natural pasture feeds, water resources and suitable ambient temperatures. Lately, Balikowa (2011) has noted that the Ankole cattle are established in the southern and Western Uganda. These regions are characterized by comparatively higher altitudes, lower ambient temperature ranges and abundant rainfall patterns (>2 100 mm). These conditions favour good pasture rangelands, resulting into more feed resource availability. The exhibition of higher linear morphometric traits among the Ankole of the SWF, PR and WHR AEZs could be partly due to the availability of comparatively higher natural pasture and water resources compared with the northeastern drylands and northwestern savannah grasslands. Indeed, Mwambene *et al.* (2012) have recently noted that variations in availability of feed resources and farmers' breeding practices plus natural breeding barriers such as detachment between different locations largely account for morphometric trait differences. Similarly, Ankole cattle keepers have memorized selective breeding criteria based on customary knowledge to enhance higher productivity, socio-cultural identity and beauty. These criteria favour larger body sizes, tall frames and large white curved horns for the cows. Similar selection criteria for bulls have been described (Ndumu *et al.*, 2008a; Kugonza *et al.* 2011, 2012), which largely accounts for socio-cultural identity of Ankole cattle populations.

The EASZ cattle exhibited comparatively lower linear morphometric trait dimensions which occurred in the NED, PS, NESG and NWSG AEZs. The northeastern, northern and northwestern regions are characterized by lower altitudes, higher ambient temperatures and lower

Table 5. Pairwise correlation coefficients and their significance levels among the linear morphometric traits.

Traits	HL	LHT	LHB	HBC	FAL	FAC	FL	MC	TL	AL
(a) Female Ankole cattle (n = 368)										
HL	1									
LHT	0.60***	1								
LHB	0.44***	0.38***	1							
HBC	0.37***	−0.37***	0.36***	1						
FAL	0.42***	0.32***	0.28***	0.15**	1					
FAC	0.47***	0.39***	0.24***	0.19***	0.35***	1				
FL	0.66***	0.45***	0.22***	0.32***	0.45***	0.45***	1			
MC	0.50***	0.30***	0.05$^{\mathrm{NS}}$	0.19***	0.31***	0.40***	0.65***	1		
TL	0.19***	0.25$^{\mathrm{NS}}$	−0.04***	0.18***	0.18***	0.17***	0.30***	0.30***	1	
AL	0.56***	0.38***	0.19***	0.19***	0.37***	0.42***	0.57***	0.57***	0.27***	1
(b) Female Nganda cattle (n = 46)										
HL	1									
LHT	0.74***	1								
LHB	0.70***	0.66***	1							
HBC	0.53***	0.60***	0.28*	1						
FAL	0.07$^{\mathrm{NS}}$	0.00$^{\mathrm{NS}}$	0.10$^{\mathrm{NS}}$	−0.04$^{\mathrm{NS}}$	1					
FAC	0.12$^{\mathrm{NS}}$	−0.09$^{\mathrm{NS}}$	−0.06$^{\mathrm{NS}}$	−0.03$^{\mathrm{NS}}$	0.32*	1				
FL	0.49***	0.40**	0.22$^{\mathrm{NS}}$	0.33*	0.11$^{\mathrm{NS}}$	0.25$^{\mathrm{NS}}$	1			
MC	0.20$^{\mathrm{NS}}$	0.05$^{\mathrm{NS}}$	−0.18$^{\mathrm{NS}}$	0.07$^{\mathrm{NS}}$	0.25$^{\mathrm{NS}}$	0.23$^{\mathrm{NS}}$	0.45**	1		
TL	0.12$^{\mathrm{NS}}$	0.06$^{\mathrm{NS}}$	−0.03$^{\mathrm{NS}}$	0.22$^{\mathrm{NS}}$	0.19$^{\mathrm{NS}}$	0.37*	0.23$^{\mathrm{NS}}$	0.44**	1	
AL	0.04$^{\mathrm{NS}}$	−0.10$^{\mathrm{NS}}$	−0.15$^{\mathrm{NS}}$	−0.04$^{\mathrm{NS}}$	0.31**	0.45**	0.29*	0.55***	0.55***	1
(b) Female EASZ cattle (n = 387)										
HL	1									
LHT	0.66***	1								
LHB	0.55***	0.73***	1							
HBC	0.73***	0.83***	0.78***	1						
FAL	0.19***	0.09$^{\mathrm{NS}}$	0.11*	0.11*	1					
FAC	0.14**	0.07$^{\mathrm{NS}}$	0.05$^{\mathrm{NS}}$	0.09$^{\mathrm{NS}}$	0.11*	1				
FL	0.43***	0.26***	0.17***	0.27***	0.22***	0.42***	1			
MC	0.20***	0.15**	0.02$^{\mathrm{NS}}$	0.08$^{\mathrm{NS}}$	0.02$^{\mathrm{NS}}$	0.32****	0.46***	1		
TL	0.33***	0.23***	0.16**	0.27***	0.14**	0.31***	0.51***	0.40***	1	
AL	0.46***	0.32***	0.23***	0.34***	0.19***	0.38***	0.67***	0.37***	0.42***	1

EASZ, East African shorthorn zebu; HL, horn length; LHT, length between the horn tips; LHB, length between the horn bases; HBC, horn base circumference; FAL, fore arm length; FAC, fore arm circumference; FL, face length; MC, muzzle circumference; TL, tail length; AL, animal length. $^{\mathrm{NS}}$, Not significant ($P > 0.05$); ***,very highly significant ($P < 0.001$); **,highly significant ($P < 0.01$); *, significant ($P \leq 0.05$).

rainfall patterns (<500 mm) which consequently lower the availability of pasture and water resources (Balikowa, 2011). Consequently, indigenous livestock farmers' selection criteria tend to favour cattle's ability to survive under lower feed and water availability (FAO, 2007; Nalule, 2010) which in turn influences lower body sizes of EASZ cattle breed types. Selection of smaller body measurements have enabled the comparatively smaller EASZ cattle to thrive under the less privileged climatic, feed and water resource conditions (Loquang and Köhler-Rollefson, 2005; FAO, 2009).

The majority of pairwise correlation coefficients between the linear morphometric measurements were positive and highly significant. This enables accurate estimation of unavailable but correlated traits. More so in case of inability to directly measure the trait at a point in time necessitating longitudinal studies to be accurately estimated such as production traits as previously observed by Kugonza *et al.* (2011), among the Ankole cattle. Most significant pairwise correlations were evident among the Ankole, followed by the EASZ and least among the Nganda cattle. The cause for the differences in the level of correlation

Table 6. Mahalanobis squared distances between the three female cattle groups.

Breed		Ankole (n = 368)	Nganda (n = 46)	EASZ (n = 387)
Ankole	Mahalanobis squared distance	0	2.09***	4.15***
Nganda	Mahalanobis squared distance		0	1.61***

EASZ, East African shorthorn zebu.
Very highly significant at $P < 0.000$.

Table 7. Percentage classifications of indigenous cattle into their breed groups using the linear morphometric traits.

Breeds	Female cattle (n = 801)		
	Ankole (n = 368)	Nganda (n = 46)	EASZ (n = 387)
Ankole	70.11	13.32	16.58
Nganda	19.57	54.35	26.09
EASZ	4.13	16.54	79.33

EASZ, East African shorthorn zebu.

Table 8. Stepwise selection summary of the five most discriminant linear morphometric traits.

Step	Trait entered	R^2	*F* value	*P* value
1	HL	0.389	587.76	0.000
2	FAL	0.040	64.14	0.000
3	LBT	0.016	26.24	0.000
4	FL	0.004	6.21	0.013
5	FAC	0.005	7.56	0.006

HL, horn length; FAL, fore arm length; LBT, length between the horn tips; FL, face length; FAC, fore arm circumference.

among the linear morphometric traits between specific cattle breeds requires more investigations.

The study of linear morphometric traits were used to classify the female cattle into their breed groups of Ankole, EASZ and Nganda resulting into variable grades of accuracy. The occurrence of inaccurate classification is largely due to interbreeding between populations as preferred by traditional farmers, for example crossbreeding the Ankole and EASZ has resulted into composite cattle breeds such as the Nganda. While interbreeding between the different EASZ has given rise to Nkedi and Nsoga cattle populations (Bett *et al.*, 2013), crossbreeding is common in AEZs harbouring more than one indigenous breed types and where exotic genotypes such as Friesians are being popularized for increased productivity, such as among smallholder dairy farmers in central Uganda. Linear morphometric traits within the same breed populations sampled from different AEZs exhibited significant differences which could be associated with morphological signatures of selection between the zones. The Ankole, EASZ and Nganda cattle exhibited high, moderate and low within breed significant differences of the study morphometric traits, respectively. This further supports previous observations in which traditional farmers' diverse selective breeding criteria within indigenous cattle populations for agro-ecological fitness resulting into evolution of unique cattle morphometric populations (FAO, 2009). This is also comparable with Ndumu *et al.* (2008b)'s findings that identified three sub-populations using micro-satellite markers and morphological analysis within Southwestern Uganda.

Figure 3. A herd of the Ankole cattle from pastoral rangelands of Southwestern Uganda.

Figure 2. (a) A herd of the East African shorthorn zebu (EASZ) cattle from northeastern drylands (NED) of Uganda. (b) A herd of the East African shorthorn zebu (EASZ) cattle from northwestern savannah grasslands (NWSG) of Uganda.

Conclusions

This study has provided insight on the extent to which traditional farmers' selective breeding practices enhance identity and agro-ecological fitness resulting into creation of unique indigenous cattle morphometric populations. Secondly, the study has revealed that indigenous cattle linear morphometric variation is structured geographically with higher linear morphometric trait dimensions being exhibited in the southern, southwestern and western regions of Uganda. Although lower trait dimensions occur towards the northern, northwestern and northeastern regions which further corresponds to lower availability of natural feed and water resources. The high morphometric diversity among indigenous cattle population can be a basis for improvement and conservation with farmers' preferences and adaptation to the different AEZs. Appropriate management practices, including feeding, disease control and selective breeding will further enhance sustainable production more so in areas where no other type of agricultural investment is possible.

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Statement of interest

The authors declare no conflict of interest.

Ethical clearance statement

This study was guided by the guidelines stated in the Guide for the Care and Use of Agricultural Animals in Research and Teaching (FASS, 2010).

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No functional sexual dimorphism in Minorcan horse assessed by geometric morphometric methods

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Summary
The existence of sexual dimorphism in the Minorcan horse, an autochthonous breed from Minorca Island in the Balearic archipelago (NW Mediterranean Sea), is established in the official standard, with females being shorter and longer than males as well as having slenderer necks and a squarer croup. However, no study so far has explored the size and shape components of this dimorphism separately. The aim of this study was to analyse the morphology of this breed using geometric morphometric methods in order to find size and shape differences between sire lines. The analysis was based on landmarks digitized in lateral view from 38 registered adult Minorcan horses (20 males and 18 females) within an age range of 3–14 years (average 7 years) with different performance goals. The analyses did not reveal any significant differences between the "shape" and "size" of male and female animals, for the landmarks studied, so the sexes are functionally similar.

Keywords: *Balearic breeds, Equus, geometric morphometrics, morphofunctional traits*

Résumé
L'existence de dimorphisme sexuel chez le cheval Minorquin, une race autochtone de l'Île de Minorque dans l'Archipel des Baléares (Nord-Ouest de la Mer Méditerranée), est reconnue dans le standard officiel, avec les femelles étant plus basses et longues que les mâles et ayant le cou plus fin et la croupe plus carrée. Cependant, aucune étude n'a, jusqu'à présent, examiné séparément les composants de taille et forme de ce dimorphisme. L'objectif de cette étude a été d'analyser la morphologie de cette race en utilisant des Méthodes de Morphométrie Géométrique (MMG) afin de déceler des différences de taille et forme entre les lignées d'étalons. L'analyse s'est basée sur des repères numérisés sur la vue latérale de 38 chevaux Minorquins adultes inscrits (20 mâles et 18 femelles), âgés de 3 à 14 ans (7 ans, en moyenne) et avec différents objectifs de performance. Pour les repères considérés, les analyses n'ont pas mis en évidence des différences significatives entre la forme et la taille des individus mâles et femelles, comme quoi les sexes sont similaires d'un point de vue fonctionnel.

Mots-clés: *races des Baléares, Equus, morphométrie géométrique, traits morpho-fonctionnels*

Resumen
La existencia de dimorfismo sexual en el caballo Menorquín, una raza autóctona de la Isla de Menorca en el Archipiélago Balear (Noroeste del Mar Mediterráneo), está recogida en el estándar oficial, siendo las hembras más bajas y largas que los machos y con un cuello más fino y una grupa más cuadrada. Sin embargo, hasta la fecha, ningún estudio ha explorado por separado los componentes de tamaño y forma de este dimorfismo. El objetivo de este estudio fue analizar la morfología de esta raza usando Métodos de Morfometría Geométrica (MMG) con el fin de dilucidar diferencias en tamaño y forma entre las líneas paternas. El análisis se basó en puntos de referencia digitalizados sobre la vista lateral de 38 caballos Menorquines adultos registrados (20 machos y 18 hembras), con edades comprendidas entre los 3 y los 14 años (7 años de media) y con diferentes fines productivos. Para los puntos de referencia estudiados, los análisis no arrojaron diferencias significativas entre la forma y el tamaño de los ejemplares machos y hembras, con lo que los sexos son similares desde un punto de vista funcional.

Palabras clave: *razas baleares, Equus, morfometría geométrica, rasgos morfofuncionales*

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Introduction

The Minorcan horse is an autochthonous horse breed from Minorca Island in the Balearic archipelago (NW Mediterranean Sea). The Minorcan is a eumetric uniform jet-black horse with a sub-convex to straight profile. The minimum rise to the withers is 1.54 m in males and 1.51 m in females. An excellent riding horse for any type of rider, they have a great capacity to adapt to different styles and are easily broken in. They are suitable for refined riding techniques and graceful handling and also suitable for lightweight harnesses. A breeding program

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for the horse was accepted in the year 1989, when it was officially recognized. Its total census (2011) is about 3 500 animals. The conformation assessment for the Minorcan horse is very important to meet its standard racial requirements, whatever the final purpose of each animal. But these judgements are basically subjective, and therefore the implementation of objective methodologies assessing functional morphology is of major importance.

Traditionally, breed studies are based on linear and angular measures: Hevia and Quiles (1993) for the Thoroughbred, Batista *et al.* (2008) for the Mangalarga, Cervantes *et al.* (2009) for the Spanish Arab, Purzyc *et al.* (2011) for the Hucul, and so on. These kinds of studies have a great value in the sense that they describe morpho-functional traits of the studied animals. But none are based on geometric morphometrics (GM).

GM is the statistical analysis of shape variation and its covariation with other variables (Bookstein, 1991). These methods quantify variation in the shape of anatomical objects using the Cartesian coordinates of anatomical landmarks, after the effects of non-shape variation have been mathematically held constant. GM studies are accomplished through what can be called the Procrustes paradigm; an approach to shape analysis that emerged from the unification of a rigorous statistical theory for shape with analytical procedures for superimposing landmark configurations to obtain shape variables. In a typical morphometric analysis, the Procrustes paradigm is implemented as a series of operations. First, from each specimen, a set of the two-dimensional landmark coordinates is obtained, which record the relative positions anatomically definable locations. These landmarks can be considered “fixed points”, as they define the locations of particular anatomical traits representing discrete biological attributes. Next, a generalized Procrustes analysis is used to superimpose the configurations of landmarks in all specimens to a common coordinate system, and to generate a set of shape variables. This least-squares procedure translates all specimens to the origin, scales them to unit centroid size (CS), and rotates them to minimize the total sums-of-squares deviations of the landmark coordinates from all specimens to the average configuration. After superimposition, the aligned Procrustes shape coordinates describe the location of each specimen in a curved space related to Kendall’s shape space (Slice, 2001). These are typically projected orthogonally into a linear tangent space yielding Kendall’s tangent space coordinates (Dryden and Mardia, 1993), on which multivariate analyses of shape variation are then conducted. An extensive introduction to the theory of GM is provided in Adams *et al.* (2008).

Then, in this study, variations in the form of the landmark configurations were examined using these Procrustes-based GM, as the angle- and distance-based classical approach has less desirable statistical properties (Franklin *et al.*, 2008) and provides an efficient separation of size and shape components of form differences (Adams, Slice and Rohlf, 2004).

Thus, although sexual dimorphism is declared for the Minorcan breed, it is based on analogical and subjective appreciations, with expressions such as “females are recognized as more stylized than the males, their heads and bodies being longer, as well as having more slender necks and a squarer croup”. So an objective degree of sexual dimorphism in the shape independently of size has never been studied for this breed.

Thus, the objective of this paper is to explore the nature of sexual dimorphism in this breed in relation to both form components (size and shape), avoiding subjective appreciations and basing this study not on profile (“silhouette” for the observer, as is normally done in judgements) but on functional points, which will be defined for this research using homologous landmarks.

Materials and methods

Material

Our data consisted of 38 registered adult Minorcan Horses (20 males and 18 females) within an age range from 3 to 14 years (average 7 years). The animals belonged to 24 different owners, and were kept in 8 different local farms and riding centres.

Data gathering

Images were collected by taking a photograph of each animal in direct view, at rest on a horizontal floor. Fifteen landmarks were indicated by white sticks placed on the lateral aspect of each animal before taking its picture. These landmarks were chosen to provide an adequate coverage of the body functionality (Table 1 and Figure 1), as they were located (except for those located on the head, which were extremal) at articulations. A scale (an stick of 200 cm) was put on each image. Withers height was also registered. The second author was responsible for landmarking all specimens and also took also pictures, using a Sony DSC-HX1 apparatus at high resolution

Table 1. Explanation of landmarks used to derive the 15 coordinates used in the morphometric analyses.

1	Tip of muzzle (the most buccal point of the head)	9	Fetlock (joint between the cannon bone and the longer pastern bone)
2	Forehead (above the eyes)	10	Hip (anterior)
3	Forelock	11	Hip (posterior)
4	Poll (the most dorsal point of the head)	12	Buttock
5	Withers (dorsal spinal processes of roughly the 3rd to the 11th thoracic vertebrae)	13	Stifle
6	Point of shoulder	14	Hock (talocrural joint)
7	Elbow	15	Ankle
8	Knee		

Figure 1. Landmarks digitized on the surface of the body. These 15 landmarks were chosen to provide an adequate coverage of the body functionality.

(3 456 × 2 304 pixels), from a distance to ensure that the animal only occupied the central portion of focal space to avoid peripheral image distortion or parallax. The images were then digitized using TpsDig software version 2.16 (Rohlf, 2010) to obtain the *x*, *y* coordinates of the landmarks. To ensure that the localization of the selected points, a Mantel test gave a $R = 0.356$, $P = 0$. So, the error for digitizing landmarks was considered negligible. To test whether the shape variation was small enough to permit the use of approximations in tangent space, a correlation between specimen distances in tangent space and Procrustes space was performed in TpsSmall (Rohlf, 2003). The correlation was very high ($r = 1$), indicating that no significant distortion was introduced by tangent space approximations.

The geometric morphometric method (GMM) requires the positions of landmarks, a finite number of points along the outline of the shape, instead of longitudinal or angular measurements. Landmark positions were converted to scaled *x* and *y* coordinates using CoordGen6f (Sheets, 2003), which was also used to translate and rotate images. CS, which was computed as the square root of the sum of squared distances of all landmarks from the centroid (Dryden and Mardia, 1993), was used as a measurement independent of shape (Bookstein, 1991). The natural log of CS was used as the size reference. The CS is the square root of the sum of squared distances of a set of landmarks from the mathematical centre (i.e., centroid) of a configuration of landmarks (Bookstein, 1991). After that the configurations are rotated to minimize the squared differences between landmarks, and the aligned coordinates (consensus configuration) are obtained. CoordGen6f (Sheets, 2003) was used to rescale, translate and rotate images. The final "shape variables" were used for further statistical analysis.

Statistical analysis

To examine the amount of differences in sexual shape dimorphism we used Procrustes Non Parametric Anova (NPMANOVA) with 9 999 permutations and the Mann–Whitney test of log CS to assess differences in size. In addition, group assignment was cross-validated by a leave-one-out cross-validation (jackknifing) procedure. Principal component analysis (PCA) involves the linear transformation of correlated variables into pairwise uncorrelated variables and is often used as an exploratory method in which scores based on the first two or three variables are plotted to investigate or display structure in the data. Components with eigenvalues smaller than the Jolliffe cut-off may be considered insignificant, but this criterion should not be given too much weight. Statistical analyses were done with the PAST v. 2.12 (Hammer, Harper and Ryan, 2001) and MorphoJ v. 1.03d (Klingenberg, 2011) packages.

Results and discussion

The Mann–Whitney test for size did not show significant differences between sexes ($P = 0.872$), so males and females can be considered of the same size. Size is not correlated with age ($r_s = -0.200$, $P = 0.228$). Procrustes ANOVA for shape also showed no significant differences between sexes ($P = 0.132$), although males are more uniform. Variation in shape can be explained by size ($F_{30,7} = 0.945$; $P = 0.586$) (Figure 2). The PCA plot for the symmetric component (individual variation) shows some differences between the populations analysed. The first two principal components (PCs) account for 64.01 percent (PC1 + PC2 = 38.14 + 25.87 percent) of the total shape variation and provide a reasonable approximation of the total amount of variation, while the other PC components each accounted for no more than 9.0 percent of the variation (Figure 3). Seven components presented eigenvalues smaller than the Jolliffe cut-off (8.271×10^{-5}). In PC1, Procrustes 30 (corresponding to the ankle) had higher values on the positive axis, and in PC2, Procrustes 16 and 18 (corresponding to the knee and fetlock, respectively) presented higher values on the positive axis, but differences between sexes did not appear for any of these three Procrustes ($P < 0.05$). Discriminant function analysis based on the shape variables revealed no misclassification among individuals but in the alternative, more stringent jackknifing classification test, 17 specimens were misclassified (this test resulted in 81 percent misclassification between the two gender groups).

Entin (cited in Van Damme *et al.*, 2008) analysed thoroughbred horses and found that sexual dimorphism was only 1.007 in the shorter races and 1.014 in the longer races. Similarly, for standard-bred horse races from American tracks, the sexual dimorphism amounted to 1.015 for trotters and less than 1.001 for pacers. Although the standard for the Minorcan horse recognizes some differences among sexes, the extent of sexual dimorphism in adult shape between them is merely 0.062.

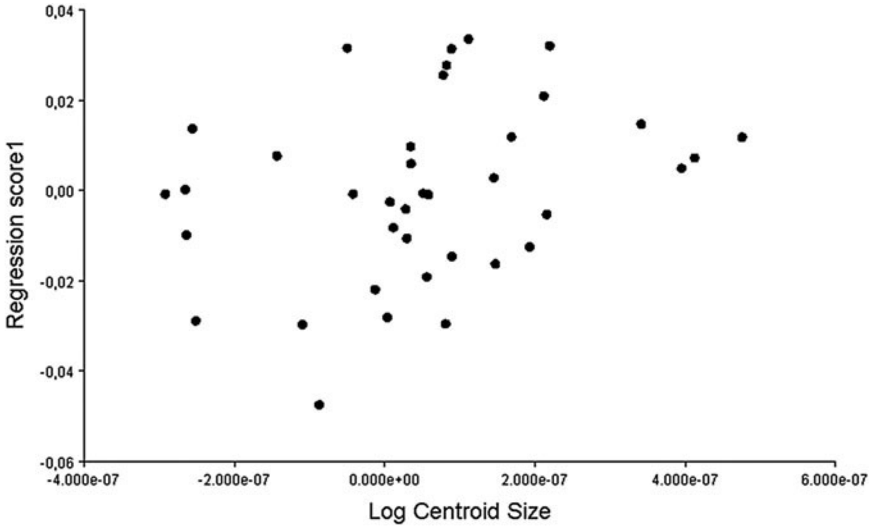

Figure 2. Relationship between log CS and size for all the specimens in this study, represented with shape scores as a function of log CS. Filled circles indicate specimens. *F*-test: $F_{30,7} = 0.945$; $P = 0.586$.

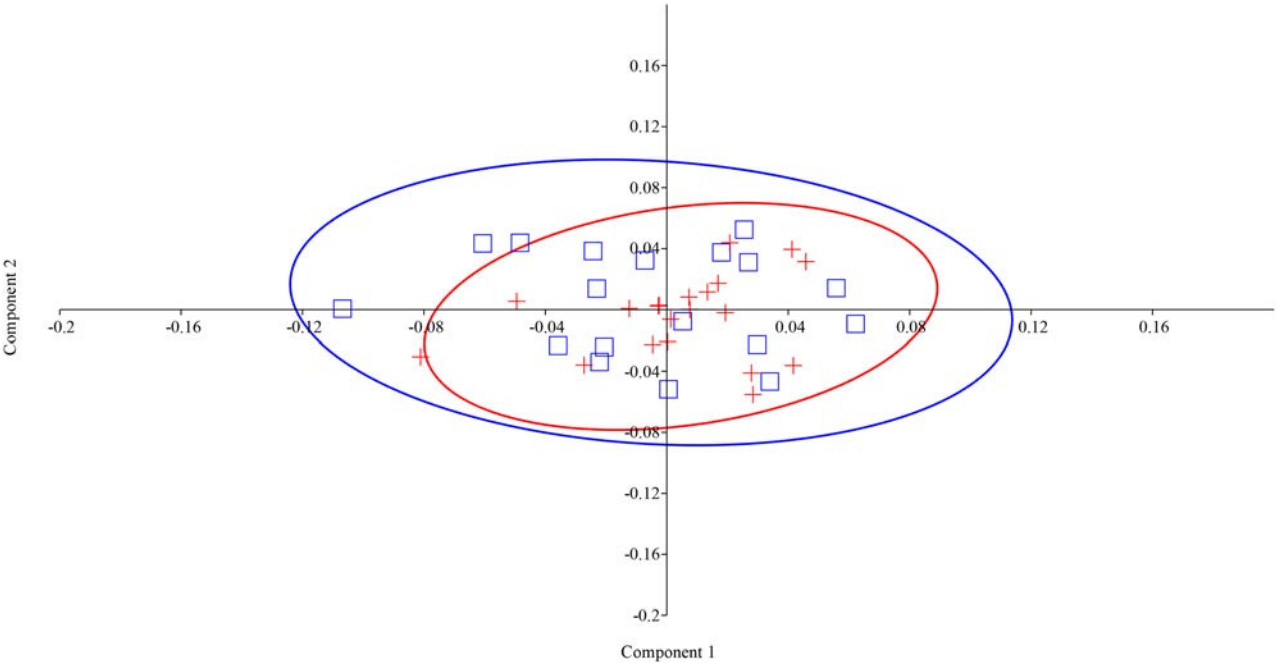

Figure 3. PCA. The first two PCs accounted for 64.01 percent (PC1 + PC2 = 38.14 + 25.87 percent) of the total shape variation. Crosses indicate males; open squares indicate females.

The conclusions are those expected for the modern horse: sexual dimorphism is very low, with males and females of the same breed having almost equal body size (Olsen, 2003). According to shape, the Minorcan horse is a low sexual dimorphism equine breed, but levels of form dimorphism (visually assessed) are probably greater than morphometric dimorphism, at least in a functional plane.

The researcher must remember, however, that "size" and "shape" are defined a priori and may not pertain directly to the geometry of the forms under study (Jungers, Falsetti and Wall, 1995). So, for instance, one must be aware that GMMs are based on the study of CS, not total body size, so perhaps if other landmarks were selected, different results could be achieved as "size" would be estimated differently. As the amount of biological information associated with constructed landmarks is dependent on the rules used for their construction, and most of the landmarks have been based upon the relative locations of the chosen functional (anatomical) points rather than upon the shape of the outline, no information relating to the curvature of form between landmarks, and

Figure 4. Vector plot. Straight lines show the consensus figure. See also Figure 1.

therefore general body curvature, was preserved. So, general and regional profiles ("silhouette") can still be visually discriminative sexual traits for horse breeds. This is why expressions in an official description such as "crest is moderately lean in mares but inclined to be more full in stallions" have sense only for a morphological description based on silhouette. Another problem is that these are empiric definitions that are moreover implicitly meshed with colloquial meanings of the same terms. The result is an imprecise and ineffective description and unclear communication for comparative studies between sexes, subpopulations or other breeds.

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Fibre quality of South American camelids in Argentina: a review

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Summary

Argentina's annual camelid fibre production is estimated at 60 000 kg for llama (*Lama glama*), somewhat more than 2 000 kg for guanaco (*Lama guanicoe*) and about 845 kg for vicuña (*Vicugna vicugna*). The potential for increasing these amounts is huge considering that barely 30 percent of llamas are shorn and considering the size of the wild camelid population in the country. A compilation of published and unpublished work confirms that almost 50 percent of the llamas are single-coated, about 40 percent have white fleeces and that average fibre diameter is about 22 µm in the main llama production area. In general, there is a wide variation in fleece weights and fibre quality between and within herds. However, a llama fleece classing and pricing system is not yet in place to motivate implementation of breeding programmes. Guanaco and vicuña fleeces are double-coated but the fine undercoat represents more than 80 percent of the fleece weight. The proportion of down fibre remaining after mechanical dehairing is only 50 percent in guanacos and 70 percent in vicuñas. The guanaco undercoat fibre diameter is about 16 µm and vicuña fibre diameter is typically between 13 and 14 µm. Both fibres are relatively short. Research is needed to establish optimum shearing season and shearing frequency that results in fibre quality demanded for handcraft and industry in each of the three species.

Keywords: *fibre, guanaco, llama, Patagonia, Puna, vicuña*

Résumé

La production annuelle de fibres de camélidés de l'Argentine est estimée à 60.000 kg pour le lama (*Lama glama*), à un peu plus de 2.000 kg pour le guanaco (*Lama guanicoe*) et à environ 845 kg pour la vigogne (*Vicugna vicugna*). Le potentiel d'accroissement de ces quantités est énorme compte tenu du fait qu'à peine le 30 pour cent des lamas sont tondus et compte tenu de la taille de la population de camélidés sauvages dans le pays. Une compilation de travaux publiés et non publiés confirme que pratiquement le 50 pour cent des lamas sont à couche unique (sans sous-poil), qu'environ le 40 pour cent ont des toisons blanches et que le diamètre moyen des fibres est de 22 µm dans la principale zone d'élevage de lamas. En général, il existe une grande variation inter- e intra-troupeaux dans le poids des toisons et dans la qualité des fibres. Malgré cela, un système de classement et de tarification des toisons des lamas n'a pas encore été mis en place pour motiver la mise en œuvre de ce genre de programmes. Les toisons des guanacos et des vigognes sont à double poil mais la bourre représente plus du 80 pour cent du poids de la toison. La proportion de fibres du duvet restantes après épilage mécanique est seulement du 50 pour cent chez les guanacos et du 70 pour cent chez les vigognes. Le diamètre des fibres du duvet est de 16 µm chez le guanaco et de 13–14 µm chez la vigogne. Dans les deux cas, les fibres sont relativement courtes. Des travaux de recherche s'avèrent nécessaires pour déterminer la saison et la fréquence de tonte optimales donnant lieu à la qualité de fibre demandée par les artisans et l'industrie pour chacune des trois espèces.

Mots-clés: *lama, guanaco, vigogne, la Puna, la Patagonie, fibres*

Resumen

La producción anual de fibras de camélidos en la Argentina se estima en 60.000 kg de llama (Lama glama), algo más de 2 000 kg de guanaco (Lama guanicoe) y unos 845 kg de vicuña (Vicugna vicugna). El potencial para aumentar esas cifras es enorme considerando que apenas el 30% de las llamas son esquiladas y considerando el tamaño de las poblaciones de camélidos silvestres de ese país. En una recopilación de trabajos publicados y trabajos inéditos se confirma que casi el 50% de las llamas tienen vellones de simple capa, el 40% de los vellones son blancos y que el promedio de diámetro de fibras es menor a 22 µm. En general se observa una gran variabilidad en pesos de vellón y en caracteres cualitativos de las fibras entre y dentro de tropas. Sin embargo todavía no hay un sistema de clasificación con precios diferenciales que motive al productor a implementar tales programas de mejora. Los vellones de guanacos y de vicuñas son de doble capa aunque la capa interior representa más del 80% del peso de vellón. El descerdado mecánico deja solo un 50% de fibras finas de guanaco y 70% de fibras finas de vicuñas. El diámetro de fibras de la capa interior de los guanacos es de aproximadamente 16 µm y el de vicuñas está entre 13 y 14 µm. Ambas fibras son relativamente cortas. Es necesario estudiar en los tres camélidos la época y la frecuencia de esquila que resulten en fibra de la calidad demandada por artesanos e industria.

Palabras clave: *llama, guanaco, vicuña, Puna, Patagonia, fibra*

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Introduction

South American camelids in Argentina include the domestic llama (*Lama glama*) and the wild guanaco (*Lama guanicoe*) and vicuña (*Vicuña vicuña*) species. Meat and fibre from llamas play an important role in securing food and cash for the most vulnerable rural population in the highlands of the Andes (Paz *et al.*, 2012). Argentina's wild camelid population of guanacos and vicuñas is the largest in the world and niche markets are developing for their fibres locally and internationally (Duba, 1999). The potential for expanding cash income from llama fibres and taking advantage from fibre niche markets appears to be big and is largely dependent on the offer of high-quality fibre (Frank *et al.*, 2006a). Quispe *et al.* (2009) and Cardellino and Mueller (2009) provide general information on South American camelid fibre production in Peru, Bolivia and Argentina. However, characterization of the quality of camelid fibres currently produced in Argentina is partial and circumscribed to specific populations (e.g. Mueller, Elvira and Sacchero, 2013). In view of the interest in designing national and regional development strategies for llama producers (PLC, 2008; MECON, 2010; PGTF, 2013) and the need of updating management programmes for vicuña and guanaco populations (MECON, 2006; Arzamendia, Baldo and Vilá, 2012), it becomes necessary to assess the quantity and quality of the fibre produced by these animal genetic resources in the country. This review examines published information and own unpublished data on domestic and wild camelid fibre quality in Argentina.

Figure 1. Map of Argentina, including provinces relevant in camelid fibre production or named in the text. Areas with llamas and vicuñas are dark shaded and correspond to "*Puna*" highland environments of Northern provinces. Areas with guanacos are light shaded and correspond to "*Patagonia*" desert environments of Southern provinces.

Population of camelids

The last national livestock census dates the year 2002 and indicates that there were 161 402 llamas in Argentina (INDEC, 2002). About 68 percent of that population was located in the province of Jujuy, 16 percent in Catamarca, 12 percent in Salta and only 4 percent in other provinces (Figure 1). A survey of 2008 in the North-Western Departments of Jujuy indicated that the llama population had increased since 2002 by 40 percent, largely at the expense of sheep (Roisinblit, 2011) and a study by FAO (2005a) shows that herd size of llamas is larger than reported in the census of 2002. It is estimated that the number of llamas by 2014 is at least 200 000 heads, with more than 90 percent reared in the Andean *Puna*. The *Puna* is a natural rangeland environment above 3 000 m above sea level occupying much of the province of Jujuy and parts of Salta and Catamarca. One can still find llamas in other, lower altitude and regions of the country, but these are likely to be in commercial or hobby farmer herds rather than in smallholder – low-input systems. It is generally accepted that there are no alpacas (*Lama pacos*) in Argentina. However, given that there are alpacas in contiguous environments of Chile and Bolivia, there may well be some alpacas in Argentina. These alpacas and llamas looking like alpacas, or perhaps crossed with alpacas, the so-called *Alpacunos*, would be included in the llama population figures.

Together with Peru, Argentina has the largest vicuña population in the world. A comprehensive survey on vicuñas yielded a total number of 131 220 animals (CNVG, 2007). This figure is much larger than expected since the previous census of 1980 estimated a population of only half of this number. Vicuñas share the *Puna* environment with llamas, 42 percent of all vicuñas are located in Jujuy, 31 percent in Catamarca and 19 percent in Salta. Only 8 percent of vicuñas are in other provinces. Guanacos inhabit the cold desert of *Patagonia* in Southern Argentina. A census carried out in the *Patagonian* provinces in 2000 estimated a population of 439 693 guanacos (Amaya, von Thüngen and De Lamo, 2001), 57 percent in Santa Cruz, 20 percent in Chubut and 23 percent in Río Negro and Neuquén. A recent survey held just in Santa Cruz Province, confirmed a guanaco population between 893 307 and 1 261 755 (Manero *et al.*, 2013). The huge jump in the estimated guanaco population of Santa Cruz may be related to the consequences of the eruption of the Hudson volcano in 1991. The ashes from the volcano covered extensive sheep grazing areas forcing the abandonment of farms and therefore facilitating the invasion of wildlife, including guanacos. The perception of experts is that the country's guanaco population may be close to 2 million, by far the largest in the world.

It should be noted that indiscriminate hunting of both camelid species in the past let to a massive reduction of the populations and risk of extinction, especially of vicuñas. Eventually Argentina subscribed the inclusion of guanacos and vicuñas in Appendix II of the "Convention on International Trade in Endangered Species of wild fauna and flora" (CITES). Hence, observing strict protection programmes which ban hunting and control fibre trade. The increasing population size of guanacos and vicuñas can therefore also be related to the successful implementation of the protection programmes. In fact, management programmes are necessary to maintain a balance of population size with available forage resources and other farming activities, such as the predominant sheep production (von Thüngen and Lanari, 2010).

Fibre production

The production of llamas is concentrated where poverty rate is high (FAO, 2005a). According to the census of 2002 there were a total of 2 803 farmers rearing llamas in mixed livestock production systems (INDEC, 2002) along Argentina. Figures from a census performed in 2008 in the province of Jujuy indicate that the number of farmers remained almost the same but the llama population increased 30 percent from 108 413 to 140 882 (Roisinblit, 2011).

The typical livestock holder in Jujuy runs 161 sheep, 69 llamas, 29 goats and 3 cows (Paz *et al.*, 2012). In the *Puna* region of Catamarca, a typical farmer holds 70 llamas in addition to about 97 sheep, 101 goats and 64 cattle (PROSAP, 2010). The main product of llamas is meat followed by fibre. In Jujuy raw fibre sales and fibre handcrafts sales contribute about 10 percent to the total income of a household (Paz *et al.*, 2012). The proportion of adult llamas which are shorn in a year varies between 20 and 40 percent, depending on the region, the price of the fibre and the needs of the farmers (Frank and Whebe, 1993). Most fibre collected from skins and from llamas for slaughter is home-used. Since a large proportion of the fibre collected is used within the households or is sold on informal markets, exact figures on the quantity of fibre produced are difficult to assess. It is estimated that the annual amount of llama fibre produced is about 60 000 kg, including about 20 000 kg home-used fibre (MECON, 2010).

Fibre and hides from vicuñas and guanacos were traditionally used for clothes, construction of shelters, textiles and decorations by indigenous people. Protection programmes were established restricting shearing to live animals under strict control and monitoring by trained wildlife authorities. Vicuña and guanaco fibre from monitored populations can be obtained either from free ranging animals or from animals kept captive in appropriately fenced paddocks. Recent research confirmed that by applying proper welfare protocols during capture and shearing, population demographics of both species are not altered (Arzamendia and Vilá, 2012; Rey *et al.*, 2012). The capture and shearing practices of vicuñas and guanacos kept in captivity were described by Amendolara (2001) and Amaya and von Thüngen (2001), respectively. Whereas the capture and shearing practices of free ranging vicuñas and guanacos were described by Rigalt, Sabadzija and Rojas (2006b) and by Lichtenstein and Carmanchahi (2012), respectively. Any farmer or community can start a wild camelid farming enterprise if the corresponding legal requirements are met. These requirements include regular controls of management plans based on population dynamics data which are difficult and expensive to obtain, therefore the actual number of farmers involved in wild camelid fibre harvest is very low. In 2013, there were only 14 farmers rearing vicuñas in captivity (DFS, 2014). In the same year, nine populations of free ranging vicuñas were captured and shorn (DFS, 2014). Owing to the wildlife management controls there are detailed figures on the amount of fibre collected from these legally shorn wild camelids. For example in 2013, a total number of 3 623 vicuñas were shorn and 845 kg of fibre was harvested (DFS, 2014). In 2008, a total number of 6 230 guanacos were shorn in 21 capture events and 2 117 kg of fibre was harvested in the two *Patagonian* provinces of Río Negro and Neuquén (Cancino, 2010, unpublished). For the remaining *Patagonian* provinces similar quantities of legally obtained guanaco fibre were estimated although guanaco fibre production figures have dropped in recent years. It is estimated that the legally obtained fibre from wild camelids represents only about two-thirds of the total fibre marketed. In any case, wild camelid fibre production is very low but it should be noted that its market price can be very high. For example, raw vicuña fibre averaged 500 USD/kg in public auctions in years 2011–2013. Table 1 shows a summary of current (2013) Argentinean domestic and wild camelid fibre production statistics.

Fleece and fibre traits

Important characteristics of the fleece and the fibre of camelids are: fleece structure, greasy fleece weight, clean washing yield, fibre colour, proportion of down fibre, mean fibre diameter, variation of down fibre diameter, fibre length and comfort factor (Frank *et al.*, 2006a; Frank, Hick and Adot, 2012). The relative importance of each of these characteristics depends on the camelid species and on the step of fibre marketing and fibre processing considered (McGregor, 2006). For llama farmers fleece

Table 1. Approximate population size, number of animals shorn, production units and fibre production of domestic and wild camelids in Argentina in 2013.

Species	Status	Animals	Animals shorn	Producers	Annual fibre production (kg)
Llama	Domestic	200 000	60 000	3 000	60 000
Guanaco	Wild	2 000 000	6 000[1]	20[2]	2 000[1]
Vicuña	Wild	131 000	3 623[1]	23[2]	845[1]

Source: Mueller *et al.* (2013) and own updated estimates.

[1] Legally shorn animals and legally marketed fibre.

[2] Management units, including breeding units and regularly captured wild populations.

weight is of major importance followed by fibre colour, fleece structure and mean fibre diameter. Mean fibre diameter is of major importance for the textile industry, followed by fibre length and fibre uniformity. For guanacos and vicuñas fleece weight is the most important trait followed by fibre length and less so the fibre diameter. The methodology used in the assessment of the various fibre traits may differ between studies and should be verified with the original publications. Our own assessments are based on standard methods applied at the INTA Bariloche Textiles fibre Laboratory in Rio Negro, Argentina (Table 2). Whenever appropriate, statistical analyses of own data were performed using mixed models with location, year, sex and age as fixed effects and considering differences in least-squares means significant at $P < 0.05$.

Fibre characteristics of llamas

In Argentina, as well as in Bolivia and Peru, there are two types of llamas. There is the *Pelado* (or *K'ara*) type and the *Lanudo* (or *T́amphulli* or *Ch'aku*) type. The two types can be differentiated phenotypically by their head, ear insertion and body structure and also by the quantity and quality of their fibre. A genetic base for this phenotypic differentiation is however not yet known (Iñiguez *et al.*, 1998). *Pelado* llamas have much less fibre on neck and extremities than *Lanudo* llamas. The *Pelado* type has a more meat animal body structure and produces less but somewhat finer fibre. The average fleece weight of *Pelados* under on-farm conditions is seldom higher than 800 g, whereas *Lanudos* have fleeces weighing more than 1 000 g (Cancino *et al.*, 2006). A comprehensive survey on llama types was undertaken by Hick *et al.* (2009) covering six sites located between 3 500 and 4 500 masl in the departments of Santa Catalina, Rinconada, Cochinoca and Yavi of the province of Jujuy. A total number of 10 760 animals from 143 herds were included in the study. About 56 percent of all animals were classified as *Lanudos*, 37 percent as intermediate and the remaining 7 percent were classified as *Pelados* and Alpacunos. The fleeces of both *Pelado* and *Lanudo* llamas may be single-coated (SC), double-coated (DC) or luster (L). Most *Lanudos* have single or luster coats and most *Pelados* have a double coat, but there are also intermediate types. SC fleeces have thick and thin crimped fibres. DC fleeces have highly visible guard fibres and crimped shorter down fibres. Luster fleeces have thick and thin straight fibres in curled staples with a thin tip (Frank, Hick and Adot, 2007). Fleeces in-between SC and L are defined as hemi-luster and fleeces in-between SC and DC are defined as intermediates. Following this definitions, Hick *et al.* (2009) classified 43 percent of llamas surveyed in Jujuy as being SC, 27 percent as DC, 18 percent as hemi-luster and the remaining fleeces as intermediate and luster.

Table 2. Camelid fibre traits and methodology of its assessment at the INTA Bariloche Textiles Fiber Laboratory in Rio Negro, Argentina.

Trait	Abbreviation	Unit	Assessment methodology
Greasy fleece weight	GFW	g	Scale
Pieces and belly wool weight	PBW	g	Scale
Total fleece weight	TFW	g	PBW + GFW
Clean washing yield	CY	%	ANZS[1]
Clean fleece weight	CFW	g	CY*GFW
Down yield	DY	%	IWTO 58[2]
Medullated fibres (kemp + med)	Med	%	IWTO 8
Mean fibre diameter	MFD	µm	IWTO 12
Coefficient variation of MFD	CVF	%	IWTO 12
Curvature	Curv	deg/mm	IWTO 12
Comfort factor	CF	%	IWTO 12
Fibre length	FL	mm	IWTO 30
Staple length	SL	mm	Ruler
Staple strength	SS	N/ktex	IWTO 30

[1] Australian – New Zealand Standards.

[2] International Wool Textile Organization.

Furthermore, the results of Hick *et al.* (2009) and Frank *et al.* (2006a) indicate that according to the coat colour 41 percent of llamas were white, 27 percent were brown or tan coloured and 16 percent chestnut coloured. Only 16 percent were of other colours such as black, grey or mixed. In the province of Catamarca, brown llamas are more common (Rigalt, 2010, unpublished). For example Frank and Nuevo Freire (1985) observed 87 brown (58 percent) and 27 black (15 percent) animals in a herd of 150 llamas in the region of Laguna Blanca in Catamarca.

Hick *et al.* (2009) classified 50 percent of llamas as superfine (<21.9 µm), 33 percent fine (22–24.9 µm), 14 percent medium (25–29.9 µm) and only 2 percent as coarse (>30

Table 3. Fibre quality of annually shorn llama males of different ages.

Age (years)	*N*	GFW (g)	CY (%)	MFD (µm)	CF (%)	FL (mm)	Med (%)	SS (N/ktex)
1	56	1 093	91.8	20.0	93.7	128	29	21.4
2	46	1 200	95.3	23.8	91.5	101	27	24.7
3	35	1 500	95.9	23.7	88.9	101	32	23.8

Source: Cancino *et al.* (2006).
See abbreviations in Table 2.

µm). The weighted average fibre diameter was 22.3 µm. Frank *et al.* (2006b) measured 22.9 µm in a mixed sex herd of Yavi, Jujuy. In Abra Pampa, Jujuy, Cancino *et al.* (2006) measured 20.0, 23.8 and 23.4 µm in samples collected from male llamas aged 13, 24 and 36 months, respectively. An increase of average fibre diameter with age was also observed by Frank *et al.* (2006b).

In the province of Catamarca, Frank and Nuevo Freire (1985) obtained a fibre diameter of 26.8 µm from a llama herd ($n = 70$) in Laguna Blanca. Rigalt (2010, unpublished) collected samples from eleven llama herds in Laguna Blanca, Antofagasta and Santa María. Fibre diameter ranged 21–25 µm and other traits also varied considerably (Table 4).

Away from their traditional rearing environment of the highlands of Jujuy, Salta and Catamarca, there are llama herds in other provinces and at lower altitude. For example, in the province of Neuquén at 800 masl, where summers are frosty and winters are cold with intensive snow cover, a large llama herd is run to produce fibre for a handcraft production company (Cancino 2010, unpublished). The foundation animals of this herd came from the highlands of Jujuy and the overall average fibre diameter of the herd is 24.4 µm ($n = 661$). Fibre diameter of males and females at first shearing is 21.8–23.8 µm and at second and third shearing between 24.9 and 29.9 µm (Table 5). In milder and more humid environments of the provinces of San Luis and Santa Fe, the fibre diameter of adult llamas is between 23.5 and 27.2 µm.

Llamas can also be found in other provinces of Argentina such as Río Negro, Córdoba and Buenos Aires. Coates and Ayerza (2004) report fibre quality of llamas in Buenos Aires, which originally were introduced from the highlands. Females and males averaged fibre diameters of 29.3 and 29.0 µm, respectively. These results for fibre diameter are much higher than figures obtained in the highlands, which might be attributed to the better feeding conditions in this environment and production system.

The observed phenotypic differences within and between herds in fleece weights and fibre diameter and the medium-to-high heritabilities reported for these traits (Wurzinger *et al.*, 2006; Frank *et al.*, 2011) enable successful selective breeding. Llama breeding programmes aimed at improving fibre traits were implemented in Abra Pampa (Jujuy) and in Santa Maria (Catamarca) but the results are not documented. In INTA Abra Pampa, the breeding programme started in 1993 with animals grouped into five coat colour herds. Total herd size by 2013 is 650 breeding animals. Birth weight and weaning weight at the age of 7–8 months are recorded and fleece samples are collected from males at first shearing. Males are selected in three stages. First on uniformity of coat colour and sound body conformation, then selection is based on records of body weight, fleece weight and mean fibre diameter. In a

Table 4. Fibre quality of adult llamas in herds of Catamarca (average ± SD).

Herd	Altitude (masl)	*n*	DY (%)	MFD (µm)	CVF (%)	CF (%)	Curv (deg/mm)	FL (mm)
L	3 800	33	n.a.	25.4 ± 3.7	28.9 ± 2.4	79.1 ± 13.8	n.a.	118 ± 33
F	3 400	7	99.8 ± 1.3	22.6 ± 4.4	29.1 ± 1.8	85.4 ± 12.9	43.0 ± 6.0	92 ± 35
I	3 300	6	n.a.	22.5 ± 2.9	29.8 ± 2.1	88.8 ± 7.5	n.a.	128 ± 22
J	3 300	17	n.a.	22.7 ± 2.7	25.6 ± 3.0	89.6± 8.5	n.a.	134 ± 50
A	3 200	30	92.4 ± 5.8	23.1 ± 3.1	31.1 ± 3.4	85.3 ± 9.2	47.5 ± 7.7	144 ± 46
B	3 200	13	94.6 ± 3.1	24.2 ± 3.4	29.7 ± 3.0	84.2 ± 11.4	47.9 ± 6.2	108 ± 32
H	3 200	7	89.7 ± 5.8	21.1 ± 2.6	28.1 ± 2.2	91.3 ± 6.7	43.6 ± 6.1	121 ± 27
K	3 200	36	n.a.	25.0 ± 4.3	28.8 ± 3.1	78.8 ± 16.5	n.a.	67 ± 33
C	1 800	9	94.9 ± 1.8	23.0 ± 5.0	31.2 ± 3.6	83.2 ± 17.2	48.4 ± 5.5	129 ± 49
D	1 800	11	92.0 ± 4.3	23.0 ± 3.7	28.0 ± 1.4	86.0 ± 11.6	46.0 ± 8.4	107 ± 37
E	1 800	7	91.0 ± 2.1	25.9 ± 4.0	29.9 ± 3.2	77.8 ± 15.2	44.1 ± 6.2	66 ± 16
G	1 800	18	91.7 ± 6.8	22.9 ± 2.5	29.6 ± 3.5	87.9 ± 8.0	50.4 ± 9.9	66 ± 24
Average			93.0 ± 4.5	23.9 ± 3.5	29.2 ± 2.9	83.6 ± 12.0	47.2 ± 7.4	106 ± 36

Source: Rigalt (2010, unpublished).
n.a.: not available.
See abbreviations in Table 2.

Table 5. Fibre quality of llamas in lowland environments.

Province	Category	Year	Age	Shearing	*n*	MFD (μm)	CVF (%)	CF (%)	FL (mm)
Neuquén	Males	2007	2 years	First	70	23.2	23.1	88.3	128.0
Neuquén	Males	2008	2 years	First	84	21.8	21.8	92.8	125.8
Neuquén	Males	2009	2 years	First	63	22.5	27.8	89.3	129.7
Neuquén	Females	2008	2 years	First	119	21.8	21.7	92.6	120.1
Neuquén	Females	2009	2 years	First	62	23.8	28.3	83.8	115.0
Neuquén	Females	2009	4 years	Second	30	24.9	27.7	83.8	107.2
Neuquén	Females	2009	6 years	Third	36	28.2	26.7	69.4	99.2
Neuquén	Females	2009	> 6 years	n.a.	79	28.6	27.3	67.3	95.4
Neuquén	Stud males	2009	4 years	Second	8	25.6	25.9	81.6	115.0
Neuquén	Stud males	2009	> 4 years	n.a.	12	29.9	23.7	62.3	113.2
Neuquén	Stud females	2009	4 years	Second	16	25.8	26.7	77.2	114.1
Neuquén	Stud females	2009	>4 years	n.a.	15	27.2	27.1	74.1	109.7
Neuquén	Males + females	2010	4 months	First	67	26.2	28.0	76.8	77.1
San Luis	Females	n.a.	Adult	n.a.	93	25.2	26.7	81.5	n.a.
San Luis	Stud males	n.a.	Adult	n.a.	17	27.2	26.7	70.8	n.a.
San Luis	Males	n.a.	Adult	n.a.	19	26.3	25.9	78.0	n.a.
San Luis	Tuis	n.a.	1–2 years	n.a.	n.a.	23.0	25.4	88.1	n.a.
Santa Fe	Females	n.a.	Adult	n.a.	43	23.4	29.6	85.2	116.0
Santa Fe	Stud males	n.a.	Adult	n.a.	4	23.5	29.3	85.3	93.0
Santa Fe	Not defined	n.a.	n.a.	n.a.	27	22.1	30.2	88.6	176.0
Average						25.0	26.5	80.8	114.7

Source: Cancino (2010, unpublished).
n.a.: not available.
See abbreviations in Table 2.

third stage, before mating or sale, a final visual inspection is done. Cancino, Rebuffi and Aller (2001b) recorded greasy fleece weights of 1 080 g ($n = 74$), 1 150 g ($n = 48$) and 1 260 g ($n = 13$) for males from the Abra Pampa base population (general herd) at the age of 1, 2 and 3 years, respectively. Selected males in the nucleus had an approximately 10 percent higher fleece weight and better fibre quality than the base population.

Fibre characteristics of guanacos

Shearing of guanacos is performed with mechanical scissors and usually includes fleece and belly sites, in general only the neck of the animal is left unshorn. It is uncommon that the same free-ranging guanaco is caught for shearing in consecutive years; therefore in a particular shearing event animals with different fibre growth periods are shorn. Shearing season seems not to affect significantly fleece weights but first shearing of an animal yields more fibre than a second shearing of the same animal (von Thüngen *et al.*, 2012). It has been shown that lifetime fibre production is higher with annual shearing's (Cancino *et al.*, 2008). Fleece weight of adult guanacos is in the range 300–700 g and animals at the age of 1 year have been recorded with fleece weights up to 420 g (Bacchi, Lanari and von Thüngen, 2010). Guanaco fleeces, such as vicuña fleeces, have two types of fibres: fine and short down fibres and coarse and long guard fibres. Although the guanaco down yield is about 80–90 percent (Table 6) the actual proportion of down fibre obtained after mechanical dehairing is usually only about 50 percent (Adot, Cossio and Maguire, 2008). Some producers clean the fleeces from soil and vegetable matter, and take out the guard fibres before selling the fleece or submitting for testing. Depending on the cleaning level, the proportion of down fibres measured in the cleaned fraction may increase to values of 65–95 percent (Sacchero, Maurino and Lanari, 2006). Fibre diameter varies between animals and age groups. Bacchi, Lanari and von Thüngen (2010) observed less fibre production (159 versus 254 g) and finer fibres (14.2 versus 15.0 μm) in guanaco calves (animals up to 1 year but with primary incisors) than in yearling guanacos (animals 1–2 years of age and with permanent incisors). Sacchero, Maurino and Lanari (2006) reported a fibre diameter ranging between 14.5 and 19.3 μm and a proportion of down fibres between 64.9 and 94.5 percent in seven different guanaco populations of the North of *Patagonia.* In that study, MFD of the whole sample was compared with the mean fibre diameter of down fibres. Down fibres were only 0.6 μm finer than all fibres in the sample. A further study of fibre quality in several guanaco populations is summarized in Table 6. It should be noted that on average the within sample fibre diameter variability (CVF = 31.3 percent) is more than four-times the between-animal fibre diameter variability (CV of MFD = 7.5 percent), whereas the between-animal variability in down fibre length is high (CV of FL = 27.0 percent). Llama herds G and J sampled for this study grazed on very poor rangelands and this may explain the particular short fibres measured (Table 6).

In another study, three guanaco populations were investigated and fibre diameters of 14.6 ± 0.7 to 16.5 ± 1.7 μm

Table 6. Fibre quality of adult guanaco herds and its between-animal coefficient of variation (CV, %).

Province	Herd	Year	*n*	MFD (μm)	CV	CVF (%)	CV	CF (%)	CV	FL (mm)	CV
Neuquén	A	2005	7	15.2	7.4	38.6	12.8	98.0	0.6	24.1	20.7
Neuquén	A	2006	23	16.0	6.4	33.6	14.6	98.2	0.5	24.2	22.5
Neuquén	A	2007	83	17.3	8.4	35.7	12.3	97.3	1.5	n.a.	n.a.
Neuquén	B	2005	101	15.0	5.8	36.6	14.5	n.a.	n.a.	n.a.	n.a.
Neuquén	B	2006	212	15.5	7.2	38.6	18.3	97.7	1.2	28.6	27.8
Neuquén	B	2007	218	16.3	10.0	18.7	9.6	99.7	1.0	n.a.	n.a.
Rio Negro	C	2005	34	13.8	6.5	21.6	17.5	95.6	1.7	n.a.	n.a.
Rio Negro	C	2006	12	15.7	5.5	45.1	8.7	97.1	0.5	35.4	25.2
Rio Negro	D	2007	165	17.6	8.7	35.9	11.9	97.1	1.6	20.0	22.2
Rio Negro	E	2007	72	15.9	5.9	35.9	13.6	n.a.	n.a.	16.8	25.6
Rio Negro	F	1998	36	15.5	5.3	32.8	11.1	n.a.	n.a.	43.0	n.a.
Rio Negro	F	1999	7	16.2	6.9	23.2	14.9	99.3	0.3	26.4	18.5
Rio Negro	F	2000	13	14.6	4.9	23.6	12.2	99.6	0.2	25.5	15.1
Rio Negro	F	2001	104	15.6	8.2	24.5	15.2	99.1	0.6	28.4	24.6
Rio Negro	F	2002	89	16.0	9.8	31.8	14.9	n.a.	n.a.	33.3	30.0
Rio Negro	F	2004	26	14.5	5.5	20.6	13.0	n.a.	n.a.	35.8	28.3
Rio Negro	F	2005	47	15.4	6.4	24.5	22.3	n.a.	n.a.	26.0	46.3
Rio Negro	F	2007	130	16.6	9.6	32.7	14.4	98.1	1.0	n.a.	n.a.
Rio Negro	G	2005	10	14.9	3.8	41.4	11.0	97.8	0.4	16.6	37.4
Rio Negro	G	2006	34	15.3	5.6	37.1	10.6	97.8	0.7	23.6	24.3
Rio Negro	G	2007	21	14.9	8.6	39.7	11.4	97.7	1.8	19.2	14.1
Rio Negro	H	2007	24	16.3	5.5	34.3	12.4	98.2	0.5	28.0	16.9
Rio Negro	I	1999	13	16.3	7.9	26.6	10.3	n.a.	n.a.	29.2	41.5
Rio Negro	I	2000	19	16.3	11.9	25.1	12.7	n.a.	n.a.	39.5	39.6
Rio Negro	I	2001	19	16.4	12.2	25.5	11.1	n.a.	n.a.	38.4	40.0
Rio Negro	I	2002	18	17.0	10.4	32.0	10.0	n.a.	n.a.	33.4	36.5
Rio Negro	J	2004	24	15.7	8.6	22.9	11.5	99.3	0.6	14.3	22.8
Rio Negro	J	2006	9	16.7	9.3	36.1	20.4	n.a.	n.a.	16.9	16.8
Santa Cruz	K	1999	27	14.7	5.6	31.8	13.4	n.a.	n.a.	38.0	23.8
Average				15.8	7.5	31.3	13.3	98.1	0.9	27.7	27.0

Source: Sacchero and Cancino (2013, unpublished).
n.a.: not available.
See abbreviations in Table 2.

and fibre length of 14.4 ± 3.3 to 38.1 ± 9.1 mm were recorded (von Thüngen *et al.*, 2005). A project run by a smallholder cooperative in the province of Mendoza managed to shear a total of 569 guanacos captured in 12 roundups in the period 2005–2010 and obtained 208.5 kg fibre with an average fibre diameter of 15.8 μm and fibre length of 36 mm (Lichtenstein and Carmanchahi, 2012). It should be noted that in some years of this study the belly area of the animals were left unshorn.

Fibre characteristics of vicuñas

Vicuñas are either shorn with scissors or with electrical or mechanical shearing equipment. It is thought that shearing with scissors or shearing only part of the animal's body reduces the risk of cold-stress but there is no research confirming this. There are also accounts on higher (up to 100 g more) fibre harvest from mechanically shorn animals rather than from animals shorn with scissors, although mechanical shearing is said to yield more contaminated fibre. For the subspecies *Vicugna vicugna vicugna*, which is the one present in Argentina, extensive information on the fibre characteristics is available from a herd kept in captivity at the INTA Abra Pampa experimental station (Rebuffi, 1999). The herd was established in 1965 with only 16 animals captured in the wild, but since then the number has increased to almost 1 300. Animals from this herd are distributed to private farmers interested in starting a commercial herd. Vicuña fibre from this station is sold to local artisans and to dehairing companies which export the processed fibre. Results from the INTA Abra Pampa herd show average MFD of 13.4 μm and FL of 47.3 mm with a high range of values between animals (Table 7). Additional information from this herd and Catamarca populations is summarized in Table 8. The Catamarca data were analysed for year and sex effect. Year effects resulted significant ($P < 0.05$) only for MFD and CVF; sex was not significant for any trait.

Figure 2 shows the development of total greasy fleece weight and fibre fineness in males according to the age of first shearing. A clear trend in increasing fleece weight with age can be observed. The linear regression shows an increase of 15.6 g/year ($r^2 = 0.97$). On the other hand the increase of fibre diameter with age is very low and seems to disappear at the age of 7–8 years. In later studies of the same herd, average fibre diameters of 13.8 μm (SD 3.0 μm) for de-haired samples and 14.1 μm (SD 4.5 μm) from complete samples were recorded (Sacchero and

Table 7. Fibre characteristics at first shearing of male vicuñas in Abra Pampa.

Trait	*n*	Average	Minimum	Maximum
Greasy fleece weight (g)	232	201	90	430
Clean fleece weight (g)	225	178	81	389
Pieces and belly wool (g)	232	111	20	235
Total fleece weight (g)	232	312	120	580
Staple length (mm)	225	49.7	25	80
Fibre length (mm)	217	47.3	25	71
Clean yield (%)	225	88.0	77.2	97.5
Mean fibre diameter (μm)	229	13.4	11.8	15.6
Comfort factor (%)	229	99.0	99.9	96.9
Continuous medullated fibres (%)	172	1.82	0	9
Discontinuous medullated fibres (%)	172	4.26	0	25
Kemp fibres (%)	172	1.89	0	7
Normal fibres (%)	172	92.0	72	100
Staple strength (N/ktex)	96	46.3	11.4	89.3

Source: Adapted from Rebuffi (1999).

Mueller, 2005). The difference being small given that down yield of vicuñas is above 85 percent (Tables 7 and 8) and few guard fibres contribute to increase fibre diameter. Mechanical dehaired vicuña fibre yields about 70 percent of down fibre (Adot, Cossio and Maguire, 2008).

Cancino, Rebuffi and Aller (2001a) analysed data from vicuñas reared in captive systems by private producers. In vicuña males, a range in fibre diameter between 11.9 and 22.0 μm with an average value of 13.6 μm (SD 4.0 μm) was observed. Production data per year of shearing and sex of animals from different producers are presented in Table 9. Note that these animals were shorn in a bi-annual interval. In Table 10, the effect of successive bi-annual shearing of the same animals is presented. One can observe that the fibre length remains more or less constant after the first shearing and females produce in general less fibre than males and castrated males.

Information on different fibre traits from vicuñas captured in the wild is still very scarce. Captures of wild vicuñas were organized by the Laguna Blanca community in Catamarca in the years 2003, 2004 and 2005. In these occasions greasy fleece weight from 169, 77 and 93 animals was measured and resulted 206, 286 and 313 g, respectively (Rigalt, Sabadzija and Rojas, 2006b). Rigalt *et al.* (2006a) took fleece samples from 61 of these vicuñas and recorded an average fibre diameter of 12.6 μm (SD 4.4 μm) and fibre length in the laboratory of 37.7 and 31.0 mm measured in the field with a ruler. Only animals, which were not shorn in the previous year, were included in the shearing. In captures of vicuñas from populations in higher altitudes (3 800 masl) in the year 2008 and 2009 values for greasy fleece weight exceeded the average values from Abra Pampa and Laguna Blanca (3 200 masl), with similar fibre diameter but longer staples. For example in Laguna Colorada (3 650 masl), the average greasy fleece weight of 207 animals reached 460 g, with some animals even reaching 1 000 g. One possible explanation for this could be that the lower temperature at higher altitudes induces more fibre production, but research is needed to determine possible confounded effects such as feed availability or body size.

Discussion

Argentine camelid fibre quality in perspective

From the available data some general observations and particularities of Argentinian llama fibres can be made. Almost half of the llamas are of the SC *Lanudo* type, whereas less than a quarter is of the double-coated, low fibre producing *Pelado* type. The advantage of SC animals is that dehairing efforts can be reduced, the fine fibre yield is higher and therefore the value of their fleece is higher. This contrasts findings in Bolivia where 74.4 percent of llamas were reported to be of the *Pelado* type (FAO, 2005b). It should be noted however that there are also llama populations in Bolivia and Peru with similar characteristics of the Argentinean highland llama populations (Maquera, 1991; Martinez, Iniguez and Rodríguez, 1995; Iñiguez *et al.*, 1998; Stemmer *et al.*, 2005). One important feature of the fibre from Argentinian llamas is that although white colour is predominant a wide range of colours is covered. A survey indicated that black, white and grey fibre fetch best prices (PROSAP, 2010). More than 80 percent of the Argentinian llama fibre is finer than 24 μm (Hick *et al.*, 2009), which is equivalent to the Peruvian “superfine” (21–24 μm) class of commercial alpaca fibre. In comparison only 10 percent of *Huacaya* alpacas of Australian herds have fibre diameter below 24 μm (McGregor, 2006).

Table 8. Fibre quality of adult vicuñas and its between-animal coefficient of variation (CV, %).

Location	Year	*n*	MFD (μm)	CV	CVF (%)	CV	CF (%)	CV	DY (%)	CV	SL (mm)	CV
Abra Pampa	2012	132	12.8	10.0	39.1	22.5	99.0	0.5	83.3	9.0	34.7	16.6
	2014	65	13.9	10.1	45.6	10.8	98.6	1.4	82.7	7.5	34.5	10.0
Catamarca	2011	93	12.1	6.8	37.1	22.3	99.1	0.9	86.0	8.7	n.a.	n.a.
	2014	21	12.8	7.4	27.8	22.6	99.5	0.5	91.2	6.2	30.8	27.9

Source: Sacchero, Lamas and Rigalt (2014, unpublished).
n.a.: not available.
See abbreviations in Table 2.

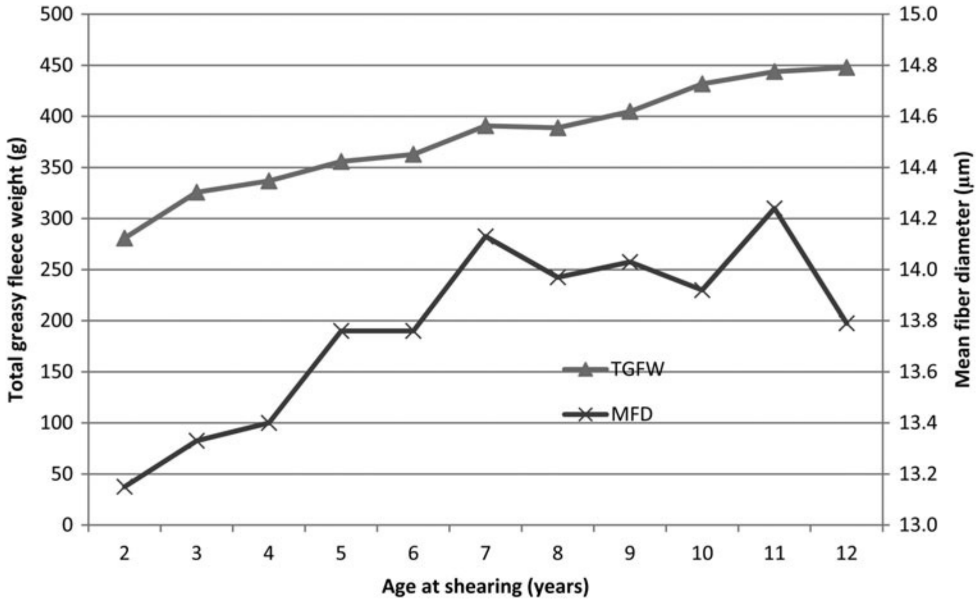

Figure 2. Total greasy fleece weight (TGFW) and mean fibre diameter (MFD) in male vicuñas shorn for the first time at different ages. *Source*: adapted from Rebuffi (1999).

Standard deviations in fibre quality traits across different herds and groups of animals are large. For example, the between animals coefficient of variation for fibre diameter in 12 different llama herds (Table 4) is on average about 15 percent (3.5/23.9). This is high if compared with the coefficient of variation for wool fibre diameter in sheep. One possible explanation for this large CV is that animals of different ages are included in the llama sampling, but it also can be a result of low selection pressure for uniformity.

Fibre length can be an issue and one of the problems in analysing reports on fibre length is that in many cases the growth period is not mentioned and in some other cases it is not clear if the fibre samples have undergone a manual dehairing before analysis. Standard IWTO 12 procedures are based on samples without previous dehairing. However, for example, results reported by Siguayro and Aliaga (2009) on fibre quality from *Pelado*-type llamas from Peru are based on previously dehaired samples. Eliminating kemp fibres from the raw fibre sample reduces the fibre diameter of the remaining fibre by 1–2 µm. Coates and Ayerza (2004) also discuss this sample preparation procedure as a possible source for differences between populations.

Little information is available on fibre quality of wild camelid populations in other countries. Quispe *et al.* (2010)

Table 9. Vicuña fibre production of private producers according to year and sex.

Year	Producers	Category	*n*	GFW (g)	PBW (g)	TFW (g)	FL (mm)
1995	2	Males	5	301	83	384	37
		Females	15	270	91	361	35
		Castrated	24	274	91	364	32
1997	10	Males	103	204	147	351	46
		Females	84	207	150	357	47
		Castrated	23	216	213	429	49
1998	5	Males	6	160	135	295	50
		Females	57	145	166	311	47
		Castrated	1	215	195	410	35
1999	11	Males	31	209	122	331	39
		Females	74	216	118	334	39
		Castrated	116	236	125	361	40
2000	5	Males	14	210	124	334	50
		Females	51	205	120	325	39
		Castrated	33	224	131	355	43
2001	10	Males	48	173	144	317	40
		Females	114	172	139	311	39
		Castrated	54	199	170	369	39

Source: Cancino *et al.* (2001a).
See abbreviations in Table 2.

Table 10. Fibre production of vicuñas according to sex and shearing stage (bi-annual) in private herds.

Shearing stage	Males (*n*=44)				Females (*n*=162)				Castrated (*n*=79)			
	GFW (g)	PBW (g)	TFW (g)	SL (mm)	GFW (g)	PBW (g)	TFW (g)	SL (mm)	GFW (g)	PBW (g)	TFW (g)	SL (mm)
First	186	128	314	48	201	130	329	43	265	133	398	43
Second	204	130	334	38	183	130	310	35	203	173	376	37
Third	205	137	340	37	162	140	297	33	218	141	359	37
Fourth	217	118	335	40	196	121	317	38	276	170	446	39

Source: Cancino *et al.* (2001a).
See abbreviations in Table 2.

sampled vicuñas in Huancavelica, Peru at 4 600 masl and obtained GFW of 189.7 g which is considerably less than most fleeces weighted in the Argentinian *Puna*. Fibre length in Huancavelica was 30.9 mm, MFD was 13.2 µm (CV 19.5 percent) and fibre curvature was 79.9 deg/mm. The lower fleece weights and shorter fibre length in this population compared to the figures from the *Puna* may be related to differences in the environment but also due to differences in the shearing system and fibre conditioning.

Improvement of camelid fibre quality

Fibre quality depends on several environmental and genetic factors. In low-input systems farmers have limited control over forage supply but can adjust shearing procedures to improve fibre quality. For example shearing on clean surface and basic conditioning and skirting as well as packing can considerably improve fibre offered. Fibre growth in llamas grazing *Puna* rangelands is affected by nutritional restrictions from July to October. If shearing is annual and during this period, instead of the regular shearing date of November, the breaking point of the fibres, due to nutritional stress, would be closer to the extremes of the fibre and therefore the effective fibre length would be larger than fibres shorn at another point of time. With bi-annual shearing regimes fibre breaking points are unavoidable and staple strength depends on health and nutritional status along the 2 years of fibre growth. Staple strength is especially important for fibre destined to mechanical dehairing, due to the tensions imposed in the process. Further studies on the profile of fibre diameter along the staples in different production areas would help to identify the best shearing dates and shearing frequencies.

Markets and processing

The llama fibre production could easily be doubled by an increase in the number of llamas shorn and by an increase in the frequency of their shearing. The main incentive for this to happen is of course the price paid for the fibre. Llama fibre is usually sold unclassified but there are some communities in Jujuy who organize a joint offer of classed fibre (Lamas, 2013). These communities clean the fleeces from soil and other contaminations and apply a basic classing protocol based on nine colour classes and four visually assessed fibre fineness classes. Homogenous groups combining colours and fineness classes are formed and tendered. Such fibre sales fetch up to double the price an individual farmer would get for his llama fibre. Thus, classing fleeces according to quality and strengthening the handling and storage capacities of communities improve income and interest to produce better and more fibre. The physical characteristics of the camelid fibres make up its commercial value, but also do so intangible features such as the association of the fibre with particular environments and exotic cultures. Llama and vicuña fibre is often associated with the Andean highlands and the remains of the Inca-culture, whereas guanacos are associated with the vast *Patagonian* desert. In order to be able to exploit these intangible values, promotion and marketing skills are needed. In Argentina, there is a lack of llama producerś organizations which promote production of high-quality fibre, especially in the regions of origin.

There is a shortage of legally produced vicuña fibre for the local artisan market, where an estimated volume of 400 kg per year is needed. If this demand cannot be satisfied with legally obtained fibre and at a reasonable price, poaching will increase. Artisans prefer processing individual vicuña fleeces rather than bulk vicuña fibre to be able to separate more easily guard hairs and classify for fibre colour. Skilled artisans separate up to six vicuña colours from a single fleece. About one-third of the fleece is white. The different colours are spun separately into yarn which is then transformed into “Ponchos” and other popular garments using traditional looms.

Guanacos produce down fibres that are at the lower limit of fibre length that is acceptable by the textile industry. Short fibres are also difficult to spin by artisans. Most guanaco fibre samples have an average fibre length in the range 25–35 mm and are processed through the woollen system. With coefficients of variation of fibre length at 30 percent there is a high proportion of fibres below 10 mm which typically would produce pilling in finished products. Often guanaco fibres are also tender and break in the carding process and therefore reduce its yield. Thus, pure guanaco fibres are difficult to get through the combing process. Local experiences indicate that guanaco fibres can be successfully blended with merino wool (in for example 20:80 proportions, respectively) in order to increase spinning performance and produce high-valued products (Guenguel, 2014). Vicuñas have a slightly higher fibre length but face similar challenges as guanaco fibres. Studies to identify fibre quality differences along the fleece of guanacos of both sexes and different ages have been performed in order to detect eventual fibre classing needs (Cancino, Mueller and Giovannini, 2011). Hick *et al.* (2005) conclude that such classing should be based on the results of differences in dehaired fibre quality along the fleece. The cost-effectiveness of such additional work remains an open question.

Fine-tuning the shearing dates and shearing regime can improve the length, down yield and fibre diameter of these special fibres. It seems also necessary to study more guanaco and vicuña ecotypes and populations to investigate if there is a relation between fleece weight, fibre length, altitude and temperature. This knowledge would help to better target wild camelid populations for capture and shearing.

Spinning camelid fibres on farm and selling the yarn can increase profit substantially (von Thüngen and Lanari, 2010). At the community level, small-scale fibre processing plants such as the “Mini-mills” (Belfast Mini-mills, 2014) are being tested in the country. At these small scale but versatile mills, yarn and felt products are already produced with cashmere, wool and camelid fibres in various blends (Sacchero, 2014).

Conclusions

The Puna highlands in the northwest of Argentina and the vast Patagonian cold desert in the South are home to llamas, vicuñas and guanacos which produce noble fibres used by artisans and the textile industry to produce high-valued textile products. Fibre production potential is high as is further improvement of fibre quality and added value.

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Analysis of pig breeding management and trait preferences in smallholder production systems in Kenya

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Summary

Data on breeding management, breed and trait preference for pigs were collected from smallholder farmers in Kiambu and Kakamega Counties of Kenya. The production systems evaluated were semi-intensive and extensive and depicted varying pig production intensities, production objectives, pig performances as well as farmers' breed and trait preferences. The perception of the importance of traits was evaluated to obtain a more balanced objective view on production and/or breeding objectives. The data collected were analysed through computation of indices, which represented a weighted average of all rankings of a particular trait. In the semi-intensive system, preference for performance traits such as size, growth rate and body weight, scored the same index (0.181), followed by the reproduction trait – prolificacy (0.161). In the extensive system, the indices for these traits were 0.187, 0.183, 0.163 and 0.106, respectively. Spearman's non-parametric rank correlations were calculated for ranking of traits of economic importance to indicate the directional effects and plausible trade-offs between traits. In the semi-intensive system, correlations were moderate between growth rate and both size and weight. In the extensive system, correlations were moderate for growth rate with both size and body weight. Appropriate breeds that suit the divergent production systems need to be identified and utilized based on performance and adaptability to ensure efficient resource use.

Keywords: *breeding objectives, extensive production system, genetic improvement, performance traits, semi-intensive production system*

Résumé

Des données sur la gestion de la reproduction et sur la préférence en matière de races et caractéristiques ont été recueillies chez des petits éleveurs de porcs des comtés de Kiambu et Kakamega au Kenya. Les systèmes de production évalués ont été le système semi-intensif et le système extensif. Des différences ont été observées entre les systèmes pour ce qui est de l'intensité de la production porcine, les objectifs de production, les performances des porcs et les préférences des éleveurs quant à la race et les caractéristiques. La perception de l'importance des différentes caractéristiques a été évaluée afin d'obtenir une vision objective plus équilibrée des objectifs de production et/ou de la sélection. Les données recueillies ont été analysées en calculant des indices consistant en une moyenne pondérée de toutes les positions d'une caractéristique donnée dans le classement. Dans le système semi-intensif, des paramètres productifs tels que la taille, le taux de croissance et le poids corporel ont atteint le même indice de préférence (0.181), suivis par le paramètre reproductif prolificité (0.161). Dans le système extensif, les indices de ces paramètres ont été 0.187, 0.183, 0.163 et 0.106, respectivement. La corrélation non paramétrique des rangs de Spearman a été calculée pour classer les caractères à importance économique dans le but de mettre en évidence les effets directionnels et de possibles compensations entre caractéristiques. Dans le système semi-intensif, ainsi que dans celui extensif, la corrélation du taux de croissance a été modérée aussi bien avec la taille qu'avec le poids corporel. Sur la base de la productivité et l'adaptabilité, il s'avère nécessaire d'identifier et d'utiliser des races appropriées s'adaptant aux systèmes de production divergents afin d'assurer une utilisation efficace des ressources.

Mots-clés: *objectifs de la sélection, système extensif de production, amélioration génétique, caractères productifs, système semi-intensif de production*

Resumen

Se tomaron datos sobre la ordenación de la reproducción y sobre la preferencia de razas y rasgos en los cerdos de pequeños ganaderos de los condados de Kiambu y Kakamega en Kenia. Los sistemas de producción evaluados fueron el semi-intensivo y el extensivo, que presentaron variaciones en la intensidad de producción porcina, en los objetivos de producción, en los rendimientos de los cerdos así como en las preferencias de los ganaderos en cuanto a la raza y los rasgos. La percepción de la importancia de las distintas características fue evaluada para obtener una visión objetiva más equilibrada sobre los objetivos de producción y/o de la cría. Los datos recogidos fueron analizados mediante el cálculo de unos índices, que consistían en una media ponderada de todas las posiciones en la clasificación de una determinada característica. En el sistema semi-intensivo, parámetros productivos tales como el tamaño, la tasa

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de crecimiento y el peso corporal alcanzaron el mismo índice de preferencia (0.181), seguidos por el parámetro reproductivo prolificidad (0.161). En el sistema extensivo, los índices de estos parámetros fueron 0.187, 0.183, 0.163 y 0.106, respectivamente. La correlación no paramétrica por rangos de Spearman fue calculada para clasificar los parámetros de importancia económica con el fin de evidenciar los efectos direccionales y posibles compensaciones entre características. En el sistema semi-intensivo, así como en el extensivo, la correlación de la tasa de crecimiento fue moderada tanto con el tamaño como con el peso corporal. Resulta necesario identificar y utilizar razas apropiadas que se adapten a los sistemas de producción divergentes, en base a la productividad y la capacidad de adaptación, para garantizar un uso eficiente de los recursos.

Palabras clave: *objetivos de la selección, sistema extensivo de producción, mejora genética, parámetros productivos, sistema semi-intensivo de producción*

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Introduction

In Kenya, pig production plays important socio-economic roles at both household and national levels. Besides income generation, pigs are assets representing a store of wealth, whereas from sociological perspective, they play roles in traditional ceremonies and beliefs (Mutua *et al.*, 2010; FAO, 2012). With regard to gender roles in agriculture, they form key income generator for women and youth within society where they are reared. Pig rearing is mainly by smallholder farmers who constitute about 70 percent of the total pig farmers (MOLD, 2006). Over the years, smallholder pig production has remained relatively unexploited despite the country having an established pig industry. The production potential remains underutilized due to lack of properly defined production practices and organized breeding programmes to facilitate genetic improvement. There is lack of systematic selection and crossbreeding programmes. The common trend is to keep bigger and 'improved' breeds because of expected higher cash revenue. However, this implies an economic risk for the resource-poor farmers due to higher-input requirement (Lemke *et al.*, 2007).

Development of sustainable pig breeding programmes should integrate appropriate breeds that can efficiently use the limited resources within specific production systems (Lemke *et al.*, 2007; Roessler *et al.*, 2008). In addition, animal selection should be based on high-value traits that farmers understand, easily measure and derive direct economic value (Tada, Muchenje and Dzama, 2013). Different animal trait preferences are influenced by various factors, including the production system, infrastructural and environmental constraints and availability of feed resources (Scarpa *et al.*, 2003; Roessler *et al.*, 2008). Kahi, Rewe and Kosgey (2005) point out that, in Kenya and other developing countries, the important components for design of breeding programmes such as definition of breeding objectives, choice of selection criteria, genetic evaluations, selection and design of appropriate mating systems and strategies for the dissemination of genetic superiority are missing. On the other hand, the lack of farmer involvement in the planning and design of breeding programmes often leads to failure of some well-intended livestock improvement initiatives (Roessler *et al.*, 2008).

For genetic improvement programmes to be successful there is the need for appropriate understanding of the production systems so as to address improvement within constraints such as feeding, breeding, health, management and marketing infrastructure. By implementing the breeding goals reflected by pig farmers, sustainable genetic improvement can be achieved through utilization of the genetic variation with the limited resources of smallholder farmers. The objective of the study was therefore, to analyse the breeding practices and breed and trait preferences necessary for the design of pig breeding programmes in Kenya.

Materials and method

Study sites

The selected study sites were Kiambu and Kakamega administrative Counties of Kenya. Kiambu County is located in Central Kenya to the north of Nairobi at 1° 10′ 0″ S/36° 50′ 0″ E and covers a total area of 1323.9 km^2. It lies at an altitude of about 1 720 m a.s.l. The annual rainfall is between 800 and 1200 mm. Kakamega County is located in Western Kenya at 0° 17′ 0″ N/34° 45′ 0″E and covers an area of 1 395 km^2. It lies within altitude 1 250–2 000 m a.s.l. The area receives an average annual rainfall of 1 250–1 750 mm.

These are among the regions with high smallholder pig production in the country but with very divergent production systems. The distinct production systems differ in remoteness, market access, resources availability and pig production intensity. In Kiambu, pig production is mainly under semi-intensive commercial systems (Wabacha *et al.*, 2004) while in Kakamega, production is mainly under smallholder extensive/free-range (Kagira *et al.*, 2010; Mutua *et al.*, 2010). Kiambu is located on the outskirts of Nairobi, the capital city and characterized by high-potential farming. Pig production is driven by the high demand for pork and pork products. Kakamega is a rural setup and production is driven by availability of farm resources. The contrasting study areas were selected assuming the economic and resource availability would

Table 1. Pig herd sizes by category in semi-intensive and extensive pig production systems in Kenya.

	Semi-intensive			Extensive		
Pig class	**Mean**	**Median**	**Range**	**Mean**	**Median**	**Range**
Piglets	12.2 ± 7.3	10	5–30	7.8 ± 1.0	7.5	7–9
Growers	10.5 ± 8.9	8	1–48	1.6 ± 1.1	1	1–5
Sows	1.9 ± 1.2	1	1–6	1.1 ± 0.4	1	1–3
Boars	1	1	–	1.3 ± 0.8	1	1–3

influence the management practices and farmers' preference for important pig breeding traits.

Data and information collection

Data and information were collected through personal interviews using a structured questionnaire and direct observations of pigs and management practices. In the two Counties, 102 pig farmers were interviewed; 52 in Kiambu and 50 in Kakamega. Data on herd structure and breeding management relied on information recalled by the farmers over the last 12 months. Pigs were classified as piglets (birth to weaning), growers (non-reproducing males and females, castrates from weaning to sale as porkers or baconers), sows (reproducing females) and boars (reproducing males). Ranking of trait preference was first done separately for performance (body weight, size and growth rate), reproduction (prolificacy and fertility), functional (disease tolerance, heat tolerance, drought tolerance and temperament) and other formal/aesthetic traits (colour, shape and meat quality). Farmers were asked to state which traits they prefer for the sows and boars and to state if they consider a number of predefined traits to be good (1), average (2), poor (3) or if they do not consider the trait (4) for the specific breed.

Data analysis

Quantitative data were analysed using descriptive and inferential statistical procedures in SAS 9.1 (SAS Institute, Cary, NC). Tests for the statistical significance or otherwise for particular comparisons were done with *Chi*-square (χ^2) or *t*-tests as appropriate. The perception of the importance of traits was done to obtain a more balanced objective view on the production and/or breeding objectives. Indices were calculated to provide an overall ranking for the traits preference. The indices represent weighted averages of all rankings for a particular trait or reason. The following equation from Bett *et al.* (2009) was adopted to calculate the index (I_i) for each trait or purpose

$$I_i = \frac{\begin{pmatrix}3\\2\\1\end{pmatrix}\left[\sum_{j=1}^{3} X_j\right]_i}{\sum_{k=1}^{n}\left[\begin{pmatrix}3\\2\\1\end{pmatrix}\sum_{j=1}^{3} X_j\right]_k},$$

where X_j is the percentage of respondents ranking the trait i in the jth rank and k is the sum of ranks for n number traits. Spearman's non-parametric correlation coefficient (r) of ranks was used to compare the ranking of traits perceived by farmers as being of primary importance and the logical trade-offs in the choice of traits.

Results and discussion

Herd structure and breeding management

Descriptive data for the pig herd structures in the semi-intensive and extensive systems are presented in Table 1. Pig production intensity differed between the systems with herd sizes higher in the semi-intensive. In the extensive system, herd sizes were generally small probably due to lack of or inadequate housing and feed resources. Pigs were sourced from within the local village or from neighbouring villages. The sources of breeding boars were: hired boar 64 percent, own bought boar 25 percent and boar bred on-farm 11 percent ($n = 44$) in the semi-intensive system. Corresponding figures for the extensive system were 72, 21 and 7 percnet ($n = 29$). In the semi-intensive system, boar services were charged in cash (|KES 1 000–1 500 per service: 1 US$ = KES 86 at the time of study), while in the extensive system the charges were cash (KES 500–1 000) or alternatively a piglet after weaning. This practice is common among smallholders in the tropics (Ajala, 2007). The reason why most farmers do not keep their own boar is related to the small number of sows kept per farm rendering it uneconomical (Wabacha *et al.*, 2004). Most farmers did not know the boar genotype and used any boar that was readily available. In breeding their pigs, all farmers practiced hand mating. Artificial insemination was not used in any of the herds surveyed. In the extensive system, relatedness of boar and sow were reported. This can be an indication of some levels of inbreeding which might be higher than in the semi-intensive system.

Across the systems, pigs were mainly removed from the herd after attaining market weight depending on the target market. However, breeding sows and boars were culled due to old age. In addition, 10 percent of the farmers in the semi-intensive system reported culling their sows due to poor fertility. Diseases also contributed to culling (4 percent) in this system. Body condition such as small size, deformities, hernia and undesired colour were the main contributors to culling at the piglet stage.

Table 2. Reproductive performance (means, medians and range) in semi-intensive and extensive pig production systems in Kenya.

	Semi-intensive			Extensive		
	Mean	**Median**	**Range**	**Mean**	**Median**	**Range**
Farrowing interval (months)	$6.0^a \pm 1.4$	6	5–7	$7.6^b \pm 2.6$	6.5	5–12
Piglets born/litter	$10.4^a \pm 2.4$	10	4–14	$7.2^b \pm 2.9$	7	3–12
Piglets weaned/litter	$8.8^a \pm 2.0$	9	3–14	$6.1^b \pm 2.6$	6	2–12

Means in rows followed by different superscripts differ significantly at $P < 0.05$.

Pig herd sizes are mainly driven by resource availability. It is common for smallholder farmers to keep small herds and to try and match the resources available to pig numbers (Halimani *et al*., 2012). Herd sizes fluctuate with season and feeds availability especially under free-ranging conditions (Chiduwa *et al.,* 2008). In the dry season, farmers cull and give away pigs to other households as a feed shortage coping strategy. After food harvesting, pigs are not confined and therefore random and uncontrolled mating take place. This results in high frequency of farrowings during the rainy season. However, this is not the case in semi-intensive system where there is total confinement of pigs. This system relies mainly on cereals and oil seeds and their by-products. These are in plenty during the rainy season and after harvesting, making the prices affordable to most pig farmers. As a result of improved nutrition, sow fertility and piglet survival are expected to improve.

Reproductive performance

The age at first mating ranged from about 4.5 to 9 months for gilts and 6 to 9 months for boars in the semi-intensive system. In the extensive system, a higher range of 5–14 months for gilts and 7–12 months for boars was reported. Some farmers attributed the wide range to a lack of breeding boars in the vicinity. In both systems, the modal age at first service for gilts was 6 months. In the semi-intensive system, weaning was done at 8 weeks whereas in the extensive system an early weaning of 4 weeks was practiced. The reported farrowing intervals differed significantly ($P < 0.05$), and were on average 6.0 and 7.6 months in the semi-intensive and extensive system respectively. Mating was done at 3–7 days post-weaning.

Litter size at birth and farrowing intervals differed significantly in the production systems. As presented in Table 2, sows in the semi-intensive system had larger litters at both farrowing and weaning and lower farrowing intervals than sows in the extensive system. The long farrowing intervals and small litter sizes could be attributed to poor husbandry practices and feeding management. Diseases such as pneumonia and adverse weather conditions were mentioned as major contributors to pre-weaning mortality.

The reproductive performance (weaning to service interval, litter/sow/year and piglets born/sow/litter) in the semi-intensive system compares well with those reported for purebred Landrace and Yorkshire and their crossbreeds in the tropics (Kunavongkrit and Heard, 2000; Tantasuparuk *et al*., 2000). The total number of piglets born per litter was also within the range reported here. Even under conditions of identical feeding, similar genetic and health status, the reproductive performance of outdoor production systems is significantly lower than of indoor systems (Akos and Bilkei, 2004). Similarly, Chiduwa *et al.* (2008) reports high incidences of farrowing under confinement than under free range in indigenous pigs. Indoor systems record lower percentage of productive days, culling rate and annual mortalities with the outdoor systems having fewer piglets born per litter, born alive and weaned. It is also reported that fluctuation in weather plays a major role in determining reproductive performance than management factors such as housing, hygiene and feeds in outdoor systems (Chiduwa *et al.,* 2008). However, these factors may be interrelated. The reproductive performance potential of sows in the tropics fail to be realized due to many interacting factors, including the environment, diseases, feed quality, poor genetics and substandard management (Kunavongkrit and Heard, 2000). The performance can be improved by investment in housing, disease control, nutrition and genetics.

Considering that most farmers kept scanty records on litter traits only, such as litter size born alive, piglets weaned per litter, it is difficult to estimate the reproductive efficiency of such herds. This is because such breeding records do not account for age at first mating, infertility, repeat breeding and conception rates and therefore time loss between farrowings all which affect the overall profits.

Breed and trait preferences

Breed preference

In the semi-intensive system, farmers mainly kept Large White and Landrace and their crossbreeds. These breeds were preferred for their faster growth rates and high mature weights. In addition, the Large White was preferred due to high prolificacy and mothering ability. Similar observations were reported by Wabacha *et al.* (2004). Their performance is good under tropical conditions if they are properly managed.

In the extensive system, pigs were usually crossbred between the Large White, Landrace Hampshire, Duroc and Pietrain and therefore could not be clearly described/classified. The Large White was the preferred sire breed in this system. The crossbreeds were preferred for the

Table 3. Ranking of traits perceived by farmers as being of primary importance in semi-intensive and extensive pig production systems in Kenya.

	Semi-intensive					Extensive				
Trait	**Rank 1**	**Rank 2**	**Rank 3**	**Sum**	**Index**	**Rank 1**	**Rank 2**	**Rank 3**	**Sum**	**Index**
Body weight	33	42	23	98	0.181	2	14	64	80	0.163
Size	37	15	46	98	0.181	52	36	4	92	0.187
Growth rate	29	40	29	98	0.181	40	38	12	90	0.183
Prolificacy	83	4	–	87	0.161	52	–	–	52	0.106
Fertility	4	46	–	50	0.092	4	20	–	24	0.049
Temperament	2	–	–	2	0.004	20	4	–	24	0.049
Disease tolerance	40	–	–	40	0.074	20	18	2	40	0.081
Drought tolerance	–	–	–	–	0.000	14	2		16	0.033
Colour	27	4	–	31	0.057	70	–	–	70	0.142
Meat quality	23	14	–	37	0.068	–	4	–	4	0.008

moderate growth rates, mature weights and disease tolerance. However, most farmers in this system preferred breeds that require low investment and maintenance cost. This is expected in such conditions where feeds are of low nutritional value and availability fluctuates with season. Given that housing is not provided throughout the year, disease tolerance and adaptability to local environment and husbandry conditions become important traits in breed selection.

It was apparent that farmers did not have elaborate plans to implement genetic improvement. Therefore their breeding management disregards the genetic and economic implications of such endeavours. Although improved breeds yield higher cash revenues due to higher biological performances and resulting higher output, they pose economic risks due to the converse high-input requirements (Lemke *et al.*, 2007). As such, appropriate breeds which suit the divergent production systems in this study need to be analysed for productivity performance and adaptability to ensure efficient resource use.

Trait preference

Farmers in the different production systems had different trait preferences. The ranking of traits perceived by farmers as being of primary importance are presented in Table 3. High body weights, large size and faster growth rates were highly preferred in the semi-intensive system. This was mainly because marketing these animals was on a weight basis. Farmers wanted pigs which attained high market weight early so as to achieve faster and higher returns per cycle. The price of meat was determined by the age of the pig and carcass quality. Prices were high for porkers and lowered as the pigs aged for those farmers who sold to the leading pig products processor in the country (Farmers Choice Limited). Carcass quality did not influence prices among the local butchers who offered an alternative market for these pigs. In the extensive system, farmers' preference was for moderate body size and faster growth rates. The breeds kept in this system are smaller in size and suspected to be indigenous or crossbreeds of indigenous and exotic (Kagira *et al.*, 2010). In such systems, breeds with traits closely related to exotic breeds are disliked due to high monetary requirement for purchase of supplementary feed (Roessler *et al.*, 2008). Under conditions of sparse feeding or low nutritional levels, small animals have an advantage over large ones because more energy is left for production when the maintenance requirements have been met. Additionally, small-sized breeds yield convenient carcass sizes for rapid disposal in such areas with limited marketing channels, inadequate transport network and freezing facilities (Philipsson, Rege and Okeyo, 2006). Market is mainly to local butchers and therefore carcass quality does not tend to affect prices.

Prolificacy was perceived as the most important reproductive trait relative to fertility. This was because additional piglets meant more income for farmers in the different production operations (farrow to weaner and farrow to finish). The trait is also easy to monitor and record compared to other reproductive traits. According to Mutua *et al.* (2010), pigs are preferred to other livestock in the extensive system because they breed easily, have a shorter gestation period and produce many piglets in a single farrowing.

Disease tolerance received a reasonable ranking in both systems indicating that farmers dislike animals that fall ill more often. This is particularly important for exotic breeds because they could be more susceptible to tropical diseases implying a high production risk through animal losses (Roessler *et al.*, 2008). However, it is reported that high-income farmers tend not to rank disease resistance highly probably due to their ability to purchase drugs for treatment (Halimani *et al.*, 2012). Drought tolerance was not ranked in the semi-intensive system. This could be because farmers do not mainly depend on fodder production to feed their pigs and normally supplement the normal diets with commercial concentrates. This was not the case in the extensive system where most of the time pigs are left to scavenge for their feeds.

In the semi-intensive system, colour, other than white was mainly associated with crossbreeding (crossbreds of Hampshire, Duroc or Pietrain) and influenced selection

Table 4. Correlations of farmer's preference rankings for traits of economic importance in semi-intensive and extensive pig production systems in Kenya.

Production system	Traits	Body weight	Size	Growth rate	Prolificacy	Fertility
Semi-intensive	Size	−0.564**				
	Growth rate	−0.286*	−0.629**			
	Prolificacy	−0.062	0.217	−0.303*		
	Fertility	−0.168	−0.255	0.390*	−1.000**	
	Meat quality	−0.229	0.000	0.169	−0.228	0.346
Extensive	Size	−0.030				
	Growth rate	−0.473**	−0.850**			
	Prolificacy	0.103	0.042	0.069		
	Fertility	0.258	0.316	−0.345	−1.000**	
	Disease tolerance	0.104	0.223	−0.254	–	0.378

*, Correlation is significant at the 0.05 level (two-tailed); **, Correlation is significant at the 0.01 level (two-tailed).

and marketing. White pigs were mainly Large White, Landrace and their crossbreds. In the extensive system, black pigs were regarded as local/indigenous breeds and the spotted as crossbreds. These form the majority of pigs in this system of production. However, these local and/or crossbreds are mainly non-descript and have not been characterized. Their preference stems from the perception that they are more tolerant to diseases. In terms of marketing local buyers prefer white-coloured pigs; therefore, the more common black-coloured pigs have a low market value (Mutua *et al.*, 2010).

As reported by Roessler *et al.* (2008), in demand-driven production systems such as the semi-intensive reported in this study, productive and reproductive performance are the most preferred pig breeding traits while adaptive traits play a lesser role. In the resource-driven extensive system adaptability to fibre-rich diets is the most important trait. In general, farmers in the semi-intensive system preferred faster growing pigs which attain high market weights to meet the high market demand for pork. Exotic genotypes with suitable adaptable traits can be effectively utilized in this system. For the farmers targeting the formal markets such as Farmers Choice Limited, crossbreeding with terminal sire genotypes is recommended for desired carcass quality to be achieved. In the extensive system, farmers should focus on medium-sized pigs which are highly adaptive to utilization of fibre-rich diets and show disease tolerance as well as being compatible with the limited resources available. Under such divergent circumstances, these preference differences should be put into consideration in order to ensure efficient design of breeding programmes (Roessler *et al.*, 2008). Prolificacy should be supported with piglet survival which is fundamental in determining the herd size and consequently farm profitability.

The Spearman's non-parametric rank correlations were calculated for ranking of traits of economic importance to indicate the directional effects and plausible trade-offs between traits (Table 4). In the semi-intensive system, correlations were moderate between growth rate and body weight, and size growth rate. Preference for body weight was negatively correlated with all other traits. This indicates the importance of this trait relative to the other traits. This is because of the marketing structure where animals are sold on weight basis and therefore a heavier animal is expected to fetch a higher market price. Fertility and prolificacy showed a very strong correlation, probably resulting from the expected genetic correlation between the traits. There was no correlation between size and meat quality.

In the extensive system, correlations were moderate for body weight and growth rate and size growth rate. Here growth rate was more important and therefore correlations were negative. Although positive, correlations between prolificacy and all other traits were too low to be meaningful. In this system, the importance of disease tolerance was the most importance functional trait. Correlations of the different traits with disease tolerance in the semi-intensive and for meat quality in the extensive systems, respectively, were not calculated due to the low ranking the traits received. In general, there were logical trade-offs in the choice of the traits by farmers in both systems.

Consideration of farmers' breed and trait preferences is important in design of sustainable improvement programmes. This would ensure that animal selection is based on traits that farmers understand, measures and records easily and derives direct economic value (Tada, Muchenje and Dzama, 2013). The biological traits preferred by the farmers in this study are variables that are partly determined by the genotype of the animals and are considered potential breeding objective traits. As a result, it is extremely important that they are set at a level where they truly reflect the needs of the locality, and that farmers support the direction of change (Philipsson, Rege and Okeyo, 2006). Development of village breeding programmes has been suggested as a key entry point in the improvement of smallholder pig production (Roessler *et al.*, 2008). These programmes should integrate appropriate breeds that can efficiently utilize available resources for the improvement of production traits in line with profit maximization. Such breeds are available in the country and can be obtained from breeders or farmers can improve their own replacement stock. In addition to concentrating on production traits improvement, reproduction rates and adaptation to farm-produced feeds should be maintained (Roessler *et al*., 2008). By developing a community-based organization for the genetic improvement of livestock (CBOGIL), a group of farmers can form a dispersed nucleus consisting of groups of elite herds among which selection decisions are made and from which improved germplasm is disseminated into populations that are not participating in the genetic improvement initiative. The group's mandate should focus on genetic evaluation, selection of parental stock and dissemination of genetic material (Kahi, Rewe and Kosgey, 2005). To support their efforts, farmers should embrace proper animal identification and performance recording. The records are important in day-to-day management activities, for genetic evaluation and improvement, performance monitoring and evaluation and increased market value (Bett *et al*., 2009).

The information on biological trait preference from this study was integrated with economic variables to develop a bio-economic model for estimating economic values in different smallholder production systems in a subsequent study.

Conclusions

In the two production systems evaluated, indices for trait preference were high for performance traits such as body weight, size and growth rate and the reproductive trait, prolificacy. In these systems opportunities exist for breeding management improvement. As such, appropriate breeds which suit the divergent production systems in this study need to be identified and utilized based on performance and adaptability to ensure efficient resource use. Further studies are required to assess the trait preferences in the different production systems that suit the farmers' production objectives and market demand.

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Managing local breeds: a dynamic connected to livestock farming systems that concerns different levels of organization

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Summary

Management of local breeds is closely linked to the global challenges involved in genetic resources management. However, it cannot be reduced to this genetic dimension alone and is an integral part of the entire farming system of which it is a part. The aim of this paper is to show why it is essential to have an approach to local breed management that takes the dynamics of livestock farming systems (LFS) into account. After a presentation of the LFS approach, we show how genetic management is strongly linked to other dimensions of farming systems, at the farm scale as well as at more comprehensive scales. We illustrate our claim with different examples of the management of local breeds of different species.

Keywords: *level of organization, livestock farming system, local breeds, selection criteria*

Résumé

La gestion des races locales renvoie aux enjeux globaux de gestion des ressources génétiques cependant elle concerne des dimensions qui dépassent la seule dimension génétique et est en relation avec les systèmes d'élevage dans lesquels ces races sont mobilisées. L'objectif de cet article est d'expliciter l'intérêt d'une approche de la gestion des races locales qui prennent en compte les dynamiques des systèmes d'élevage. Après avoir présenté le concept de système d'élevage, nous présentons les liens entre gestion génétique des populations animales et autres dimensions des systèmes d'élevage, au niveau de l'exploitation mais aussi à des niveaux plus englobant. Nous illustrons notre propos de différents exemples de gestion de races locales dans diverses espèces.

Mots-clés: *système d'élevage, races locales, critères de sélection, niveau d'organisation*

Resumen

La ordenación de las razas locales está intrínsecamente vinculada a los desafíos globales que conlleva la gestión de los recursos genéticos. Sin embargo, no se puede reducir exclusivamente a su dimensión genética ya que las razas ganaderas influyen sobre la totalidad de elementos de los sistemas agropecuarios de los que forman parte. El objetivo de este artículo es el de mostrar por qué resulta esencial adoptar un enfoque que tenga en cuenta las dinámicas de los Sistemas Agropecuarios (SA) en la ordenación de las razas locales. Tras una presentación del enfoque SA, mostramos cómo la gestión genética está fuertemente relacionada con otras dimensiones de los sistemas agropecuarios, tanto a nivel de granja como también a escalas mayores. Ilustramos nuestra propuesta con diferentes ejemplos de ordenación de razas locales de distintas especies.

Palabras clave: *sistema agropecuario, razas locales, criterios de selección, nivel de organización*

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Introduction

Management of local breeds is closely linked to the global challenges of genetic resources management (FAO, 2007). The first challenge when dealing with genetic resources concerns the conservation of a potential from a genetic point of view. In this perspective, importance is given to the uniqueness of a breed from a genetic point of view (e.g. Tapio *et al.*, 2006). However, it has been emphasized in numerous research projects that the question of local breed management cannot be reduced to this genetic dimension alone (Audiot, 1995; Vissac, 2002; Lambert-Derkimba, 2007; Labatut, 2009; Lauvie, Gonzalo-Turpin and Labatut, 2009). The breed can be a resource for specific farming systems and is, at the same time, a product of long-time breeding practices within farming systems. Genetic management practices, going from the level of the animal to that of the whole population, are strongly linked to the aims of the farmers who use these animals,

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and to their expectations. The management practices are themselves a key component of the global livestock farming systems (LFS) of which the animals of the breed are an integral part.

The aim of this paper is to show why it is essential to have an approach to local breed management that takes the dynamics of LFS into account and does not just reduce them to their genetic aspect. We will show that if we consider those two dynamics as being linked, the analysis of local breed management dynamics raises the question of the articulation of several organization levels, i.e. several scales at which we consider the systems. We will then illustrate our statements and questions using French examples from the literature.

The main principles of the LFS approach

The system approach (von Bertalanffy, 1968) has been used since the 1980s in the agricultural sciences. It is based on the definition of a system as a complex organization of components in interaction. The system is a whole, indivisible, and it is more than just the sum of its parts. A change in one of its components leads to a change in the other components and in the system as a whole. The systemic approach focuses on the interactions between components in order to describe and understand the behaviour of the whole system as a unit, rather than studying each component and its causal relationships with other components as in an analytic approach.

A LFS is a conceptual model of the whole livestock farm. It represents a duality between the view of a farm as a human activity system, with a farm family (or an enterprise) seeking to satisfy specific objectives, and the view of a farm as a production process, with the transformation of physical inputs to physical outputs (Gibon *et al.*, 1999). Practices are a key component that links these two views of LFS. They are the result of the farm family's decision-making process, through the perception of its context, and ultimately determine the production process. We distinguish five categories of practices (Figure 1, from Moulin and Bocquier, 2005).

First, over the years, the farm family configures the herd (choice of species and breeds, culling and replacement, etc.). It also configures the farmland: acquiring or relinquishing land areas, creating equipment or buildings (fencing, trails, water points, outbuildings, etc.) and rehabilitating some plots (stone removal, bush clearance, etc.). Then, over an annual cycle, the family farm operates the system. It links the herd and the farmland through rearing practices (breeding, feeding, etc.) and land-use practices (assigning a crop to a plot or a batch to a pen). It also collects the outputs of the herd and markets animal products, possibly after processing.

The use of several levels of organization is also a classic principle of the systemic approach, extensively used in ecology. As an example, in order to understand the localization of an animal on a specific vegetation unit in a landscape, Bourbouze (1986) used several spatial organization levels: from a plot where the vegetation, a flock and a shepherd interact, to a large area within a geographic space where a human society maintains a population of domestic animals.

Understanding local breed management dynamics in relation to other dimensions of LFS

Articulation of genetic management and other dimensions of LFS at the farm level

At the organization level of the farm, the farmer's aims and choices are of the utmost importance. Of course, the first point concerns the choice of the genetic resource itself, consistent with the motives and aims of the farmer (Gandini *et al.*, 2010). Several studies have attempted to develop a better understanding of those choices (e.g. Bebe *et al.*, 2003; Mwacharo and Drucker, 2005). The second point concerns all of the decision making involved in breeding practices. This decision-making process is linked to the other dimensions of the production system (marketing, feeding, etc.). As a consequence, to understand decision making in terms of breeding, it is necessary to understand links with other dimensions of the farming system, which is a crucial aspect of the systemic approach.

Feeding systems can have an impact on the choice of a specific breed or on breeding choices, as illustrated in the case of the *Bretonne Pie Noire* cattle breed (reared in the western part of France). As a motive for choosing that breed, many farmers mention that it is well adapted to their low-input systems that are mainly based on grassland (Quéméré, 2006). Another example is given by Lambert-Derkimba, Verrier and Casabianca (2011) concerning the *Nustrale* pig breed, a local Corsican breed that is used in extensive farming systems based on the use of natural resources.

Breeding practices can be linked to marketing choices, as illustrated in the case of the *Gascon* pig breed. This breed is a rare pig breed from the southwestern part of France. In this case, a group of stakeholders (localized in a specific area known as Bigorre) has expressed the desire to use the breed to produce high-quality dried ham. A Protected Designation of Origin (PDO) project has been built and has led to the development of a new selection criterion – leg slenderness – directly linked to the product. As a consequence, the farmers involved in this project have a marketing opportunity as a result of the good reputation of the *Noir de Bigorre* ham product (even if the PDO is still pending), and it has led them to take this selection criterion into account in their selection practices (Audiot *et al.*, 2005).

Another example is the one of the Merino sheep breed. Sheep farming in the Crau Region (southeastern part of France) is based on a long transhumance (several hundred kilometres covered to reach high mountains), valorizing several resources depending on the season: high mountain

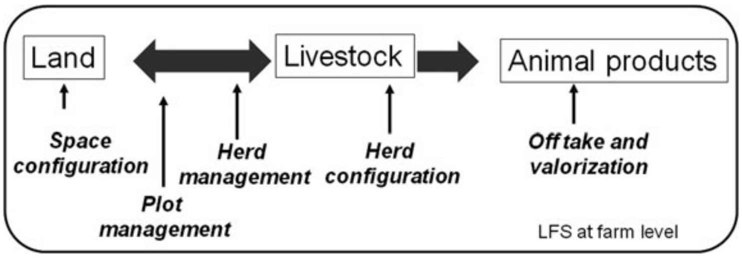

Figure 1. The LFS approach at the farm level (from Moulin and Bocquier, 2005).

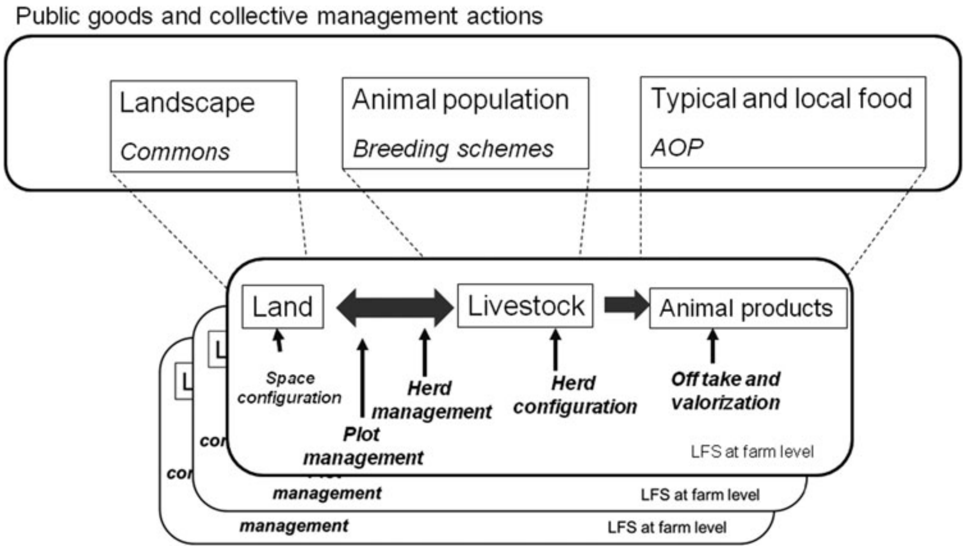

Figure 2. Interactions between genetic management and other dimensions of LFS at the collective level.

pastures in summer, irrigated grassland in autumn and winter, steppic rangeland and cereals in spring (Moulin, Pluvinage and Bocquier, 2004). The local *Merino* breed is considered to be well adapted for rangeland use and transhumance, but the lamb carcasses do not comply with the standard market expectations, particularly because of their small size. As a consequence, cross-breeding is used to produce lambs with the desired conformation, and this practice is encouraged by the operators of the lamb supply chain. Farmers who use cross-breeding have smaller flocks within the diversity of the systems encountered in the area (300–500 ewes). These farmers aim at selling more effectively valorized carcasses (considering the limited size of the flock), and at selling all their lambs for meat. They then buy ewes to replace them in order to have a simpler type of management, with only one breed of rams to manage (Moulin, Pluvinage and Bocquier, 2004). They buy pure Merinos ewes because they still use transhumance with their flocks of ewes, even if they respond to a specific market demand with cross-bred lambs.

Articulation of genetic management and other dimensions of LFS at the collective action level

The evolution of the animal population is also linked to decision making at the collective level (selection criteria can be defined at an individual level, but also at a collective level, e.g. in official breeding schemes where the breeders involved have to agree on common selection criteria). The constitution of networks for exchanging, buying and selling breeding animals can also have an impact on the evolution of the animal population. This decision making at collective levels and the way individual practices are articulated at the scale of the animal population is also linked to the characteristics of the farming systems. In the same way, several dimensions of the farming system may be concerned by specific collective management systems such as, in the case of landscape, questions of collective land management, or in the case of product marketing, Geographical Indication projects (e.g. like PDOs). These different collective dynamics can interact as well (see Figure 2).

The *Tarentaise* cattle breed is an example of this question of decision making based on selection criteria at a collective level, in relation to the characteristics of the LFS. This breed is involved in the production of cheeses with a PDO (including cheeses with a production limit mentioned in the specification, like Beaufort). It has an official selection scheme in which it was chosen to give less weight to milk production in the selection index, compared to most French dairy cattle breeds. With that decision, breeders underline the fact that their breed is adapted to a mountain farming system (since they give more weight in their selection to criteria other than the quantity of product), and take the marketing process into account (PDO cheese and the associated production limits) (Lambert-Derkimba, 2007). In this example, the collective decision making in the breeding scheme is clearly linked to the collective decision for product valorization (PDO). The collective decision making is also linked to a global dynamics of the territory (maintaining mountain pastures considered as a heritage landscape of the area).

Links between LFS and local breed management: the articulation between levels of organization

From the farm to the collective level: where system diversity co-exists

The articulation of different levels of organization and, in particular, the articulation between expectations at the farm level and decision making at the collective level, can take several shapes and dynamics. At the scale of the animal population, several systems (farming systems, products valorized) generally co-exist.

The *Aubrac* cattle breed, a rustic and multi-purpose breed (draught, milk, meat) from the mountainous central part of France, was threatened with extinction in the 1950s and 1960s, during the period of modernization of French agriculture and the spread of the use of tractors, replacing draught animals. This is a good example of the use of cross-breeding to add value to local breeds by producing cross-bred animals better suited to market expectations. Such a strategy involves, in parallel to the cross-breeding practices, to continue to strictly manage the pure breed (Vissac, 2002). Such a collective strategy has led to a considerable increase in the animal population. The same breed produces a diversity of products. Very few dairy cows remain but a conservation program for milk production does exist. Most of the animals are instead used for meat production and, in particular, for the valorization of cross-bred animals in fattening channels in other areas such as Italy, as well as for the production of local (*Fleur d'Aubrac*), and pure-bred animals (*Boeuf Fermier d'Aubrac*). The maintenance of the breed in its territory is linked to the maintenance of local farming systems based on grazing.

In Corsica, a mountainous island in the Mediterranean Sea, the local sheep breed, known as the *Corsican Sheep*, is the object of an official breeding scheme that only involves a part of the sheep farmers (55 in 2014 out of a total of about 400 sheep breeders in Corsica[1]). However, even if the part of the breeders involved in the breeding scheme is limited, and even if the tools proposed by this breeding scheme, e.g. artificial insemination, are practically not used by farmers outside of the breeding scheme, this single local sheep breed is involved in a diversity of LFS types, including feeding systems. A first step in the identification of the types of systems has made it possible to distinguish four types briefly described in Table 1 (Paoli *et al*., 2014). Breeders of the official scheme are found in all of the types except the most traditional, based only on rangeland grazing. The official breeding scheme co-exists using management practices from farmers who are not involved in this scheme. Stakeholders in the breeding scheme consider taking the diversity of systems into account since they work with farmers from a diversity of systems. However, the breeding scheme is mainly oriented towards increasing milk production, even if they are considering the introduction of new criteria to more effectively take account of the diversity of farmers' expectations. Except for a few farmers that want to avoid animals from the selection scheme, there are exchanges of animals among farmers involved or not in the selection scheme. Some farmers outside of the scheme buy rams from the selection scheme, and breeders and farmers exchange breeding animals, whether they are part of the scheme or not.

Table 1. The four farming systems using the Corsican Sheep breed identified.

System	Description	Geographical area
1	Low stocking rate system on rangeland with little farm equipment	Slopes of inland valleys and rocky coasts
2	Systems with forage crop intensification limited by tillable areas	Slopes and base of inland valleys
3	Low-intensity systems on grassland with medium farm equipment	Coastal plains
4	Systems with forage crop intensification where surplus fodder is sold	Coastal plains

In the second case, the collective action encompasses a wide variety of LFS throughout the territory of the *Corsican Sheep* breed, but a large part of the interrelations also occurs outside of the official management system. This example raises the question of the extent to which the breeding program can be made flexible enough to accommodate different production goals.

Our paper focuses on local breeds, but we can nevertheless observe that in most of the highly represented breeds such as the *Holstein Friesian*, the selection index built at a collective level produces a specialized population that can be used in a diversity of systems (as witnessed by the geographical extension of those breeds). However, the maximal expression of the genetic potential of the animals of such breeds is implicitly linked to specific farming systems (feeding systems to express the potential of the breed, specialization systems, etc.).

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[1] 421 sheep breeders registered with the RGA (2010), the French General Agricultural Census, cited by the OS (the selection organization).

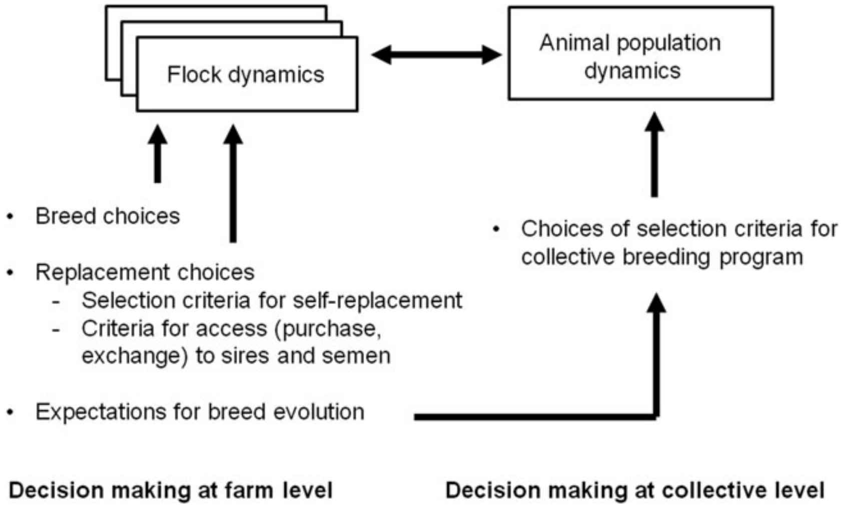

Figure 3. Local breed management and LFS.

From the farm to the collective level: when tensions are expressed

The articulation of points of view at one level of organization may sometimes lead to tensions at another level of organization.

In the *Maraîchine* cattle breed, for example, a rare breed from the Atlantic marshland area in western France, we can see the link between breed management and other dimensions of LFS at a collective level. The association created for the breed conservation mentions the link between breed management and marshland management in its very name. The breed was also faced with the challenge of finding outlets for products of the breed, and this challenge was discussed at the collective level (Steyaert, 2006). Two types of tensions between breeders were identified by Steyaert (2006). The first concerns the animals' conformation. Some of the breeders prefer hardy animals with good qualities for grazing (but lacking conformity for the standard meat market), whereas others consider conformity for meat. The second is linked to the feeding systems associated with the breed, some of which are in favour of grazing systems, whereas others are in favour of more intensive fodder systems (use of silage maize, in particular) (Steyaert, 2006). Consequently, a debate exists among these farmers as to the management criteria and different visions of the relevant type of animal in the breed, in relation to the feeding system that they consider to be relevant, and the type of product valorization they desire.

The *Manech Tête Noire* is a dairy sheep breed from the western part of the French Pyrenees. Labatut (2013) identified two ways to collectively manage the breed: the first one is the official breeding scheme that emphasizes milk production in quantity and quality and that is based on milk recordings and index calculations. The second one concerns a group of breeders who practice transhumance, use other collective tools such as livestock shows, and focus on the hardiness of the breed and its "standard" (i.e. a description of some traits of the breed's phenotype such as the morphological characteristics and the colour of the animals). The vision of the relevant animal is different here as well, depending on the breeders and their systems (Labatut, 2009).

Slow growth is a characteristic of the *Nustrale* breed mentioned earlier. This local pig breed from Corsica is associated with extensive systems that use natural resources and, in particular, chestnuts and acorns. Lambert-Derkimba, Verrier and Casabianca (2011) showed that for some farmers who have less chestnuts or acorns available during the finishing period, they can supplement their animals' feed with purchased barley. In this case, the farmers can select animals that more effectively valorize this barley and, by doing so, run the risk of losing the slow growth rate, which is considered by other breeders as a characteristic of the breed that should not be lost (linked by farmers to the ability to valorize natural resources).

In the *Merino* example presented earlier, at the collective level, debates have arisen among *Mérinos d'Arles* breeders as:

(i) What products for what market (the pure-bred lambs are used for non-standard markets and these niche strategies are linked to reinforced pure-breeding strategies).
(ii) The definition of the good *Merino* ewe (there are different opinions as to the size of the good ewe)

Discussion and conclusion

Finally, Figure 3 illustrates the fact that dealing with local breed management in a systemic approach makes it possible to better understand the decision-making process: what is the impact of feeding strategies, the use of the territory by the herd, marketing processes and sanitary issues on the breeding choices of the farmer? On the contrary, what are the consequences of breeding practices on the herd composition and on the way it valorizes the resources in the farming system?

Such an approach also involves questioning the articulation of levels of organization from the animal to collective action. It is essential to take decision making at the farm level into account, as well as to analyze the diversity of points of view and practices at a larger level (the animal population). At a collective level, it is necessary to question the forms of coordination that lead to shared selection criteria or to the exchange of breeding animals.

To address those questions raised by the articulation of the different levels of organization, we need to take a systemic and global approach to those dynamics, linking the general dynamics underlying farming systems, to a deeper analysis of genetic management practices.

Moreover, methodological tools from the social sciences can be useful for dealing with tensions at the collective level, for example, the *"dispositif"* notion[2], controversy analysis and organization science tools such as design workshops.

A first step is to analyze how collective action is built at the collective level (how breeders interact and are associated with animals, tools, products, etc., as proposed, e.g. with the "dispositif" notion defined by Foucault). In this collective action, it is necessary to understand the controversies expressed by stakeholders, the challenges they face, and how they establish practices that can cause tension at the scale of the animal population (e.g. Lauvie *et al.*, 2008).

A step further can be taken with research action practices as in the example of the *Manech Tête Noire* mentioned earlier, where Labatut (2013) has organized design workshops to gather all of the stakeholders involved in breed management to overcome the tensions in their projects and to build a common project. This approach has led to the establishment of a new association that brings together farmers from the two previous groups around a common project describing the relevant animal as "a beautiful ewe that allows them to make a good living."

Our statements are illustrated in this article with examples taken from a diversity of species and geographical areas in France, including areas qualified as having "harsh conditions", such as marshlands, mountains and the Mediterranean region. As a consequence, the scope of our statements extends beyond French territory and may concern any area where local breeds are raised.

Acknowledgements

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[2] We can define a "*dispositif*" to manage an animal population as a network that links stakeholders, animals, various tools and objects, knowledge and know-how, for the purpose of managing the population. Mormont (2003) reports that the first person to propose this notion was Michel Foucault, and that the notion is now used in several areas such as environmental management.

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Is crossbreeding of cattle beneficial for mixed farming systems in Central Java?

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Summary

From 1980s onwards, Indonesia's government has been implementing crossbreeding with European beef breeds through artificial insemination to improve the beef performance of local cattle, in response to the increasing demand for meat. Crossbreeding is promoted and implemented throughout the country, regardless of the various agro-ecological zones, each endowed with different feed resources in the smallholder farming systems. This study analyses the impact at farm level of crossbreeding in the different mixed farming conditions in Central Java. Quantitative and qualitative information was collected through participatory approaches involving famers ($n = 252$) in four study areas representing three agro-ecological zones: Wet lowlands (subdivided in two areas based on the history of breeding local cattle and crossbreeding), Wet uplands and Dry uplands. Phenotypic characteristics, reproductive performances, and carcass characteristics of Ongole and crossbred cattle were assessed, together with farmers' reasons for keeping Ongole or crossbred breeding stock, the functions of cattle on the farms and the Gross Margins (GM) of the cattle component on Ongole and crossbred farms. Across different agro-ecological zones, crossbreeding is not changing the farming systems: herd sizes, farm types, experience in cattle keeping and functions of cattle were about the same for Ongole and crossbred farms. The agro-ecological zones differed in the cropping pattern and feed resources; however, they did not differ in amounts of dry matter and crude protein fed to individual animals. Crossbreeding is changing the individual characteristics of cattle and consequently the market prices of animals. In general, mature female crossbred cattle were approximately 25 percent heavier than mature female local cattle. Male crossbred progeny was 16 percent heavier their local counterparts, whereas female crossbred progeny was 24 percent heavier than female local cattle. In terms of reproduction performances, both local and crossbred cows performed well with calf crops ranging between 73 and 86 percent per year. Most farmers preferred crossbred over Ongole cattle. Simmental cross is the most preferred. GM for crossbred and Ongole farms were comparable within the different study areas; selling prices of crossbreds are higher, but feed costs too. Crossbreeding will continue. It is promoted by government policies and farmers are motivated to keep crossbred cattle as body weights and market prices are higher than for Ongole cattle; however, farmers said that they do not prefer upgrading to very high levels of Simmental. A viable Ongole population is needed to reduce the risk of upgrading to too high levels of Simmental.

Keywords: *agro-ecological zones, benefits, Indonesia, Ongole cattle, Simmental crossbreeding*

Résumé

Depuis les années 80 du XXème siècle, le gouvernement de l'Indonésie a promu le croisement avec des races bovines à viande d'Europe par le biais de l'insémination artificielle afin d'améliorer les performances bouchères des bovins locaux et pour répondre à une demande croissante de viande. Les croisements ont été promus et mis en application partout dans le pays, sans tenir compte de la diversité de zones agro-écologiques, chacune desquelles offre différentes ressources alimentaires aux petits exploitants. Cette étude analyse, au niveau de la ferme, l'impact des croisements pour différentes conditions de production mixte en Java Central. Des données quantitatives et qualitatives ont été recueillies en adoptant une approche participative qui cherchait à impliquer des éleveurs ($n = 252$) de quatre domaines représentant trois zones agro-écologiques: les Zones Humides des terres basses (subdivisées elles-mêmes en deux zones selon l'élevage traditionnel de bovins locaux ou d'animaux croisés), les Zones Humides des terres hautes et les Zones Arides des terres hautes. Des caractéristiques phénotypiques, des performances reproductives et des paramètres de la carcasse ont été évalués chez des bovins Ongole et croisés ainsi que les raisons des éleveurs pour le maintien de reproducteurs Ongole ou croisés, les fonctions du bétail bovin dans les fermes et la Marge Brute (MB) dégagée de l'élevage de bovins dans les exploitations élevant des bovins Ongole ou croisés. En aucune des zones agro-écologiques considérées, les croisements n'ont affecté le système productif: la taille des troupeaux, le type d'exploitation, les pratiques d'élevage et les fonctions des bovins ont été très similaires entre les fermes élevant du bétail Ongole et celles élevant des animaux croisés. Même si les quantités de matière sèche et de protéines brutes allouées par animal n'ont pas différé, des différences ont été décelées entre les zones agro-écologiques pour ce qui est des cultures et des ressources alimentaires. Les croisements ont affecté les caractéristiques individuelles des bovins et, ainsi, les prix de marché des animaux. Dans l'ensemble, les femelles adultes croisées ont été environ un 25 pour cent plus lourdes que les femelles adultes locales. La progéniture des mâles croisés a été un 16 pour cent plus lourde que ses équivalents locaux, alors que la progéniture des femelles croisées a été un 24 pour cent plus lourde que les femelles locales. Pour ce qui est des performances reproductives, aussi bien les vaches locales que celles croisées ont atteint de bons résultats annuels de fertilité (entre 73 et 86 pour cent). La

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plupart des éleveurs ont préféré les bovins croisés au bétail Ongole; en particulier, le croisement avec la race Simmental a été le plus apprécié. Dans les différentes zones étudiées, la MB a été similaire entre les fermes élevant des bovins croisés et celles élevant du bétail Ongole; le prix de vente des animaux croisés a été plus élevé mais aussi leur coût d'alimentation. Les éleveurs continueront vraisemblablement à croiser leurs animaux, compte tenu du fait que le gouvernement promeut les croisements et que les éleveurs préfèrent les animaux croisés en raison de leurs plus grands poids corporels et des prix de marché plus élevés par rapport au bétail Ongole. Les éleveurs ont quand même fait savoir qu'ils ne souhaitent pas arriver à des taux très élevés de sang Simmental chez les animaux croisés. Ainsi, pour éviter un pourcentage trop élevé de sang Simmental, il s'avère nécessaire de maintenir une population Ongole viable.

Mots-clés: *Indonésie, zones agro-écologiques, bovins Ongole, croisement avec Simmental, bénéfices*

Resumen

Desde los años 80 del siglo XX, el gobierno de Indonesia ha promovido el cruzamiento con razas europeas de ganado bovino de carne mediante inseminación artificial, con el fin de mejorar los rendimientos cárnicos del ganado bovino local y para, así, dar respuesta a la creciente demanda de carne. Los cruzamientos se han promovido e implementado por todo el país, sin tener en cuenta la diversidad de zonas agroecológicas, cada una de las cuales ofrece diferentes recursos alimenticios a los pequeños productores. Este estudio analiza, a nivel de granja, el impacto de los cruzamientos en las diversas condiciones de producción mixta en Java Central. Se recogió información cuantitativa y cualitativa mediante un enfoque participativo que implicó a ganaderos ($n = 252$) de cuatro áreas de estudio, que a su vez representaban tres zonas agroecológicas: los Humedales de las tierras bajas (subdivididos en dos áreas de acuerdo con la cría tradicional de ganado local o de animales cruzados), los Humedales de las tierras altas y las Zonas Áridas de las tierras altas. Se evaluaron características fenotípicas, rendimientos reproductivos y parámetros de la canal en ganado Ongole y cruzado, así como la motivación de los ganaderos por mantener reproductores Ongole o cruzados, las funciones del ganado bovino en las granjas y el Margen Bruto (MB) asociado al ganado bovino en las granjas criadoras de ganado Ongole o cruzado. En ninguna de las diferentes zonas agroecológicas consideradas están los cruzamientos cambiando el sistema productivo: el tamaño de los rebaños, el tipo de granja y el manejo y las funciones del ganado bovino fueron muy similares entre las granjas criadores de ganado Ongole y las criadoras de ganado cruzado. Si bien no hubo diferencias en las cantidades de materia seca y proteína bruta suministradas a cada animal, las zonas agroecológicas difirieron en los cultivos y en los recursos alimenticios. Los cruzamientos están cambiando las características individuales del ganado bovino y, en consecuencia, los precios de mercado de los animales. En términos generales, las hembras maduras cruzadas fueron aproximadamente un 25 por ciento más pesadas que las hembras maduras locales. La descendencia de los machos cruzados fue un 16 por ciento más pesada que sus homólogos locales, mientras que la descendencia de las hembras cruzadas fue un 24 por ciento más pesada que las hembras locales. En cuanto a los rendimientos reproductivos, tanto las vacas locales como las cruzadas alcanzaron buenos resultados anuales de fertilidad (entre el 73 y el 86 por ciento). La mayoría de los ganaderos prefirieron el ganado cruzado al ganado Ongole; en concreto, el cruzamiento con la raza Simmental fue el más apreciado. En las diferentes áreas de estudio, el MB fue similar entre las granjas criadoras de ganado cruzado y las criadoras de ganado Ongole; los precios de venta de los animales cruzados fueron mayores pero también lo fueron los costes de alimentación. Se cree que se seguirán dando los cruzamientos ya que las políticas gubernamentales los promueven y los ganaderos prefieren los animales cruzados en razón de sus mayores pesos corporales y precios de mercado en comparación con el ganado Ongole. No obstante, los ganaderos puntualizaron que no desean llegar a niveles muy elevados de sangre Simmental en los ejemplares cruzados. Así, para evitar el riesgo de mejora hasta un elevado grado de pureza Simmental, se hace necesaria una población Ongole viable.

Palabras clave: *Indonesia, zonas agroecológicas, ganado bovino Ongole, cruzamiento con Simmental, beneficios*

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Introduction

Crossbreeding with exotic breeds is a major driving force for livestock intensification in developing countries (Udo *et al.*, 2011). Most studies on the impact of crossbreeding are focused on dairy cattle (Syrstad, 1996; Kahi *et al.*, 2000; Samdup *et al.*, 2010). Ideally, crossbreeding strategies have to match the production environment, of which the feed resources are a main determinant (Kahi *et al.*, 2000; Wollny, 2003). In practice, crossbreeding schemes are characterized by un-systematic use of exotic semen, irrespective of agro-ecological and socio-economic settings (Wollny, 2003).

In Indonesia, crossbreeding is widely applied for beef production. The high human population increase and increased purchasing power are major factors driving the rising demand for red meat from ruminants. In 2010 the human population was about 237 million (BPS, 2010). More than 50 percent of all cattle are kept on Java, the main island with 57 percent of the human population of Indonesia (Kementan, 2010). To satisfy the demand for meat, the government has been importing meat and live animals. Particularly in Java, from the 1980s onwards, the government has been promoting artificial insemination using exotic breeds from temperate regions, such as Simmental, Limousin, Aberdeen Angus and Hereford to improve the beef performance of the local cattle.

In Indonesia, farmers keep cattle not only for meat production, but also for financial security, manure for cropping, social status and draught power (Widi, 2004). About 95 percent of cattle are in smallholder crop–livestock farmers' hands, with fewer than five cattle per farm.

During the colonial period the Dutch administration introduced Ongole cattle from India to replace the indigenous Javanese cattle (*Bos javanicus*) (Barwegen, 2004). The male and female Ongole cattle were bought from areas surrounding Madras. Ongole were considered more suitable for carrying the heavy loads for the sugar industry. Javanese farmers initially disliked the Ongole breed, because they could not work in forests like the Javanese cattle (Barwegen, 2004). The pure Ongole was brought to Sumba Island and became the purebred Sumba-Ongole. In Java, the Sumba-Ongole were crossed with Javanese cattle and formed the Ongole-grade (in Indonesia called *Peranakan Ongole*, PO). Added to this, the Dutch administration introduced Ongole cattle in areas along a main concrete road, '*Daendels* road', located along the south coast in Central Java; the Ongole has been developed and favoured by farmers in this area (Sudardjat and Pambudy, 2003). In the course of the twentieth century, Ongole became the prominent cattle breed in Java (Maule, 1990).

Characteristics of Ongole cattle are: a big body, strong power, docile and a quiet temperament, good heat tolerance and ability to survive under restricted feed conditions (Maule, 1990). This makes them good animals for draught power. Ongole cattle grow faster than Madura or Bali cattle. However, they are less fertile than the indigenous Javanese cattle (Barwegen, 2002; Widi *et al.*, 2006), and Madura and Bali cattle (Maule, 1990). In 2003, the Ongole population was estimated at about 4.4 million. About 90 percent of them are on Java (Deptan, 2003). Their numbers are, however, rapidly decreasing, mainly because in the period 2006–2011, the percentages of semen from exotic and local breeds distributed by AI centres all around Indonesia were 85 and 15 percent, respectively (BIB, 2011). In Java, AI is the dominant breeding method for cows. About 85 percent female cattle in Java Island have been served with AI (Sudardjat and Pambudy, 2003).

The performance of breeds depends on environmental conditions and farming systems (Frisch and Vercoe, 1978). In Java, there are broadly speaking two agro-ecological zones, based on the altitude: the uplands and the lowlands; and based on the annual rainfall dry and wet subdivisions can be made. Each zone has a different topography, soil type, soil fertility and agro-climatic conditions. The result is a different cropping pattern, land use management, production potential and consequently variation in feed resources (Budisatria, 2006). Crossbreeding is promoted and implemented throughout the country regardless of the different resources in the various agro-ecological zones and the different functions of cattle in the smallholder farming systems.

Central Java is one of the prominent areas in Indonesia with beef cattle. Crossbreds are already a major part of the cattle population, but also the original breeding areas of Ongole cattle are found here (Widi *et al.*, 2008). In Central Java, feeding conditions are relatively good in the lowlands and Wet uplands, and poor in the Dry uplands (Sutresniwati, 2006).

Given the large utilization of crossbreds, irrespective of the different mixed farming conditions, we studied the relative performance of Ongole and crossbred cattle to address the question: is crossbreeding an appropriate breeding strategy in the different agro-ecological zones endowed with different feed resources?

Materials and methods

Study areas

This study was conducted in Yogyakarta and Central Java Provinces, situated in the southern part of Central Java (Figure 1). Both provinces have large cattle numbers.

The study areas represented two agro-ecological zones, the lowlands and the uplands, with different rainfall patterns: Wet lowlands, Wet uplands and Dry uplands. Wet lowlands are found at less than 100 m above sea level (asl) and their annual rainfall ranges from 2 400 to 3 000 mm (BPS, 2009). Lowlands have fertile soils and are characterized by irrigated farming systems with paddy and maize as the main crops. Wet uplands are defined as areas above 500 m asl with annual rainfall ranging from 3 000 to 3 600 mm (BPS, 2009). This zone has fertile soils and is characterized by both irrigated and rain-fed farming systems, with paddy fields, horticulture and forest. Dry uplands are also situated above 500 m asl but have less fertile soils and low annual rainfall: 1 800–2 400 mm (BPS, 2009). This zone is characterized by rain-fed farming systems with cassava and dry land paddy as the main crops.

There are two rainfall seasons over the year. The wet season usually begins in September and lasts until about April. No grazing areas are available, as all land is used for cropping. The types of forages used include improved grasses, such as Napier and Elephant grasses, rice straw, maize straw, many kinds of tree leaves, cassava leaves and tree legumes. Native forages, such as weeds and grasses, are collected from farmers' own fields and backyards, roadsides, riversides and forest edges. During the dry season, when forage sources are limited, farmers buy forages from other areas. The Dry uplands are relatively far away from the input markets, approximately 60 km, 1.5 h by truck.

For this study, Wet lowlands were divided into two areas, namely Wet lowlands I and II (Figure 1). In Wet lowlands I, located in Yogyakarta Province, crossbreeding is broadly applied in contrast to Wet lowlands II, located in Central Java, where crossbreeding is practiced less frequently. In this area, the local government allocated different locations for maintaining Ongole and for crossbreeding in order to maintain the Ongole in this zone, which is an original

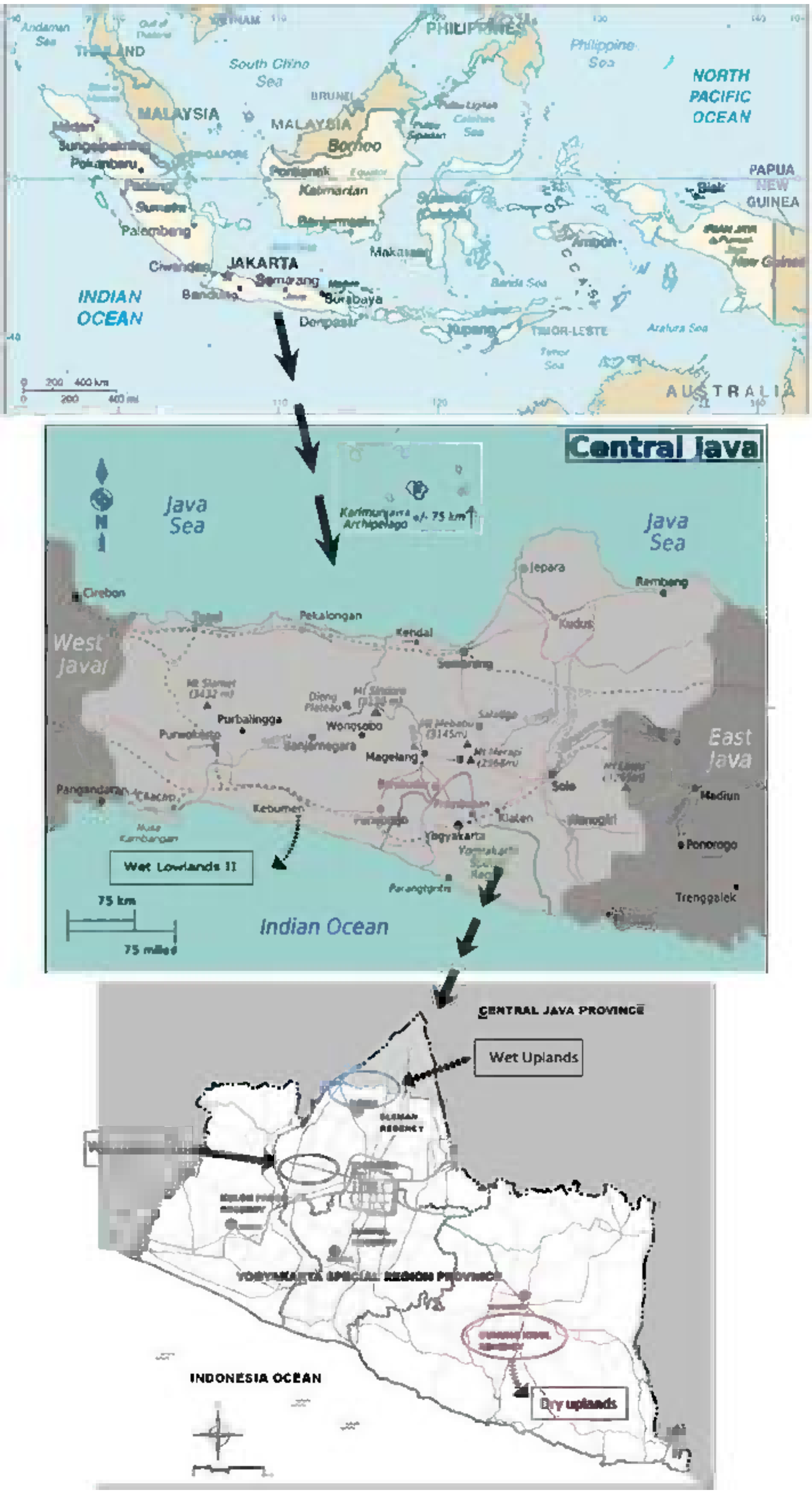

Figure 1. Map of Indonesia, Central Java and Yogyakarta Province (Source: Anonymous, 2007 and Pemda-DIY, 2005, cited by Budisatria, 2006).

Ongole breeding area from colonial times onwards. In each zone, the farmers could be divided into Ongole and crossbred farmers, based on the breed of cattle they kept as breeding stock.

Before 1990, mostly Ongole cows were used for breeding; they were inseminated with Simmental or Limousin semen which resulted in F_1 Simmental or Limousin crossbreds. From 1990 onwards the majority of F_1 and F_2 cows were inseminated using Simmental or Limousin semen, which resulted in F_2 and F_3 Simmental and Limousin crossbreds. Consequently, the number of Ongole cattle has been sharply decreasing since 1990 (Widi *et al.*, 2008).

Data collection

Secondary data collection

Secondary data related to geographical situation of study areas, cattle population, distribution of semen and local implementation of national and local policies were collected from The Agricultural Department of Indonesia, Animal Husbandry Office of Yogyakarta Province and Central Java Province, government websites, publications and reports from institutes. Secondary data provided insight in the recent local situations.

Focus group discussions (FGDs) and farmers' interviews

Participatory approaches started by conducting FGDs amongst farmers and the key persons such as head of farmers' group and village elders in each area. The purpose of the FGDs was to introduce the study and identify the issues regarding the local and crossbred cattle keeping. In total 296 participants (60 in Wet lowlands I, 86 in Wet lowlands II, 65 in Wet uplands and 85 in Dry uplands) were randomly selected and involved in the FGDs.

The issues which were obtained in the FGDs were used for making a checklist for guidance of semi structured interviews for the farmers. In total 252 farmers from 296 FGDs' participants in the four study areas (56 farmers in Wet lowlands I; 63 farmers in Wet lowlands II; 59 farmers in Wet uplands and 74 farmers in Dry uplands) were purposively selected. The farmers had an experience of minimum 10 years in keeping their own herd of cattle. Most farmer respondents were men, only four of them were women, widows. Men are doing all of the management activities of large animals, such as cattle and buffaloes, while women are responsible for smaller animals, such as chickens, goats and sheep. The 252 farmers were interviewed individually about their background, technical aspects, their motivations for keeping animals and reasons to choose Ongole or crossbred cattle as breeding stock. Household members contributed to recall information during the interviews. These data were collected during the first farm visit in the period July–November 2009.

Phenotypic characteristics of Ongole and crossbred cattle

Each animal on all 252 farms was characterized by observing the body, face, nose, leg, tails' hair and vulva colours; existence of dewlap, backline and hump; shape of horns and the thickness of body and heads' hairs. Ongole and crossbred cattle were distinguished based on these characteristics, using a checklist (Maule, 1990; Porter, 1991; Supiyono, 1998; Sumadi *et al.*, 2003; Triyono, 2003; Widayanti, 2008) with specific conformation traits, and on information from the farmer on breeding background of the animal concerned.

Quantitative phenotypic characteristics of 294 female cattle of the 252 farms were collected by taking length of the body (LB), girth of chest (GC), height at withers (HW), height at hip (HH), head index (HI) and estimation of body weight (BWe), using a measurement tape with cm and the transformation of chest girth in cm into weight in kg (developed by FHK Ogawa Seki Co. Ltd, Tokyo, Japan), over the period January 2010 to July 2011. Body condition score (BCS) was visually assessed (Ferguson *et al.*, 1994 cited by Lassen *et al.*, 2003). The age of each animal (in years) was determined by inspecting its teeth (Widi *et al.*, 2014). Similar measurements were done for calves ($n = 127$) at weaning and at approximately 11 months of age. Eleven months of age was chosen because most calves are sold before they reach the age of 1 year.

Feeding practices

Many different feeds were offered. The feeds were categorized in fresh forages, dry forages and supplementary feeds. The proportions of the different fresh forages were estimated by separating the fresh forages again in its components. Feed inputs were calculated based on farmers' estimates and direct observation on kinds and amounts of feeds offered to each individual adult animal, over 1 year (January 2011–January 2012). The estimations of kind and amount of fresh and dry forages offered were recorded by farmers every day. Enumerators checked the farm recording once a month. Dry forages and supplementary feeds that were bought were estimated from the amounts bought. These estimates were translated into kg dry matter (DM) and crude protein (CP) intake per animal, applying the feed composition tables for feeds available in Central Java of Hartadi, Soedomo and Tillman (2005).

Reproductive performances

Reproductive data were collected over the period January 2010 to July 2011. This recording was done by farmers, guided and assisted by enumerators ($n = 8$) at the start of the monitoring period. Enumerators visited the farmers every month to collect and check the recorded information. Reproductive performances determined were days to postpartum estrus (PPE) days to postpartum mating (PPM), services per conception (S/C), calving interval (CI), weaning age and calf crop. CI estimates were based on calving dates of animals with two calvings in the reporting period or on calving date in the reporting period and a previous calving from before the recording started derived from recall information. Calf crop per study area was calculated as follows:

$$\text{Calf crop in each study area} = \frac{\sum \text{calves born} - \sum \text{pre} - \text{weaning calves died}}{\sum \text{cows}} \times (365/\text{CI}).$$

The reproductive performances of 114 Ongole and 156 crossbred cows were recorded. Cows were defined as female cattle that had calved at least once. The farmers observed and recorded the reproduction cycle of their cows over a period of 1.5 years. Farmers in all study areas have relatively similar knowledge on reproductive management. They obtained it through information sharing amongst farmers, farmers' community groups and formal training from the local extension officer. Farmers do not routinely record reproductive information. For this survey, we asked farmers to fill in a recording sheet for the reproductive data of their cattle. They were explained beforehand and enumerators visited them every month to assist them in recording the reproductive activities. Information on age at first estrus and calving (if available) were also collected by recall. The number of infertile female cattle was very small, not more than 2 percent. Farmers immediately sold infertile heifers and the cows which are failing to have a next calving ($S/C > 5$). Artificial insemination is applied in all the study areas, particularly to crossbred cows.

Carcass characteristics of Ongole and crossbred cattle

We visited the biggest slaughter house in Yogyakarta, and measured the slaughter cattle belonging to two butchers over a period of 15 days. Carcass weight and meat bone ratio (MBR) were measured on 55 cattle (13 Ongole, 29 Simmental cross and 13 Limousin cross animals). They consisted of 14 female and 41 male cattle. The scales used to weigh the cattle and carcasses had an accuracy of 1 kg and the scale used to weigh the meat had an accuracy of 20 g.

Gross margins analysis

Farmers recorded the inputs and outputs of their cattle over a period of 1.5 year (January 2011–July 2012). Enumerators ($n = 8$) visited the farmers every month to collect and check the recorded information. This particular period was representative of an average period in terms of rainfall and perceptions of farmers that the revenues from their cattle covered their financial requirements. Only 184 of the 252 farmers sold cattle during the monitoring period. Most farmers used only family labour, only few farmers ($n = 20$) used hired labour, either regularly or on an *ad hoc* basis.

The Gross Margins (GM) analysis was done for each farm for the reporting period. It was based on financial revenues minus variable costs. Procedures in the GM calculations included:

- Fresh forage costs comprising cultivated grasses and maize foliage bought from forage sellers in the livestock markets or alongside roads.
- Dry forage costs comprising rice and maize straws bought from dry forage sellers or collected from the fields and loaded on trucks, involving costs for the fuel, or hiring the trucks and drivers.
- Supplementary feeds costs comprising concentrates, rice bran, cassava meal, cassava, tofu (soybean curd) waste and soybean hulls bought from poultry shops, markets and soy-processing factories.
- Costs for veterinary services and medicines.
- Costs for artificial insemination or mating services.
- Hired labour costs.
- Feeds collected by farmers from communal sources (road sides, forests, communal lands) and transported on the back of farmers or on bicycles were not valued.
- Revenues of cattle sales; local traders buy the cattle and bring these to cattle markets.
- Revenues from the sale of manure; manure in the form of compost is sold to horticulture farmers, ornamental plants farmers, producers of organic fertilizer, or plantations.
- Opportunity value of manure used for crops was not included.
- Actual farm gate prices were used for accounting in IDR (Indonesian Rupiah; US\$ 1 = 9 200 IDR in 2011).

Data analysis

The qualitative data were analysed descriptively. Ranking was used to determine the level of agreement of farmers' motivations for keeping cattle. Frequency distribution was used to analyse the reasons of the farmers in choosing Ongole or crossbred breeding stock. The quantitative data were analysed using analysis of variance (ANOVA) 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.

Results and discussion

Phenotypic characteristics of Ongole and crossbred cattle

By observing the phenotypic characteristics in the study areas, the cattle were identified as Ongole or crossbred, while the crossbred cattle were Simmental or Limousin crosses. The diversity in phenotypic characteristics of crossbred cattle is presented in Figure 2. There was not sufficient information to distinguish subsequent crossbred generations, since there is no pedigree recording system kept by farmers nor inseminators. Farmers could also not distinguish subsequent crossbred generations; they purchased their animals from the market or middle men without any pedigree information.

Body sizes of female Ongole and crossbred cattle older than 2.5 years, which most of them were cows, in the four areas are presented in Table 2. Simmental crossbred female cattle in all areas were significantly bigger and higher than female Ongole cattle ($P < 0.05$). The height and weight estimates for the Limousin crossbred females did not differ from the Simmental crossbreds.

Body sizes of calves at weaning (approximately at 7 months of age) and at approximately 11 months of age in the study areas are presented in Table 3. Weaned crossbred male calves were 16 percent heavier than Ongole male calves, for female calves this figure was 24 percent. These differences were significant ($P < 0.05$). At 11 months of age crossbred males were only 2 percent heavier than Ongole males, for females this difference was 18 percent ($P < 0.05$). The number of Ongole calves ($n = 1$) in Wet lowlands I was not sufficient for testing of differences between breed types.

Body condition scores of Ongole cows were lower ($P < 0.05$) than those of crossbred cows in the Wet lowlands I,

Figure 2. Diversity of phenotypic characteristics of crossbred cattle in the study areas. Code 'A' is for Simmental cross and 'B' is for Limousin cross.

Table 1. Characteristics of Ongole and crossbred households in the four study areas, established in July–November 2009.

	Area/breed								*P* value*
	Wet lowlands I ($N=56$)		Wet lowlands II ($N=63$)		Wet uplands ($N=59$)		Dry uplands ($N=74$)		
	Ongole ($N=17$)	Crossbred ($N=39$)	Ongole ($N=31$)	Crossbred ($N=32$)	Ongole ($N=12$)	Crossbred ($N=47$)	Ongole ($N=30$)	Crossbred ($N=44$)	
Age of household head (years)	$54.6^{a} \pm 11.0$	$51.3^{a} \pm 10.3$	$50.4^{a} \pm 9.9$	$49.1^{a} \pm 7.1$	$44.3^{a} \pm 11.8$	$51.2^{b} \pm 13.8$	$58.6^{a} \pm 14.5$	$56.9^{a} \pm 11.4$	0.00
Land size (ha)	$0.13^{a} \pm 0.13$	$0.14^{a} \pm 0.09$	$0.36^{a} \pm 0.8$	$0.21^{a} \pm 0.12$	$0.17^{a} \pm 0.06$	$0.16^{a} \pm 0.16$	$0.44^{a} \pm 0.29$	$0.55^{b} \pm 0.50$	0.00
Family size (person)	$4.5^{a} \pm 1.6$	$4.3^{a} \pm 1.5$	$4.7^{a} \pm 1.4$	$5.1^{a} \pm 1.6$	$4.7^{a} \pm 1.5$	$4.4^{a} \pm 1.3$	$4.0^{a} \pm 1.6$	$3.9^{a} \pm 1.4$	0.02
Education level (%)									
No school	0.0	2.6	3.2	0.0	0.0	0.0	16.7	9.1	
Elementary school	52.9	41.0	64.5	68.8	33.3	38.3	53.30	3.8	
Junior high school	35.7	28.2	22.6	21.9	41.7	14.9	26.7	20.6	
Senior high school	11.4	23.1	9.7	6.3	25.0	23.4	3.3	27.3	
Higher education	0.0	5.1	0.0	3.1	0.0	23.4	0.0	11.4	
Experience in cattle keeping (years)	$19.3^{a} \pm 7.6$	$17.6^{a} \pm 10.9$	$16.6^{a} \pm 10.5$	$12.4^{b} \pm 3.8$	$23.6^{a} \pm 12.6$	$21.1^{a} \pm 15.0$	$31.2^{a} \pm 14.5$	$29.0^{a} \pm 10.4$	0.19
Livestock ownership									
Cattle (head)	$2.2^{a} \pm 1.0$	$2.2^{a} \pm 0.9$	$2.0^{a} \pm 0.9$	$3.1^{b} \pm 1.7$	$2.3^{a} \pm 1.0$	$2.5^{a} \pm 1.0$	$2.2^{a} \pm 1.0$	$2.5^{a} \pm 1.6$	0.37
Cow (%)	64.7	58.6	57.4	47.5	57.1	58.9	46.1	56.1	0.13
Small ruminants (head)	$0.8^{a} \pm 1.4$	$1.4^{a} \pm 1.9$	$0.9^{a} \pm 1.9$	$0.8^{a} \pm 1.3$	$1.2^{a} \pm 1.5$	$0.7^{a} \pm 1.4$	$1.9^{a} \pm 1.7$	$1.4^{a} \pm 1.7$	0.02
Poultry (head)	$0.5^{a} \pm 1.2$	$2.1^{b} \pm 2.4$	$1.1^{a} \pm 1.7$	$1.6^{a} \pm 2.1$	$1.3^{a} \pm 2.3$	$1.4^{a} \pm 2.2$	$1.5^{a} \pm 1.8$	$1.4^{a} \pm 2.0$	0.91
Cattle ownership status (%)									
Owning	100	100.0	80.6	59.3	83.4	93.6	90.0	86.4	
Sharing	0	0	16.1	18.8	8.3	6.4	10.0	11.4	
Both	0	0	3.3	21.9	8.3	0.0	0	2.2	
Main occupation (%)									
Farming	47.1	46.2	77.4	75.0	75.0	61.7	83.3	61.4	
Government official	0.0	7.7	3.2	6.3	0.0	17.1	3.3	11.4	
Trader/private business	0.0	15.4	19.4	0.0	0.0	10.6	3.3	20.5	
Labourer	52.9	30.8	0.0	18.8	25.0	10.6	10.0	6.8	

[a,b] Different superscripts indicate significant differences among breeds within areas ($P < 0.05$).

*P value among areas.

Table 2. Physical characteristics (Mean ± s.d.) of female Ongole and crossbred cattle with minimum age 2.5 years in four areas in Central Java.

Physical characteristic	Area/breed									
	Wet lowlands I		Wet lowlands II			Wet uplands			Dry uplands		
	Ongole ($N = 21$)	Sim-cross ($N = 38$)	Ongole ($N = 36$)	Sim-cross ($N = 36$)	Lim-cross ($N = 4$)	Ongole ($N = 16$)	Sim-cross ($N = 76$)	Lim-cross ($N = 3$)	Ongole ($N = 22$)	Sim-cross ($N = 32$)	Lim-cross ($N = 10$)
Age (year)	6.8^{a} ± 3.1	4.7^{b} ± 1.6	5.3^{a} ± 2.5	4.0^{b} ± 1.6	3.4^{b} ± 1.4	5.7^{a} ± 2.0	4.1^{b} ± 1.6	3.0^{b} ± 0.5	5.7^{a} ± 3.0	4.3^{b} ± 1.7	5.9^{a} ± 1,4
GC (cms)	159.9^{a} ± 9.8	175.2^{b} ± 5.0	167.4^{a} ± 8.6	175.7^{b} ± 9.6	169.3^{ab} ± 8.2	157.9^{a} ± 9.0	172.3^{b} ± 12.3	172.7^{b} ± 8.6	159.7^{a} ± 10.1	176.7^{b} ± 16.7	176.2^{b} ± 13.5
HW (cms)	125.1^{a} ± 3.9	128.2^{b} ± 5.0	130.4^{a} ± 5.8	129.7^{a} ± 6.3	122.8^{b} ± 6.2	120.8^{a} ± 3.9	129.3^{b} ± 6.7	129.8^{b} ± 6.9	120.9^{a} ± 6.8	126.7^{b} ± 7.5	126.9^{b} ± 4.9
LB (cms)	107.3^{a} ± 11.1	116.9^{b} ± 10.3	111.3^{a} ± 7.8	121.2^{b} ± 7.7	119.4^{b} ± 7.1	104.1^{a} ± 4.2	120.4^{b} ± 9.9	115.0^{b} ± 7.8	108.7^{a} ± 8.6	115.7^{b} ± 12.6	120.1 ± 9.8
HI (%)	39.2^{a} ± 3.5	45.6^{b} ± 2.8	40.8^{a} ± 4.1	43.1^{b} ± 2.9	41.8^{a} ± 1.4	42.1^{a} ± 2.9	42.3^{a} ± 4.1	42.4^{a} ± 4.0	39.1^{a} ± 3.0	43.1^{b} ± 4.4	44.3^{b} ± 3.9
BWe (kg)	325^{a} ± 48.2	396^{b} ± 67.7	368^{a} ± 51.0	420^{b} ± 65.4	380^{a,b} ± 45.7	304^{a} ± 82.3	403^{b} ± 74.4	399^{b} ± 57.1	321^{a} ± 55.5	434^{b} ± 116.7	427^{b} ± 30.4
BCS	2.7^{a} ± 0.5	3.2^{b} ± 0.5	3.3^{a} ± 0.4	3.2^{a} ± 0.4	3.9^{b} ± 0.2	3.2^{a} ± 0.4	3.2^{a} ± 0.4	3.8^{b} ± 0.3	3.1^{a} ± 0.5	3.1^{a} ± 0.6	3.3^{a} ± 0.2

Sim-cross, Simmental cross; Lim-cross, Limousin cross; CG, girth of chest; HW, height at the withers; LB, length of the body; HI, head index, is calculated by dividing length of head from the width of head in percentage; BCS, body condition score, is visual assessment of body tissues (Ferguson *et al.*, 1994 cited by Lassen *et al.*, 2003). The range is 1–5, where 1 is the lowest and 5 is the highest (Baliarti, 1999); BWe, body weight estimation.

[a,b,c]Different superscripts indicate significant differences among breeds within the same area ($P < 0.05$).

Table 3. Physical characteristics (Mean ± s.d.) of progeny at weaning and at about 11 months of age of Ongole and crossbred cows in three study areas in Central Java.

Physical characteristics	Area						Overall average (sex/breed)			
	Wet lowlands II		Wet uplands		Dry uplands		Male		Female	
	Ongole ($N = 32$)	Crossbred ($N = 12$)	Ongole ($N = 2$)	Crossbred ($N = 28$)	Ongole ($N = 11$)	Crossbred ($N = 42$)	Ongole ($N = 15$)	Crossbred ($N = 65$)	Ongole ($N = 30$)	Crossbred ($N = 38$)
At weaning										
Age (month)^{ns}	5.9 ± 1.5	5.8 ± 1.3	5.5 ± 0.7	6.8 ± 1.3	7.1 ± 1.4	6.1 ± 1.0	5.7 ± 1.6	6.4 ± 1.3	6.4 ± 1.4	6.1 ± 1.4
GC (cms)	110.2^{a} ± 11.3	121.7^{b} ± 9.3	129.0^{a} ± 18.4	125.2^{a} ± 9.0	119.0^{a} ± 11.2	120.0^{a} ± 12.1	115.3^{a} ± 14.1	122.1^{b} ± 10.3	112^{a} ± 11.7	121.0^{b} ± 12.3
HW (cms)^{ns}	110.6 ± 7.7	100.0 ± 6.5	108.0 ± 18.4	100.4 ± 6.6	99.5 ± 8.3	97.2 ± 6.9	100.9 ± 7.9	99.3 ± 6.7	100.5 ± 7.8	98.3 ± 7.7
LB (cms)	78.2^{a} ± 7.4	86.4^{b} ± 8.2	84.0^{a} ± 11.3	86.8^{a} ± 5.8	77.8^{a} ± 8.1	82.5^{a} ± 10.2	76.9^{a} ± 7.9	85.0^{b} ± 8.5	79.1^{a} ± 7.4	84.1^{b} ± 10.0
HI (%)^{ns}	45.0 ± 5.5	42.9 ± 7.7	43.0 ± 4.2	45.1 ± 3.9	42.9 ± 3.4	45.3 ± 4.8	45.7 ± 5.2	44.6 ± 4.5	43.8 ± 4.9	45.7 ± 5.5
BWe (kg)	116^{a} ± 35.1	154^{b} ± 31.1	185^{a} ± 71.4	167^{a} ± 33.0	148^{a} ± 39.3	150^{a} ± 44.7	135^{a} ± 44.4	157^{b} ± 37.4	123^{a} ± 39.2	152^{b} ± 42.6
At approximately 11 months of ages										
Age (month)^{ns}	10.5 ± 1.6	10.3 ± 2.1	9.5 ± 0.7	11.1 ± 1.4	11.7 ± 2.7	10.4 ± 2.0	10.8 ± 2.1	10.5 ± 1.7	10.8 ± 1.9	10.6 ± 1.9
GC (cms)	126.0^{a} ± 9.2	136.8^{b} ± 9.3	136.0^{a} ± 18.4	132.6^{a} ± 9.2	134.2^{a} ± 12.3	133.5^{a} ± 16.5	130.3^{a} ± 11.3	131.4^{b} ± 12.7	127.5^{a} ± 10.7	134.7^{b} ± 13.5
HW (cms)	110.2^{a} ± 6.9	111.5^{a} ± 6.2	113.5^{a} ± 3.5	107.6^{a} ± 5.8	109.4^{a} ± 7.6	107.5^{a} ± 8.8	111.7^{a} ± 7.9	107.2^{b} ± 7.1	109.1^{a} ± 6.4	109.1^{a} ± 8.2
LB (cms)	90.5^{a} ± 9.7	98.1^{b} ± 10.0	90.0^{a} ± 11.3	93.4^{a} ± 6.1	89.2^{a} ± 9.7	92.1^{a} ± 11.2	90.9^{a} ± 10.6	92.0^{a} ± 8.7	89.8^{a} ± 9.2	94.1^{a} ± 11.1
HI (%)	44.8^{a} ± 4.7	46.4^{a} ± 4.9	45.9^{a} ± 0.6	46.7^{a} ± 3.3	44.8^{a} ± 3.0	46.4^{a} ± 3.4	45.7^{a} ± 3.6	46.7^{a} ± 3.6	44.4^{a} ± 4.4	46.4^{a} ± 3.4
BWe (kg)	170^{a} ± 34.4	214^{b} ± 37.9	213^{a} ± 79.2	197^{a} ± 36.6	205^{a} ± 54.2	202^{a} ± 65.6	188^{a} ± 45.6	192^{a} ± 49.1	177^{a} ± 43.2	208^{b} ± 57.1

CG, girth of chest; HW, height at the withers; LB, length of the body; HI, head index, is calculated by dividing length of head from the width of head in percentage; BWe, body weight estimation.

[a,b]Different superscripts indicate significant differences among breeds within the same area and in all areas ($P < 0.05$).

[ns]non-significant.

indicating that crossbred cows may have been fed better than Ongole cows in this area. Overall, the body condition scores indicated that cows were in a good body condition (2.7–3.9 in the BCS range of 1–5).

Livestock farming systems and motivations of keeping cattle

Table 1 gives household and farm characteristics for the livestock farming systems in the four study areas. The land sizes of the farms in Dry uplands were significantly larger than in the other areas, but most of this land is infertile. Crossbred farmers had significantly more (crop) land than Ongole farmers in the Dry uplands (0.6 versus 0.4 ha), but in the other areas the farms sizes were the same for both farm types. Farmers had on average 21 years' experience in cattle keeping. The experience in cattle keeping was not different between Ongole and crossbred farms within the areas, except in Wet lowlands II where the crossbred farmers had 4 years less experience in cattle keeping than Ongole farmers. Experience in cattle keeping differed significantly between the areas with the longest experience in keeping cattle in the Dry uplands; farmers in this area were also slightly older (58 years) than in other areas (50 years). However, no differences ($P < 0.05$) were found in uptake of crossbreeding in relation to experience of cattle keeping. Cattle are the main livestock. Goats, sheep and chickens are of secondary importance. The herd sizes of Ongole (2.0–2.5 head) and crossbred (2.2–3.2 head) farms were the same in the areas, except in Wet lowlands II where crossbred farmers had significantly ($P < 0.05$) more cattle (3.2) than Ongole farmers (2.0). Education level only seemed to have affected uptake of crossbreeding ($P < 0.05$) in the Dry uplands (Table 1). On average, more than 50 percent of the cattle were cows. About 10 percent of farmers were sharing cattle (sharing implies the cattle on the farms were owned by other parties; the benefits are shared by mutual agreement); only in Wet lowlands I, no sharing took place (Table 1). There was no difference between Ongole and crossbred farms in the proportion of farmers sharing cattle with owners within the areas. In Wet lowlands I, less than 50 percent of farmers had farming as their main occupation. Many were labourers (53 percent for Ongole farmers and 31 percent for crossbred farmers, since the access to employment in the capital city, Yogyakarta, is near. In the other areas, the percentage of farming as main occupation varied from 61 to 83. However, the percentage distribution between Ongole and crossbred farms was not significantly different within areas ($P < 0.05$). It could be speculated that the relatively low body condition scores of Ongole cattle in Wet lowlands I may be the result of the fact that many of the farmers working as labourer could pay less attention to their cattle than fulltime farmers.

Most of the Ongole cattle were cows. In the Dry uplands and Wet lowlands II area also a substantial number of Ongole calves were kept. Wet lowlands II is an area with specific Ongole breeding tracts. In Wet lowlands I and Wet uplands, there were very few Ongole calves. This indicates that farmers who were still keeping Ongole cows, in these two areas, had their cows inseminated with exotic semen.

As in other areas in Indonesia, in Central Java cattle keeping serves various objectives. Both Ongole and crossbred farmers reported that capital savings, additional income and manure were the main motivations for keeping cattle (Table 4). Farmers consider security (capital savings) as being able to sell cattle to meet unexpected or large expenditures, such as sending children to school, financing a wedding or circumcision party, or buying a motorcycle. They consider income as the cash they receive relatively regularly from the sale of progeny (weaners). Most farmers considered manure the third important motive for keeping cattle. As with farmers in other areas in Java, farmers in the four study areas depend on livestock manure to fertilize soils. It is also common in Java that farmers sell excess manure to horticulture and ornamental plants farmers, producers of organic fertilizer, or plantations. Draught power was the least important motivation in all areas and for all types of cattle. Nowadays farmers use hand tractors to plough their land.

Tables 5 and 6 show the reasons of farmers to choose Ongole or crossbred cattle as their main breeding stock. The most frequent reasons for choosing local Ongole cattle were lack of capital, less feed required, easy management and most knowledge/custom. While the most frequent reasons for choosing crossbreds were big body size and the high prices when progeny were sold. In general, farmers keep only one or two cows. When farmers have enough money to purchase a crossbred animal, they tend to replace an Ongole cow by a crossbred cow. The Simmental crossbred is preferred because of its nice appearance, the shiny red coat and rectangle head shape (Sutresniwati, 2006). Crossbred farmers (75–86 percent) preferred F_1 cows; the preference for specific crossbred generation for young animals was less pronounced (Table 6).

Feeding

All farms used stall-feeding. The feed types, the fresh feed intakes, and DM and CP intake estimates of Ongole and crossbred cattle are shown in Table 7. In most cases, the forage collected by farmers was a mixture, rather than a single type. The majority of the feeds offered were the locally available forages. The proportion of the forages in a ration varied between the areas, reflecting the different cropping patterns. In the Dry uplands, proportion of native grass in the forage ration was about 40 percent, while in other study areas this was lower (25–30 percent). Cassava leaves, ground nut haulm and legumes were offered more frequently in this area, compared with other areas. The maize foliage in Dry uplands came partly from outside this area. Rice bran was the most common supplementary feed in all study areas. Tofu waste and compound concentrates were supplementary

Table 4. Farmer's ranking motivations for keeping cattle in four study areas in Central Java.

Motivation	Area/Breed															
	Wet lowlands I ($N = 56$)				Wet lowlands II ($N = 63$)				Wet uplands ($N = 59$)				Dry uplands ($N = 74$)			
	Ongole ($N = 17$)		Crossbred ($N = 39$)		Ongole ($N = 31$)		Crossbred ($N = 32$)		Ongole ($N = 12$)		Crossbreed ($N = 47$)		Ongole ($N = 30$)		Crossbred ($N = 44$)	
	Average score	Rank*	Average score	Rank*	Average score	Rank*	Average score	Rank*	Average score	Rank*	Average score	Rank*	Average score	Rank*	Average score	Rank*
1. Saving	1.5 ± 0.7	1	1.4 ± 0.7	1	1.7 ± 0.8	1	1.8 ± 0.6	2	1.1 ± 0.3	1	1.8 ± 0.8	1	1.5 ± 0.6	1	1.4 ± 0.6	1
2. Income	2.3 ± 1.3	2	1.8 ± 0.6	2	1.8 ± 0.9	2	1.5 ± 0.8	1	2.3 ± 1.1	2	1.9 ± 1.1	2	2.5 ± 1.3	2	2.9 ± 1,7	2
3. Hobby	4.9 ± 1.9	4	5.0 ± 1.6	5	5.3 ± 1.9	6	5.3 ± 1.7	6	5.2 ± 0.9	6	4.5 ± 1.9	5	5.0 ± 1.8	5	4.9 ± 1.7	5
4. Utilization crop by-product or back yard	5.4 ± 1.6	6	4.7 ± 1.4	4	4.0 ± 1.6	4	5.2 ± 1.2	5	5.0 ± 1.3	5	4.3 ± 1.4	4	5.6 ± 1.2	6	5.4 ± 1.2	6
5. Manure	3.8 ± 0.9	3	3.8 ± 0.9	3	3.9 ± 0.9	3	3.6 ± 0.9	3	3.2 ± 0.6	3	3.9 ± 1.2	3	2.9 ± 0.7	3	2.8 ± 1.0	3
6. Social/status	5.0 ± 1.2	5	5.2 ± 0.9	6	5.1 ± 1.0	5	4.1 ± 0.9	4	3.9 ± 0.8	4	4.8 ± 0.9	6	4.2 ± 0.5	4	4.5 ± 1.2	4
7. Draught power	6.1 ± 1.9	7	6.7 ± 1.4	7	6.3 ± 1.3	7	7.0 ± 0.0	7	7.0 ± 0.0	7	6.9 ± 0.4	7	7.0 ± 0.0	7	6.9 ± 0.2	7

*Rank = the smallest score of rank (1) means the most important motivation and the highest score of rank (7) means the least important motivation.

feeds fed in Wet lowlands I and Wet uplands. In Wet lowlands II and Dry uplands, farmers offered cassava to their cattle as supplementary feed. Cassava is more abundant in Dry uplands.

Crossbred cattle were fed more ($P < 0.05$) in terms of DM, on average, 10.5 versus 8.7 kg DM per day for Ongole cattle. Overall, the estimates of DM and CP offered per kg metabolic body weight of crossbred cattle were significantly higher than for Ongole cows. So, in general farmers were able to collect extra forages and buy extra supplementary feed for the crossbred stock. Both Ongole and crossbred cows consumed DM at 2.6 percent of their body weight. Ongole and Crossbred cows consumed CP 8.9 and 9.3 percent of DM, respectively. Feeding guidelines for beef cattle (both Ongole and crossbred) show that DM and CP requirements for maintenance are 2.5–3 percent of body weight (Tillman *et al*., 1998) and 9.76 percent of DM (NRC, 1996). So, the current feeding levels are in the range of the maintenance requirements.

Reproductive performances

Table 8 presents the reproductive performances of Ongole and crossbred cows in the four study areas. In the Wet and Dry uplands, Simmental and Limousin crossbred cows expressed PPE significantly earlier than Ongole cows. In the other two areas, Simmental and Limousin crossbred cows also expressed PPE earlier than local cows, but these differences were not significant. Farmers usually had their cows inseminated immediately after PPE was expressed. In the Wet and Dry upland areas the S/C of Ongole cows were relatively fewer than those of crossbred cows. In Wet lowlands II and Dry uplands, natural mating was used, in particular for Ongole cows (86 and 24 percent). Ongole cows expressed PPE later than Simmental cross herd mates. This resulted in longer CI in Ongole cows than in Simmental cross cows in the Wet uplands area. Overall, CI of Ongole cows was 448 days and of crossbred cows 436 days. In the end, the estimates for calf crops of Ongole and crossbred cows were the same in all areas: 81–85 percent for Ongole farms and 73–86 percent for crossbred farms. Both Ongole and crossbred cows performed well compared with, e.g. Bali cattle in Bali and Nusa Tenggara Provinces which had an estimated calf crop of 47 percent (Bamualim and Wirahayati, 2002; Toilehere, 2002).

About one-third of crossbred farmers complained about repeat breeding (high number of S/C), mostly after the fourth or fifth calving. This is in agreement with the relatively higher S/C of crossbred cows. Purwo (personal communication, 2010) and Budiyanto (2012) suggested that reproductive problems occur, in particular, in F_2 and F_3 generation cows. Farmers usually decide to sell the cows with these problems to middle men who sell these animals to local butchers as soon as possible, and buy a pregnant cow or heifer. The farmers complained also about silent heat, but this was not directly reflected in our reproduction

Table 5. Farmer's reasons to choose Ongole cattle in four study areas in Central Java.

Reason	Area							
	Wet lowlands I ($N = 17$)		Wet lowlands II ($N = 31$)		Wet uplands ($N = 12$)		Dry uplands ($N = 30$)	
	Average score	Rank*	Average score	Rank*	Average score	Rank*	Average score	Rank*
1. Lack of capital	2.1 ± 1.6	2	2.6 ± 1.4	2	2.7 ± 1.4	3	2.5 ± 1.6	2
2. Less feed required	1.8 ± 0.6	1	2.3 ± 0.9	1	1.5 ± 0.7	1	1.9 ± 1.1	1
3. Easy management	3.1 ± 1.0	3	3.4 ± 0.9	3	2.6 ± 0.8	2	3.4 ± 1.1	3
4. Most knowledge/custom	3.8 ± 0.9	4	2.3 ± 1.5	1	5.9 ± 1.7	6	4.3 ± 1.4	4
5. Good reproduction performance	4.3 ± 1.1	5	4.8 ± 1.3	4	5.7 ± 2.0	4	5.4 ± 1.9	6
6. Government program	6.4 ± 1.2	6	5.4 ± 0.8	5	5.8 ± 2.2	5	6.5 ± 0.9	8
7. Draught power	7.0 ± 1.0	8	6.5 ± 0.9	6	5.9 ± 1.4	6	5.9 ± 1.3	7
8. *Idul Adha* Festivity	6.9 ± 1.1	7	6.5 ± 0.9	6	6.3 ± 1.7	7	4.8 ± 2.2	5
9. Good meat quality	8.1 ± 1.4	9	6.8 ± 1.2	7	7.8 ± 1.5	8	6.8 ± 1.5	9

*Rank = the smallest score of rank (1) means the highest priority and the highest score of rank (9) means the lowest priority.

data. In 2003, Hasbullah (2003) found that 28 percent of Ongole and 38 percent of Simmental cross cows (most likely F_2 and F_3 cows) had repeat breeding problems.

The farmers reported that they usually sell the 'good' calves, as soon as possible after weaning, in order to obtain a high price with very few inputs. The farmers defined 'good' or 'poor' from body conformation and the visibility of ribs, which is also used to measure BCS. They want to avoid the risk of low growth rates in crossbred calves when they are not able to provide the calves good feed. Good weaned crossbred calves are bought by local traders who sell them to other farmers or commercial feedlot farmers.

Carcass characteristics of Ongole and crossbred cattle

Table 9 presents the sex-specific carcass characteristics of Ongole and crossbred cattle. In the same sex, the ages of Ongole and crossbred cattle which were slaughtered in a slaughterhouse in Yogyakarta Province did not differ. Male cattle were slaughtered at younger ages compared with female cattle.

At similar ages, in both males and females, the body weight at slaughter and total carcass and meat weights of Ongole cattle were significantly lower ($P < 0.05$) than those of their crossbred mates. However, carcass and meat percentages did not differ among breeds in the same sex. MBR was significantly higher in male Ongole and Limousin crosses than in Simmental crosses, while the MBR of female cattle was not different among breeds.

On average, the meat weights of crossbred cattle were 1.42 times higher compared to local cattle (Table 9). Local small-scale butchers said that slaughtering crossbred cattle is not always more profitable than slaughtering Ongole cattle. It depends on the condition of the cattle and how accurately they estimated the weight and the price of the cattle. In contrast, the feedlot and slaughterhouse companies prefer to slaughter crossbred cattle, because of their higher

Table 6. Farmer's reasons to choose crossbred cattle and preferences of crossbred level in four study areas in Central Java.

Reason	Area							
	Wet lowlands I ($N = 39$)		Wet lowlands II ($N = 32$)		Wet uplands ($N = 47$)		Dry uplands ($N = 44$)	
	Average score	Rank*	Average score	Rank*	Average score	Rank*	Average score	Rank*
1. High growth rate	1.1 ± 0.9	1	1.0 ± 0.0	1	1.3 ± 0.8	1	2.0 ± 1.1	2
2. High price of sold progeny	1.9 ± 0.2	2	2.0 ± 0.0	2	2.0 ± 0.5	2	1.5 ± 0.6	1
3. Not picky eaters	4.3 ± 0.9	4	4.1 ± 0.8	4	4.0 ± 0.9	4	2.7 ± 0.7	3
4. Trend	3.5 ± 0.8	3	3.5 ± 0.7	3	3.3 ± 0.9	3	4.4 ± 0.8	5
5. Appearance	4.0 ± 0.7	5	4.6 ± 0.5	5	4.3 ± 0.8	5	4.3 ± 0.6	4

Preference of crossbred level	Area			
	Wet lowlands I ($N = 39$)	Wet lowlands II ($N = 32$)	Wet uplands ($N = 47$)	Dry uplands ($N = 44$)
• For breeding stock (%)				
- F_1	77	81	75	86
- Does not matter	23	19	25	14
• For fattening (%)				
- $>F_1$	82	47	77	36
- Does not matter	18	53	23	67

*Rank = the smallest score of rank (1) means the highest priority and the highest score of rank (5) means the lowest priority.

Table 7. Feeding practices, feed intake (FI), DM and CP intake (in kg/day and g BW^{-0}.^{75} /day) (Mean ± s.d.) for Ongole and crossbreds cows in four study areas in Central Java.

Type of feeds	**Area**			
	Wet lowlands I	**Wet lowlands II**	**Wet uplands**	**Dry uplands**
Fresh forages fed and proportion in the forage ration (%)	*Pennisetumpurpureum*(30%) *Panicum maximum* (25%) Maize foliage (10%) Native grass (30%) Ground nut haulm (5%)	*Pennisetumpurpureum* (25%) *Panicum maximum* (20%) Maize foliage (10%) Native grass (35%) Rice stalk and ground nut haulm (10%)	*Pennisetumpurpureum*(30%) *Panicum maximum* (30%) Maize foliage (10%) Native grass (25%) Cassava leaves, ground nut haulm (5%)	*Pennisetumpurpureum*(25%) *Panicum maximum* (10%) Maize foliage (10%) Native grass (40%) Cassava leaves, ground nut haulm, legumes (15%)
Dry forages fed	Rice straw	Rice straw	Rice straw	Rice straw Maize straw
Supplementary feeds fed	Rice bran Concentrate Wheat bran Tofu waste	Rice bran Cassava	Rice bran Concentrate Tofu waste Soy bean hull	Rice bran Cassava

Intake	**Breed**								**Overall average**	
	Ongole (N = 17)	**Crossbred (N = 39)**	**Ongole (N = 31)**	**Crossbred (N = 32)**	**Ongole (N = 12)**	**Crossbred (N = 47)**	**Ongole (N = 30)**	**Crossbred (N = 44)**	**Ongole (N = 90)**	**Crossbred (N = 162)**
Average body weight (BW)(kg)	308^{a} ± 47.8	370^{b} ± 47.8	357^{a} ± 45.6	404^{b} ± 55.8	305^{a} ± 32.7	398^{b} ± 54.3	347^{a} ± 46.6	440^{b} ± 72.2	337^{a} ± 49.2	404^{b} ± 66.5
FI of fresh forage (kg/day)	24.5^{a} ± 1.2	29.6^{b} ± 1.9	23.8^{a} ± 2.0	31.1^{b} ± 2.8	27.4^{a} ± 2.0	32.6^{b} ± 2.4	24.5^{a} ± 1.9	28.2^{b} ± 2.1	24.6^{a} ± 2.1	30.4^{b} ± 2.8
FI of dry forage (kg/day)	3.1^{a} ± 0.3	3.5^{b} ± 1.1	4.9^{a} ± 0.9	6.0^{b} ± 1.8	4.7^{a} ± 1.1	4.8^{a} ± 1.8	4.4^{a} ± 1.2	5.7^{a} ± 2.2	4.4^{a} ± 1.1	5.0^{b} ± 2.0
FI of supplementary feed (kg/day)	0.4^{a} ± 0.3	1.2^{b} ± 0.7	0.2^{a} ± 0.1	0.6^{b} ± 0.6	0.6^{a} ± 0.4	1.0^{b} ± 0.5	0.8^{a} ± 0.3	1.0^{a} ± 0.4	0.5^{a} ± 0.4	0.9^{b} ± 0.6
DM (kg/day)	7.5^{a} ± 0.4	9.7^{b} ± 0.9	8.4^{a} ± 0.7	10.7^{b} ± 1.2	8.8^{a} ± 0.7	10.3^{b} ± 1.0	9.6^{a} ± 0.7	11.2^{b} ± 0.9	8.7^{a} ± 1.0	10.5^{b} ± 1.1
CP (kg d^{-1})	0.9^{a} ± 0.0	1.2^{b} ± 0.1	0.6^{a} ± 0.1	0.9^{b} ± 0.1	0.7^{a} ± 0.4	1.0^{b} ± 0.5	0.9^{a} ± 0.1	1.0^{b} ± 0.1	0.8^{a} ± 0.1	1.0^{b} ± 0.1
DM (g BW$^{-0.75}$ /day)	103.9^{a} ± 11.6	115.8^{b} ± 13.9	103.6^{a} ± 11.7	119.3^{b} ± 10.7	120.5^{a} ± 6.9	115.8^{a} ± 8.9	120.2^{a} ± 9.6	117.8^{a} ± 10.2	111.6^{a} ± 13.1	117.1^{b} ± 10.9
CP (g BW$^{-0.75}$/day)	12.4^{a} ± 1.5	14.0^{b} ± 1.6	7.9^{a} ± 0.8	9.5^{b} ± 0.9	9.6^{a} ± 0.5	9.6^{a} ± 1.0	10.8^{a} ± 1.9	10.5^{a} ± 0.9	9.9^{a} ± 2.0	10.9^{b} ± 2.1
DM (% BW)	2.5^{a} ± 0.4	2.7^{a} ± 0.4	2.4^{a} ± 0.3	2.7^{b} ± 0.4	2.9^{a} ± 0.2	2.6^{b} ± 0.3	2.8^{a} ± 0.3	2.6^{b} ± 0.3	2.6^{a} ± 0.4	2.6^{a} ± 0.3
CP (% DM)	12.0^{a} ± 0.2	12.1^{a} ± 0.6	7.6^{a} ± 0.2	8.0^{b} ± 0.3	7.9^{a} ± 0.2	8.3^{a} ± 0.8	9.0^{a} ± 0.2	8.9^{a} ± 0.3	8.9^{a} ± 1.6	9.3^{a} ± 1.7

^{a,b}Different superscripts indicate significant differences between breeds within areas ($P < 0.05$).

Table 8. Reproductive performances (Mean ± s.d.) of Ongole and crossbred cows in four study areas in Central Java, over the period January 2010–July 2011.

Reproductive performance parameter	**Area/Breed**						
	Wet lowlands I ($N = 61$)		**Wet lowlands II ($N = 80$)**		**Wet uplands ($N = 62$)**		**Dry uplands ($N = 67$)**
	Ongole ($N = 22$)	**Sim-cross^{1} ($N = 39$)**	**Ongole ($N = 48$)**	**Sim-cross ($N = 32$)**	**Ongole ($N = 19$)**	**Sim-cross ($N = 43$)**	**Ongole ($N = 25$)**	**Sim-cross ($N = 33$)**	**Lim-cross ($N = 9$)**
PPE (days)	$122.7^{a} \pm 52.9$	$99.2^{b} \pm 36.0$	$121.9^{a} \pm 37.8$	$117.2^{a} \pm 29.4$	$151.2^{a} \pm 61.6$	$103.0^{b} \pm 45.8$	$151.2^{a} \pm 63.8$	$112.7^{b} \pm 49.6$	$97.8^{b} \pm 50.5$
PPM (days)	$128.2^{a} \pm 51.5$	$101.1^{a} \pm 35.8$	$130.0^{a} \pm 36.3$	$123.8^{a} \pm 31.6$	$155.6^{a} \pm 58.3$	$115.7^{b} \pm 43.5$	$153.2^{a} \pm 62.3$	$119.5^{b} \pm 52.4$	$140.7^{a,b} \pm 55.4$
S/C	$2.2^{a} \pm 1.0$	$2.8^{a} \pm 1.9$	$1.9^{a} \pm 1.3$	$2.3^{a} \pm 1.1$	$1.9^{a} \pm 0.9$	$2.4^{b} \pm 1.3$	$2.0^{a} \pm 0.9$	$3.1^{b} \pm 2.2$	$2.0^{a} \pm 0.9$
CI (days)	$440.2^{a} \pm 58.9$	$422.1^{a} \pm 53.3$	$433.3^{a} \pm 47.4$	$435.0^{a} \pm 38.7$	$457.7^{a} \pm 65.8$	$428.2^{b} \pm 48.1$	$459.5^{a} \pm 64.3$	$446.2^{a} \pm 73.7$	$447.8^{a} \pm 56.2$
BCS	$2.8^{a} \pm 0.4$	$2.9^{a} \pm 0.5$	$2.6^{a} \pm 0.4$	$2.9^{a} \pm 0.3$	$2.0^{a} \pm 0.3$	$2.7^{b} \pm 0.5$	$2.4^{a} \pm 0.3$	$2.8^{b} \pm 0.4$	$2.9^{b} \pm 0.6$
WA (months)	$4.6^{a} \pm 0.6$	$5.1^{a} \pm 1.6$	$4.0^{a} \pm 0.7$	$3.9^{a} \pm 0.7$	$4.9^{a} \pm 2.0$	$4.3^{b} \pm 1.2$	$5.9^{a} \pm 2.3$	$6.1^{a} \pm 1.0$	$6.0^{a} \pm 0.9$
Calf crop (%/year)^{ns}	84.5 ± 12.1	85.8 ± 17.2	85.3 ± 10.1	84.6 ± 7.8	81.2 ± 10.8	86.2 ± 8.7	80.8 ± 10.6	75.5 ± 26.7	73.0 ± 22.3
Methods of mating (%)									
AI	100	100	8	100	100	100	40	98	100
Natural	0	0	86	0	0	0	24	0	0
Mix (AI and natural)	0	0	6	0	0	0	36	2	0

Sim-cross, Simmental cross; Lim-cross, Limousin cross; PPE, post-partum estrus; PPM, post-partum mating; S/C, services per conception; CI, calving interval; WA, weaning age; BCS, Body condition score, is visual assessment of body tissues (Ferguson *et al.*, 1994 cited by Lassen *et al.*, 2003). The range is 1–5, where 1 is the lowest and 5 is the highest (Baliarti, 1999); AI, artificial insemination.

^{a,b}Different superscripts indicate significant differences among breeds within the same area ($P < 0.05$).

^{ns}non-significant.

body weights which provide economies of scale in slaughtering processes.

Gross margins

Table 10 shows the financial results of the cattle component of Ongole and crossbred farms over a period of 1.5 years. The biggest expenses of both Ongole and crossbred farmers were forages and supplementary feeds. No significant differences in GM were observed between local and crossbred farms within the same area. The GM of cattle, Ongole or crossbred, in the dry upland area was the lowest of the four areas, since total variable costs were the highest in this area due to higher costs for forages and supplementary feeds. The variation between farms in supplementary feeds used was large, see the large SDs (coefficient of variation 173 percent). Mainly during the dry season, the availability of forages is limited, especially in the Dry uplands area. About 6 years ago farmers in the Dry uplands still preferred local cattle because of the shortage of forages in the dry season (Sutresniwati, 2006). Currently, the infrastructure in this area, as well as in other areas, is improving and gives the farmers easy access to feed resources and cattle markets. Trade in forages that come from outside the local land-use systems, has become big business (Paryadi, personal communication, 2010). In the Dry uplands area, cassava meal is an opportunity to reduce feed costs, since it is abundant in this area. Currently, the demand for cassava meal is increasing to produce bio-ethanol (Suradal, personal communication, 2010). It remains to be seen what effect the reduced access to cassava meal will have on the GM in the Dry uplands area. During the dry season, farmers in the Dry uplands area sell some of their livestock to buy forages and additional feeds. The higher feed costs have negatively affected the GM compared to the wet areas, but the difference in the GM between crossbred and Ongole farms in the Dry uplands is negligible. Overall, GM per h of family labour input was significantly higher for Ongole farms than for crossbred farms (1 319 versus 880 IDR per h d^{-1}).

Future of crossbreeding

Government started to promote crossbreeding in the 1980s in order to improve the meat production of Ongole cattle and the productivity of smallholder farmers (Deptan, 2003). Only exotic semen was provided; there was no assistance in terms of feeding and breeding management.

In the early years of crossbreeding crossbred animals fetched a much higher price than the meat value, as there was a big demand for crossbred breeding stock (Barwegen, 2004; Sutresniwati, 2006). This gave a big boost to crossbreeding. When the importation of frozen meat and live cattle from Australia was high, however, the price of cattle, both local and crossbreds decreased.

Table 9. Quantity of carcass and meat and MBR (Mean ± s.d.) of slaughtered Ongole and crossbred cattle in Yogyakarta Province.

Parameter	**Sex/Breed**					
	Male			**Female**		
	Ongole ($N = 5$)	**Sim-cross ($N = 25$)**	**Lim-cross ($N = 11$)**	**Ongole ($N = 8$)**	**Sim-cross ($N = 4$)**	**Lim-cross ($N = 2$)**
Age (y)	$2.8^{a} \pm 0.5$	$2.6^{a} \pm 0.7$	$2.5^{a} \pm 0.7$	$4.3^{a} \pm 1.5$	$4.0^{a} \pm 1.5$	$4.5^{a} \pm 0.7$
Body weight at slaughter (kg)	$386^{a} \pm 105.5$	$517^{b} \pm 87.0$	$516^{b} \pm 87.3$	$335^{a} \pm 58.0$	$480^{b} \pm 103.2$	$526^{b} \pm 33.9$
Carcass weight (kg)	$203^{a} \pm 35.8$	$279^{b} \pm 51.3$	$272^{b} \pm 27.1$	$168^{a} \pm 34.0$	$246^{b} \pm 46.3$	$268^{b} \pm 17.7$
Carcass percentage (%)	$54.2^{a} \pm 8.5$	$54.3^{a} \pm 7.7$	$53.7^{a} \pm 7.8$	$50.1^{a} \pm 4.0$	$51.6^{a} \pm 2.3$	$50.9^{a} \pm 0.1$
Meat weight (kg)	$168^{a} \pm 29.4$	$217^{b} \pm 46.8$	$226^{b} \pm 24.1$	$128^{a} \pm 26.6$	$189^{b} \pm 58.1$	$209^{b} \pm 15.6$
Meat percentage (%)	$45.0^{a} \pm 7.2$	$41.9^{a} \pm 5.0$	$44.6^{a} \pm 7.0$	$38.5^{a} \pm 5.9$	$38.7^{a} \pm 3.9$	$39.7^{a} \pm 0.4$
MBR	$4.8^{ab} \pm 0.3$	$3.9^{b} \pm 1.3$	$4.9^{a} \pm 0.5$	$3.6^{a} \pm 1.3$	$3.6^{a} \pm 1.7$	$3.6^{a} \pm 0.1$

Sim-cross, Simmental cross; Lim-cross, Limousin cross.

^{a,b}Different superscripts among breeds within the same sex indicate significant difference ($P < 0.05$).

For example, during 2009–2011, the volume of imported frozen meat was high, and it was distributed to the wet market which depressed the sale price of cattle. Farmers were disappointed that the prices of crossbred cattle decreased more than of local cattle (40 percent vs 25 percent) (Suseno, personal communication, 2011). This was either due to their high price expectation or high initial price paid for crossbred cattle. Crossbreeding is now a routine practice and prices for both crossbred and local cattle are based on body weight estimates, being their actual meat value in the market.

Good fertility of the cows, high survival of calves and good quality weaned calves are very important for the farmers. The productivity of the herds can be expressed by combining the calf crop estimates with the weaning weight estimates. On average the Ongole farms produced 129 kg weaner weight per year, whereas the crossbred farms are more productive from this point of view: 154 kg weaner weight per year. Most farmers said they prefer crossbreds over Ongole, because of bigger body sizes and higher selling prices. Prices of crossbred weaners are in the range of approximately 5.0–7.5 million IDR, whereas Ongole weaners are sold for prices in the range of 3.5–4.5 million IDR. Most farmers do not consider the higher feed requirements of crossbreds (Table 10). The higher selling prices are much more tangible than the economic evaluation in terms of GM. So, crossbreeding will continue.

The crossbreeding of 'beef' cattle in smallholder mixed farms in Java confirms the general trend of crossbreeding in dairy type animals by smallholders in many different areas, that it is done rather un-controlled (Wollny, 2003). Systemic crossbreeding seems not possible, as there is no reliable pedigree information available and Simmental semen is used, irrespective of the crossbred generation type of the cows (Widi *et al.*, 2008). Farmers in all zones said they do not prefer upgrading to very high levels of Simmental, as they expect poorer growth and less optimal reproductive performances of high levels of upgraded cattle. They are already satisfied with the performance of existing crossbred cattle. This implies that in future Ongole semen has to be used on higher grade crossbred animals. The local government has started a breeding initiative '*Return to Ongole*'. The main aim of this programme is to contribute to maintaining a viable Ongole population. In this programme farmers get a subsidy for every pregnant Ongole cow. This programme is only carried out in the Wet lowlands II and Dry uplands. The Return to Ongole breeding plan was set up in areas with a minimum Ongole productive cow population of 2000 head. The selection goal is growth rate from weaning to one year of age. The best yearling calves are transferred to a Performance Test Station from which the best bulls and cows are selected. This programme has resulted in an increasing demand for Ongole cattle.

In Indonesia meat production has increased from 399.7 tonnes in 2005 to 593.5 tonnes in 2013 (BPS, 2013). In the same period the total number of cattle has increased from 10.6 to 14.2 million (BPS, 2013). Crossbreeding has certainly contributed to the increase in meat production. In Central Java the majority of the cattle are already crossbreds. The productivity of crossbreds in terms of the productivity parameter weaned weight per farm is higher than in Ongole farms.

The assumption in literature that the introduction of more productive breeds will result in keeping fewer animals and so lessening the impact on the environment (Steinfeld *et al.*, 2006; Marshall, 2014) is not confirmed by the cattle herd sizes in the smallholder mixed farming systems in Central Java. The herds at the farms have always been very small, crossbreeding will not change that situation. Farmers keep a specific number of animals in relation to their limited resources. There is no information of numbers of specific crossbreeding generations and Ongole cattle in Indonesia. Marshall (2014) concludes that the impact of the introduction of new breed types on indigenous populations should be monitored by regular census. Such information is needed to support informed decision making on future (cross) breeding strategies. In Indonesia, census data on livestock numbers are available,

Table 10. Inputs, revenues and GM (in Million IDR)[1] of Ongole and crossbred cattle farms in four areas in Central Java for the period of January 2011–July 2012.

	Area/Breed																*P* value*
	Wet lowlands I (*N* = 56)				Wet lowlands II (*N* = 63)				Wet uplands (*N* = 59)				Dry uplands (*N* = 74)				
	Ongole (*N* = 17)		Crossbred (*N* = 39)		Ongole (*N* = 31)		Crossbred (*N* = 32)		Ongole (*N* = 12)		Crossbred (*N* = 47)		Ongole (*N* = 30)		Crossbred (*N* = 44)		
	Mean	s.d.	Mean	s.d.	Mean	s.d.	Mean	s.d.	Mean	s.d.	Mean	s.d.	Mean	s.d.	Mean	s.d.	
Number of cattle kept (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	0.70
Total time spent per day (h/day)	4.5^{a}	0.7	5.0^{b}	0.7	4.9^{a}	0.9	5.4^{a}	1.4	4.9^{a}	0.9	4.8^{a}	1.0	4.0^{a}	1.5	4.4^{a}	1.4	0.03
• Cleaning cattle (%)	4.4		3.2		5.6		4.7		5.7		4.2		3.2		4.2		
• Cleaning the barn (%)	17.0		16.7		18.4		16.3		15.8		17.5		3.3		4.8		
• Collecting feed (%)	51.7		54.0		47.8		50.5		45.0		47.4		65.8		60.4		
• Offering feed (%)	26.9		26.1		28.2		28.5		33.5		30.9		27.7		30.6		
Total variable costs (Million IDR)	0.88^{a}	0.30	1.56^{b}	0.80	0.58^{a}	0.16	0.87^{b}	0.50	1.46^{a}	0.72	1.92^{a}	1.50	1.00^{a}	0.58	2.42^{b}	3.62	0.01
• Forage	0.31^{a}	0.04	0.32^{a}	0.09	0.40^{a}	0.10	0.38^{a}	0.12	0.40^{a}	0.07	0.43^{a}	0.07	0.66^{a}	0.48	1.28^{b}	0.94	0.00
• Supplementary feed	0.42^{a}	0.32	1.05^{b}	0.80	0.13^{a}	0.13	0.25^{b}	0.25	0.89^{a}	0.69	1.33^{a}	1.67	0.27^{a}	0.20	0.91^{a}	2.03	0.00
• Artificial insemination/mating and reproduction services	0.08^{a}	0.03	0.10^{a}	0.08	0.04^{a}	0.04	0.22^{b}	0.24	0.09^{a}	0.03	0.11^{a}	0.02	0.07^{a}	0.03	0.11^{a}	0.16	0.32
• Other costs (hired labour, veterinary services, other)^{ns}	0.06^{a}	0.01	0.09^{a}	0.12	0.01^{a}	0.04	0.02^{a}	0.05	0.08^{a}	0.13	0.13^{a}	0.26	0.002^{a}	0.009	0.12^{a}	0.56	0.18
Total output (Million IDR)	4.19^{a}	3.04	4.11^{a}	3.12	3.58^{a}	2.14	5.04^{b}	2.33	5.17^{a}	3.18	3.48^{a}	3.41	3.48^{a}	2.47	4.20^{a}	5.16	0.84
• Selling cattle	4.04^{a}	3.03	3.97^{a}	3.17	3.51^{a}	2.17	4.91^{b}	2.31	4.94^{a}	3.12	3.37^{a}	3.38	3.48^{a}	2.47	4.20^{a}	5.16	0.86
• Selling manure	0.16^{a}	0.48	0.13^{a}	0.17	0.08^{a}	0.13	0.13^{a}	0.20	0.23^{a}	0.19	0.11^{b}	0.17	0.00	0.00	0.00	0.00	0.00
Gross Margins^{2} (Million IDR)	3.32^{a}	2.98	2.55^{a}	2.93	3.01^{a}	2.15	4.17^{b}	2.30	3.71^{a}	2.87	1.56^{a}	3.68	2.47^{a}	2.34	1.78^{a}	3.22	0.01
GM per family labour time^{3} (Thousand IDR/h/day)	1.41^{a}	1.36	0.97^{a}	1.14	1.26^{a}	1.21	1.54^{a}	0.97	1.43^{a}	1.02	0.53^{b}	0.14	1.29^{a}	1.49	0.69^{a}	1.59	0.03

[1] One US$ = 9 200 IDR.

[2] GM (Million IDR) = Total output (Million IDR) − Total variable costs (Million IDR).

[3] GM per family labour time, GM per day/total time spent per day (Thousand IDR).

[a,b] Different superscripts indicate significant differences between breeds within an area.

[ns] non-significant.

**P* value among areas.

however, unfortunately census data do not distinguish different breed or crossbred generation types.

Limitations of the impact analysis used

Marshall (2014) suggests that strategic research is needed to assess the impact of different breed types from a range of viewpoints: household level, food and nutrition security at different scales and environmental sustainability. The present analysis of the impact of crossbred animals on smallholder cattle keeping in Central Java considers only farm level developments, such as animal performances, herd sizes, objectives of keeping cattle and financial results. These data helped to understand why crossbred farmers opt for crossbreds. Research at other levels is needed to complete the picture of the impact of crossbreeding. Our farm level data on animal weights and feed intakes might lack in accuracy, as detailed measurements are not possible on large numbers of animals in the field. The GM analysis only included the financial flows on the farms, the additional benefits of cattle in terms of manure use on own crop land and the security function of the cattle are not included. We expect no differences between the farm types in manure use, however the security function of crossbred cattle might be slightly higher than for Ongole, as estimates of this are generally based on financial value of the cattle kept and sold (Udo *et al.*, 2011). So, crossbred cattle present a higher capital asset value than Ongole cattle.

Conclusions

In Indonesia, crossbreeding has become a common practise over a period of about 30 years. The question whether or not crossbreeding is beneficial for the mixed farming systems in Central Java can be looked at from farmers' points of view and from national level point of view. The comparisons of households with Ongole and crossbred cattle in different agro-ecological zones in Central Java show that crossbreeding is not changing such farming systems: household and farm characteristics, and herd sizes and structures were not really different between farmers keeping Ongole or crossbred breeding stock. Crossbreeding has also not changed the basic motives of keeping cattle. The main motives for keeping cattle, either Ongole or crossbreds, were the capital asset function (saving), income and manure production. The reasons for choosing either type of breeding stock, however, differed: lack of feed and capital are reasons for not choosing crossbreds, whereas expectations of better growth and better selling prices trigger keeping crossbreds.

In all agro-ecological areas included in this study, the crossbreds reached considerably higher body weights and consequently fetched higher sale prices, but they also required more feed resulting in comparable GM for farmers with crossbred or Ongole breeding stock. So, crossbreeding is not bringing financial gains for the farmers. Nevertheless, in all study areas, farmers prefer Simmental crosses because of their nice appearance, high growth rate and high price of progeny sold compared to Ongole.

At national level crossbreeding is contributing to increased meat production. The amount of weaned weight per farm was 16.2 percent higher on crossbred farms than on Ongole farms. Hence, crossbreeding will continue in Indonesia, since farmers are satisfied with the performances of crossbred cattle, such as their higher body weights and consequently higher market prices across agro-ecological zones. Government bodies continue to promote crossbreeding, however, at the same time conservation of Ongole has started three years ago in its original breeding area and is supported by a structured breeding program. There is no breeding strategy to maintain current crossbred levels. A viable Ongole population is needed to reduce the risk of upgrading to too high levels of Simmental.

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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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Options for enhancing efficiency and effectiveness of research capacity for livestock genetics in, and for, sub-Saharan Africa

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Summary

Animal breeding for increased productivity over the past 50 to 60 years has been very successful in terms of increasing growth rate, milk yield and egg production in most livestock producing regions of the world (Rauw *et al*., 1998). However, this success has not registered that well in most countries in sub-Saharan Africa (SSA). Ironically, just like most developing regions, SSA is faced with the challenge to increase rapidly the agricultural productivity to help feed their growing human populations without depleting the natural resource base (Rege, 2005). Genetic improvement of livestock depends on access to genetic variation and effective methods for exploiting this variation (Rege, 2005). This is where human capacity and infrastructure for decision-support systems in animal breeding are required. This paper provides a synthesis of views from a cross-section of livestock production experts working in SSA. These views were collated through an e-conference which was held from 8th March to 20th April 2011. The e-conference discussed future research and development (R&D) needs for animal breeding and genetics in SSA and how they can be met. The e-conference attracted 43 participants from 17 countries. Results from the e-conference demonstrated that the R&D institutions and infrastructure in SSA vary widely in terms of both the physical and human capacity. Equally varied is the level of utilization of these institutions. In terms of training in Animal Breeding and Genetics, although most universities/colleges have programmes in Animal Science and teach animal breeding and genetics, there are very few practicing animal breeders. Lack of mentorship programmes and collaboration, and in some cases lack of appropriate jobs, continue to contribute to this 'leaking pipeline' phenomenon. The following is a summary of the consensus stemming from the conference on how the efficiency and effectiveness of livestock genetic improvement in SSA could be enhanced. First, the need to augment the approach that promotes animal breeding and genetics as part of a wider agriculture and rural development system, second, collaboration both within Africa and with those in the Diaspora should be further tapped into and utilized as a source of capacity for R&D and third, initiative of sharing resources and research platforms such as pooling data for genetic analysis from across institutions, and even across countries, should be encouraged in case where this is advantageous to do so.

Keywords: *capacity development, institutional framework, sub-Saharan Africa*

Résumé

La sélection animale réalisée dans les 50 à 60 dernières années en vue d'accroître la productivité a connu un grand succès, notamment en termes d'augmentation de la vitesse de croissance, la production laitière et la production d'œufs, dans la plupart des régions d'élevage du monde (Rauw *et al.*, 1998). Cependant, ce succès n'a guère été remarqué dans la plupart des pays d'Afrique Subsaharienne (ASS). Paradoxalement, comme c'est aussi le cas dans beaucoup d'autres régions en développement, l'ASS doit relever le défi d'accroître rapidement sa productivité agricole pour répondre aux besoins alimentaires croissants de sa population humaine sans pour autant épuiser ses ressources naturelles de base (Rege, 2005). L'amélioration génétique des animaux d'élevage est conditionnée par l'accès à la variabilité génétique et à des méthodes efficaces pour exploiter cette variabilité (Rege, 2005). C'est là qu'interviennent le capital humain et l'infrastructure de systèmes d'aide à la prise de décisions dans la sélection animale. Cet article résume les opinions d'un échantillon représentatif d'experts travaillant dans le domaine de la production animale en ASS. Ces opinions ont été collectées par le biais d'une conférence web tenue du 8 Mars au 20 Avril 2011. Dans le cadre de la conférence, il a été question des besoins futurs en recherche et développement (R&D) dans le domaine de l'amélioration génétique animale en ASS et des voies pour répondre à ces besoins. La conférence web a attiré 43 participants de 17 pays. Les résultats de la conférence web ont montré qu'il existe de grandes différences aussi bien pour ce qui est des moyens physiques que pour les ressources humaines entre les institutions de R&D en ASS. Le degré d'utilisation de ces institutions est aussi très variable. En ce qui concerne la formation en Amélioration Génétique Animale, bien que la plupart des universités ou écoles ont des programmes en Sciences Animales et enseignent la sélection et la génétique animales, il y a très peu de sélectionneurs en exercice. Le manque de programmes de mentorat et de collaboration, ainsi que dans certains cas le manque d'emplois appropriés, contribuent toujours à ce phénomène de « tuyau qui fuit ». Ce qui suit est un résumé du consensus issu de la conférence sur la façon dont l'amélioration génétique animale pourrait être rendue plus efficace et efficiente en ASS. En premier lieu, il s'avère nécessaire de promouvoir l'approche selon laquelle l'amélioration génétique animale fait partie d'un système agricole plus ample de développement rural; deuxièmement, la collaboration devrait être renforcée tant au sein de l'Afrique qu'avec ceux qui

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ont émigré afin d'augmenter la capacité de R&D et troisièmement, les initiatives de partage de ressources et de plates-formes de recherche, comme par exemple la mise en commun de données de différentes institutions ou même de différents pays pour la réalisation d'analyses génétiques, devraient être encouragées.

Mots-clés: *cadre institutionnel, développement des capacités, Afrique Subsaharienne*

Resumen

La selección animal llevada a cabo en los últimos 50–60 años con el fin de incrementar la productividad ha sido muy exitosa, en términos de aumento de la velocidad de crecimiento, la producción de leche y la puesta de huevos, en la mayoría de las regiones ganaderas del mundo (Rauw *et al.*, 1998). Sin embargo, este éxito apenas se ha notado en la mayoría de los países de África Subsahariana (ASS). Paradójicamente, tal y como sucede en muchas otras regiones en vías de desarrollo, ASS se enfrenta al reto de incrementar rápidamente su productividad agrícola para dar respuesta a las crecientes necesidades alimenticias de su población humana pero sin por ello agotar sus recursos naturales de base (Rege, 2005). La mejora genética del ganado está condicionada por el acceso a la variabilidad genética y a métodos eficaces de explotación de esta variabilidad (Rege, 2005). Es aquí donde intervienen el capital humano y la infraestructura de sistemas de apoyo a la toma de decisiones en la selección animal. Este artículo recapitula las opiniones de una muestra representativa de expertos en producción animal que trabajan en ASS. Estas opiniones fueron recopiladas mediante un congreso web que se celebró del 8 de marzo al 20 de abril de 2011. En este congreso se abordaron las necesidades futuras en investigación y desarrollo (I + D) en el ámbito de la mejora genética animal en ASS y cómo satisfacer dichas necesidades. El congreso web atrajo a 43 participantes de 17 países. Los resultados del congreso web demostraron que existen grandes diferencias tanto en medios físicos como en recursos humanos entre las instituciones de I + D en ASS. También es muy variable el nivel de utilización de dichas instituciones. En términos de formación en Mejora Genética Animal, hay muy pocos mejoradores en activo, si bien la mayoría de universidades o escuelas tienen programas de Ciencia Animal y enseñan selección y genética animal. La falta de programas de tutoría y de colaboración, así como también en algunos casos la falta de empleos apropiados, siguen contribuyendo a este fenómeno de "tubería con fugas". A continuación se ofrece un resumen del consenso alcanzado en el congreso acerca de cómo lograr una mejora genética animal más eficaz y eficiente en ASS. En primer lugar, se hace necesario fomentar el enfoque que contempla la mejora genética animal como parte de un sistema agrícola más amplio de desarrollo rural; en segundo lugar, se debería consolidar la colaboración tanto dentro de África como con aquéllos que han emigrado para así incrementar la capacidad en I + D y terceramente, se deben alentar las iniciativas para el uso compartido de recursos y plataformas de investigación, tales como la puesta en común de datos para los análisis genéticos entre instituciones o incluso entre países.

Palabras clave: *marco institucional, desarrollo de capacidades, África Subsahariana*

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Introduction

Livestock are an important asset in sub-Saharan Africa (SSA) and have been shown to contribute significantly to rural development through the provision of food, cash, manure and general livelihoods in the rural and peri-urban households (Agyemang, 2005; Zaibet *et al.*, 2011). Despite the rapid growth, the livestock sector in SSA is faced with several challenges and hence livestock's contribution to sustainable livelihoods is neither optimal nor sustained in most parts. These include limited breeding stock, low productivity, poor management and inadequate access to extension, health and other support services (Goyder and Mang'anya, 2009). These challenges have negative impacts on productivity and genetic improvement initiatives (Rege, 2005). With respect to genetic improvement initiatives, some of the reasons for their sub-optimal contribution are: low capacity (human and infrastructural) for livestock genetics; high cost of livestock genetics and breeding research and development (R&D) infrastructure; limited and disjointed R&D efforts within countries; limited effort to share the available capacity between countries; and inappropriate imported genetic technologies (genotypes and genetic improvement technologies and methods) which have often failed to deliver the expected results. However, there are some technologies developed elsewhere (in either the North or South) which offer opportunities for Africa. These may need to be tested in, and adapted for, local contexts. Further rapid developments in genetics and genomics offer opportunities which remain relatively unharnessed in, and for, Africa's development.

Sustainable options that would enhance the efficiency and effectiveness of future research needs for livestock genetics is urgently required. These are the kind of options that would interface with overall livestock and agriculture development in SSA. Robust strategies would enhance the efficiency and effectiveness for delivering the R&D that would address high priority constraints for SSA. However, generating such strategies requires the involvement of a wide range of players. Establishing avenues of consultation, engagement and support from local and international R&D community is a vital part of this process. From 8th March to 20th April 2011, an e-conference aimed at collating views that would inform the development of such strategies was conducted. The current paper provides a synthesis of the e-conference, analyses the situation and outlines the drivers that were identified to have the potential to enhance the efficiency and effectiveness of livestock genetics research for development in, and for, SSA.

Methodology

Prior to the e-conference, announcements were sent through animal genetics associated discussion groups such as Domestic Animal Diversity Network (DAD-Net), Animal Geneticists Discussion Group (AnGenMap) and animalgenetics listserv. Prospective participants were requested to circulate the announcement to anyone in their network and as widely as was possible. Animal Scientists, Agricultural Economists, Agronomists and experts in Agricultural Research not only from Africa but also from other countries around the globe participated in the e-conference. The 43 experts who participated in the e-conference were from Bangladesh, Cameroon, Canada, Egypt, Ethiopia, Ghana, Italy, Kenya, Malawi, Nigeria, South Africa, Spain, Sudan, Sweden, Tanzania, United Kingdom, and Zimbabwe. The e-conference was hosted by the animalgenetics listserv (animalgenetics@sympa.sun.ac.za) based at Stellenbosch University in South Africa. In the e-conference, a framework was defined as ‘a basic structure underlying a system’ and could take a variety of forms. The scope and definition of the framework were introduced at the beginning of the e-conference. Following were the envisioned aims of the framework for the discussion: (a) to provide a mechanism for leveraging available individual expertise and institutional capacities on the continent; (b) to create functioning and effective mechanisms for harnessing available collaborative opportunities within Africa and between Africa and the international R&D community, including Africa’s Diaspora; (c) to highlight ongoing development of technical and human capacity in genetics and breeding on the continent to provide the required critical mass; (d) to generate technologies that can be applied at scale in multiple countries (i.e. international public goods) to address high priority constraints; (e) increasing efficiency and return to R&D investments; and (f) to catalyse the evolution of sustainable R&D platform(s) on the continent. During the e-conference, a moderator introduced the theme based on each aim for discussion, together with some guiding questions for the participants as shown in Table 1. The moderator neither censored nor limited the level of debate and discussion. Rather, the moderator asked questions that would bring up either more information or different perspectives. At the end of each theme, the moderator produced a summary that was shared back to all participants and all on the networks by email, to allow corrections, additions and even more in-depth discussion. Towards the end of the e-conference, a request for information that would enable the start of the process for developing a database of experts in animal breeding and genetics in Africa was made. The information requested was: name (including title), institutional affiliation, physical and postal address, telephone contacts, email address and, areas of training, expertise and current work focus.

Table 1. Main themes covered in the e-conference’

Theme	Specific questions
Leveraging available individual expertise and institutional capacities on the continent’.	1. What animal breeding and genetic R&D institutions are available and functional in African countries? Are these fully utilized? 2. What are the major underlying causes of continuing human capacity constraints for animal genetics and breeding in Africa? 3. How can Africa best use the scarce human and institutional (including infrastructural) capacity it has in the area of animal genetics and breeding?
Available expertise and how this can be used to best serve sub-Saharan Africa (SSA);	1. Do we have an estimate of the number of animal genetics and breeding experts available on the continent? If so, is this information available in public domain – e.g. in databases – at country, sub-regional or continental level (please provide the web addresses or e-mail contacts where available)? 2. What options/models are available (give specific examples), or could be explored, for longer term collaboration between African institutions and other parts of the world?
How to leverage collaborative opportunities outside the continent, including tapping into the substantial African Diaspora.	What options/models are available (give specific examples), or could be explored, for effectively engaging the Diaspora?
Generating technologies that can be applied at scale in multiple countries (i.e. *international* public goods) to address high priority constraints;	1. What are the highest priority technology-related constraints to animal genetics and breeding in SSA and what technological solutions currently or potentially (in the near-term) available with the global research community can be applied/adapted to address these constraints? 2. How best can existing or emerging technological solutions be ‘adapted’ and scaled out for wider application (in multiple countries) in SSA?
Increasing efficiency and return to R&D investments. Following are the specific questions:	How can animal genetics and breeding R&D efficiency be increased to get better returns to investment targeting SSA?

Current status

Institutional capacity

Participants highlighted that infrastructure in animal breeding and genetics comprises hard and soft infrastructure. Hard infrastructure is the physical and organizational structures needed for the delivery of technological innovations and R&D in animal breeding and genetics. Soft infrastructure is made up of all the operational and quality assurance capacity that promotes and facilitates the implementation of the technological know-how generated from the R&D. In the e-conference there was a general consensus that some premier and other potentially premier institutions for animal genetics and breeding R&D exist on the continent. However, these institutions are very varied in terms of both the physical and human capacity. Equally varied is the level of utilization of these institutions. Specific examples that were given were from countries like Zimbabwe, South Africa, Malawi, Kenya and Nigeria. The majority of these are public institutions in the form of universities and research centres. Very few of these have long-term experiments and research programmes running. Where some long-term experiments and research programmes are running, they do not seem to be well supported and their value not well appreciated.

Although difficult to maintain and at times to economically justify, long-term experiments and research programmes have valuable scientific resources providing data and continuity. The following are some examples of long-term experiments spanning over a decade and research programs that are still running albeit not at full capacity. In Zimbabwe, Matopos Research Station runs a beef crossbreeding experiment and is also home to the only known flock of indigenous Sabi sheep; Makhoholi Research Station maintains a Mashona beef herd; while the Grassland Research Station keeps a Tuli cattle herd. In Malawi, Mbawa Research station has a pure Malawi Zebu breed which is used in a cross-breeding programme with the Brahman breed. These centres have the potential of hosting and maintaining nucleus herds of farm animal genetic resources (FAnGR) in an either open or closed nucleus breeding system. Long-term experiments also have the potential to provide unique data sets that may provide a huge resource for ongoing analysis and also provide a case of best practice. However, the value of long-term datasets can only be noticed when such data are utilized. One issue that was raised in the e-conference is that most of the institutions are not effectively utilized.

Most countries in SSA have artificial insemination (AI) centres. Most of these produce and distribute semen to farmers. However, AI centres are mostly considered as semen and support service providers to the genetic improvement sector. The e-conference participants noted that functioning AI and livestock breeding programmes exist where there was a market oriented (commercial) livestock sector. An example is South Africa where there are functioning and well developed breeding programmes and support infrastructure such as stud breeders and breeders associations for many species, national performance recording and genetic evaluation.

Human resources

Databases of animal breeding and geneticists exist at different levels of detail. For example there is a relatively comprehensive database in South Africa where there are about 45 Animal Breeders and Geneticists. Lack of proper databases and lists of animal breeders could mainly be attributed to the fact that in some countries there are very few animal breeders and hence co-workers know each other. Currently, most animal breeders and geneticists work for universities and research institutions (Table 2). Although there are animal breeders and geneticist in the different countries, it was noted that there are very few animal breeding organizations (implementers of genetic improvements) on the continent. The absence of animal

Table 2. The landscape of human capacity in animal breeding and genetics in the different countries.

Country	Type of institution			
	University	Research and development	Other	Total[1]
Benin		1		1
Botswana	2	2		4
Burkina Faso	2	2		4
Burundi		1	1	2
Cameroon	2	4		6
Chad		1		1
Cote d'Ivoire	1	4		5
DR Congo	1	1		2
Egypt				0
Ethiopia	7	13	2	22
Gambia		1		1
Ghana	5	1		6
Kenya	4	11		15
Madagasca		2		2
Malawi	2	2		4
Mali	1	1		2
Mauritius		1		1
Mozambique		3		3
Namibia	1	1		2
Nigeria	25	2		27
Rwanda		3		3
Seira Leon	2			2
Senegal		2		2
Somalia	1			1
South Africa	12	11		23
Sudan		3		3
Swaziland	1	1		2
Tanzania	1	9		10
Uganda	1	3		4
Zambia		1		1
Zimbabwe	3	3		6
Total	**74**	**90**	**3**	**167**

[1] Data were based on what the e-conference participants could recall and not on a head-count. Although the absolute numbers may not be accurate, they are precise enough to present the overall picture.

breeding organizations may be one reason why in most countries, the advantages of using new improvements and technologies are neither appreciated nor utilized under field conditions. This may also be the reason as to why there are only a few organized breeding programmes on the continent.

Ongoing human and technical capacity development

In terms of training in Animal Breeding and Genetics, most universities/colleges in SSA had programmes in Animal Science, and teach Animal Breeding and Genetics. Training is mostly at first degree level. Postgraduate training opportunities in animal breeding and genetics in Africa are very limited. Only a few universities have post graduate programs, and these universities have less than optimum capacity in terms of expertise and facilities, to deliver high quality M.Sc. or Ph.D. training. Regional programmes have been initiated in the past. An example is the M.Sc. in Animal Science programme that was hosted by Bunda College in Malawi on behalf of the Southern Africa Centre for Coordination of Agricultural Research (SACCAR) and financially supported by GTZ from 1990 to 2000 (Wollny *et al*., 2002). Through that programme, which now continues as a local programme, animal scientists including animal geneticists mainly from the Southern Africa Development Community (SADC) region received tuition from Bunda College and were allowed to travel back to their home countries to conduct research. Another successful programme was the training of trainers' project that was launched in 1999 by the International Livestock Research Institute (ILRI) in collaboration with the Swedish University of Agricultural Sciences and supported by the Swedish International Development Cooperation Agency (Sida). This project was based on an approach that targeted university lecturers and researchers who were actively involved in teaching and supervising research in animal breeding and genetics (Ojango *et al*., 2011).

Even with these within country and regional training and educational programmes, there is a general deficit in the numbers of animal geneticists on the continent. Two problems exist in this respect. One is the lack of strategies to maintain and retain the trained personnel and the other is the failure to attract the numbers from young scientists to join the field. Quite a good number of animal geneticists are now gainfully employed either in other countries or in other organizations that do not deal in animal breeding and genetics. There is outward migration of personnel to other fields such as relief and development non-governmental organizations (NGOs). Different reasons were given in the e-conference for this situation. Some of these are: low remuneration, limited career development prospects, and lack of appreciation for work output. Further, there is a general decline in the numbers of students in animal breeding and genetics. The discipline seems not to attract high numbers of new students who would be the next generation of movers and shakers. Ironically, the quantitative and numerate skills that animal geneticists possess are highly appreciated when moved into other fields.

There is need for innovative regional graduate programs that harness collective capacities of multiple universities (Gibson, Rege and Chagunda, 2014). Such an initiative could be linked to advanced research institutes/universities in the developed world. One fundamental difference between successful livestock genetic professionals (researchers, industry and extension) in the developed world vs those in Africa is that after receiving their M.Sc. or Ph.D., the former generally receive strong mentoring and continuous 'learning-through-doing', while there is limited or no opportunity to gain deep experience and high-level mentoring for most African graduates of livestock genetics training. This is an area that needs some attention if the sector is to retain its human resources.

Breeding programmes

In most African countries R&D related to animal breeding is under the control and support of government institutions. These institutions were established with the aim of providing improved stock and technologies to the farmers. The majority of these institutions were established with either little or no participation of the end users (farmers). As a result, most of the organizations seem not to address directly the needs of the smallholder farming community. Therefore, their contribution to the nations as well as to the farming community is very low relative to the cost incurred in either establishing or running these institutions. In addition to the government institutions, in some countries there are private breeding companies and NGOs that are selling germplasm (semen and embryo) and live animals imported from the Europe, America and to a limited extent from South Africa. This is mainly for dairy cattle and poultry.

Apart from a few commercially orientated operations in a handful of countries, in the rest of Africa there are no strong breeding institutions. As the result of this weakness, farmers are dependent on imported animals for the replacement stock. However, several studies on genotype by environmental (G × E) interaction have shown the strong negative effect of the indiscriminate importation of germplasm (e.g. Chagunda *et al*., 2004; Friggens and Newbold, 2007). In very few countries there is targeted livestock genetics research meant for the local environment (Rege, 2005). One of the consequences of the disjoined R&D activities is the lack of coherent breeding policies. This has resulted in a mismatch of genotypes with production systems. Private sector, farmer organizations and the emerging commercial farmers are mostly disconnected to the research programmes. Most R&D initiatives seem to be developed with little attention paid to the production environment. The issue of identifying and matching the animal genetics and breeding R&D to the existing and appropriate farming systems was emphasised during the e-conference. This was identified to have been a major problem in small-scale and communal farming systems. The paradox is that in most African countries, the dominant type of livestock farming is either small scale or subsistence, where animals are managed under communal farming system with no control mating. In most cases, there is no controlled breeding in this sector. However, where planned breeding takes place, the breeding stock predominantly come from research station based breeding programs and Government run multiplication centres. There is strong need for studies to determine not only the optimal breeds and genotypes for different production systems but also the methodologies and tools for determining these optimal combinations. Further, there was recognition in the e-conference that the subsistence farmer keeps his/her livestock for multiple purpose use – food, power, cash, etc. The animal numbers per farm in this sector are small, sometimes mixed species. The vital questions are: how to define breeding objectives that would be appropriate for the multi-functional production systems, and how to implement such an improvement program? Answering these questions would help inform the debate on making animal breeding and genetics relevant and appropriate to the existing and future production systems. This is where robust and clear breeding policies are needed. As indicated by Zonabend *et al.* (2013), a livestock breeding policy is an important tool to show the direction of priorities and activities to be conducted in livestock breeding. For such breeding policies to have sustainable contribution to rural livelihoods, they would need to be informed by a broader livestock development policy. Together with R&D organizations, breeding organizations and performance recording organizations there is need to take the new developments forward to the users and feedback to the R&D organizations. The existence of institutional herds at research and multiplication centres would act as nucleus herds for spreading genetically improved germplasm across commercial herds. However, if the appropriate infrastructure for the gene flow is not available the advantages of using the new improvements and technologies cannot be proven at farm level.

Low profile

Participants in the e-conference expressed concerns over the low profile of animal breeding and genetics in the different SSA countries. Despite the fact that this is one of the few disciplines that brings about permanent change and improvement in livestock, it is very often considered as a technology that may not respond to urgent needs especially to the policy makers. This picture, however, may reflect more the fact that it takes a considerable number of years to reap the benefits of genetic improvement and yet there may be other more urgent system constraints which need to be addressed. This may apply even more to smallholder and subsistence livestock production systems than to large multinational companies that are now increasing their presence mainly in the poultry sector. Their investment in animal genetics is growing faster than in animal nutrition and animal health (KPMG, 2013). It was noted that the production sector and society do not appreciate research as a part of their activity and hence researchers are not rewarded with reasonable remuneration. However, it was also noted that animal scientists and more specifically animal geneticists have themselves not demonstrated the value of animal breeding to society. In summary, it was pointed out that animal breeding and genetics should not only be done but should be seen to be done. Another issue may be that the many failed animal breeding programs in Africa have reduced confidence. There is need to investigate and implement strategies that may help to avoid these failures in the future. An example is by better targeting in terms of where and when to apply breeding interventions.

Some possible ways to raise the profile of animal breeding and genetics are:

- Animal Breeding and Genetics courses in different universities and colleges should be made more attractive while maintaining its relevance and robustness.
- Teaching and research facilities and equipment should be established in order to make the course more practical than theoretical which is often the case when practical facilities are lacking.
- The importance of within-country collaboration is that it would enable students do practical work or placement in research institutions. This could be extended to formal scientific exchange programme between institutions.
- The need for clear information on career path and expected returns from the career are crucial in creating not only a clear demand for and place of animal breeding on the market but also helping to develop the area.
- Use already existing resources and forums such as, All Africa Conference of Animal Agriculture (AACAA), World Congress (WCGALP), pedigree of animal breeders. These resources should be utilized more to increase the profile and visibility of the activities that animal breeders undertake in Africa.

Sociological and ecological differences

The need to recognize regional social, economic and environmental differences and similarities was highlighted and acknowledged during the e-conference. This line of discussion extended to sociological and ecological differences among countries. This means that it might be more efficient to promote regional collaboration. However, caution should be taken not to breakdown the regions too much, resulting in hindering any benefits that could be accrued from collective effort. Similarities and common platforms are worth exploiting because the similarities may outweigh differences. Gibson, Rege and Chagunda (*2014*) pointed out that cross-institution collaboration, within and between countries in livestock genetics is extremely limited.

Ironically, SSA has a continent-wide level of cohesion and shared vision. This is facilitated by among other things, use of a limited number of shared languages. A number of well-functioning pan-African institutions and mechanisms for collaboration have arisen in recent decades. This indicates that there are good opportunities to establish regional or pan-African institutions and collaborations to promote more effective training and delivery in livestock genetic improvement (Gibson, Rege and Chagunda, 2014). Strong national human capacity begets strong regional human capacity. Animal Geneticists need to work together to improve each other's weaknesses and build each other's strengths. Mentoring of young scientists should be done at both national and regional levels.

Harnessing available collaborative opportunities

Collaboration both within Africa and with those in the Diaspora remains an untapped potential source of capacity. There are some initiatives that require regional collaboration in order to achieve sustained impact. Some useful observations in this regard were made by Wollny *et al.* (2002). Even with some within-country initiatives, there is need to break-down the traditional subject boundaries among research, extension and training. In most of the countries, NGOs have contributed substantially to change the gene pool through the importation of different genotypes especially in dairy cattle, pigs and goats. Animal geneticists need to integrate their activities with those of the NGOs through taking the work forward and adding the genetic improvement dimension to rural development work. This can be, for example, through setting up systematic animal performance recording; conducting genetic evaluation, and sire selection; and carrying out breed comparison research that would inform the decisions on the genotypes that would be appropriate for different production systems, all of which are lacking in most countries in SSA. To compliment this kind of initiative, there is need for a robust and functioning extension service. This would bring out the comparative advantage of an innovation such as genetic improvement (Agwu, Dimelu and Madukwe, 2008).

Since quantitative genetic analyses rely on availability of high volumes of routinely collected data, initiatives such as pooling data from either across institutions or across countries and analysing such data with appropriate statistical models that account for regional and country differences, would not only provide some fundamental information but also work as a training ground for students and young scientists. This would be even more useful for training if different methodologies and procedures would be used to harmonize data and account for different data collection protocols. Not every country would have the human resources with such skills. Skill sharing and knowledge exchange would help Africa best use the scarce human and institutional capacity it has in the area of animal genetics and breeding. Some models of collaboration exist between African institutions and other parts of the world. Most of these could be explored further for longer term benefits on institutional capacity. This is because most of the collaboration efforts that go a long way start as researcher-to-researcher initiatives. Although this is the case, other formidable collaboration initiatives have been those that have been initiated through bilateral agreements. Clearly articulating the R&D needs helps to identify relevant projects and work-areas. Forming project consortia and responding to specific research calls has been another very successful strategy for collaboration. Involving both Africa-based scientists and those in the Diaspora has a synergistic effect to the collaboration effort. Simpler networks and approaches that are affordable in Africa must also be encouraged and funded, for example, strengthening the African Animal Production Association, initiating e-forums and discussion groups. Formal scientific exchange programs for researchers between institutes should be considered as a catalyst for further long-term collaboration. SSA is in a unique position for potential joint and regional postgraduate training programmes. As was noted by Gibson, Rege and Chagunda, (*2014*), there are vast regions that share language, cultural and political diversity. Utilizing African scientists that are in the Diaspora can take several forms that need institutional involvement. Initiatives like joint supervision of graduate students, joint projects, and joint short to medium-term appointments would promote knowledge exchange and skills-sharing.

Generating technologies and increasing efficiency

Research in animal breeding should be attractive to the private sector and funding community in order to attract investment and innovation. It should also give political mileage to Governments so that they can justify spending scarce financial resources in supporting the research. There is need to recast animal breeding and genetics as part of a bigger dynamic innovation system in agriculture and rural development. An innovation systems' approach should be taken in order to reshape the pathway through which animal breeding and genetics can contribute to poverty alleviation in Africa. An innovation system approach offers a holistic and multi-disciplinary approach to innovation and processes, incorporating emerging reforms and approaches for agricultural development (Agwu, Dimelu and Madukwe, 2008). Following are some considerations that should be encompassed in livestock innovation systems:

- Animal breeding and genetics must focus on innovations not merely research or science and technology. Innovation is defined as 'the application of knowledge to achieve social and economic outcomes'.

- Animal breeding and genetics must develop working styles and practices, both as individuals and as organizations and the incentives, support structures and policy environments that encourage innovation.
- Breeders and geneticists in Africa must be responsive to stakeholder demands and agendas, not their own religiously guarded pet projects or academic interests. In other words, think beyond the 'laboratory' or 'experimental field' to find out what clients really need out there.
- Breeders and geneticists in Africa need to be dynamic – new challenges require new partners and new ways of working. Institutional learning is central to this process and will ensure successes and failures of the past are used to inspire future solutions. 'If you cannot change you will soon become irrelevant'.

Institutions like African Union Information Bureau for Animal Resources (AU-IBAR) and ILRI should continue to take the lead and create opportunities to motivate scientists on the continent to come up with solutions to the numerous challenges of Animal Genetics. They need to continue to support capacity building and also to bring a fair balance of projects on Animal Genetic Resources across the continent.

Catalysing the evolution of sustainable R&D platforms

Essential to any breeding programme is the accurate and appropriate estimation of genetic parameters and the consequent formulation of breeding goals. Currently, there are no such breeding programmes at both national and regional level in most of SSA (Rege *et al.*, 2011). Mostly, this is due to lack of infrastructure and functioning animal recording systems. The inevitable consequence of the lack of coherent and well-grounded breeding strategies is the use of inappropriate genotypes and germplasm. There is need to take a concerted effort and have a relook in order to incorporate different and novel approaches that may not only improve productivity but also promote the implementation of livestock genetic improvement in SSA. Some of the questions that would guide this evolution are: are there any easy-to measure phenotypes that would be used as indicator and proxy traits, are there any new and readily available easy-to-use technologies that would help in gathering the required phenotypes, is it possible for several institutions to initiate a joint animal recording system, and would it add value to any potential breeding scheme to pool together any existing phenotypic data from across institutions and countries and analyse such data with appropriate statistical models that will account for regional and country differences? Affirmative responses to these questions would create the needed platform that would provide the footing for fundamental information in terms of genetic parameters, breeding values and the basis for the formulation of national and regional breeding programmes. An alternative breeding program could be one changing the genetic merit of the population by increasing the proportion of animals that are of the most appropriate breed-type, be it either pure-bred or cross-bred for any given production system. Although institutional herds and flocks have a role to play in generating new knowledge, they tend not to be managed in a similar manner as local farmers' herd and flocks. Where this is the case, the differential management strategies may lead to significant G × E resulting in re-ranking of sires. However, institutional herds and flocks, as well as on-farm livestock populations are valuable resources. For example, in some smallholder farms, with small numbers of animals per farm, the lack of contemporary groups becomes important, and hence institutional herds and flocks may be more appropriate. An alternative would be on-farm livestock populations managed in a scientist-farmer partnership. This would provide a valuable resource in an open nucleus breeding scheme. Collaborative efforts would provide the technical expertise needed for such initiatives and analyses.

Conclusion

This paper provides a synthesis of an international e-conference on one of the fundamental issues in livestock development in SSA. Participants expressed gratitude at the usefulness of the exercise that brought out a lot of issues and constructive suggestions that would inform the development of a framework for enhancing the efficiency and effectiveness for delivering livestock genetics R&D. General consensus was towards developing fundamental soft infrastructure and capacity that would form the basis of vital R&D with minimal bureaucratic constraints.

Capacity should be developed around systems for organizing, collecting and utilizing livestock performance data. Improved communication and coordination of efforts within and across countries should be in the centre for these developments. The conference highlighted that animal breeders and geneticists within SSA should be the ones to 'kick-start' the process and raise the profile of the profession. This is because they are the ones who have the political contacts and local knowledge to obtain the buy-in on different R&D initiatives from the key people within Governments and the farming community. Colleagues in the Diaspora should be involved on initiatives in transferable-skills and help to identify new project opportunities.

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Statement of interest

There is no conflict of interest.

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Animal Genetic Resources, 2015, 56, 155. © Food and Agriculture Organization of the United Nations, 2015

Recent Publications

An introduction to heritage breeds

D.P. Sponenberg, J. Beranger and A. Martin Edited by D. Burns & A. Larkin Hansen Storey Publishing, North Adams Published in 2014, pp. 240
ISBN 978-1-61212-125-3 (pbk.: alk. Paper)
ISBN 978-1-61212-130-7 (Hardcover: alk. Paper)
e-ISBN 978-1-61212-462-9

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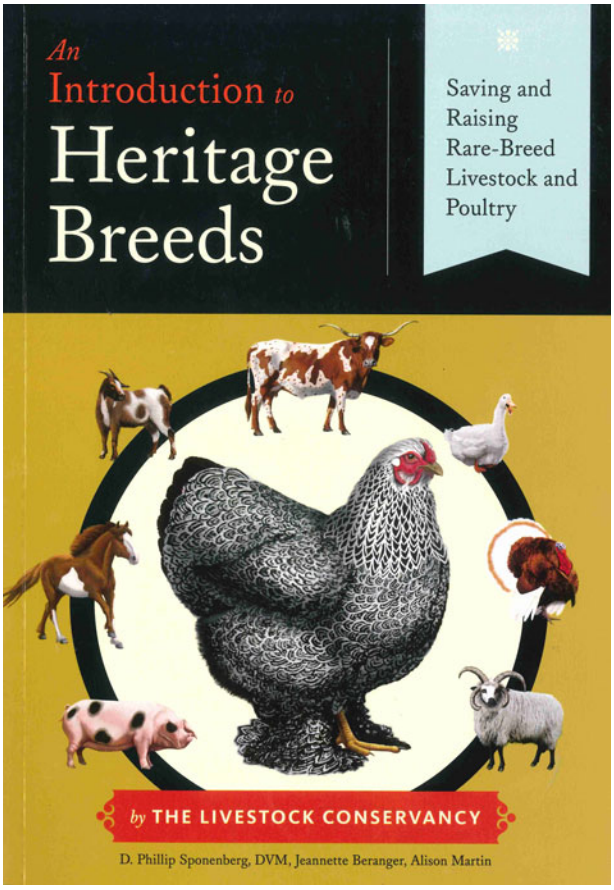


The book is a product of The Livestock Conservancy, a non-profit organization focused on preserving and promoting rare breeds of livestock. The authors explain that heritage breeds were developed thousands of years to fit with local environments, farming methods and purposes and provide interesting choices for today's small scale sustainable farms. This eloquent, inviting, visual guide explains why conserving heritage breeds is important and shows how one can raise such breeds him or herself, and by this helping to preserve them and benefiting from them at the same time. Written by three experts from the Livestock Conservancy, this book includes chickens, turkeys, ducks, geese, rabbits, pigs, sheep, goats, cattle, donkeys and horses, detailing each breed's specific characteristics. In one chapter the specific needs of each species, in order of size from smallest to largest, are discussed showing that about anyone can manage the smallest species while as size increases, so does the complexity of managing and housing animals. The reader is guided from the selection of the right species, to the selection of breed and even to exit strategies to avoid that a breed undergoes huge losses when producers buy up uniquely breed animals and then hastily disperse them after a few year of involvement. The book represents a guide for a new generation of farmers.

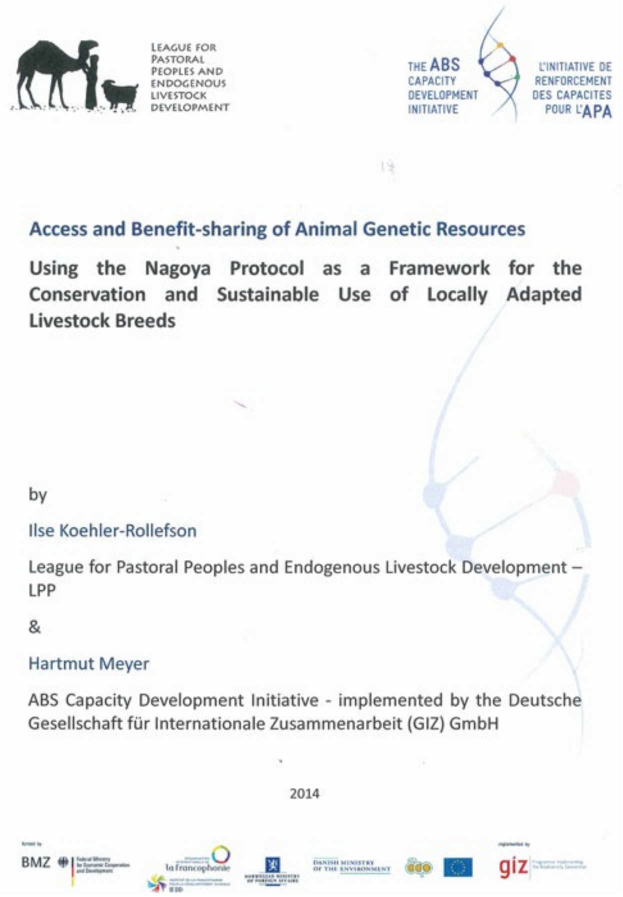
Animal Genetic Resources, 2015, 56, 157–157. © Food and Agriculture Organization of the United Nations, 2015

Recent Publication

Access and benefit-sharing of animal genetic resources – using the Nagoya Protocol as a framework for the conservation and sustainable use of locally adapted livestock breeds

I. Koehler-Rollefson and H. Mayer League for Pastoral Peoples and Endogenous Livestock Development (LPP) ABS Capacity Development Initiative Published in 2014, pp. 45
Available at http://www.fao.org/ag/againfo/programmes/en/genetics/documents/ITWG_AnGR_8/side-event/01_Invitation-ABS_for_AnGR_GIZ_LPP.pdf

doi:10.1017/S2078633615000077



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POUR L'APA

Access and Benefit-sharing of Animal Genetic Resources

Using the Nagoya Protocol as a Framework for the Conservation and Sustainable Use of Locally Adapted Livestock Breeds

by

Ilse Koehler-Rollefson

League for Pastoral Peoples and Endogenous Livestock Development – LPP

&

Hartmut Meyer

ABS Capacity Development Initiative - implemented by the Deutsche Gesellschaft für Internationale Zusammenarbeit (GIZ) GmbH

2014

This study seeks to investigate the cornerstones of an international access and benefit-sharing regime for animal genetic resources that would be fair and equitable as well as workable, considering the distinctive features of animal genetic resources, as well as the urgent need for maintaining and conserving domestic animal diversity for future generations.

Various stakeholder groups have different opinions on access and benefit-sharing. Governments are mostly concerned with developing the right kind of material transfer agreements and preventing any disruption in the flow of animal genetic resources. They also see the need for addressing Livestock keepers' Rights and support (Biocultural) Community protocols, as stipulated by the Nagoya protocol. Among scientists, some are worried that their access to research materials may be jeopardized; others warn about the deleterious impact of the indiscriminate export of exotics into developing countries threatening the integrity of local breeds. Indigenous and local livestock keepers have been advocating for fair and equitable benefit-sharing since 2003, requesting for their breeds to be recognized as product of their traditional knowledge and as community property.

While the Global Plan of Action for Animal Genetic Resources provides a comprehensive framework for the management of animal genetic resources, the Nagoya protocol adds important dimensions. By mandating prior informed consent and mutually agreed terms not only by provider countries but also by local and indigenous communities it enforces Strategic Priority 5 of the Global Plan of Action to support indigenous and local production systems and associated knowledge systems of importance to the maintenance and sustainable use of animal genetic resources.

The components of a specific international regime for animal genetic resources are suggested, including the need for the decoupling of benefits from specific cases to sharing and managing benefits on a collective basis. The 'International Regime' would include support for community protocols by communities that conserve specific breeds and agro-ecosystems, creation of a 'Community breed repository' (in analogy to the Global Seed Vault), enactment of Livestock keepers' Rights and the establishment of a benefit-sharing fund. Provisions would have to be made to protect traditional knowledge with respect to animal genetic resources to put it on an even footing with scientific knowledge and give it protection. Recommended is also the regular use of genetic impact assessments as well as a monitoring mechanism.

Animal Genetic Resources, 2015, 56, 159–159. © Food and Agriculture Organization of the United Nations, 2015

Recent Publication

Study of origin and conservation strategy of the pramenka sheep breeds as a regional transboundary breed

Edited by A. Ivankoviç and J. Ramljak European Regional Focal Point for Animal Genetic Resources (ERFP) Published in 2014, pp. 103
ISBN 978-3-00-046512-3

doi:10.1017/S2078633615000089

This small booklet comprises the results of a study on the pramenka sheep, a regional transboundary breed spread over the southeast of Europe. The study was supported by the European Regional Focal Point for Animal Genetic Resources. The major part of the publication is a collection of the power point presentations given within the frame work of the project showing the situation of the pramenka sheep populations in Croatia, Bosnia and Herzegovina, Serbia, Greece, Macedonia, Montenegro, Romania, Turkey, Slovenia and Albania.

A summary of the project results is provided as well as an article on the phylogenesis of the pramenka sheep breeds. The pramenka sheep represents a valuable resource of genetic diversity in sheep. Its national breed populations are well adapted to the local conditions. The populations can be found in mountainous regions, rocky and karst areas, Mediterranean coastal area and islands. The animals are usually kept in traditional semi-extensive or extensive production systems.

European Regional Focal Point for Animal Genetic Resources
RFP
EUROPE
STUDY OF ORIGIN AND CONSERVATION STRATEGY OF THE PRAMENKA SHEEP BREEDS AS REGIONAL TRANSBOUNDARY BREEDS
Final Project Report
Edited by:
Ante Ivanković & Jelena Ramljak
2014

Animal Genetic Resources, 2015, 56, 161. © Food and Agriculture Organization of the United Nations, 2015

Recent Publications

Coping with climate change – the roles of genetic resources for food and agriculture

Food and Agriculture Organization of the United Nations, Rome, Italy Published in 2015, pp. 110
ISBN 978-92-5-108441-0 e-ISBN 978-92-5-108442-7
Available at http://www.fao.org/3/a-i3866e.pdf

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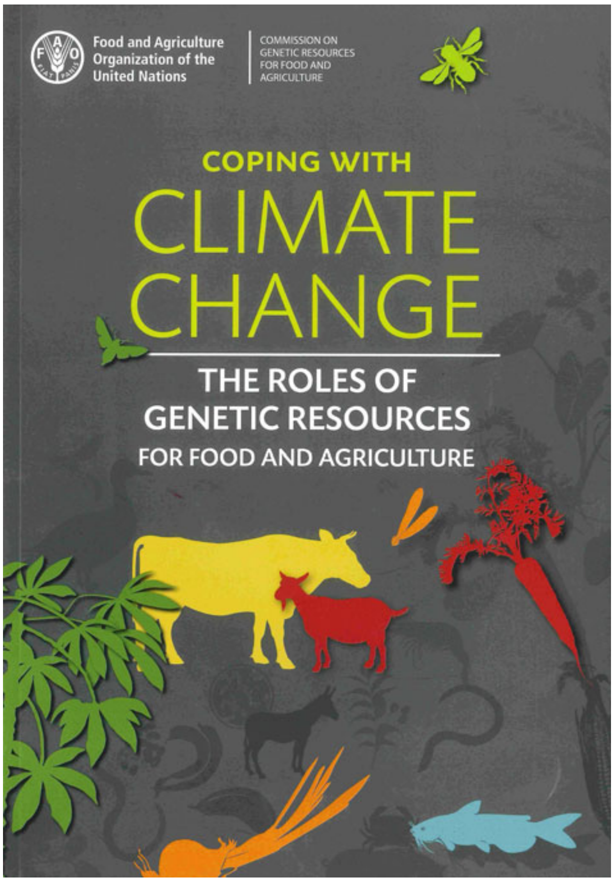

Biodiversity for food and agriculture is among the earth's most important resources. Crops, livestock, aquatic organisms, forest trees, micro-organisms and invertebrates – thousands of species and their genetic variability – make up the web of biodiversity upon which the world's food production depends.

Biodiversity is indispensable: be it the insects that pollinate plants, the microscopic bacteria used for making cheese, the diverse livestock breeds used to make a living in harsh environments, or the thousands of varieties of crops that sustain food security worldwide. Biodiversity is essential for achieving nutritional diversity in diets – a diverse food basket – which is important for human health and development.

However, biodiversity, and in particular genetic diversity, is being lost at an alarming rate. The threats to genetic diversity include: (i) a focus on the development and use of only a few commercial crop varieties and breeds of livestock, neglecting locally adapted varieties and breeds and their important characteristics; (ii) the effects of increasing population pressure; (iii) the loss of natural habitats and environmental degradation, including deforestation, desertification and river-basin modification; and (iv) climate change.

Genetic resources are the raw materials that local communities and researchers rely upon to improve the quality and output of food production. When these resources are eroded, humankind loses potential means of adapting agriculture to new socio-economic and environmental conditions. It is because of their genetic variability that plants, animals, micro-organisms and invertebrates are able to adapt and survive when their environments change. Maintaining and using a wide range of diversity – both diversity among species and genetic diversity within species – therefore means maintaining capacity to respond to future challenges. For example, plants and animals that is genetically tolerant of high temperatures or droughts, or resistant to pests and diseases, are of great importance in climate change adaptation.

Maintaining biodiversity for food and agriculture is a global responsibility. As countries seek to diversify and adapt their agricultural and food-production systems, the exchange of genetic resources and the interdependence of countries increases. With climate change, the conservation and sustainable use of genetic diversity has become more critical than ever. The challenge of conserving and sustainably using genetic resources extends across all continents and ecosystems and demands a broad-based response. At the request of the Commission on Genetic Resources for Food and Agriculture, FAO prepared thematic studies on the interactions between climate change and plant, animal, forests, aquatic, invertebrate and micro-organism genetic resources. This publication summarizes the results of these studies including a chapter on animal genetic resources describing in detail the effects of climate change on animal genetic resources and their management, the roles animal genetic resources play in coping with climate change and provides recommendations for policy makers.

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Recent Publication

The green quarter – a decade of progress across the world in sustainable pastoralism

H. de Jode IUCN, International Union for Conservation of Nature – WISP, World Initiative for Sustainable Pastoralism Published in 2014, pp. 52
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Available at https://portals.iucn.org/library/node/44903

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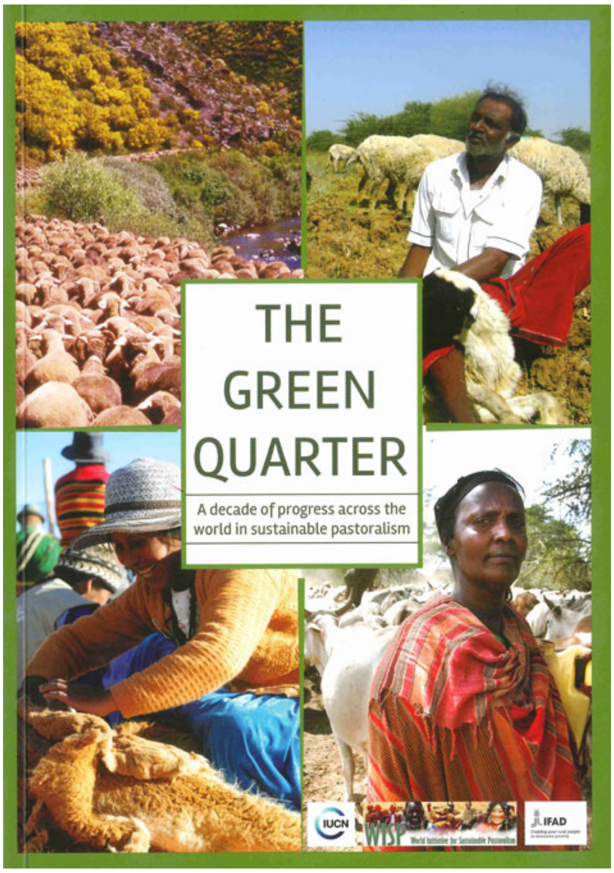

The World Initiative for Sustainable Pastoralism (WISP) has now been in existence for a decade, a period during which considerable progress has been made globally towards sustainable pastoral development. Many challenges remain for pastoralists, but in the areas where gains have been made it is vital these are built upon and achievements are not squandered. This book follows WISP's global approach and highlights key examples from its work with partners around the world. It identifies the impact of WISP's work in empowering pastoralists through improved advocacy skills and better knowledge, and in helping to change policy and practice. Through case studies, testimonies and photos, this book aims to bring WISP's global stories of pastoralism to a wider audience and identify opportunities for future success.

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