55
2014
ISSN 2078-6336

ANIMAL GENETIC RESOURCES

an international journal

RESSOURCES GÉNÉTIQUES ANIMALES

un journal international

RECURSOS GENÉTICOS ANIMALES

una revista internacional

United Nations Decade on Biodiversity

E-ISBN 978-92-5-008571-5

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

Ressources génétiques animales est un journal international publié sous les auspices de la Sous-Division des ressources génétiques animales de la Division de la production et de la santé animales, Organisation des Nations Unies pour l'alimentation et l'agriculture (FAO).

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

Print edition and institutional subscriptions / Édition imprimée et abonnements pour institutions / Edición de la impresión y suscripciones institucionales: Sales and Marketing Group, Office of Knowledge Exchange, Research and Extension, FAO, Viale delle Terme di Caracalla, 00153 Rome, Italy; Fax: (39) 06 5705 3360; E-mail / courrier électronique / correo: Publications-Sales@fao.org or through FAO sales agents / ou auprès des agents de vente des publications de la FAO / o a través de los agentes de venta de la FAO.

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Animal Genetic Resources, 2014, 55, i. © Food and Agriculture Organization of the United Nations, 2014
doi:10.1017/S207863361400037X

Editorial

Dear reader,

While writing these lines the Animal Genetic Resources Branch of the Food and Agriculture Organization of the United Nations (FAO)[1] is busy with the preparation of the Eighth Session of the *Intergovernmental Technical Working Group on Animal Genetic Resources for Food and Agriculture* which will take place in Rome in November 2014. The Working Group was established in 1997 by the *Commission on Genetic Resources for Food and Agriculture*[2] to support its work in the animal genetic resources sector.

This year the Working Group will discuss topics such as

- The second report on *The State of the World's Animal Genetic Resources for Food and Agriculture*
- Implementation and update of the *Global Plan of Action for Animal Genetic Resources*
- Ecosystem services provided by livestock species and breeds
- Access and benefit-sharing for animal genetic resources
- Genetic diversity and climate change

Draft documents for the Session will be made available at the Working Group webpage[3] and you are warmly invited to have a look at them. The draft document on *TheState of the World's Animal Genetic Resources for Food and Agriculture* might be of special interest to you. This report is a comprehensive global assessment of livestock biodiversity and its management. Such assessments are necessary to coordinate international efforts to improve the management of animal genetic resources for food and agriculture. The Commission on Genetic Resources for Food and Agriculture has established a series of global "State of the World" assessments[4] . The first report on animal genetic resources was published in 2007[5]. In 2013, the Commission requested FAO to prepare the second report on *The State of the World's Animal Genetic Resources for Food and Agriculture*, as an update of the first report, for publication in 2015. Amongst others, the update is based on reports received from 129 countries and 15 international organizations.

On the Working Group webpage you will also find information on the Global Databank for Animal Genetic Resources DAD-IS[6] which currently contains data from 182 countries and 38 species. Based on DAD-IS data, trends in genetic erosion of breeds since the publication of the first report on *The State of the World's Animal Genetic Resources for Food and Agriculture* are presented. Since the year 2006, the proportion of breeds classified 'as at risk of extinction' increased from 15 to 17 percent, the breeds classified as 'not at risk' decreased from 21 to 18 percent and the percentage of breeds reported to be extinct remained stable at seven percent. The number of breeds where no risk status can be calculated due to either complete lack of information on population sizes or lack of updating of population data for a period of more than ten years is high with almost 60 percent .

The editors would like to encourage the readership of *Animal Genetic Resources* to have a look at the content of the Global Databank for Animal Genetic Resources and contribute, in collaboration with the respective National Coordinators for the Management of Animal Genetic Resources[7], to its improvement. In case you do have any comments to the draft version of the second report on *The State of the World's Animal Genetic Resources for Food and Agriculture* please send them to SoWAnGR2@fao.org

Yours sincerely,

Roswitha Baumung

[1] http://www.fao.org/AG/AGAInfo/themes/en/AnGR.html
[2] http://www.fao.org/nr/cgrfa/en/
[3] http://www.fao.org/AG/AGAInfo/programmes/en/genetics/angrvent.html
[4] http://www.fao.org/AG/AGAInfo/programmes/en/genetics/global_assessments.html
[5] http://www.fao.org/AG/AGAInfo/programmes/en/genetics/First_state.html
[6] http://www.fao.org/dad-is
[7] http://dad.fao.org/cgi-bin/EfabisWeb.cgi?sid=-1,contacts

Animal Genetic Resources, 2014, 55, iii.
doi:10.1017/S2078633614000381

Editorial

Estimado lector,

A la hora en que escribo estas líneas, la Subdivisión de Recursos Zoogenéticos de la Organización de las Naciones Unidas para la Alimentación y la Agricultura (FAO)[1] se emplea a fondo en la preparación de la Octava Reunión del *Grupo de Trabajo Técnico Intergubernamental sobre los Recursos Zoogenéticos para la Alimentación y la Agricultura*, que tendrá lugar en Roma en Noviembre de 2014. El Grupo de Trabajo fue establecido en 1997 por la *Comisión de Recursos Genéticos para la Alimentación y la Agricultura*[2] para apoyar su labor en el campo de los recursos zoogenéticos.

Este año el Grupo de Trabajo abordará temas tales como:

- El segundo informe sobre *La Situación de los Recursos Zoogenéticos Mundiales para la Alimentación y la Agricultura*
- La aplicación y puesta al día del *Plan de Acción Mundial sobre los Recursos Zoogenéticos*
- Los servicios ecosistémicos prestados por las especies y razas ganaderas
- El acceso a los recursos zoogenéticos y el reparto de los beneficios que resultan de su utilización
- La diversidad genética y el cambio climático

Los borradores de los documentos de esta Reunión van a ser puestos a su disposición en la página web[3] del Grupo de Trabajo y le invitamos cordialmente a darles un vistazo. El borrador del documento sobre *La Situación de los Recursos Zoogenéticos Mundiales para la Alimentación y la Agricultura* puede ser de especial interés para Usted. Este informe constituye una exhaustiva evaluación mundial de la biodiversidad ganadera y su gestión. Tales evaluaciones se hacen necesarias para coordinar los esfuerzos internacionales por mejorar la gestión de los recursos zoogenéticos para la alimentación y la agricultura. La Comisión de Recursos Genéticos para la Alimentación y la Agricultura ha establecido una serie de evaluaciones de la "Situación Mundial"[4]. El primer informe sobre los recursos zoogenéticos fue publicado en 2007[5]. En 2013, la Comisión solicitó a la FAO la preparación del segundo informe sobre *La Situación de los Recursos Zoogenéticos Mundiales para la Alimentación y la Agricultura*, como una actualización del primer informe, para su publicación en 2015. Entre otros, la actualización se basa en los informes remitidos por 129 países y 15 organizaciones internacionales.

En la página web del Grupo de Trabajo, también podrá encontrar información acerca de la Base Mundial de Datos para los Recursos Zoogenéticos DAD-IS[6], que actualmente contiene datos de 182 países y 38 especies. De acuerdo con los datos introducidos en DAD-IS, la evolución de la erosión genética de las razas desde la publicación del primer informe sobre *La Situación de los Recursos Zoogenéticos Mundiales para la Alimentación y la Agricultura* se presenta tal como sigue. Desde el año 2006, la proporción de razas clasificadas como "en peligro de extinción" ha aumentado del 15 al 17 por ciento, las razas clasificadas como "no amenazadas" han disminuido del 21 al 18 por ciento y el porcentaje de razas registradas como extinguidas se mantiene estable en un 7 por ciento. El número de razas para las cuales no se puede determinar el estado de riesgo, ya sea por una falta completa de información sobre los tamaños de población o por no haberse actualizado la información de la población en un periodo superior a los diez años, es elevado, suponiendo cerca del 60 por ciento.

Los editores desean animar a los lectores de *Recursos Genéticos Animales* a consultar los contenidos de la Base Mundial de Datos para los Recursos Zoogenéticos y a contribuir a su mejora, en colaboración con los respectivos Coordinadores Nacionales para la Gestión de los Recursos Zoogenéticos[7]. En caso de que quisiese formular cualquier comentario en relación con la versión preliminar del segundo informe sobre *La Situación de los Recursos Zoogenéticos Mundiales para la Alimentación y la Agricultura*, escriba por favor a la siguiente dirección: SoWAnGR2@fao.org.

Atentamente,

Roswitha Baumung

[1] http://www.fao.org/AG/AGAInfo/themes/es/AnGR.html
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Animal Genetic Resources, 2014, 55, v. © Food and Agriculture Organization of the United Nations, 2014
doi:10.1017/S2078633614000393

Editorial

Cher lecteur,

À l'heure où j'écris ces lignes, la Sous-division des Ressources Zoogénétiques de l'Organisation des Nations Unies pour l'Alimentation et l'Agriculture (FAO)[1] se dépense pour préparer la Huitième Session du *Groupe de Travail Technique Intergouvernemental sur les Ressources Zoogénétiques pour l'Alimentation et l'Agriculture*, qui se tiendra à Rome en Novembre 2014. Le Groupe de Travail a été mis en place en 1997 par la *Commission des Ressources Génétiques pour l'Alimentation et l'Agriculture*[2] pour soutenir son travail dans le secteur des ressources zoogénétiques.

Cette année le Groupe de Travail abordera des sujets tels que

- Le deuxième rapport sur *L'État des Ressources Zoogénétiques pour l'Alimentation et l'Agriculture dans le Monde*
- La mise en œuvre et la mise à jour du *Plan d'Action Mondial pour les Ressources Zoogénétiques*
- Les services écosystémiques fournis par les espèces et les races d'animaux d'élevage
- L'accès aux ressources zoogénétiques et le partage des avantages en découlant
- La diversité génétique et le changement climatique

Les ébauches des documents de la Session seront mises à votre disposition sur la page web[3] du Groupe de Travail et nous vous invitons cordialement à leur jeter un coup d'œil. L'ébauche du document sur *L'État des Ressources Zoogénétiques pour l'Alimentation et l'Agriculture dans le Monde* peut tout particulièrement vous intéresser. Ce rapport est une exhaustive évaluation mondiale de la biodiversité des animaux d'élevage et sa gestion. De telles évaluations s'avèrent nécessaires afin de coordonner les efforts internationaux pour améliorer la gestion des ressources zoogénétiques pour l'alimentation et l'agriculture. La Commission des Ressources Génétiques pour l'Alimentation et l'Agriculture a mis en place une série d'évaluations de "l'État des Ressources Zoogénétiques dans le Monde"[4]. Le premier rapport sur les ressources zoogénétiques a été publié en 2007[5]. En 2013, la Commission a sollicité à la FAO de préparer le deuxième rapport sur *L'État des Ressources Zoogénétiques pour l'Alimentation et l'Agriculture dans le Monde*, comme une mise à jour du premier rapport, pour être publié en 2015. Entre autres, l'actualisation se base sur les rapports fournis par 129 pays et 15 organisations internationales.

Sur la page web du Groupe de Travail vous trouverez aussi des informations sur la Base Mondiale de Données pour les Ressources Zoogénétiques DAD-IS[6] qui contient actuellement des données de 182 pays et 38 espèces. L'évolution de l'érosion génétique des races depuis la publication du premier rapport sur *L'État des Ressources Zoogénétiques pour l'Alimentation et l'Agriculture dans le Monde* est présentée ci-après, conformément aux données saisies sur DAD-IS. Depuis l'année 2006, la proportion de races classées comme "menacées d'extinction" a augmenté de 15 à 17 pour cent, les races classées comme "non menacées" ont diminué de 21 à 18 pour cent et le pourcentage de races signalées comme éteintes demeure stable à 7 pour cent. Le nombre de races pour lesquelles l'état de risque ne peut pas être jaugé, soit parce qu'il y a un manque complet d'information sur la taille des populations ou parce que les données populationnelles n'ont pas été actualisées pendant plus de dix ans, est assez élevé (près de 60 pour cent des races).

Les rédacteurs voudraient encourager les lecteurs de *Ressources Génétiques Animales* à parcourir les contenus de la Base Mondiale de Données pour les Ressources Zoogénétiques et à contribuer à son amélioration, en collaboration avec les respectifs Coordonnateurs Nationaux pour la Gestion des Ressources Zoogénétiques[7]. Au cas vous souhaiteriez faire un commentaire à propos de l'ébauche du deuxième rapport sur *L'État des Ressources Zoogénétiques pour l'Alimentation et l'Agriculture dans le Monde*, veuillez vous adresser à: SoWAnGR2@fao.org

Cordialement,

Roswitha Baumung

[1] http://www.fao.org/AG/AGAInfo/themes/fr/AnGR.html
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Animal Genetic Resources, 2014, 55, 1–7. © Food and Agriculture Organization of the United Nations, 2014
doi:10.1017/S2078633614000241

Chemical composition of colostrum from Azawak cow in Niger compared with meta-analytical data

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Summary

This study aimed at comparing data obtained from Azawak zebu colostrum with literature data. The comparison was performed by a meta-analytical approach. Colostrum samples were hand-collected after 5 h from seven Azawak cows at calving between August 27 and September 10, 2009 in the Sahel. For data from literature, 21 references were identified in the following analytical databases: PubMed, Science Direct, Google scholar, Collection from University of Liege. The references were selected according to the following two criteria: (i) only studies reported on bovine colostrum were used irrespective of breeds, and (ii) among the selected studies, those not providing complete information to allow meta-analytical calculation were excluded. Samples were analysed for immunoglobulins (IgG, IgM and IgA), lactoferrin and chemical composition (dry mater, protein, fat, lactose, ash, Ca, P, NA, K and Mg). The mean levels of IgG, IgM, dry matter, protein and fat for Azawak cows were lower ($P < 0.001$) than those obtained in other breeds; however, colostrum from the Azawak was higher in IgA but the difference was not significant. For lactose and ash, mean values for Azawak cows were higher ($P < 0.001$) than those from the literature. Contents of Ca, P, Na and Mg in Azawak bovine colostrum were significantly higher ($P < 0.001$) than the mean levels in form the literature data. In conclusion, the colostrum from Azawak cows appears to be lower in most immunoglobulins, in fat and in protein than the values reported in the literature, but higher in lactose and minerals. This could be an adaptation to Sahelian constraints.

Keywords: *Azawak, bovine breeds, chemical composition, colostrum, immunoglobulin*

Résumé

Ce travail vise à comparer les données obtenues avec le colostrum du zébu Azawak à celles obtenues dans la littérature aux fins d'une utilisation hétérologue chez les petits ruminants, et ceci en utilisant une approche méta-analytique. Des échantillons de colostrum ont été récoltés par traite manuelle au cours des vêlages entre le 27 août et le 10 septembre 2009 dans le Sahel, à partir de 7 zébus Azawak. Pour les données de la littérature, vingt et un (21) des références ont été identifiées dans les bases de données analytiques (PubMed, Science Direct, Google Scholar, Collection de l'Université de Liège). Les références ont été sélectionnées selon les deux critères suivants: (i) les études rapportées sur le colostrum bovin ont été utilisées sans distinction de races, et (II) parmi les études sélectionnées celles ne comportant pas des informations complètes pour permettre le calcul méta-analyse ont été exclues. Les échantillons ont été analysés pour immunoglobulines (IgG, IgM, IgA), lactoferrine, et la composition chimique (matière sèche, protéines, lipide, lactose, cendre brute, calcium, phosphore, sodium, potassium, magnésium). Les concentrations moyennes d'IgG, d'IgM de matière sèche, de protéines et matières grasses pour le zébu Azawak présentaient des valeurs plus faibles ($P < 0.001$) que celles obtenues chez d'autres races, mais elles ont des niveaux plus élevés en IgA ($P > 0.05$), lactose et cendre brut ($P < 0{,}001$). Les teneurs en minéraux solubles (Ca, P, K, Na et Mg) du colostrum du zébu Azawak étaient significativement plus élevées ($P < 0.001$) que les niveaux moyens des données de la littérature recueillies. En conclusion, comparé aux données de littérature, le colostrum de vache Azawak semble être plus pauvre en immunoglobuline, en lipides et en protéines, mais plus riche en lactose et en minéraux. Il se pourrait qu'il s'agisse d'une adaptation de la race au milieu sahélien.

Mots-clés: *Azawak, races bovines, colostrum, composition chimique, immunoglobulines*

Resumen

Este estudio tiene como objetivo comparar los datos obtenidos a partir de cebú Azawak calostro con datos de la literatura, para uso heterólogo en pequeños rumiantes. La comparación se realiza, utilizando un enfoque meta-analítico. Muestras de calostro fueron recogidos a mano durante el parto entre agosto 27 y septiembre, el 10 de 2009 en el Sahel, de 7 Azawak vacas. Para los datos de la literatura, veintiuno (21) referencias se identificaron en las siguientes bases de datos analíticos: PubMed, Science Direct, Google scholar, Colección de la Universidad de Lieja. Las referencias han sido seleccionados de acuerdo con los dos criterios siguientes: (i) sólo estudios informaron sobre el calostro bovino se utilizaron independientemente de razas, y (ii) entre los estudios seleccionados los que no proporcionan información completa para permitir el cálculo meta-analítica fueron excluidos. Las muestras se ensayaron para inmunoglobulinas (IgG, IgM, IgA), lactoferrina, y la composición química (materia seca, proteína, lípido, lactosa, ceniza bruta, calcio, fósforo, sodio, potasio, magnesio). Los niveles medios de IgG, IgM, materia seca, proteína y grasa de vaca Azawak fueron menores ($P < 0.001$) que los obtenidos en otras razas, pero fue mayor para IgA ($P > 0.05$). En el caso de la lactosa y cenizas, los valores medios de las vacas

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Azawak fueron más altos ($P < 0.001$) que los de la literatura. Contenido de Ca, P, Na y Mg en Azawak calostro bovino fueron significativamente mayores ($P < 0.001$) que los niveles medios en datos de la literatura.. El calostro de Azawak se aparece contenir menos immunoglobulin, gasa y proteína que los datos de la literatura, pero mas lactose y cenizas. A lo mejor, se podría estar un adaptacio al medio Sahelian.

Palabras clave: *Azawak, bovino razas, calostro, la composición química, las inmunoglobulinas*

Submitted 10 September 2013; accepted 16 April 2014

Introduction

In Niger, breeding of small ruminants is the main economic activity for more than 6 million farmers. The health of their livestock is of paramount importance. At birth, the survival of newborns is essentially determined by the ingestion of colostrum (Berge *et al.*, 2009). It provides nutrients and antibodies for the transitional protection against external aggressions, but also growth factors and hormones (Kuralkar and Kuralkar, 2010). In ruminants, a high variability and rapid changes in the composition of colostrum over time, as well as inter-specific differences have been reported (Hadjipanayiotou, 1995; Abdel-Fattah *et al.*, 2012; Hawken *et al.*, 2012). This variability may be related to factors such as nutrition (Kaewlamun *et al.*, 2011), especially during the last week before parturition (Hawken *et al.*, 2012). In addition, it is known from the literature that colostrum production is abundant in cattle, and that it is possible to use it to improve the health status of small ruminants (Godden *et al.*, 2009; Machado-Neto *et al.*, 2011). This study aimed at comparing data obtained from Azawak zebu colostrum with literature data. The comparison was performed by a meta-analytical approach. Zebu Azawak, whose females are known in Sahel for their good milking skills (Seydou, 1981) is native from North Niger (Joshi, Mclaughline and Phillips, 1957). This breed also spread in other countries, especially in the area of Menaka (Mali), Burkina Faso and North of Nigeria (Gouro and Yenikoye, 1991). The zebu Azawak is an animal of medium size (1.3 m at the withers). In very good conditions and intensive breeding, Azawak cow can produce on average 12 litres of milk per day (Seydou, 1981). The dressing out percentage is 50–60 percent (Oumarou, 2004).

A meta-analysis was performed. Meta-analysis is a statistical method that synthesizes data from studies on a particular subject where there are contrasting results. This statistical method shows the effect of treatment in cases where the studies taken individually do not lead to a conclusion because there are no statistically significant results. Meta-analysis seeks to gather an exhaustive list of conflicting data and to remove possible mistakes. In addition, it highlights study data by comparing them with those of trials referring to similar experiments as it is the case in the present study.

Materials and methods

Animals

Seven multiparous cows (mean age 8 ± 0.8 years) of Azawak zebu breed were used during calving between August 27 and September 10, 2009. Animals had lactation numbers between 2 and 4. Except one animal coming from a private farm in Niamey, four cows were from the Farm Station of Kirkissoye (FSK) in Niamey and two from the Sahelian experimental station of Toukounous (SSET) located 200 km North of Niamey (14°31 North and Longitude 3°18 East). They were vaccinated against Contagious Bovine Pleuropneumonia (CBPP). At FSK, farming was conducted in stables where the main diet consists of *Echinochloa stagnina* complemented, with wheat, cottonseed, cottonseed meal, peanut meal, brewer's spent grains and licks. Feed was done *ad libitum*. Animals of SSET were on pasture, dominated by grasses (*Aristida mutabilis*, *Cenchrus biflorus*, *Eragrostis tremula*, *Schoenfeldia gracilis*, *Panicum laetum*) and woody (*Maerua crassifolia*, *Salvadora persica*), according to Chaibou (2005). Pregnant and lactating females were supplemented with cotton seed (2 kg) during the dry season.

Colostrum collection

Colostral samples were taken in the first 5 h after calving by hand milking before calves suckled, collected in containers and packed in appropriate tubes, being stored in a freezer at −20 °C before analysis. The cold chain was never interrupted during this period. During the journey from Niamey to Liege, samples were taken in a thermos with ice.

Chemical analysis

Immunoglobulin (Ig) and lactoferrin (Lf) contents (g/l) in colostrum were measured at the Center of Rural Economy of Marloie (Belgium) by ELISA, following the manufacturer's recommendations (Bethyl® quantitative sandwich ELISA, USA). Dry matter (DM), crude ash, nitrogen-free extract (NFE), ether extract (EE) and total nitrogenous matter (TNM) were measured according to the methods of the Association of Official Analytical Chemists

(AOAC, 2006). Calcium (Ca) and magnesium (Mg) were determined by atomic absorption, potassium (K) and sodium (Na) by flame emission and phosphorus (P) by spectrophotometry.

Meta-analytic data collection

Meta-analytical means were calculated from data collected from the literature. Only studies on bovine colostrum were used, regardless of breed. Among the selected studies, those not providing complete information to allow meta-analytical calculation were excluded. In other words, all studies that do not indicate the number of animals used or in which average values are not accompanied by indicators of variation (standard deviation, standard error) were discarded. Twenty one references were identified in analytical databases (PubMed, Science Direct, Google scholar, Collection from University of Liege). Table 1 summarizes the materials (animals and experimental design) used by the authors during their studies. It refers to number of animals used, area or country, time of colostrum collection after birth, stage of lactation and feed.

Data analysis

Averages and standard deviations of data were calculated

Meta-analytical data were obtained according to the method proposed by Cucherat *et al.* (2000), in which a literature general mean is obtained by the following formula:

$$M = \frac{\sum M_i W_i}{\sum W_i},$$

where M_i is the published mean related to author I, and W_i is the inverse of the variance of the mean associated with M_i.

$$W_i = \frac{n_i}{s^2_{x_i}},$$

Table 1. List and characteristics of the 21 references identified in analytical databases.

References	Bovine breed	Country	NA	TCAB (h)	SL	Feed
Parrish *et al.* (1950)	Holstein	USA	10	3	NI	Concentrate mixture, Atlas sorgo silage and hay
Stott *et al.* (1981)	Holstein	USA	12	BFM	NI	NI
Klimes *et al.* (1986)	Bohemian Pied Lowland	Czech Republic	13	2–4	2	NI
Quigley and Martin (1994)	Jersey	USA	88	BFM	2	NI
Quigley *et al.* (1995)	Jersey	USA	49	BFM	NI	Pasture
Nardone *et al.* (1997)	Holstein	Italy	6		NI	Mixture of forages and concentrates on an *ad libitum* basis
Maunsell *et al.* (1998)	Holstein	USA	33	BFM	NI	NI
Klobasa, Goel and Werhahn (1998)	Holstein–Friesian	Germany	8	NI		NI
Kume *et al.* (1998)	Holstein	Japan	24	BFM	NI	Mixed ration
Beighle (1999)	Friesian cows	South African	60	NI	1–3	Animals were fed *ad libitum* a mixture of 50 percent Lucerne and 50 percent blue buffalo grass
Andrew (2001)	Holstein Heifers	USA	25	0–6	NI	NI
Elfstrand *et al.* (2002)	Swedish Friesian	Sweden	20	0–6	1	NI
Ontsouka *et al.* (2003)	Red Holstein	Switzerland	60	BFM	1, 2 and more	Consisting of grass silage, hay, and concentrates
Georgiev (2005)	Cows (black and white)	Bulgaria	5		2–4	Consisting of alfalfa, maize silage, brewers grain and concentrates
Tsloulpas *et al.* (2007)	Friesian cows	UK	8	1–3	3	NI
Strekozov *et al.* (2008)	Black Pied third	Russia	43	1	NI	NI
Ferdowski Nia *et al.* (2010)	Holstein	Iran	69	1	NI	NI
Zagorska *et al.* (2011)	Latvian Brown (76 percent)	Lettonia	29	NI	NI	NI
Morill *et al.* (2012)	Holstein	USA	494	NI	NI	NI
Abdel-Fattah *et al.* (2012)	Holstein	Egypt	12	6	1–3	Rice straw and concentrate (16 percent protein), and housed in free stalls
Sacerdote *et al.* (2013)	Holstein	Italy	30	1–12	2	Mix containing wheat and corn silage mix plus 25.7 percent row proteins and 2.4 percent row fats)
					2–4	

BFM, before first milking; NA, number of animals; NI, no information; SL, stage of lactation; TCAB, time collection after birth.

where n_i is thenumber of animals used to obtain the published value M_i, and S^2 the variance of the mean M_i.

When the standard deviation (SD) was available, W_i was calculated as n_i/SD^2.

When the standard error (SE) was available, W_i was computed as $1/\mathrm{SE}^2$.

Finally, the confidence intervals of the meta-analytic mean (CI) was estimated by:

$$IC = \pm 1.96\sqrt{\frac{1}{\sum w_i}}, \sqrt{\frac{1}{\sum w_i}}$$

representing the synthetic SE from the literature.

The experimental and meta-analytic means were finally compared by the Student's *t*-test.

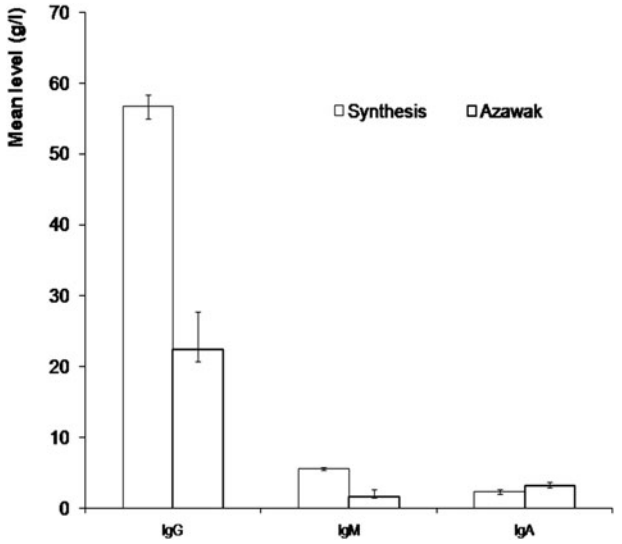

Figure 1. The mean level concentration ± standard deviation (SD) of immunoglobulins in colostrum of Azawak cow ($n = 7$) and other bovine breeds (21 references).

Results

Figure 1 presents the mean levels ± standard error of immunoglobulins and lactoferrin in the colostrum of Azawak and other bovine breeds. The value for IgA, obtained in the current study was numerically higher than the mean value of the synthesized data. For IgG and IgM, the mean value of data obtained in the literature was significantly higher ($P < 0.001$) than the mean obtained for Azawak, while for lactoferrin the means were not significantly different (0.2 ± 0.1 g/l versus 0.03 ± 0.003 g/l).

In the case of DM, the mean of data reported in literature was significantly higher ($P < 0.001$) than that of Azawak (Figure 2). For protein and fat, the mean levels found in the literature were also higher ($P < 0.05$) than those of Azawak zebu cows (Figure 2). In the case of lactose and ash, mean values of Azawak cows were higher (+12.2 g/kg DM; +1.3 g/kg DM; $P < 0.001$, respectively) than those from literature.

As far as soluble minerals are concerned, colostrum contents from Azawak for Ca, P, K, Na and Mg were significantly higher (+0.7 g/kg DM; +0.9 g/kg DM; +0.1 g/kg DM, +0.3 g/kg DM; +0.2 g/kg DM; $P < 0.001$, respectively) than the mean levels of literature data (Figure 3).

Discussion

The meta-analysis showed that the average values of the synthesized data were significantly higher than that of

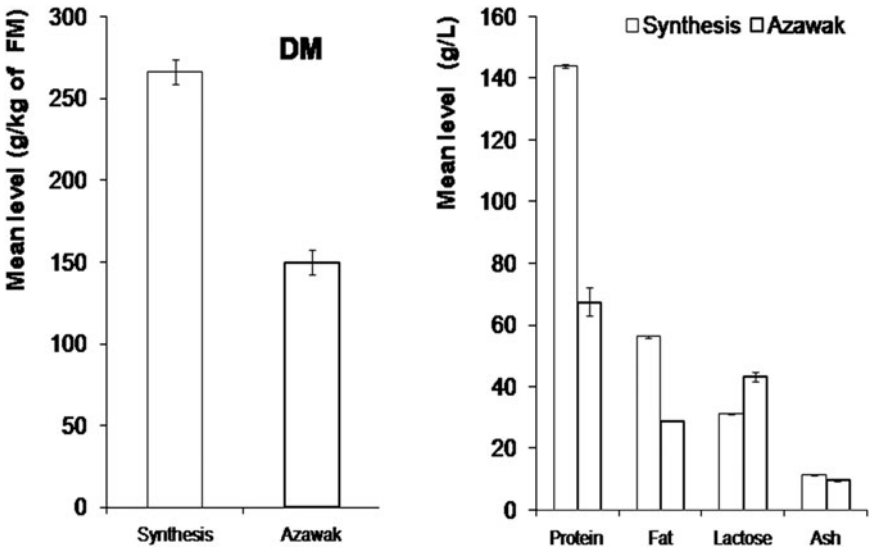

Figure 2. The mean level concentration ± standard deviation (SD) of dry matter and nutrients in colostrum of Azawak cow ($n = 7$) and other bovine breeds (21 references).

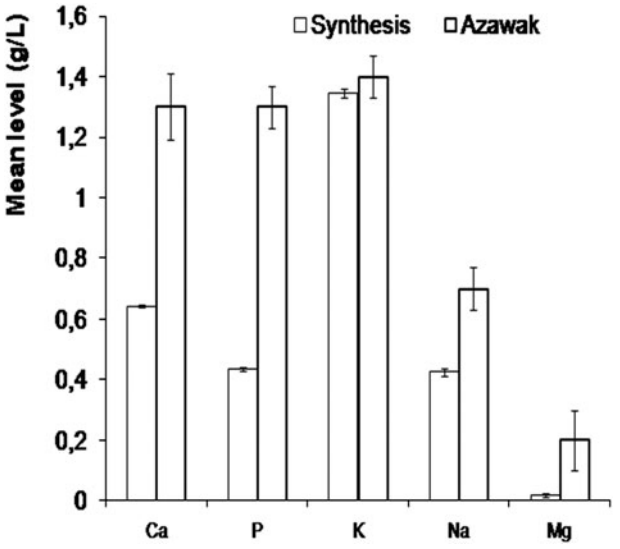

Figure 3. The mean level concentration ± standard deviation of soluble minerals in colostrum of Azawak cow and other bovine breeds.

Azawak zebu for immunoglobulins (IgG and IgM), DM, protein and ether extract. By contrast, IgA, lactose, ash and all soluble mineral contents observed in the Azawak colostrum were numerically or significantly higher than those reported in other breeds of cattle. These differences may be related to several factors. It is well known that nutrients, minerals and immunoglobulin in colostrum vary according to rank of lactation (Zarculas *et al.*, 2010; Abdou *et al.*, 2012), breed, nutritional status (Kaewlamun *et al.*, 2011), climate (Westra and Wahyudi, 2009) and season (Abdel-Fattah *et al.*, 2012).

At first sight, these variations may be related to *pre-partum* (pregnancy) management of cow. The antibody concentration may vary due to a period of abnormal dry, or non-stop milking before calving, or pathogen pressure. It was reported in literature (Brandon and Lascelles, 1975; Remond and Bonnefoy 1997; Rastani *et al.*, 2005) that cows which are milked during late pregnancy do not renew their secretory epithelium and are unable to concentrate their IgG1 secretion. According to Serieys (1993), in cows, a minimum of 25 days of drying is necessary for a renewal of the mammary epithelium cells that are responsible for the transfer and accumulation of Ig in the udder.

The rank of lactation could probably not explain the results of this study because the two groups of animals were generally at a similar rank (2–4). However, it is possible to establish a relationship between breed and the effects observed. It is known from the literature (West, 2003; Chaibou, 2005) that breeds in tropical countries have a lower genetic merit than those in areas with temperate climates. The majority of breeds listed in this meta-analysis are from countries with temperate climates. This may explain the low level of some Ig in Azawak bovine colostrum (Nardone *et al.*, 1997; West, 2003).

Environmental (Nardone *et al.*, 1997; West, 2003) effects, particularly feed, could also explain the difference in Ig observed between Azawak cow and other breeds. Although Azawak cows are reared on farms, their maintenance requirements are provided through natural pasture and crop residues with low nutritional value and agro-industrial by-products. Breeding conditions are so precarious that the animals are hardly able to fulfil all of their performances. In addition, climatic factors could directly affect animal performance (West, 2003) since they interfere with homeothermy. Prolonged hyperthermic stress causes a reduction in the secretion of many hormones (thyroxine, growth hormone, insulin, sex hormones and prolactin) involved in the metabolism (Wolfensohn, Flamenbaum and Berman, 1988; Collier *et al.*, 1991).

It appears that changes in these hormones are sensitive to change (high or low) in prevailing temperature. Thermal variation in Niger ranges from a minimum of 25 °C and a maximum of 45 °C and even 47 °C. It is possible that in the Azawak cow, the levels of some hormones involved in the mechanism of colostrum secretion were reduced. All these reasons indicated above could explain the differences observed between the composition of Azawak cow colostrum and that of other breeds used in the meta-analysis. Several studies (Hadjipanayiotou, 1995; Abdel-Fattah *et al.*, 2012; Hawken *et al.*, 2012) have focused on changes in the chemical composition of cow colostrum after calving. Thus, the variations observed could be finally attributed to factors such as endocrine hormones alteration. It is known that oestrogens, especially 17-estradiol, the serum concentration of which increases during the dry period, achieve a peak just before parturition, and have an essential role in the development of new mammary epithelial cells (Derivaux Ectors and Beckers, 1976; Tucker, 2000), which also possess receptors for IgG1 (Serieys, 1993). A study conducted by Sheldrake *et al.* (1984) showed that exogenous 17-estradiol and progesterone in non-pregnant dry cows induce a lobulo-alveolar development of the mammary gland. In a previous study, Delouis (1978) found that rapid induction of parturition in cows in late gestation by administration of corticosteroids or a combination of steroids and estradiol may bring colostrum a best one.

Regarding the determination of immunoglobulins (IgG, IgA and IgM) and lactoferrin, some authors used the radial immunodiffusion technique while others applied the ELISA method, but from different manufacturers. For example, Elfstrand *et al.* (2002) measured all individual colostrum samples through the IR technique (CombiFoss 5 000, Foss Electric A/S, and Hillerïod, Denmark). Nutrients (protein, fat, lactose and ash) and soluble minerals (Ca, P, K, Na and Mg) were analysed with methods similar to those used in the current study.

By contrast to other Ig whose levels from Azawak were lower than synthesized data, the average IgA concentration in the current study was similar to literature. There exist relationships between IgA production and the exposure of mucosas of the mother to external antibody. May be a

high ambient infectious pressure existing in Niger could explain the proportionaly higher IgA levels when compared to IgG and IgM. The average concentration of lactoferrin in Azawak bovine colostrum was similar to that obtained in the colostrum of cattle breeds used in the meta-analysis.

Colostrum quality can also be influenced by diseases such as mastitis (Maunsell *et al.*, 1998) or/and dietary imbalance (e.g. vitamin E or selenium) during the dry period (Zarcula *et al.*, 2010). The differences observed between the Azawak cows and the mean of synthesis data from the literature can be also explained either by the fact that the Azawak cow would naturally tend to produce a rather poor colostrum dry matter, in order to bring out quickly water to his young. Colostrum sampling could also be performed too late relative to calving but it is not the case in this experiment. The distribution of means from the literature, although normal, was very narrow. However, the statistical test used in meta-analysis take into account this distribution. Colostrum of goat tends to be poorer in solids and immunoglobulins than cow (Hadjipanayiotou, 1995; Levieux *et al.*, 2001; Machado-Neto *et al.*, 2011). It can therefore be inferred that the kid could tolerate adequately the Azawak colostrum. However, there are some uncertainties with respect to the justification of using Azawak colostrum in goats, based only on the dry matter content. Further experiments should be performed in that senses.

Conclusion

The current study has shown that the level of antibodies and nutrients in Azawak colostrum is lower to those reported in the literature. By contrast, for IgA, lactose and soluble minerals, are at similar levels or significantly different in favour of Azawak cow. In conclusion, the colostrum from Azawak cows appears to be lower in most immunoglobulins, in fat and in protein than the values reported in the literature, but higher in lactose and minerals. This could be an adaptation to the Sahelian constraints. Administration of heterologous colostrum also has been yet experienced in pig with good results. This study was conducted to test the hypothesis that bovine colostrum seems to be a potential source for improving weight performance and health of other species such as lambs and kids. In conclusion, the results of this study show that bovine colostrum of Azawak can be used in other species such as goats and lambs.

Acknowledgements

This work was funded by the Belgian Technical Cooperation (BTC). The authors wish to acknowledge the organization. My thanks are also addressed to the laboratory team of Marloie (Belgium) for their collaboration.

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Animal Genetic Resources, 2014, 55, 9–17. © Food and Agriculture Organization of the United Nations, 2014
doi:10.1017/S2078633614000149

Exploring the genetic diversity and substructure of the Portuguese cattle breed "Brava de Lide" using microsatellites

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Summary
The genetic structure and diversity of nine *ganadarias* (the Portuguese word for bull farmer) of the Portuguese "Brava de Lide" (Bullfighting) breed were assessed with 30 microsatellites. Allelic richness per locus was low, with an overall average of 2 547. The mean number of alleles corrected for the size of the smaller sample ranged between 2,4 in *ganadaria* Jorge Mendes and 1,9 in *ganadaria* Vaz Monteiro. The mean expected and observed heterozygosities ranged between 0.627 in *ganadaria* Palha and 0.461 in *ganadaria* Vaz Monteiro and between 0.617 in *ganadaria* Cabral D'Ascension and 0.4485 in *ganadaria* Vaz Monteiro, respectively. The *ganadaria* Vaz Monteiro was the one that systematically showed the lowest values of genetic diversity. To analyse the substructure among the 51 animals studied, a factorial correspondence analysis and a Bayesian approach were performed using the Genetix and STRUCTURE programs, respectively. The outcome of the factorial correspondence analysis resulted in the formation of four well-defined clusters. On the other hand, the analysis with the STRUCTURE program has allowed us to obtain six well-defined clusters. One well-defined cluster corresponded to the oldest Portuguese *ganadaria,* the Vaz Monteiro. This *ganadaria* was established, at its inception in 1843, with bulls and cows of pure Portuguese caste and has been kept in the same family owing to its formation without the introduction of any other blood, constituting a unique caste that must be preserved, which is the true offspring of the Portuguese cattle breed "Brava de Lide". In turn, the other clusters formed corresponded to the *ganadarias* Mario Vinhas, Murteira Grave, Nuno Casquinha, Palha and Jorge Carvalho.

Keywords: *Brava de Lide breed, genetic diversity, population substructure, Portuguese cattle*

Résumé
La structure et la diversité génétiques ont été évaluées avec 30 microsatellites chez neuf élevages portugais de taureaux de combat. La richesse allélique par locus a été faible, avec une moyenne générale de 2 547. Le nombre moyen d'allèles, corrigé selon la taille du plus petit échantillon, a varié entre 2,4 chez l'élevage Jorge Mendes et 1,9 chez l'élevage Vaz Monteiro. Les hétérozygoties moyennes observée et attendue ont varié respectivement entre 0.627 chez l'élevage Palha et 0.461 chez l'élevage Vaz Monteiro et entre 0.617 chez l'élevage Cabral D'Ascension et 0.4485 chez l'élevage Vaz Monteiro. L'élevage Vaz Monteiro a été celui qui a présenté systématiquement les plus faibles valeurs de diversité génétique. Pour analyser la sous-structure entre les 51 animaux étudiés, une analyse factorielle des correspondances et une approche bayésienne ont été appliquées respectivement avec les programmes Genetix et STRUCTURE. L'analyse factorielle des correspondances a donné comme résultat la formation de quatre grappes bien définies alors que l'analyse avec le programme STRUCTURE en a données six. Un des groupes définis a correspondu à l'élevage de taureaux de combat le plus ancien du Portugal, l'élevage Vaz Monteiro. Cet élevage a été établi en 1 843 avec des taureaux et des vaches de pure caste portugaise et a été conservé dans la même famille depuis sa création sans l'introduction d'un autre sang. L'élevage possède donc une caste unique devant être conservée en tant que descendante directe de la vraie race bovine portugaise de combat, la race « Brava de Lide ». D'un autre côté, les autres grappes constituées ont correspondu aux élevages Mario Vinhas, Murteira Grave, Nuno Casquinha, Palha et Jorge Carvalho.

Mots-clés: *race bovine Brava de Lide, diversité génétique, sous-structure populationnelle, bovins portugais*

Resumen
Se estudió la estructura y la diversidad genética de nueve ganaderías de la raza bovina portuguesa de Lidia usando 30 microsatélites. La riqueza alélica por locus fue baja, siendo la media general de 2 547. El número medio de alelos, corregido por el tamaño de la menor muestra, varió entre 2,4 en la ganadería Jorge Mendes y 1,9 en la ganadería Vaz Monteiro. La heterocigosis media esperada y la observada oscilaron entre 0.627 en la ganadería Palha y 0.461 en la ganadería Vaz Monteiro y entre 0.617 en la ganadería Cabral D'Ascension y 0.4485 en la ganadería Vaz Monteiro, respectivamente. La ganadería Vaz Monteiro fue la que sistemáticamente presentó los menores valores de diversidad genética. Para analizar la subestructura entre los 51 animales estudiados, se llevó a cabo un análisis factorial de correspondencias y se adoptó un enfoque bayesiano, empleando respectivamente los programas Genetix y

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STRUCTURE. El análisis factorial de correspondencias resultó en la constitución de cuatro conglomerados bien definidos mientras que el análisis con el programa STRUCTURE permitió la obtención de seis conglomerados bien diferenciados. Uno de los conglomerados formados se correspondió con la ganadería de Lidia más antigua de Portugal, la Vaz Monteiro. Esta ganadería fue creada en 1 843 con toros y vacas de pura casta portuguesa y, desde entonces, se ha mantenido en la misma familia sin la introducción de ninguna otra sangre, representando así una casta única que debe ser conservada. Esta ganadería está por tanto formada por la descendencia directa de la verdadera raza bovina portuguesa de Lidia. Por otro lado, los otros conglomerados formados se correspondieron con las ganaderías Mario Vinhas, Murteira Grave, Nuno Casquinha, Palha y Jorge Carvalho.

Palabras clave: *raza bovina de Lidia, diversidad genética, subestructura poblacional, ganado bovino portugués*

Submitted 24 October 2013; accepted 17 March 2014

Introduction

"Brava de Lide" is a Portuguese cattle breed with great significance beyond its home borders because of bullfighting in Spain using Portuguese bulls. The breed owes its name to its aggressive character, unwilling to be domesticated and resisting to forms of traditional management, i.e. its behaviour is not gregarious and rebellious with no natural tendency to subjection by man (Lucas, 2004). For their leadership, technical and aesthetic parameters are applied that embody the bullfighting, the main objective for the existence of these animals (Lucas, 2004). As regards its ethnic framework, the breed Brava de Lide is affiliated to the evolutive branch Black Orthoide, having had its origin in the evolutionary path of the North African domestic cattle (Alves, 2004; Cymbron *et al.*, 2005; Mateus, 2008) having been established in Portugal in Prehistoric times (Felius, 1995; Anderung *et al.*, 2005; Bollongino *et al.*, 2006; Ginja, Gama and Penedo, 2009*a*). Indeed, the discovery of mtDNA haplotypes of African origin in several varieties of the Spanish Fighting Bulls (Cortés *et al.*, 2007), and more recently in the Portuguese "Brava de Lide" (Ginja *et al.*, 2009*b*) could substantiate this hypothesis. The "Brava de Lide" breed is bred in large farms designated as *ganadarias*, avoiding as much as possible any contact with humans. In 2012, the Portuguese Association of Breeders of the Lide Bulls contemplated 104 *ganadarias* (Lucas, personal communication), distributed through the Alentejo, Ribatejo and Oeste, Beira Interior and Beira Litoral, the oldest of which was established in 1843 (Lucas, 1996, 2004). The unique production system, along with a very diverse product demand depending on the type of celebration, has given rise to a characteristic population structure, divided into lines or castes, even in herds within castes. The increasing import into Portugal of the main castes of the Spanish Fighting Bulls has led to the disappearance of the true Portuguese "Brava de Lide" breed. However, there is a *ganadaria*, the oldest in Portugal, the *ganadaria* Vaz Monteiro, which has remained faithful to the breeding of genuine Portuguese bulls of "Brava de Lide".

The objectives of this study are to study the genetic diversity and the substructure in the "Brava de Lide" breed using 30 microsatellite markers and to evaluate the hypothesis that the animals of *ganadaria* Vaz Monteiro are really different from other bulls of Lide raised in Portugal. Moreover, we also draw attention to those responsible for the importance of conserving the genetic diversity of the cattle breed "Brava de Lide".

Material and methods

Animals

In this work, 51 pure animals, registered in the Herd Book of the "Brava de Lide" breed sampled in nine *ganadarias*, were used. This included *ganadaria* Palha (PA) ($n = 6$), *ganadaria* Vaz Monteiro (VM) ($n = 11$), *ganadaria* Jorge Carvalho (JC) ($n = 7$), *ganadaria* Jorge Mendes (JM) ($n = 2$), *ganadaria* Nuno Casquinha (NC) ($n = 3$), *ganadaria* Cabral D'Ascenção (CD) ($n = 2$), *ganadaria* Mário Vinhas e Herdeiros de Manuel Vinhas (MV) ($n = 6$), *ganadaria* Paulo Caetano (PC) ($n = 2$) and *ganadaria* Murteira Grave (MG) ($n = 12$). It should be noted that of those ganadarias referred to here, where only two animals were included is owing to the fact that these *ganadaria*s have only two paternal lines. It is not preferable to use highly related animals in diversity studies and, therefore, only two animals, one as reference to one of the parental lines and the other as a son of the other paternal line, were used. Table 1 summarizes the sampled procedures.

Table 1. Sampling origin.

Ganadaria	Sampled	Used		
		♂	♀	Total
PA	13	4	2	6
VM	14	1	10	11
JC	9	1	6	7
JM	7	2	0	2
NC	6	2	1	3
CD	4	1	1	2
MV	6	2	4	6
PC	7	1	1	2
MG	13	0	12	12
Total	79	14	37	51

Microsatellites

The microsatellites used were BM1824, BM2113, BM2613, BM1818, BM203 RM067, RM006, ETH131, ETH10, ETH225, ETH152, ETH185, ETH03, ILSTS035, ILSTS065 HEL9, HEL13, HEL11, SPS113, SPS115, TGLA345, TGLA53, TGLA227, TGLA126, TGLA122, BRRIBO, INRA023, MGTG4B, CSSM036 and CYP21.

Polymerase chain reaction (PCR) conditions and detection of PCR products

Microsatellite markers were combined in multiplex-PCRs using fluorescently labelled primers and amplified in 12.5 µl reaction volume containing 2.5 mM $MgCl_2$, 200 µM DNTPs, 50–100 ng template DNA, 0.5 U Taq polymerase and primers at the appropriate concentration (Table 2). The plates containing the DNA template, the primers multiplexes and 20 µl of Chill-out were initially incubated at 90 °C for 5 min. Subsequently, the temperature was reduced to 85 °C and held for 10 min for the addition of the remaining reagents prepared together. Amplification was done with five cycles of 1 min at 94 °C, 30 s at specific annealing temperatures (Table 2) and 30 s at 72 °C followed by 25 cycles where the denaturation step at 94 °C was reduced to 45 s. We carried out a final 30 min extension. PCR products were separated in denaturing polyacrylamide gels run on ABI 373 DNA Sequencers (Applied Biosystems, Foster City, CA, USA). Fragment size analysis was performed with the STRAND software (Hughes, 2000). The internal size standard GeneScan TM-ROX 350 (PE-Applied Biosystems, Warrington, UK) was used for sizing alleles. In addition, sample no. 1 from the International Society for Animal Genetics (ISAG) 1997/98 comparison test was used as the reference to standardize allele sizes.

Table 2. Microsatellites used, its autossomic location, number of alleles detected, allele size range, temperature of annealing and primers concentration.

Locus	BTA	Number of allele size		T_a (°C)	Primers
		Alleles	Range (bp)		Concentration (µM)
BM1824	1	7	178–190	58	0.22
BM 2113	2	11	121–143	58	0.11
INRA023	3	12	183–220	58	0.40
MGTG4B	4	12	129–153	60	0.15
RM067	4	8	90–106	58	0.75
ETH10	5	8	209–225	60	0.15
ETH152	5	9	193–211	58	0.12
ILSTS035	6	20	210–268	58	0.80
RM006	7	7	110–134	58	0.25
HEL9	8	11	147–169	52	0.03
ETH225	9	7	140–152	60	0.15
SPS113	10	13	133–157	60	0.15
BRRIBO	10	13	238–262	58	0.30
HEL13	11	6	185–195	52	0.03
TGLA345	12	7	112–142	58	0.05
CSSM036	14	11	162–188	60	0.08
SPS115	15	8	246–260	58	0.40
TGLA53	16	17	154–188	60	0.15
ETH185	17	11	221–245	66	0.03
TGLA227	18	11	77–97	58	0.35
ETH3	19	10	109–131	60	0.20
TGLA126	20	6	113–123	58	0.50
TGLA122	21	17	137–181	58	0.32
ETH131	21	26	142–171	58	0.50
BM2613	22	11	159–179	58	0.16
CYP21	23	29	183–222	58	0.20
BM1818	23	7	258–270	58	0.30
ILSTS065	24	10	126–146	58	0.08
HEL11	26	11	184–210	58	0.10
BM203	27	13	207–241	58	0.04

Microsatellites included in the FAO–MoDAD programme are given in bold.

Data analysis

Allele frequencies for all locus population combinations are obtained with the Fstat Program 2.9.3 (Goudet, 2001), while the number of population-specific alleles (Private-Alleles, PA) was counted manually. To test whether the populations were in Hardy–Weinberg equilibrium (HWE, Ho: *random union of gametes*) exact tests were performed using the program GENEPOP version 4.0 (Raymond and Rousset, 1995*b*). The non-biased estimates of the exact *P* value were obtained by Markov chain Monte Carlo developed by Guo and Thompson (1992). The excess or deficiency in heterozygosity for each locus in each population was analysed using a *U*-test (Rousset and Raymond, 1995). To test the between population differentiation, the null hypothesis was Ho: *the alleles were taken from the same distribution in all populations* and the test used to reject or accept the null hypothesis was the *G*-test (Raymond and Rousset, 1995*a*). The test was repeated for differentiation of populations, but considering population pairs. For all those tests, the Markov chain parameters chosen were: dememorization 100 00, batches 2 000 and 5 000 interactions per batch. For each population the level of significance was adjusted by a strict Bonferoni procedure for multiple comparisons, which allowed us to reduce type II errors (Weir, 1996).

The classical genetic diversity parameters were calculated by the GENETIX program, version 4.05.2 (Belkhir *et al.*, 1998). Thus, the average observed and unbiased expected heterozygosities within the breeds and the total and mean number of alleles were calculated per population, with a correction being made to these two last parameters with all the possible combinations of two animals (smaller size of an analysed sample) within each *ganadaria*. The Fstat program (2001) allowed us to calculate the inbreeding coefficient (F_{IS}), the gene diversity and the allelic richness.

The population structure was evaluated using the parameters of hierarchical *F*-statistics (F_{ST}, F_{IT}, F_{IS}) estimated according to those proposed by Weir and Cockerham (1984) and implemented in the Fstat program, version 2.9.3.2. (Goudet, 2001). The null hypothesis (Ho): *the*

estimates are not significantly different from zero was tested using permutations as proposed by Goudet (2001). To test the $F_{IS}(f)$, the alleles were exchanged between individuals within populations. To test the $F_{IT}(F)$, the alleles were exchanged between populations. Finally, to test the $F_{ST}(\theta)$ individuals were exchanged between populations. The F_{ST} parameter that measures the proportion of different alleles between all population pairs was also calculated.

To have an idea of the degree of genetic separation between the *ganadaria*s studied, the D_A genetic distances between all pairs of populations using the Populations program (Langella, 2002) were also calculated.

Multivariate analysis of correspondences

The graphical representation of genetic relationships among a group of individuals can be obtained through multivariate techniques, which can condense the variance of allele frequencies of loci analysed in a set of two, three or four synthetic variables. The factorial analyses of correspondences allowed us to see what the dispersion of the individuals in the space defined by the three major hypergeometric axes, depending on the variance of its allele frequencies and, thus, analyse whether or not there is some kind of substructure within a population and to see the genetic differences among all the individuals analysed. The analysis of correspondence was performed using the module AFC (Analyse Factorielle Correspondance) implemented by the GENETIX program (Belkhir *et al.*, 1998).

Analyse with the STRUCTURE Program

The structure of the Brava the Lide was also analysed using the STUCTURE Program, version 3.0 (Pritchard, Stephens and Donnelly, 2000) to estimate the number of population clusters (K), more likely among the nine *ganadarias* studied. Data were analysed using the Alpha and Lambda parameters defined by the default program. The definition of clusters was based on the admixture model and the assumption that allele frequencies were correlated between the breeds, as is convenient for closely related populations. To estimate the K value (number of population clusters inferred by the data), its value was made to vary between $K = 1$ and $K = 10$ and the program set to run with a Burn-in of 50 000 and a number of MCMC repetitions after burn-in of 200 000. It was empirically determined that these values for the size of the run were enough to ensure the convergence of the parameters to be estimated (Pritchard and Wen, 2003). For each value of K, ten runs were performed, the most likely value of K was determined by the highest average of the maximum likelihood of the data (Ln $P(D)$) with smaller variance. The STRUCTURE program was used to allocate individuals to their population of origin, using the strict Bayesian method implemented by the program. To determine the number of animals classified in each cluster a run was made with a longer burn-in of 100 000 and a number of repetitions of MCMC after a burn-in of 1 000 000 for the most likely value of K.

The percentage of individuals classified in each cluster was determined by considering the estimated proportion of the association of each individual genotype (Q) to each of the clusters. The percentage of subjects not included in their population of origin and misclassified in other cluster population was also calculated. Tests of individual allocation were also performed by the STRUCTURE program using *a priori* information about the source population of individuals, as the subjects were sampled from bull farmers with a specific breeding program and a specific reproductive program. The run had the same characteristics as before, with the K being equal to 9 because nine was the number of the sampled *ganadarias*.

Results

The diversity parameters are shown in Table 3 where one can observe that the average expected and observed heterozygosity was relatively low when compared with all other Portuguese cattle breeds (Mateus *et al.*, 2004; Ginja, Gama and Penedo, 2010). The expected heterozygosity ranged

Table 3. Summary of genetic diversity parameters, including, the observed and expected heterozygosity, total (TNA) and mean number (MNA) of alleles, mean (MNA_C) and total (TNA_C) number of alleles corrected for the size of the smaller sample, number of private alleles (PA), gene diversity and allelic richness, inbreeding coefficient (F_{IS}) and deviations from Hardy–Weinberg equilibrium (Dev. HWE) observed among the ganadarias studied.

Ganadaria	H. Exp.	H. Obs.	MNA	MNAc[1]	TNA	TNAc[1]	PA	Gene diversity	Allelic richness	F_{IS}	Dev. HWE
PA	0.63	0.61	3.6	2.3	109	68.0	6	0.63	2.41	0.037	0
JC	0.54	0.56	3.5	2.2	105	66.3	8	0.54	2.19	−0.138	0
JM	0.61	0.57	2.4	2.4	71	71.0	3	0.63	2.37	0.105	0
NC	0.53	0.53	2.3	2.1	70	62.0	0	0.53	2.06	−0.005	0
CD	0.59	0.62	2.3	2.3	69	69.0	0	0.58	2.30	0.015	0
PC	0.60	0.57	2.3	2.3	69	69.0	2	0.62	2.30	0.081	0
MG	0.58	0.56	3.9	2.3	119	68.2	7	0.58	2.26	0.026	0
VM	0.46	0.45	3.0	1.9	90	57.8	20	0.46	1.95	0.028	0
MV	0.53	0.51	3.0	2.1	91	63.0	14	0.53	2.12	0.042	0

[1]Average of all possible combinations of two animals within each *ganadaria*.

Table 4. D_A genetic distances above the diagonal F_{ST} between pairs below the diagonal.

Ganadarias	PA	JC	JM	NC	CD	PC	MG	VM	MV
PA	0	0.1316	0.2396	0.3454	0.2347	0.2307	**0.1303**	0.3906	0.3606
JC	0.0367	0	0.2310	0.3171	0.2236	0.2764	0.1519	0.4170	0.3881
JM	0.0268	0.0549	0	0.3696	0.2170	0.2457	0.2106	0.4823	0.3558
NC	0.1597†	0.1871†	0.1482‡	0	0.3841	0.3387	0.2982	0.5117	0.3414
CD	0.0160	0.0767	−0.0821	0.1689‡	0	0.3041	0.2277	0.4521	0.3892
PC	0.0101	0.1072	**−0.0601**	0.1074	0.0104	0	0.2558	**0.5243**	0.3748
MG	0.0489†	0.0672†	0.0478	0.1614†	0.0693	0.0851‡	0	0.4112	0.3462
VM	0.2512†	0.3132†	0.3148†	**0.3757**†	0.2954†	0.3439†	0.285†	0	0.4770
MV	0.2086†	0.2511†	0.1849†	0.2159†	0.2225†	0.1993†	0.2362†	0.3543†	0

Bold values indicates the maximum and minimum DA genetic distance and the highest and lowest F_{ST} values.
‡$P < 0.01$.
†$P < 0.001$.

from its highest value observed in *ganadaria* Palha (0.627) and the minimum value observed in *ganadaria* Vaz Monteiro (0.461). Regarding the observed heterozygosity, it ranged from a maximum of 0.617 observed in *ganadaria* Cabral D'Ascenção and a minimum of 0.448 observed in the *ganadaria* Vaz Monteiro. Incidentally, the *ganadaria* Vaz Monteiro was the one that systematically showed the lower variability (MNAc, TNAc, Gene Diversity and Allelic Richeness). The F_{IS} values were all close to zero, an indication that in the *ganadarias* studied, an excess or a deficiency in heterozygotes did not exist, which would be confirmed by tests carried out by the Genepop program regarding the excess and deficiency of heterozygotes, with all P values being not significant. All loci and population combinations are in HWE.

The D_A genetic distances and the coefficient of genetic differentiation (F_{ST}) are shown in Table 4. In general, all D_A genetic distances are relatively larger than those found among all populations of the Portuguese cattle (Mateus *et al.*, 2004; Mateus, 2008), indicative of the large genetic separation between the nine *ganadarias* studied. The largest D_A genetic distance was found between the *ganadarias* Vaz Monteiro and Paulo Caetano, while the shortest D_A distance was established between the pair Murteira Grave and Palha. In what concerns the coefficients of genetic differentiation F_{ST}, the maximum has been established between *ganadarias* Vaz Monteiro and Nuno Casquinha, while the minimum was found between the pair Jorge Mendes and Paul Caetano. Regarding the genetic differentiation among the nine *ganadarias* studied, the global test was significant at least for all loci population combinations, having the P value varied between zero and 0.00149, which allowed us to reject the null hypothesis: *the alleles are drawn from the same distribution in all populations*. But when the populations were considered in pairs (Table 4), the *ganadarias* that showed the highest degree of genetic differentiation were the *ganadarias* Vaz Monteiro and Mário Vinhas with both presenting highly significant P values for all other *ganadarias*. The other two *ganadarias* that showed considerable degree of genetic differentiation were the *ganadarias* Nuno Casquinha and Murteira Grave, being the first to obtain P values between very and highly significant for all other *ganadarias* except for *ganadaria* Paulo Caetano, while *ganadaria* Murteira Grave also presented P values between very and highly significant for all other *ganadarias* with the exception of *ganadarias* Jorge Mendes and Cabral D'Ascension.

Table 5. Indices of Wright of genetic differentiation for the ganadarias studied.

Locus	*f*	*F*	*θ*
BM1818	0.200	0.297	0.121†
BRRIBO	0.020	0.161	0.143†
SPS115	0.200	0.313	0.142
INRA23	0.033	0.257	0.231†
CYP21	−0.085	0.18‡	0.244†
ETH152	0.099	0.283	0.205†
BM1824	0.149	0.482†	0.391†
ETH131	0.198	0.337†	0.173†
TGLA122	0.019	0.402†	0.391†
BM2113	−0.256	−0.040	0.172†
RM067	0.137	0.42†	0.328†
TGLA227	0.026	0.199‡	0.177†
ETH3	−0.151	0.059	0.182†
ETH225	0.007	0.200	0.194†
TGLA53	−0.095	0.123	0.199†
MGTG4B	−0.140	0.082	0.195†
SPS113	−0.040	0.152	0.185†
ETH10	0.051	0.092	0.044
CSSM36	0.131	0.414†	0.325†
ILSTS035	0.319	0.416†	0.143†
BM2613	0.059	0.067	0.009
ILSTS065	−0.041	0.175	0.208†
RM006	−0.030	0.257	0.279†
BM203	−0.082	0.157	0.221†
HEL11	0.021	0.211	0.195†
TGLA345	−0.043	0.112	0.149
TGLA126	−0.001	0.109	0.109‡
ETH185	−0.085	0.165	0.23†
HEL13	−0.051	0.372	0.402†
HEL9	0.011	0.100	0.091
Média	0.017	0.217†	0.204†

†$P < 0.001$.
‡$P < 0.05$.

The Wright estimators of genetic differentiation $F_{IS}(f)$ $F_{IT}(F)$ and $F_{ST}(\theta)$ are presented in Table 5. None of the estimates of the inbreeding coefficient f was significantly different from zero. The levels of the genetic differentiation θ obtained by locus were relatively high and ranged between 0.009 and 0.402 for locus BM2613 and HEL13, respectively. For all the loci analysed, estimates of θ were highly significant different from zero ($P < 0.001$) except for the loci SPS115, ETH10, BM2613 and TGLA345, HEL9. The locus TGLA126 was only significantly ($P < 0.05$) different from zero. The average proportion of genetic variation explained by differences among *ganadarias* was 20.4 percent, which is considerably high when compared with the variation observed among all populations of the Portuguese cattle (Mateus *et al.*, 2004; Mateus, 2008; Ginja Gama and Penedo, 2010). The remaining variation was attributed to individual differences existing within each of the studied *ganadarias*.

The outcomes of the factorial analysis of correspondence to the "Brava de Lide" breed is shown in Figure 1. As can be seen, the "Brava de Lide" breed shows a clear substructure among the individuals, which justified their grouping into four well-defined clusters. It was interesting to note that the cluster at the bottom left of Figure 1 was exclusively composed by animals sampled in *ganadaria* Vaz Monteiro, considered by the bullfighting experts as the most Portuguese of all bull farmers in the country. In turn, the cluster located in the upper right side of Figure 1 consists of animals sampled in *ganadaria* Mário Vinhas e Herdeiros de Manuel Vinhas and the cluster formed in the middle upper side comprehends two animals sampled in g*anadaria* Nuno Casquinha. All other animals are grouped in the fourth cluster that appears at the bottom right side of the space defined by the three main axes of the FCA.

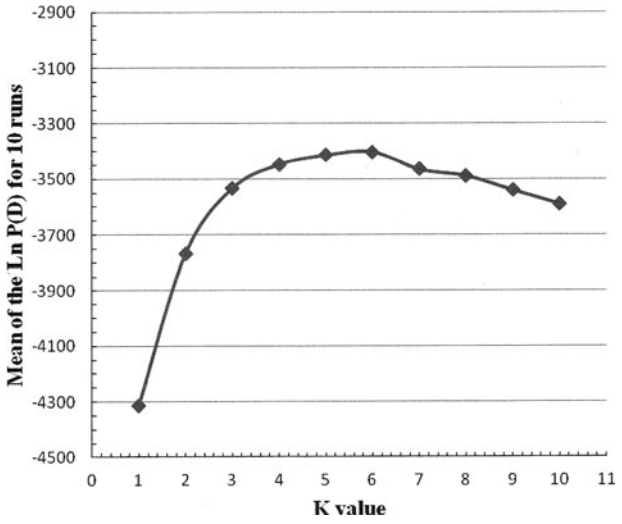

Figure 2. Average value of Ln $P(D)$ for ten runs without information regarding the source populations of the animals.

Runs originally made with the STRUCTURE program with no information regarding the source populations of the animals allowed us to define the most probable value of K and identify the population clusters that best explain the partitioning of all data analysed. The Ln $P(D)$ increased as the K values increased, but tended to its maximum value when K was equal to 6, followed by a sharp decline, which remained constant for the remaining values of K tested (Figure 2). The results of the longest run performed with the STRUCTURE program without information on the population of origin of animals with $K = 6$ is summarized in Table 6. When the assignment to a cluster was defined as the most likely value of the occurrence of its genotype in this cluster (Q_{max}), the percentage of correctly classified individuals in their population of origin

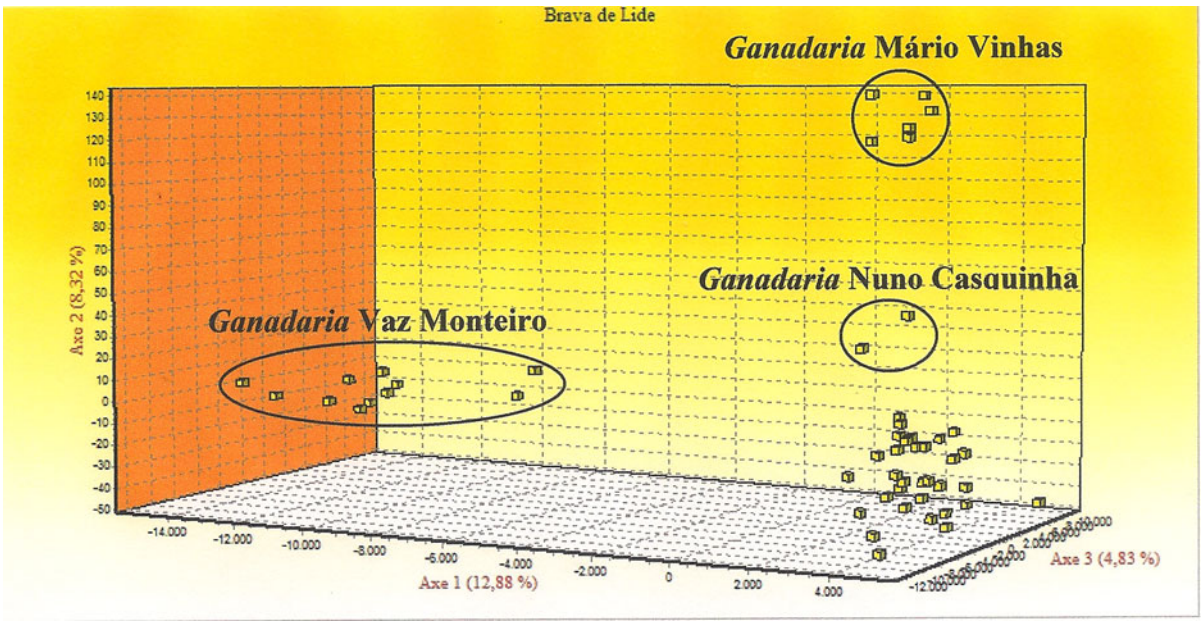

Figure 1. Factorial correspondence analysis carried out on the "Brava de Lide" Breed.

Table 6. Allocation of individuals for the longest run with STRUCTURE without the information regarding the source population of the animals and $K = 6$.

Ganadarias	Q_{max} (%)	$Q \geq 0.8$ (%)	$Q \geq 0.9$ (%)	Mean (%)
Palha (PL)	33	17	17	22
Jorge Carvalho (JC)	86	57	57	67
Nuno Casquinha (NC)	100	100	67	89
Murteira Grave (MG)	83	67	42	64
Vaz Monteiro (VM)	100	91	82	91
Mário Vinhas (MV)	100	100	83	94
Mean	84	72	58	71

Table 8. Allocation of individuals for the longest run with STRUCTURE regarding the information about the source population of the animals and $K = 9$.

Ganadarias	Q_{max} (%)	$Q \geq 0.8$ (%)	$Q \geq 0.9$ (%)	Mean (%)
Palha (PL)	67	50	33	50
Jorge Carvalho (JC)	86	71	71	76
Jorge Mendes (JM)	100	100	100	100
Nuno Casquinha (NC)	100	100	100	100
Cabral D'Ascenção (CD)	100	100	100	100
Paulo Caetano (PC)	100	100	100	100
Murteira Grave (MG)	100	92	83	92
Vaz Monteiro (VM)	100	91	82	91
Mário Vinhas (MV)	100	83	83	89
Mean	95	87	84	89

ranged from 33 percent in *ganadaria* Palha to 100 percent in *ganadaria* Nuno Casquinha, Vaz Monteiro e Mário Vinhas. The other *ganadarias* to be identified by the program as having distinct populations were the *ganadarias* Jorge Carvalho and Murteira Grave. Table 7 summarizes the individuals correctly classified and misclassified in other clusters. As can be seen, the *ganadaria* Palha was the one with more misclassified individuals, three of them were classified as belonging to *ganadaria* Jorge Carvalho and one as belonging to *ganadaria* Murteira Grave. All the animals of the *ganadaria* Nuno Casquinha Vaz Monetiro e Mário Vinhas are correctly classified in their respective population of origin and with high Q values.

When the allocation of individuals was performed with the STRUCTURE program with prior knowledge of the source population of the animals and $K = 9$, it was possible to differentiate each of the *ganadarias* studied (Table 8). Approximately 95.0 percent of the animals were assigned to their respective source populations (Table 8). Only three individuals were incorrectly classified, two animals of the *ganadaria* Palha were classified as belonging to *ganadaria* Jorge Carvalho and one animal of the *ganadaria* Jorge Carvalho was incorrectly classified as belonging to *ganadaria* Cabral D'Ascenção (results not shown). All the other individuals were correctly classified in their source population. It is important to note that all animals belonging to the *ganadarias* not recognized by the STRUCTURE program as being distinct populations, respectively, the *ganadarias* Jorge Mendes, Cabral D'Ascension and Paulo Caetano, were all classified in their source population of origin with huge odds (e.g. >0.9). This could mean that if the sample in these *ganadarias* contemplates more animals these *ganadarias* could be considered as distinct populations when we run the STRUCTURE Program to find the most probable number of distinct populations among our data.

Discussion and conclusions

The low patterns of genetic diversity are characteristic of a breed that is subdivided into castes well defined in genetic terms. No other Portuguese breed achieves a level of genetic differentiation as high as that seen in the Brava Lide breed. 20.4 percent of the genetic variation was due to differences between the *ganadarias*, but otherwise the diversity within each *ganadaria* is considerably low as evidenced by indexes of genetic diversity presented in this study. The high genetic distances D_A also seem to point to a high degree of genetic isolation among the different *ganadarias* studied in this work. In particular, the *ganadaria* that genetically moves further away from all the others *ganadarias* is the *ganadaria* Vaz Monteiro with an average of D_A genetic distance of 0.458 and an

Table 7. Individuals correctly classified and misclassified in other clusters made with the STRUCTURE program without knowing the source population of the animals and with $K = 6$.

	PL	JC	JM	NC	CDA	PC	MG	VM	MV	N	%
Palha (PL)	**2**	3	0	0	0	0	1	0	0	6	33
Jorge Carvalho (JC)	0	**6**	0	1	0	0	0	0	0	7	86
Jorge Mendes (JM)	1	1	**0**	0	0	0	0	0	0	2	0
Nuno Casquinha (NC)	0	0	0	**3**	0	0	0	0	0	3	100
Cabral D'Ascenção (CD)	1	1	0	0	**0**	0	0	0	0	2	0
Paulo Caetano (PC)	1	1	0	0	0	**0**	0	0	0	2	0
Murteira Grave (MG)	2	0	0	0	0	0	**10**	0	0	12	83
Vaz Monteiro (VM)	0	0	0	0	0	0	0	**11**	0	11	100
Mário Vinhas (MV)	0	0	0	0	0	0	0	0	**6**	6	100

Bold values indicates the animals correctly classified in his respective cluster.

average coefficient of genetic differentiation F_{ST} of 0.317, also being the one with more private alleles (20). Let us remember here that the *ganadaria* Vaz Monteiro is considered by all breeders of "Brava de Lide" as the most Portuguese of all *ganadarias* existing in Portugal, so its genetic separation from all other *ganadarias* was somehow expected.

An unexpected result in this study was the zero deviations from HWE, unlike the results reported by Mateus *et al.* (2004), where the breed "Brava de Lide" was the one that showed more deviations (five deviations) to the HWE. Maybe the deviations found in that study were due to the substructure characteristic of this breed and when this substructure was dismantled in this work, it resulted in zero deviations from HWE.

As we can see, there is a clear substructure within the breed "Brava de Lide", which resulted in obtaining the four clusters achieved by FCA and the six clusters obtained with STRUCTURE. A similar result was presented by Cañón *el al.* (2007), who obtained 31 different clusters for the 77 *ganadarias* covered by their study, having the genetic variability among the studied *ganadarias* reached 20 percent, a similar result to that obtained in the present study, despite the much smaller number of *ganadarias* covered, which only confirms the enormous genetic diversity found among the various *ganadarias* constituting this cattle breed.

In this study, and using the STRUCTURE program, we were able to identify six of the nine *ganadarias* used, which is a considerable number. But when we run the STRUCTURE program knowing the source populations of the animals, we were able to identify all the nine *ganadarias* studied. The variation among groups was 20,4 (F_{ST} = 0.204) and for this level of differentiation among the populations we believe that all *ganadarias* studied would be well differentiated, as was proven when the STRUCTURE program was run with the *a priori* knowledge of the source populations of the animals. Notice that the animals of those *ganadarias* not recognized by the STRUCTURE program are classified with high percentages (>0.9) in their populations of origin when the program was run with the knowledge of the source populations of animals. These results were not at all unexpected if we consider that this breed began to be selected during the eighteenth century (Felius, 1995). As a result of the selection process and creation schemes, the breed gave rise to a small number of well-differentiated lines or castes, traditionally raised on farms, where the reproductive isolation was imposed. Strategies for establishment of this breed also favoured the prevalence of breeding or breeding lines, selected for behavioural traits (e.g. aggressiveness and nobility), which contributed to an increase in inbreeding and a reduction in heterozygosity. This farming system led to a divergence between farms and produced several subpopulations among which it is even possible to observe morphological differences. Regarding the results achieved in this study, the low levels of within genetic diversity in contrast with the high level of genetic differentiation among all the *ganadarias* tested in the present work seems to point at genetically different populations where the reproductive isolation is working well and it is, therefore, this isolation the determining factor of the substructure found in this cattle breed. The change of animals between the *ganadaria* Jorge Carvalho and Palha was expected because both shared breeders of the same origins (Lucas, personal communication). The *ganadarias* better differentiated genetically are, without any doubt, *ganadarias* Nuno Casquinha, Mário Vinhas and *ganadaria* Vaz Monteiro. Note the fact that only these *ganadarias* include all their animals in the same cluster, when the STRUCTURE Program was run without *a priori* knowledge of the source populations of the animals. The *ganadaria* Mário Vinhas e Heirdeiros de Manuel Vinhas because its caste is pure Santacoloma, one of the main Spanish castes, although lately have entered reproducers Los Caminos and Buendia. The *ganadaria* Vaz Monteiro, the oldest in Portugal, was incorporated in its beginning in 1843, with cows and breeders of the pure Portuguese caste, coming from the Marquês de Vagos and has been kept in the same family without the introduction of any other blood, constituting a unique caste that must be preserved, which is the true offspring of the Portuguese "Brava de Lide" breed. Mateus (2008), when proceeding to the classification of animals of Portuguese cattle breeds in their populations of origin using the STRUCTURE program, systematically classified the four animals of "Brava de Lide" breed sampled in the *ganadaria* Vaz Monteiro in another population, running the program either with or without the knowledge of their source populations. Therefore, special attention should be given to animals of this *ganadaria* if we do not want to miss a valuable genetic resource, which is the true Portuguese cattle breed "Brava de Lide". We also believe that we have confirmed the importance of preserving these genetic resources to enrich the animal genetic resources of the country, due to the great variability between *ganadarias*.

Acknowledgements

This work was supported by the Fundação para a Ciência e Tecnologia (FCT), Project: PRAXIS XXI 3/3.2/CA/2005/95. J. C. Mateus was supported by a Fellowship of the FCT ref: PRAXIS XXI BD/18354/98.

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Animal Genetic Resources, 2014, 55, 19–27. © Food and Agriculture Organization of the United Nations, 2014
doi:10.1017/S2078633614000277

Traditional breeding practices and trait preferences of cattle farmers in Gamo Goffa Zone, Southern Ethiopia

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Summary
The study was conducted in Gamo Goffa Zone of Southern Ethiopia to characterize traditional cattle breeding practices and cattle trait preferences of the Gamo Highland and Gamo Lowland cattle types. Data collected through group discussions and individual interviews were synthesized and summarized using descriptive statistics. Indigenous cattle in the study area provide multiple functions, are well adapted to their production environments, and managed under traditional and subsistent modes of production. Farmers' cattle trait preferences slightly differ across highland and lowland sites. Whereas lowland farmers prefer carcass yield and traction capacity, cattle farmers in highland areas give more weight to adaptation, milk production and manure contributions. Common breeding system in all sites was pure breeding, although very few farmers residing in mid and highland areas exercise crossbreeding with introduced Holstein Friesian bulls for dairy improvement. The main reported selection criteria of farmers for breeding their animals were body size and conformation, milk production, fertility and breeding history of animals. Cattle breeding and management practices of the study area are traditional and low input.

Keywords: *breeding practices, cattle, farmers' trait preferences, Southern Ethiopia*

Résumé
El estudio fue llevado a cabo en la región de Gamo-Gofa del Sur de Etiopía con el fin de caracterizar las prácticas tradicionales de selección y los rasgos preferidos en las variedades bovinas Gamo de las Tierras Altas y Gamo de las Tierras Bajas. Se sintetizó y resumió la información, obtenida mediante debates de grupo y entrevistas individuales, con estadísticos descriptivos. El ganado bovino autóctono del área de estudio desempeña múltiples funciones, está bien adaptado a sus entornos de producción y es manejado según modelos de producción tradicionales y de subsistencia. Los rasgos preferidos en los animales por los ganaderos difirieron ligeramente entre la zona de las Tierras Altas y la de las Tierras Bajas. Mientras que los ganaderos de las Tierras Bajas prefieren el rendimiento a la canal y la capacidad de tracción, los ganaderos de las Tierras Altas dan mayor peso a la adaptación, la producción lechera y el aporte de estiércol. En todas las zonas, lo más habitual fue la cría en pureza, habiendo también unos pocos ganaderos afincados en áreas de altitud media y alta que cruzan el ganado con toros Frisones Holstein para mejorar el rendimiento lechero. Los principales criterios de selección identificados fueron el tamaño corporal y la conformación, la producción lechera, la fertilidad y la ascendencia de los animales. La selección del ganado y las técnicas de manejo siguieron un modelo tradicional y de bajos insumos en el área de estudio.

Mots-clés: *bovins, caractères préférés par les éleveurs, méthodes de sélection, Sud de l'Éthiopie*

Resumen
L'étude a été menée dans la région du Gamu-Gofa dans le Sud de l'Éthiopie pour caractériser les méthodes de sélection et les caractères préférés chez les variétés bovines Gamu des Hautes Terres et Gamu des Terres Basses. Les données obtenues au moyen de groupes de discussion et d'interviews individuels ont été synthétisées et résumées avec des statistiques descriptives. Les bovins autochtones de la région d'étude remplissent de nombreuses fonctions, sont bien adaptés aux systèmes de production et sont élevés selon des modes de production traditionnels et de subsistance. Les caractères préférés par les éleveurs n'ont pas été tout à fait les mêmes dans les Hautes Terres et les Terres Basses. Alors que les éleveurs des Terres Basses préfèrent le rendement de la carcasse et la capacité de trait, les éleveurs des Hautes Terres donnent plus d'importance à l'adaptation, la production laitière et l'apport de fumier. Dans toutes les zones, l'élevage en race pure a été le système le plus commun. Pourtant, quelques éleveurs résidant dans des zones à altitude moyenne et élevée font du croisement avec des taureaux Holstein pour améliorer le rendement laitier. Les principaux critères de sélection identifiés ont été la taille corporelle et la conformation, la production laitière, la fertilité et l'ascendance des animaux. La sélection des bovins et les pratiques d'élevage dans la région d'étude ont été traditionnelles et à faible intensité d'intrants.

Palabras clave: *ganado bovino, prácticas de selección, rasgos preferidos por los ganaderos, Sur de Etiopía*

Submitted 16 February 2014; accepted 28 May 2014

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Introduction

The urgent need to increase livestock production in sub-Saharan Africa in order to keep pace with expected increases in demand for meat and milk is very topical (Delgado *et al.*, 1999a, b). Breed improvement provides key entry points for increasing production and productivity in cattle populations (Ouma, 2005). The functions required of indigenous cattle influence the selection of traits for genetic improvement. Knowledge of traditional animal breeding practices and techniques is important to develop sustainable genetic improvement schemes under smallholder settings (Wuletaw, Ayalew and Sölkner, 2006). The issue, however, is how to design sustainable breeding schemes for indigenous breeds under inherent tropical conditions (Rege *et al.*, 2011) where resources are limited, and feed availability as well as quality vary greatly depending on the breed type of animals, geographical location and season. Well-designed breeding programmes including crossbreeding schemes enable effective utilization of desirable characteristics of the breeds or strains involved (López-Villalobos, 1998).

In developing countries, such as Ethiopia, where the majority of indigenous cattle are raised for multipurpose production and service functions, developing breeding programmes entails the selection of multiple priority traits and their precise definition (Haile *et al.*, 2011). Regardless of the scale of the operation, designing of genetic improvement programmes involves careful analysis of the short- and long-term objectives for improvement, as well as the socio-economic and environmental contexts in which the programmes are to operate (FAO, 2007; p215–241). Breeding objectives need to be defined in the context of the existing production conditions, applicable legal frameworks and current relevant market relations (Belihu, 2002). Traditional breeding practices, such as controlled mating, selection of breeding males or keeping pedigree information determine the extent to which expressed breeding goals can be achieved (Bittner *et al.*, 2000).

In developing countries, many important functions of livestock are embedded in traits that are not traded in the market (Scarpa *et al.*, 2003). These important traits can be revealed through surveys of farmers' trait preferences and assessment of livestock production systems. Only a few priority traits that can help optimize the overall gain should be considered as objective traits in order to design simple but effective breeding plans for easy implementation under farmers' conditions. Involving livestock producers in the identification of these traits and incorporating the identified traits in the design of breeding plans encourage them to actively participate in their implementation (Duguma *et al.*, 2010). Elucidation of objective traits using the tools with active involvement of producers can result in appropriate livestock genetic improvement that truly reflects owners' preferences (Duguma *et al.*, 2010). On that basis, as part of a larger study (Chebo, 2012), this study set out to survey traditional breeding practices of cattle keepers of Gamo Gofa Zone in Southern Ethiopia to reveal farmers' trait preferences and lay the ground for design of appropriate improvement schemes.

Materials and methods

The study area

This study follows an earlier study on phenotypic characterization of the Gamo Highland and Gamo Lowland cattle in Gamo Goffa Zone of Southern Ethiopia (Chebo, 2012; Chebo, Ayalew and Wuletaw, 2013). The study area (Figure 1) is described in detail in the earlier report (Chebo, Ayalew and Wuletaw, 2013). Topography of the study area is characterized by undulating landscapes and variable climate. The total human population in the Zone was reported recently to be about 1.6 million (CSA, 2008/09) with an average population density of 80 inhabitants per km^2. The estimated livestock population in 2010 was 1.44 million cattle, 800 thousand sheep, 337 thousand goats, 128 thousand equines and 1.1 million chickens (CSA, 2010/11).

Farming practices of the study area are mainly mixed crop–livestock type, with crops being more dominant in the higher altitude areas and livestock being more significant in lowland areas. In the highlands, cattle provide traction power for ploughing crop fields and manure as fertilizer, whereas crop harvest leftover and residue is used to feed livestock. Sheep are important sources of cash; mules are used as pack animals. In the lowland areas, cattle are regarded as the most important livestock asset followed by goats, poultry and donkeys, and provide milk, meat, cash, traction power and socio-economic values (Chebo, 2012).

Sampling and data collection

Based on information generated through single rapid exploratory field visits of the Zone coupled with key informant interviews and review of available secondary information, the 15 districts were categorized into three groups matching the highlands, mid-altitude areas and the lowland areas of the study area. Three sample districts (Bonke, Chencha and Boreda) from highlands and two districts (Arba-Minch Zuria and Mirab-Abaya) from lowlands were purposively selected for actual data collection, by taking into account the dominant agro-ecological zone of the districts, local knowledge on cattle population types and size of the cattle populations. As reported earlier (Chebo, Ayalew and Wuletaw, 2013), cattle populations of the mid-altitude areas did not show distinct features that make them different from those of the highland and lowland areas and instead appeared to have intermediate features of the other two types. Therefore, samples were not taken from mid-altitude districts.

Sampling of study households took account of early indications noted during the rapid survey and key informant

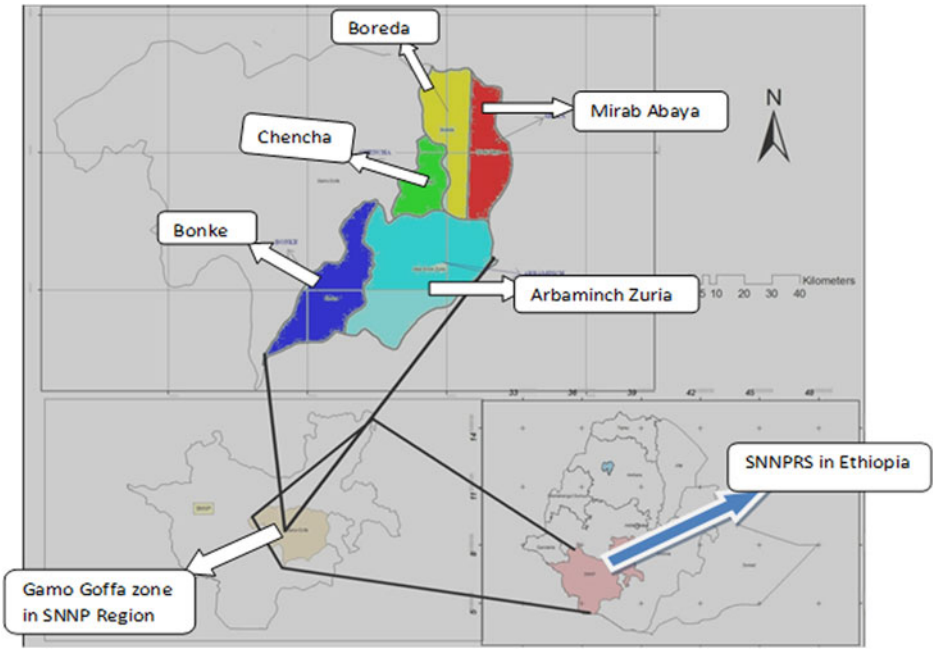

Figure 1. Location of the study area.

interviews that cattle keepers attach high value to adaptation to local environment and milk production. From each of the five study districts, cattle raising villages were randomly selected, and in each of these only cattle farmers who at the time of the survey were maintaining lactating cows were purposively selected for formal interviews using semi-structured questionnaires. These are a subset of sample herds selected for phenotypic characterization of the cattle population (Table 1). The questionnaires covered socio-economic characteristic of the sample households, cattle husbandry practices, herd structure and dynamics, cattle trait preferences, breed choices, breeding practices and constraints in cattle production. From 40 to 49 questionnaires per district were completed. Local agricultural extension staff who speak the local language were trained together and administered the questionnaires. In addition, within each district two focus group discussions involving 8–12 selected key informant farmers per session were facilitated by the researcher in the presence of the local agricultural extension officers. The topics for discussion were cattle trait preferences of the locality, practices for selection of replacement breeding stock, level of control of cattle breeding processes and known undesirable characteristics of cattle.

Table 1. Sample households and group discussions by study districts.

Sites	Households involved	Focus group discussions
Chencha	41	2
Bonke	40	2
Boreda	40	2
Mirab Abaya	49	2
Arbaminch Zuria	45	2
Total	215	10

Statistical analysis

Data were transcribed into computer for checking and processing using MSExcel© before detailed analysis using descriptive statistics of SAS (2002) version 9.0.

Results and discussion

Herd size and sex and age structure

The mean cattle herd size per sample district ranged from 3.3 in Chencha to 9.8 in Mirab Abaya, with an overall mean for the study area of 6.83 cattle per household (Table 2). This average is similar to that of the 7.4 cattle/household reported by Tassew and Seifu (2009) for Mecha district of Amhara Region, an agrarian district. It is also within ranges of mean values of 5–14 cattle/household reported by Tadesse (2005) for South and North Wollo zones of Amhara Region and 2.82–7.44 cattle/household reported by Wuletaw (2004) from highland districts of South and North Gondar zones, but much lower than the 44.76 cattle/household for largely pastoral lowland district. The overall average cattle holding is higher than 5.2 heads per household reported by Taye, Ayalew and Hedge (2007) for Sheko breed in Benchi Maji zone of Southern Ethiopia. As presented in Table 2, the proportion in the herd of female cattle ranged from 69.8 to 72.9 percent, whereas that of males ranged from 27.07 to 30.2 percent. A larger proportion of the males are oxen, followed by breeding bulls. Commonly, young bulls not

Table 2. Age and sex structure (%) of sample cattle herds by breed type and site.

Sex and age category	Highland sites			Lowland sites	
	Bonke	Chencha	Boreda	M/Abaya	A/Zuria
Sample herds	40	41	40	49	45
Total males	30.2	27.07	29.0	30.0	29.7
Oxen	39.72	30.56	47.14	52.3	58.14
Breeding bulls (>3 years)	23.29	30.56	21.43	21.2	17.0
Young males (1–3 years)	17.8	13.89	18.57	14.4	13.2
Male calves (<1 year)	19.18	27.8	15.71	11.3	11.6
Total females	69.8	72.93	71.0	70.0	70.3
Cow-total	55.30	61.86	57.9	64.1	67.0
Lactating	22.0	23.71	17.54	18.9	14.4
Dry	34.3	38.14	40.35	45.6	52.6
Heifers	20.45	18.56	24.5	22.6	22.5
Female calves	15.9	11.56	14.0	13.2	10.4
Male:female ratio	1:2.3	1:2.8	1:2.6	1:2.2	1:2.4
Breeding male:female	1: 2.2	1:2.0	1:2.6	1:3	1:4
Average holding	5.1	3.3	6.1	9.8	9.03

needed for breeding are either castrated or sold out by about sexual maturity. The overall adult male to female ratio ranged from two to three females per one breeding male for highland and two to four breeding females to one breeding male for lowland sites (Table 3). The average breeding male-to-female ratio indicated lower number of bulls per cow available compared with the 1:1.97 reported by Mukasa-Mugerwa (1989) for Ethiopian highlands, but higher than that of 1:1.02 to 1:1.07 reported by Getachew (2006) for Awi, East and West Gojjam zones and 1:1.04 to 1:1.73 reported by Tadesse (2005) for South and North Wollo zones.

Based on recalls of cattle herd owners, annual herd dynamics within sample cattle herds was calculated (Table 3). During the reference year, there was a slight (1.56 percent) net increase in cattle numbers. Overall mortality during the year was 7.2 percent, due mainly to very high levels of especially male but also female calf mortality.

The proportion of herds disposed of in the form of sale, gift and transfer (altogether referred to in Table 3 as off-take) was 8 percent overall, but 16 percent among males and only 4.4 percent for females. On the other hand, farmers purchased 45 more animals than they sold during the year, and hence net production was actually negative during the reference year. It was noted that in the study area animals are sold just to meet immediate cash needs, i.e. distress sales, rather than as means of continual income.

Functions of indigenous cattle

The major functions of cattle of the highlands of the study area are manure, milk, income generation (albeit small and intermittent), traction power, meat and social values in that order of importance. In the lowlands, on other hand, manure does not appear on the list of main functions, whereas milk, traction power, income generation, meat and social value are identified as more or less equally important (Table 4).

Trait preferences

Adaptation to local environment (i.e. variability in weather, type and seasonality of feed supply as well as disease

Table 3. Annual cattle herd dynamics (frequency and percentages) of the study area reconstructed from recalls of herd owners.

Sex and age category	Beginning of the year		Calved		Died		Off-take		Purchased		Total end of the year	
	n	%	*n*	%	*N*	%	*n*	%	*n*	%	*n*	%
Female total	959	68.4	192	20.0	41	4.3	42	4.4	83	8.7	982	68.9
Cow	643	67.0	192	29.9	15	2.3	14	2.2	37	5.8	636	64.8
Heifer	227	23.7	–		7	3.1	28	12.3	43	18.9	217	22.1
Female calves	89	9.3	–		19	21.3	–	0.0	3	3.4	129	13.1
Male total	444	31.6	0	0.0	60	13.5	71	16.0	75	16.9	443	31.1
Oxen	220	49.5	–		12	5.5	26	11.8	37	16.8	214	48.3
Breeding bulls	102	23.0	–		7	6.9	14	13.7	10	9.8	91	20.5
Young male	90	20.3	–		10	11.1	26	28.9	17	18.9	78	17.6
Male calves	32	7.2	–		31	96.9	5	15.6	11	34.4	60	13.5
Total	1403		192		101	7.2	113	8.05	158	11.3	1425	

Table 4. Frequency (percent in brackets) of reported functions of cattle by cattle type and district.

Reported functions	Highland Zebu type			Lowland Zebu type	
	Bonke	Chencha	Boreda	A/Zuria	M/Abaya
N	40	41	40	45	49
Traction	27 (67.5%)	24 (58.5%)	31 (77.5%)	40 (88.9%)	40 (81.6%)
Milk	36 (90%)	37 (90.2%)	40 (100%)	40 (88.9%)	40 (81.6%)
Manure	40 (100%)	40 (97.6%)	40 (100%)	–	–
Income generation	32 (80%)	25 (61.0%)	28 (70%)	40 (89.9%)	40 (81.6%)
Beef	16 (40%)	13 (31.7%)	17 (42.5%)	34 (75.6%)	36 (73.5%)
Social values	12 (30%)	9 (22.0%)	15 (37.5%)	27 (60.0%)	39 (79.6%)

and parasite burden) was the most preferred trait (45.6 percent) of cattle in all five sites, followed by milk production (23 percent) and traction capacity (17.7 percent) (Table 5). Reflecting the low emphasis placed on the traits, carcass yield did not appear on the list of preferred traits in the highland sites, as was docility in the lowlands sites. Getachew (2006) reported a similar preference for adaptation traits of local cattle of Eastern and Western Gojjam Zones of central Ethiopia. Wuletaw (2004) also reported a similar but much wider variation in cattle trait references in an adjacent area in Northwestern Ethiopia, ranging from 20 to 96 percent for adaptation and from 0 to 50 percent for milk production. It is interesting to note that despite the long-established and common tradition of using cattle for traction in the study areas of all the three studies, traction did not rank high on the list of preferred traits. One possible explanation for this is the worsening feed scarcity especially during the long dry seasons as crop fields encroach into communal pastures. Under these circumstances, cattle keepers place higher importance to their adaptation to local environment to continue to produce and reproduce, rather than for instance to body size and conformation.

Criteria for selecting breeding animals

Focus group discussions revealed that cattle keepers select breeding animals mainly for milk production, reproduction, body conformation and coat colour. Milk production capacity is assessed based on production history (of animal and its parents), large navel flap, medium size of dewlap, large udder, well-placed teats and thin slender neck. Farmers give more weight to known milk production levels than to body size of the cow.

Reported criteria for identifying better reproducing cows include displaying clear signs of heat, attainment of early sexual maturity, early age at first calving, short calving interval and good milk production. Animals with history of abortion are selected against. Bulls with long prepuce and good libido during mating are considered good for reproduction.

Body conformation traits considered for selecting replacement breeding heifers include size and attachment of the udder, teat placement, size of the navel flap and thin legs.

Black coat colour of cattle is a preferred attribute in the highland areas which have cool and seasonally cold weather. In contrast, farmers of lowlands select against cattle with black coat colour, even when milk production and body size are much better. It was also noted that local market prices are strongly influenced by coat colour.

Mating practices

Except for some areas where cross-breeding with Holstein Friesians has been promoted since the 1990s through artificial insemination and bull services, technical services in cattle breeding from local agricultural extension offices has been very limited. Mating of cattle is mostly uncontrolled and free. This is similar to the report by Wuletaw (2004) and Getachew (2006) from Northwestern Ethiopia. Cited reasons for uncontrolled mating are lack of awareness of possible options (60.4 percent), shortage of grazing land (32 percent), shortage of labour and scarcity of breeding

Table 5. Respondents' reported cattle trait preferences (per cent).

Preferred cattle traits	Highland sites			Lowland sites		Overall
	Bonke (*N* = 40)	Chencha (*N* = 41)	Boreda (*N* = 40)	A/Zuria (*N* = 44)	M/Abaya (*N* = 49)	
Adaptation	50.8	55.5	48.3	40.5	32.8	45.57
Milk production	22.0	22.4	23.3	26.5	20.6	22.96
Traction capacity	13.2	12.8	26.4	18.4	17.7	17.70
Conformation and size	6.5	8.2	–	21.6	18.0	13.57
Reproduction	11.25	–	11.5	10.6	12.7	11.12
Carcass yield	–	–	–	17.6	22.0	19.80
Docility	14.4	10.9	13.2	–	–	12.83

bulls (7.2 percent). Some farmers in the highland areas are aware of the consequences of mating their cows with unknown bulls, and attempt to control mating mainly to ensure that cows give birth during the wet season when feed is relatively more abundant. Of those who practice controlled mating, including artificial insemination, 23.6 percent of respondents mate cows soon after detecting signs of heat, 28.7 percent within half a day after the first sign of heat, 36.5 percent within a day and the rest 11.2 percent take cows to mate after 2 days. Some of these farmers practice tethered feeding of the cows and reported that these cows manifest clear physical signs when they are in heat, such as restlessness, bellowing, mucus discharges and swelling of the vulva, lifting up of the tail, reduction in milk yield and frequent urination.

Reported sources of breeding bull are own herd (21 percent), neighbour (52 percent), relatives (14 percent) and sometimes paid bull service (13 percent). Purposeful rearing and management of breeding bulls is not a common practice in the study area.

Feeds and feeding management

Communal and private unimproved natural pastures are the major source of animal feed in the study area (Table 6). Farmers indicated that more and more pasture land is being converted into cropping fields. Communal pastures are more common in the lowland areas, and often groups of cattle herds are tended together on communal lands known locally as "*wude*".

During the cropping season, especially in the highlands, cattle are fed tethered on the fringes of crop fields; both grazing lands and labour are scarcer during the cropping season than the dry season. Farmers say tethering allows better control of animals from otherwise straying into gardens.

Throughout the study area, selected cattle are supplemented with a variety of feeds such as spent grain of local brew (*Atella*), natural mineral leak (*bolle*), leaf of a local staple known as *Enset* (*Ensete Ventricosum*), bamboo leaf, vines and leaves of sweet potato and leftover grains. *Enset* leaves are fed to all classes of cattle especially during the dry season. Farmers believe *Enset* is particularly good for lactating cows. Improved forages such as elephant grass, vetch, clover, tree Lucerne, *Sesbania* and *Desmodium* species are grown and used by a few model farmers in the highland districts. Feed conservation is commonly practiced in the form of crop residues (cereal straws) and hay in both highlands and lowlands areas. During the traction season, oxen are supplemented with barley and wheat grain, natural mineral leak, *Enset*, straw of barley and wheat and even raw sliced potato, signifying the importance they attach to farm traction. Fattening cattle and lactating cows are also fed purchased agro-industrial by-products such as mill run as well as kitchen residue.

Water is often freely available from streams and springs. During the peak dry season herders take cattle to river watering points two to three times per day.

Housing

Two types of cattle housing practices were observed in the study area. In the cool highland areas cattle are sheltered in houses, mostly in a sector of the family house, but in the warmer lowland areas cattle are kept overnight in simple fenced open kraals, locally known as *Dirsa*, with no separation for calves, near homesteads.

Reported animal health problems

The common animal health problems of cattle as reported by sample cattle owners and local extension staff involved in this study were classified to known diseases based on local names of the reported problems as well as knowledge of reported symptoms. The relative reported prevalence of these problems are presented in Table 7, and are discussed further under three categories: infectious diseases, parasites and nutritional ailments.

Infectious diseases

Blackleg or black quarter

Blackleg is known in lowlands of the study area as "*Abagorba*" and in highlands it is called "*Kantso or Tsilike*". Occurrence is common during dry periods of the year from December to March. The reported symptoms are depression, anorexia, rumen stasis, high fever,

Table 6. Reported frequency (per cent) of use of major feed resource for cattle by district.

Feed sources	Highland sites			Lowland sites	
	Bonke ($n = 40$)	Chencha ($n = 41$)	Boreda ($n = 40$)	A/Zuria ($n = 45$)	M/Abaya ($n = 49$)
Communal grazing land	77.5	63.4	87.5	100	100
Private grazing land	87.5	85.3	92.5	88.9	89.8
Enset	100	100	100	–	–
Crop by products	100	100	100	100	100
Hay (*haffa*)	70	78	62.5	93.3	93.8
Improved forage	30	41.5	25	–	–
Cut and carry fodder	82.5	87.8	87.5	–	–
Supplementary feed	100	100	100	100	100

Table 7. Reported level of prevalence of diseases and parasites of cattle across the study sites.

Disease and parasite	Lowland sites		Highland sites		
	A/Zuria	M/Abaya	Chencha	Bonke	Boreda
Anthrax	Low	Low	Medium	Medium	High
Blackleg	Low	Medium	High	High	Medium
CBPP	Medium	High	Low	Low	Low
Trypanosomosis	High	High	–	–	–
Tuberculosis	Medium	Medium	Low	Low	Low
Pasteurellosis	Medium	Medium	Low	Low	Low
Rabies	Medium	High	Low	Low	Medium
Babesiosis	Medium	High	Low	Low	Medium
Abortion	Medium	Medium	Low	Low	Low
Bloating	Low	Low	Medium	Medium	Low
Grain overload	Low	Low	High	High	Low
Plant poising	Low	Low	High	Medium	Medium
Mastitis	Medium	High	Low	Low	Low
Ecto-parasites	Medium	Medium	Low	Medium	Low
Endo-parasites	Medium	Medium	Medium	Low	Low
Pneumonic Pasteurellosis	Medium	Medium	Low	Low	Medium
Foreign materials	Low	Low	Low	Low	Low

tachycardia and marked lameness with pronounced muscle swelling of the upper part of the affected leg.

Young animals were said to be more susceptible to the disease. Farmers use both traditional and veterinary drugs to treat diseased cattle. The traditional way of treating is slashing of the gas pockets with sharp blade or knife to draw the pus and wash the localized site with salt followed by smoking or burning the wound with hot metal plate. Sometimes a smear of ground garlic, sesame and salt is applied on the wound. After the treatment, farmers keep the animals without drinking water for a few days in the traditional belief that healing would progress faster when the animal stays thirsty.

Anthrax

Anthrax is reported to be fairly common with low to high relative prevalence across districts. It is known locally as "*Abasanga*" or "*Tsade*". Reported symptoms such as abrupt onset of fever, trembling, haematuria and blood-tinged diarrhoea are used to confirm that this disease is indeed Anthrax. All groups of cattle are infected. Veterinary treatment is sought from assistant veterinarians and animal health technicians based at district agricultural extension offices when animals are suspected of having contracted the disease. Increasingly rare traditional ways of treating diseased animals involve cutting skin open using sharp objects at body parts that show signs of shivering to draw (dark) blood in the belief that it would limit disease progression. The wound is then treated with garlic juice and salt. Sample communities are now aware of the possible risk of disease cross-infection to humans but no case of human infection was reported.

Tuberculosis

This disease was reported as having low to medium relative prevalence in the sample districts, affecting all classes of cattle throughout a year. It was said to occur more often in overcrowded cattle barns both during the dry and wet seasons. No traditional treatment practices were reported or known in the study area, and farmers invariably seek veterinary treatment or administer illicit drugs that are often available in rural village kiosks.

Rabies

Rabies is known to also affect cattle in the study area, especially in lowland villages located close to forested and bushy areas frequented by sick stray and wild dogs. Disease occurrence was reported to be on the decline with the clearing of natural forests and bush lands, but its reported prevalence in the sample districts ranges from low to high. Diseased animals are likely to die from it and the carcass of dead animals is condemned and disposed off promptly in the belief that the disease can be transmitted to humans.

Contagious bovine Pleuro-pneumonia (CBPP)

The disease was said to be prevalent mainly in lowland areas. Fever, loss of appetite, difficult breathing, chronic coughing when forced to move and standing with the elbows apart were identified as common symptoms of the disease.

Disease outbreak is expected in the study area with reported prevalence by district ranging from low to high during the dry season when pastures have deteriorated and animals are in poor body condition. Farmers reported that there is no known effective treatment for the disease and they continue to use traditional ways of treating diseased animals with herbs.

Pneumonic Pasteurellosis (shipping fever)

Shipping fever is known in the study area as one triggered by severe stress, for instance, on excessive work load on cattle during the traction season and long trekking of animals to distant markets. The disease was characterized by

Table 8. Reported frequency of use of curative measures by cattle farmers to deal with known diseases and parasites by sites.

Curative measures	Lowlands		Highlands			Overall
	A/Zuria	M/Abaya	Chencha	Bonke	Boreda	
N	45	49	41	40	40	125
Veterinary treatment	28.9	26.5	24.4	22.5	20.0	24.48
Use of traditional herbs	20.0	20.4	29.3	32.5	35.0	31.44
Informal drug vendors	33.3	30.6	29.2	27.5	30.0	30.12
Cured naturally	4.4	10.2	7.3	10.0	2.5	6.90
Quarantine	7.5	12.2	9.6	13.4	10.0	10.60

depression, loss of appetite, fever, increased respiratory rate and shallow respiration.

Parasites

Both internal and external parasites of cattle were reported to occur in the study area with low to medium prevalence (Table 7). The two major internal parasites were *Fasciola* and *Trypanosoma*. Among the ectoparasites mentioned were ticks, lice, leech and mange mites.

Trypanosomosis was reported to be a prevalent disease in the lowland districts where communal pastures are known to have low to medium challenge levels of the vector Tsetse fly, *Glossina* spp.

Leeches are common endoparasites in wet areas and often found attached to the underside of the tongue. Farmers remove the parasite manually using hot ash or alcohol.

Lice infestations occur at beginning of wet season, most commonly on young calves. Traditionally farmers smear the infested area with tobacco juice mixed with mud.

Nutritional ailments

Bloating and grain overload were the most commonly reported cases of non-infectious ailments in the study area. Bloating occurs very commonly during the rainy season when bloat producing legumes grow abundantly. Grain overload or rumen acidosis is a common incident during the grain harvest season when cattle accidentally ingest large quantities of readily digestible wheat and barley grains especially in the highlands. Farmers treat sick cattle with drenching of juice of local herbs mixed with salt.

Cattle farmers use a variety of curative means to treat their sick animals (Table 8). The frequency of reported use of veterinary treatment from public and private clinics ranged from 20 to 29 percent between the sample districts. Popular drugs are widely marketed informally in the sample districts through village kiosks and unauthorized drugs vendors. A greater proportion of the lowland farmers tend to use traditional herbs.

Conclusions

Cattle production of the study area is subsistence oriented and characterized by mixed crop-livestock farming in which cattle provide the traction and manure to support crop production and the crop residues serve as supplementary sources of feed for cattle. Management inputs on cattle are minimal, although cattle play multiple production and service roles in support of rural livelihoods.

Straight pure breeding is a common breeding practice in all study sites except Bonke and Chencha districts where some cross-breeding with Holstein Frisians is known to occur. Reported mating practices in the study districts are mostly uncontrolled, but some in the highland areas also practice artificial insemination with Holstein Friesian semen for dairy improvement. Expansion of cropland, diminishing feed resources, prevalence of various diseases and parasites, poor housing management, weak extension and training service were some of reported constraints of cattle production in the study area. For these cattle farmers to realize greater benefits from their cattle, the current husbandry and breeding practices should be gradually improved.

Acknowledgements

This paper is a part of the completed M.Sc. thesis of the first author under the academic supervision of the other authors, which was completed at Bahir Dar University, Bahir Dar, Ethiopia in June 2012. The Ethiopian Ministry of Education and Bahir Dar University jointly covered incremental costs of this study. Numerous cattle farmers and agricultural extension staff in the study area supported this study by sharing their knowledge and opinion and by granting permission for use of that information for purposes of this study, for which we express our sincere gratitude.

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Animal Genetic Resources, 2014, 55, 29–38. © Food and Agriculture Organization of the United Nations, 2014
doi:10.1017/S2078633614000265

Multivariate characterization of morphological traits in local Tunisian oases goats

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Summary
This paper describes some of the morphological characteristics of the Tunisian native goat. Data were collected on 1 247 goats from 202 holdings in two oases areas (Jerid and Nefzawa). These included body length, heart girth, height at withers, ear length, horn and hairs length, as well as qualitative characters such as colour, and the presence or absence of horns, wattles and beard, ears type and curling, horns form, hair type and the facial profile. Quantitative variables were then submitted to a principal component analysis (PCA) to reduce data dimensionality and enable discrimination of groups by individuals and populations. The multiple correspondence analysis was used with qualitative variables to allow further distinction within subpopulations. A discriminant canonical analysis was also conducted discrimination between subpopulations. Wither height, heart girth and ear length were the most determinant traits in differentiating between subpopulations with the PCA. The parameters that best segregate the subpopulations in the multiple correspondences analysis are the hair length and the subpopulation. Therefore, multivariate analyses were useful in the morphological characterization of the native goat from Tunisian oases. Canonical analyses showed that hair length, ear length and wither height are the best linear measurements for discrimination between goat subpopulations. The largest Mahalanobis distance was between Arbi Jerid and Serti Nefzawa goats, whereas the closest distance was between Serti Jerid and Serti Nefzawa subpopulations.

Keywords: *Jerid and Nefzawa, morphological characteristics, multivariate analyses, native goat*

Résumé
Notre étude portait sur la caractérisation phénotypique des caprins locaux (quatre sous-populations; Arbi Jerid, Arbi Nefzawa, serti Jerid et Serti Nefzawa) dans les régions oasiennes de la Tunisie. Un échantillon de 1 247 animaux ont été analysés pour 14 caractères morphologiques; six caractères quantitatifs (hauteur au garrot, périmètre thoracique, longueur du corps, longueur des poils, longueur des cornes et longueur des oreilles) et huit caractères qualitatifs (le type et la couleur du pelage, la présence de la barbe et la présence des pampilles, la forme et la taille des cornes, la forme des oreilles, type de chanfrein). Aussi des méthodes d'analyse de données multivariées (analyse en composantes principales analyse factorielle de correspondances multiples et analyse discriminante canonique) ont été utilisées pour analyser les variables étudiées à fin de pouvoir distinguer entre les groupes génétiques ainsi qu'entre les zones d'élevage. Les chèvres Arbi Jerid possédaient les valeurs de longueur du corps les plus grandes tandis que les chèvres Arbi Nefzawa avaient les valeurs les plus importantes pour toutes les autres mesures. D'après les analyses multivariées, ces sous-populations ont été divisées en deux grands groupes génétiques. La hauteur au garrot, le périmètre thoracique et de la longueur des oreilles étaient les caractéristiques les plus déterminantes pour différencier entre les sous-populations avec l'analyse en composantes principales. Les paramètres qui correspondaient le mieux pour différencier les sous-populations de l'analyse des correspondances multiples sont la longueur des poils et les sous groupes génétiques. L'analyse canonique a montré que la longueur des poils, la longueur des oreilles et la hauteur au garrot sont les meilleures mesures linéaires permettant la discrimination entre les quatre sous-populations étudiées. La plus grande distance de Mahalanobis était entre les chèvres Arbi Jerid et Serti Nefzawa, tandis que la distance la plus proche se situait entre Serti Jerid et Serti Nefzawa.

Mots-clés: *caractérisation phénotypique, caprins, analyse multivariée, Jérid et Nefzaoua*

Resumen
Este artículo describe algunos de los rasgos morfológicos de la cabra autóctona tunecina. Los datos fueron tomados sobre un total de 1 247 cabras de 202 propietarios en dos zonas de oasis (Jerid y Nefzawa). En concreto, se midió la longitud corporal, la circunferencia torácica, la altura a la cruz y la longitud de las orejas, los cuernos y el pelo. También se registraron caracteres cualitativos como el color, la presencia o ausencia de cuernos, mamellas y barba, la forma y curvatura de las orejas, la forma de los cuernos, el tipo de pelo y el perfil facial. Las variables cuantitativas fueron después sometidas a un análisis de componentes principales para reducir la dimensionalidad de los datos y permitir la diferenciación de grupos por individuos y poblaciones. Se empleó el Análisis de Correspondencias Múltiples con las variables cualitativas para facilitar una mayor distinción dentro de las subpoblaciones. Se llevó también a cabo un análisis canónico discriminante para diferenciar las subpoblaciones. La altura a la cruz, la circunferencia torácica y la longitud de las orejas resultaron ser los rasgos más determinantes en la diferenciación de las subpoblaciones mediante el análisis de componentes

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principales. Los parámetros que mejor segregaron las subpoblaciones en el análisis de correspondencias múltiples fueron la longitud del pelo y la subpoblación. Así, los análisis multivariantes resultaron útiles en la caracterización morfológica de la cabra autóctona de los oasis tunecinos. Los análisis canónicos mostraron que la longitud del pelo y de las orejas y la altura a la cruz eran las mejores medidas lineales para la diferenciación entre subpoblaciones de cabras. La mayor distancia de Mahalanobis se dio entre las cabras Arbi Jerid y Serti Nefzawa, mientras que la menor distancia se obtuvo entre las subpoblaciones Serti Jerid y Serti Nefzawa.

Palabras clave: *características morfológicas, cabra autóctona, análisis multivariantes, Jerid y Nefzawa*

Submitted 28 October 2013; accepted 30 May 2014

Introduction

Local goat breeds constitute a valuable source of income in rural areas, and they play a crucial role in economic, environment and social domains. FAO (2007) reported that traditional production systems required multipurpose animals, which, although less productive than high-output breeds, may contain valuable functional traits. Modern agriculture has developed specialized breeds, optimizing specific production traits. Modern animal breeders have achieved striking productivity increases in high external input production systems. Livestock currently contribute about 30 percent of agricultural gross domestic production in developing countries. Only 14 of the more than 30 domesticated mammalian and bird species provide 90 percent of human food supply from animals. The five main livestock species: cattle, sheep, goats, pigs and chickens provide the majority of food produced worldwide. Among these, a small number of international transboundary breeds account for an ever-increasing share of total production (FAO, 2007).

External appearance (morphology) is still commonly used by researchers and practitioners in identifying, characterization and selection of farm animals (Khan *et al.*, 2006; Dossa, Wollny and Gauly, 2007; Alade, Raji and Atiku, 2008; Nafti *et al.*, 2009; Jimmy *et al.*, 2010). Observations on the outside view traits are the easiest to do, but this morphology is heavily influenced by external environmental factors such as availability of food and climate (Anderson, 2001; Lanari *et al.*, 2003; Salako, 2006; Jing *et al.*, 2010). Animal presence (existence) is due to their ability of adaptation with their environments or ecosystems. This property of being able to live in different areas and climates is explained by the production of more than one alternative form of morphology, physical status and or behaviour. This is considerate as a reaction or adaptation to environment changes (in the form of regulation of gene expression) and changes in shape (phenotype). (Karna, Koul and Bisht, 2001; Noor, 2002; Riva *et al.*, 2004; Mansjoer, Kertanugraha and Sumantri, 2007).

Thus genetic and phenotypic characterization remains the most powerful tools to detect, quantify and try to improve or develop these domestic mammalian species. In this context, the aim of our paper is the multivariate characterization of morphological traits in local Tunisian oases goats, which is a contribution to the study of the diversity of goat populations in Tunisia.

Material and methods

Experimental animals and location of study

Sampling was carried out on 202 local (Arbi (Figure 1) and Serti (Figure 2) goat flocks, selected at random, located in 17 different locations (rural areas and towns) in the two main Tunisian oases regions (Jérid and Nefzawa areas) (Figure 3). The study was conducted in four subpopulations (Arbi Jérid, Arbi Nefzawa, Serti Jérid and Serti Nefzawa) in the two regions (in localities of; El Hamma Jérid, Tozeur, Ibn Chabat, Degueche, Legwifla, Nefta and Tamerza in the first region and Bechri, Souk Lahad, Fatnassa, Kébili, Douz, Rjim Maàtoug, Jemna, Bechni, Fawar and Gataâya & Tombar in the second region).

A total of 1 247 caprine individuals were measured, 698 belonging to the first region (404 and 294, respectively for Arbi Jerid and Serti Jerid) and 549 from the second region (242 and 307 for Arbi Nefzawa and Serti Nefzawa, respectively). In total, 98 and 104 flocks were measured for the Jerid and Nefzawa areas, respectively. The sample was constituted by 85 male and 1 162 female adult goats (age > 2 years). Six body measurements or quantitative traits were determined, in addition to eight qualitative traits or variables. Data collected on each goat included: body length, wither height, heart girth, ear

Figure 1. Arbi Nefzawa doe.

Figure 2. Serti Nefzawa doe.

length, hair length and horn length for the quantitative variables, as well as the colour of hair, ear form and curling, presence and shape of horns, wattle presence, beard presence and the facial profile as qualitative traits.

The methodology used for measuring the morphological traits was those described by Lauvergne (1986), Cogovica (1987), Lauvergne, Renieri and Audiot (1987) and (FAO, 2012).

Statistical analysis

Before the collected physical measurements were subjected to analysis using multivariate methods, they were submitted to preliminary univariate analyses using the procedures UNIVARIATE and FREQ from SAS statistical package SAS 9.0 (SAS, 2002, SAS Institute Inc., Cary, NC, USA). Biometric data were first analysed using simple descriptive statistics (mean, mode, median, variance, standard deviation and coefficient of variation). Quantitative variables were then submitted to principal component analysis (PCA) (PROC PRINCOMP) to so reduce data dimensionality and enable facilitates analysis by grouping the data into smaller sets as first differentiation between subpopulations. The multiple correspondence analysis (MCA – PROC CORRESP) was used with qualitative variables to allow further distinction within subpopulations. Stepwise discriminant procedure was applied using PROC STEPDISC to determine which morphological traits have more discriminant power. The relative importance of the morphometric variables in discriminating the four subpopulations of goats was assessed using the level of significance ($p < 0.05$) and partial R^2 values ≥ 0.01. The CANDISC procedure was used to enable differentiation between subpopulations, calculating the Mahalanobis distances of the morphological traits, and derived canonical functions. Mahalanobis distances generated during the canonical discriminant analysis were used to construct a dendrogram using the unweighted pairs group method analysis (UPGMA). All measurements were analysed under the following linear model:

$$Y_{ijkl} = \mu + \text{locality}_i + \text{breed}_j + \text{sex}_k + \text{age}_l + \text{breed (locality)}_{ij} + \text{sex (breed)}_{jk} + \text{sex (locality)}_{ik} + \varepsilon_{ijkl}$$

where Y_{ijkl} is a quantitative variable (body length, wither height, heart girth, ear length, horns length and hair length); μ the general mean of subpopulation or population; locality_i the effect of the ith locality; breed_j the effect

Figure 3. Different areas of study.

Table 1. Descriptive statistics of morphological traits of the overall population in the two regions.

Parameters	Mean	Median	Mode	Variance	Standard deviation	Coefficient of variation	Range
Body length (cm)	98.43	99	100	69.50	8.33	8.47	49
Wither height (cm)	66.34	66	65	25.30	5.03	7.58	41
Heart girth (cm)	75.21	75	77	39.10	6.25	8.31	47
Ear length (cm)	18.55	19	19	8.91	2.98	16.09	28
Horns length (cm)	22.46	22	21	43.97	6.63	29.53	53
Hairs length (cm)	6.83	5	3	17.80	4.21	61.63	21

of the jth subpopulation; sex_k the effect of the kth sex; age_l the effect of the lth age; breed (locality)$_{ij}$ the effect of subpopulation within locality; sex (breed)$_{jk}$ the effect of sex within subpopulation; sex (locality)$_{ik}$ the effect of sex within locality and ε_{ijkl} the residual error of a null average and a constant variance.

The locality, breed, sex, age, breed (locality), sex (breed) and sex (locality) effects were contrasted by procedure GLM du SAS followed by the Student Newman–Keuls multiple comparison test, implemented in the General Linear Model procedure of SAS 9.0 (SAS, 2002, SAS Institute Inc., Cary, NC, USA).

Results and discussion

Results

Morphological diversity

In our study, a relative moderate variability was seen (Coefficient of variation (CV) ranging between 7 and 16 percent) for the traits: height at withers, heart girth and body length. The highest CVs were obtained for hair (61.63 percent) and horn (29.53 percent) length (Table 1). The smaller is the coefficient of variation better is the accuracy of the test and smaller is the errors of the results (Acourene *et al.*, 2001).

The body length did not show any significant differences between subpopulations Arbi and Serti while the horn and hair lengths displayed significant difference only between subpopulations of Arbi and Serti, i.e. neither significant difference between the Arbi Jerid and Arbi Nefzawa nor between Serti Jerid and Serti Nefzawa, but the differences are between Arbi and Serti groups (Table 2). It is expected that all animal populations have certain variability between groups or subpopulations. These differences could be attributed to the geographic location and specific feeding conditions of each location, combined with morphostructural differences.

The four analysed subpopulations the wither height and the heart girth were the most significantly different parameters within and between the subpopulations (Table 3).

The native Tunisian oases goats where characterized by an important morphological diversity between localities (Tables 3 and 4). The Arbi goats are mainly black, black and white or brown (together representing 78.64 percent of the population), with "Intermediary" horn type (67.57 percent for the Arbi Jerid goat and 64.46 percent the Arbi Nefzawa), frequent absence of beard 70.8 percent (Arbi) and wattles 78.56 percent (Arbi). With long hair 64.19 percent (Arbi) and dropping ears (more than 75 percent). Some characteristics such as short hairs were found (96.16 and 99.67 percent) for the Serti Jerid and Serti Nefzawa subpopulations, respectively, to distinguish between Serti and Arbi subpopulations.

Serti goats, with short hairs, are mostly light brown to dark brown, 34.69 and 14.99 percent, respectively, and they are white for 10 percent of goats. These subpopulations have drooping ears in 56 percent of individuals where 23.5 percent of the animals present erected ears. Their ears are not curly (60 percent) in both subpopulations. The intermediary horn type is the most frequent (58.34 percent). Generally these goats do not have beards (84.48 percent) and without wattles (76.15 percent) and their facial profile are straight (82.12 percent).

Principal components analysis

The PCA allowed us to spatially characterize the relationships among goat subpopulations from different localities according to a plan delimited by two main axes, PC1 and

Table 2. Descriptive statistics of morphological traits (raw mean and standard deviation) of Arbi Jérid & Arbi Nefzawa and Serti Jérid & Serti Nefzawa goats.

Parameters	Arbi Jérid	Arbi Nefzawa	Serti Jérid	Serti Nefzawa
Body length (cm)	98.0 ± 8.8^{a}	99.1 ± 7.54^{a}	97.82 ± 9.3^{a}	98.8 ± 7.1^{a}
Wither height (cm)	67.6 ± 5.6^{a}	65.6 ± 4.52^{b}	66.03 ± 4.9^{bc}	65.8 ± 4.3^{bc}
Heart girth (cm)	76.6 ± 6.7^{a}	74.5 ± 6.03^{bc}	75.05 ± 6.1^{cb}	74.0 ± 5.4^{d}
Ear length (cm)	18.6 ± 2.8^{a}	19.6 ± 3.22^{b}	17.49 ± 2.7^{c}	18.5 ± 2.8^{da}
Horns length (cm)	23.7 ± 7.2^{a}	22.5 ± 5.86^{a}	21.72 ± 6.8^{b}	21.1 ± 5.5^{b}
Hairs length (cm)	10.2 ± 3.6^{a}	9.6 ± 3.10^{a}	3.61 ± 1.2^{b}	3.2 ± 1.1^{b}

Letters in rows indicate significant differences ($p \leq 0.05$) upon applying the multiple comparison of means test (Student–Newman–Keuls test).

Table 3. Descriptive statistics of morphological traits (mean) within the studied localities.

Region	Oases	Body length	Wither height	Heart girth	Ear length	Hairs length	Horns length
JÉRID	El Hamma Jérid	93.8^{e}	64.9^{cdef}	73.7^{def}	17.8^{cd}	20.9^{abc}	6.5^{de}
	Tozeur	98.9^{bcd}	65.0^{cdef}	75.3^{abcde}	17.8^{cd}	23.5^{abc}	5.7^{def}
	Ibn Chabat	99.6^{abcd}	68.1^{ab}	77.4^{abc}	18.6^{bcd}	24.8^{a}	9.2^{b}
	Degueche	100.6^{abc}	66.3^{cdef}	74.9^{bcde}	17.2^{d}	22.4^{abc}	4.6^{f}
	Legwifla	95.3^{de}	68.0^{ab}	76.6^{abcd}	17.8^{cd}	22.5^{abc}	10.3^{a}
	Nefta	101.3^{abc}	66.9^{abcd}	77.2^{abc}	18.7^{bcd}	24.3^{ab}	5.4^{ef}
	Tamerza	102.3^{ab}	69.0^{a}	77.6^{ab}	20.4^{a}	23.0^{abc}	8.3^{c}
NEFZAWA	Bechri	99.2^{a}	64.1^{ab}	78.3^{a}	19.6^{ab}	22.2^{abc}	6.5^{de}
	Souk Lahad	103.8^{bcd}	68.1^{ef}	78.3^{ef}	19.6^{ab}	22.2^{abc}	6.5^{de}
	Fatnassa	100.5^{abc}	66.4^{cbde}	75.6^{abcde}	19.7^{ab}	23.2^{abc}	7.0^{d}
	Kébili	95.4^{de}	65.0^{cdef}	75.4^{f}	17.5^{cd}	21.4^{abc}	5.8^{def}
	Douz	100.8^{abc}	67.3^{abc}	75.9^{abcde}	19.0^{abc}	22.8^{abc}	5.5^{ef}
	Rjim Maâtoug	97.4c^{cde}	63.8^{f}	72.6^{ef}	20.1^{ab}	21.1^{abc}	8^{c}
	Jemna	101.6^{cde}	64.3^{ef}	75.1^{abcde}	19.6^{ab}	19.9^{c}	6.2^{de}
	Fawar	97.5^{abc}	64.4^{ef}	74.3^{cdef}	19^{abc}	20.1^{bc}	5.6^{ef}
	Bechni	98.2^{bcd}	67.0^{abcd}	73.9^{def}	19.5^{ab}	21.4^{abc}	6.4^{de}
	Gatâaya &Tombar	98.9^{bcd}	64.8^{def}	73.7^{def}	18.8^{bcd}	21.2^{abc}	4.6^{f}

Letters in rows indicate significant differences ($p \leq 0.05$) upon applying the multiple comparison of means test (Student–Newman–Keuls test).

PC2, which accounted for 50.1 and 16.8 percent of the phenotypic variance, respectively. PC1 axis (Table 5) could be linked to the variables related to higher wither measurement, larger heart girth, longer body length of the animals, whereas the PC2 axis gave a major relevance to the hair lengths. Some traits were highly correlated whereas; others weakly correlated (Table 6). The variables with the highest correlations were chest circumference, height at withers, body length and horn length. The highest correlations were between chest girth and height at withers (0.740), thoracic perimeter and body length (0.664) and between thoracic perimeter and horn length (0.636). Hair length was the less correlated trait with all others: 0.03 with body length and with length of the ears and chest girth were 0.15 and 0.16, respectively (Table 6).

Table 4. Total frequency (and percentage in brackets) for each level of the qualitative traits scored in Arbi Jérid & Arbi Nefzawa and Serti Jérid & Serti Nefzawa goats.

Variables	Class level	Arbi Jerid	Arbi Nefzawa	Serti Jerid	Serti Nefzawa
	Long	315 (77.9%)	122 (50.4%)	0 (0%)	0 (0%)
Hair type	Medium length	89 (22.0%)	120 (49.5%)	11 (3.7%)	1 (0.3%)
	Short/close-cropped	0 (0%)	0 (0%)	283 (96.1%)	306 (99.6%)
	Brown and white	14 (3.4%)	19 (7.8%)	18 (6.1%)	30 (9.7%)
	Dark brown	43 (10.6%)	35 (14.4%)	38 (12.9%)	54 (17.5%)
	White	25 (6.1%)	21 (8.6%)	25 (8.5%)	39 (12.7%)
	Light brown	39 (9.6%)	26 (10.7%)	113 (38.4%)	95 (30.9%)
Coat pattern	Grey	43 (10.6%)	12 (4.9%)	31 (10.5%)	6 (1.9%)
	Black and brown and white	5 (1.2%)	2 (0.8%)	4 (1.3%)	2 (0.6%)
	Black dominant	186 (46.0%)	107 (44.2%)	53 (18.0%)	71 (23.1%)
	Black and white	49 (12.1%)	20 (8.2%)	12 (4.0%)	10 (3.2%)
Ear position	Vertical/erected	30 (7.4%)	19 (7.8%)	83 (28.2%)	59 (19.2%)
	Semi-pendulous	56 (13.8)	39 (16.1%)	61 (20.7%)	58 (18.8%)
	Drooping	318 (78.7)	184 (76.0%)	150 (51.0%)	190 (61.8%)
Ear curling	Absence	195 (48.2%)	136 (56.2%)	186 (63.2%)	176 (57.3%)
	Presence	209 (51.7%)	106 (43.8%)	108 (36.7%)	131 (42.6%)
Horn type	Absence	75 (19.5%)	59 (24.38%)	59 (20.0%)	107 (34.8%)
	Intermediary	273 (67.5%)	156 (64.4%)	174 (59.1%)	152 (49.5%)
	Ibex	9 (2.2%)	10 (4.1%)	49 (16.6%)	25 (8.1%)
	Markhar	47 (11.6%)	17 (7.0%)	12 (4.0%)	23 (7.4%)
Beard	Absence	213 (52.7%)	203 (83.8%)	243 (82.6%)	265 (86.3%)
	Presence	191 (47.2%)	39 (16.1%)	51 (17.3%)	42 (13.6%)
Wattles	Absence	351 (86.8%)	170 (70.2%)	238 (80.9%)	219 (71.3%)
	Presence	53 (13.1%)	72 (29.7%)	56 (19.0%)	88 (28.6%)
Facial profile	Straight	310 (76.7%)	231 (95.4%)	209 (71.0%)	286 (93.1%)
	Convex	67 (16.5%)	10 (4.1%)	48 (16.3%)	12 (3.9%)
	Concave	27 (6.6%)	1 (0.4%)	37 (12.5%)	9 (2.9%)

Table 5. Eigenvectors.

	PC1	PC2	PC3	PC4	PC5	PC6
Body length	0.461	−0.255	0.123	0.032	0.809	0.225
Wither height	0.484	−0.061	−0.080	−0.584	−0.400	0.503
Heart girth	0.517	−0.116	−0.107	−0.191	−0.081	−0.815
Ear length	0.246	0.362	0.875	0.132	−0.158	−0.025
Horn length	0.449	−0.037	−0.277	0.773	−0.3041	0.175
Hair length	0.152	0.886	−0.353	−0.078	0.247	0.010

Nevertheless, as can be seen in the graphical representation of goats according to principal components 1 and 2 (Figure 4), goats from the subpopulation Arbi Jerid and Arbi Nefzawa occupied the upper part of the representation and the Serti Jerid and Serti Nefzawa were grouped in the lower part of the graphic except they overlap in the middle of the distribution. So, the results from the PCA did not allow for a clear-cut grouping of all of the different subpopulations but showed a certain degree of homogeneity between the groups Arbi and Serti, which would suggest that current flocks could be a mixture of animals from different origins with a heterogeneous contribution from each original subpopulation.

Multiple correspondence analyses of qualitative traits

Figure 5 shows association among the categories of the different variables considered. The first and the second dimensions, respectively, explained 10.41 and 6.59 percent of the total variation.

Two first dimensions (Figure 5) show clear relationship between the traits, in which the subpopulations are divided onto two main groups. The first including animals belonging to subpopulations Arbi Jerid and Arbi Nefzawa having essentially long or medium length hairs that are gray, black or black and white. While the second unites Serti animals (Serti Jerid and Serti Nefzawa) with erected ears, ibex horns and light brown close-cropped hairs.

The straight facial profile, within the studied subpopulations showed very low quality of representation, being very close to the middle line. This low quality of representation is explained by the fact that this head profile is predominant in all subpopulations.

Table 6. Phenotypic correlations among body measurements of the overall population.

	Body length	Wither height	Heart girth	Ear length	Horn length	Hair length
Body length	*1.00*					
Wither height	**0.56**	*1.00*				
Heart girth	**0.66**	**0.74**	*1.00*			
Ear length	0.29	0.26	0.26	*1.00*		
Horns length	**0.52**	**0.53**	**0.63**	0.17	*1.00*	
Hairs length	0.03	0.17	0.16	0.15	0.20	*1.00*

Discriminant analyses of the quantitative variables

Results of the stepwise discriminant analysis are presented in Table 7. The discriminant analysis based on significant *F*-values indicated hair length, ear length and wither height as the linear measures permitting discrimination between goat subpopulations. When the three most important morphometric traits for separating the two goat subpopulations were selected, Wilk's Lambda dropped to 0.484, with a significant difference between the goat subpopulations ($F = 2.59$; $P < 0.001$). The unstandardized stepwise discriminant function was used to classify individual goats (Table 7). The discriminating variables earlier extracted were the variables included in the discriminant (D) equation:

$$D = 0.38 \times \text{hair length} + 0.043 \times \text{ear length} - 0.02 \times \text{wither height}$$

In the canonical discriminant analysis, all the three canonical variables generated (CAN1, CAN2 and CAN3) were significant ($p < 0.0001$). The CAN1 and CAN2 accounted for 99.75 percent of the total variation (Table 8). CAN1 was dominated essentially by the hair length and a smaller loading for ear length and CAN2 was dominated by large loadings from the ear length and relatively important loading from the wither height.

The canonical discriminant analysis allowed a good distinction between the studied individuals in the oasis regions (Jerid and Nefzawa). This analysis permitted a full view of the distribution of studied goat groups that distinguishes four independent zones (subpopulations) more or less distant from each other.

All pair wise distances were significant ($p < 0.0001$). The largest was between Arbi Jerid goats and Serti Nefzawa goats, whereas the closest distance was between Serti Jerid and Serti Nefzawa subpopulations. The dendrogram (Figure 6) shows two main populations. The first population includes the two Serti subpopulations which showed a Mahalanobis genetic distance of 0.19. The second population presents a distance of 0.33 between the two subpopulations Arbi Jerid and Arbi Nefzawa. Table 9 shows Mahalanobis genetic distances between different subpopulations.

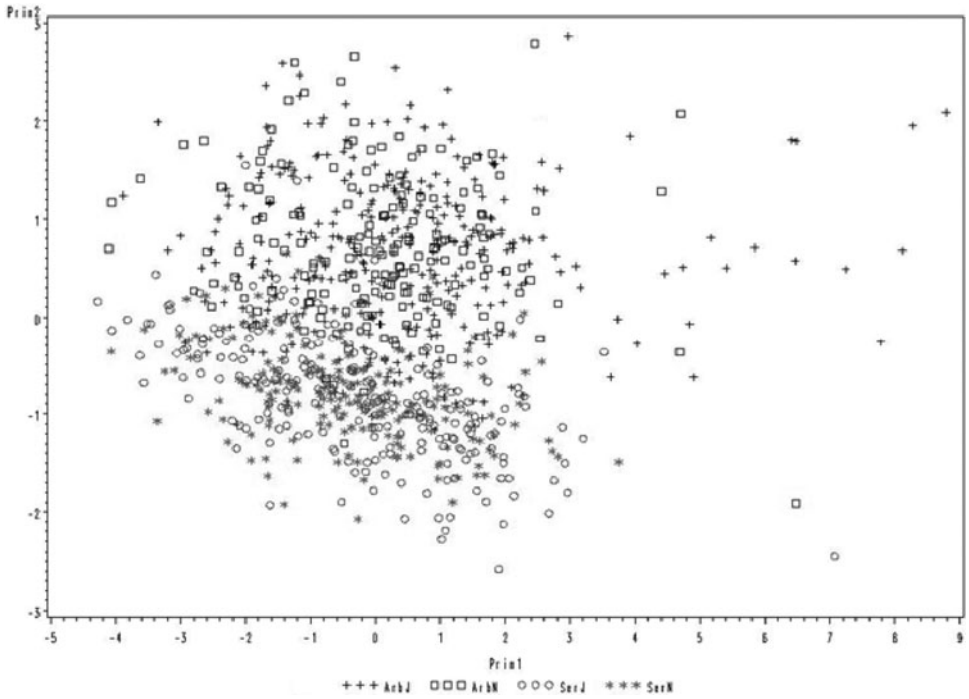

Figure 4. Graphical dispersion of scores of 4 subpopulations of goats in Tunisian oasis, related to principal components (PC) 1 (abscissa) and 2 (ordinate). ArbJ: Arbi Jerid goat, ArbN: Arbi Nefzawa, goat SerN: Serti Nefzawa goat, SerJ: Serti Jerid goat.

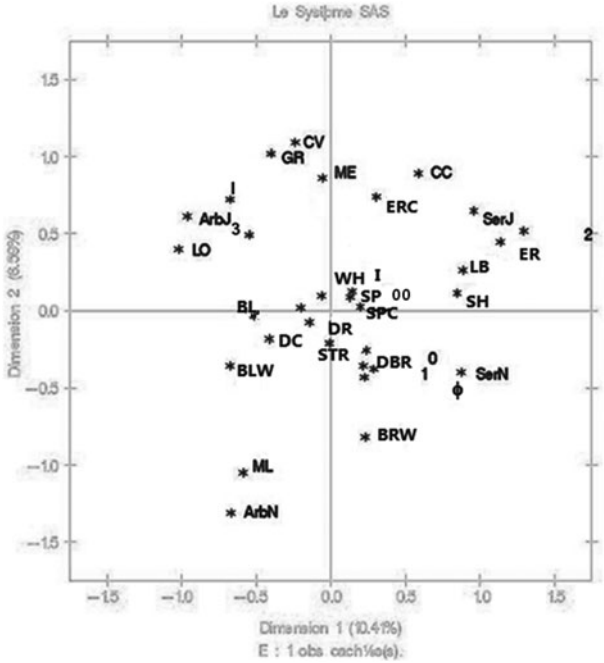

Figure 5. Association among qualitative variables revealed by multiple correspondence analyses (MCA). ArbJ: Arbi Jérid goat. CV, CC and STR: convex, concave and straight facial profile. ArbN: Arbi Nefzawa goat. LO: long hairs, ML: medium-long hairs, SH: short hairs. SerJ: Serti Jérid goat. DR, DC: dropping and dropping curly ears. SerN: Serti Nefzawa goat. SP, SPC: semi-pendulous and semi-pendulous curly ears. 1: presence of bear. ER, ERC: erected and erected curly ears. I: presence of wattles. φ: absence of bear; 00: absence of wattles; 0: absence of horns. I: intermediary form of horns.2, 3: Ibex and markhar forms of horns. ME: mixture colour of goats. DB, BRW and LB: dark Brown, brown and white and light brown colours of goats. WH, BLW and BL: white, black and white and dominant black colours of goats.

Discussion

Morphological diversity

Type trait standards are needed to define specific breeds. Phenotypic description is based on measurements and qualitative traits and essential for defining these. In the four Tunisian oases goat subpopulations studied here, body measurements showed relative moderate degrees of variation for each trait except the body length.

Similar results were cited by Nafti *et al.* (2009) in studying same goat population in the Jerid area. Also these results were found with six Indonesian breeds (Benggala, Jawarandu, Kacang, Marica, Muara and Samosir) especially great similarities were noticed with Mura breed (Batubara *et al.*, 2011). Chacón *et al.* (2011) and La O-Arias *et al.* (2012) reported smaller values of wither height, body length, ear length and coat length but higher measures of heart girth when they studied the morphological measurements and body indices for Cuban Creole goats and Traoré *et al.* (2008) within Burkina Faso goats. Also Dossa, Wollny and Gauly (2007) found smaller measurements while studying goats from four vegetation zones ranging from south towards north Benin. The four populations studied here were characterized as distinct and may be referred to as ecotypes. Herrera *et al.* (1996), worked on Mediterranean goats with a total of 634 adult goats (>3 years old) from five Andalusian caprine breeds (Malaga, Granada, Florida, Andalusian White and Andalusian Black), had found greater withers height (ranged from 68.22 to 77.91 cm) and of chest girth (from 85.59 to 96.24 cm) but smaller values of body length (from 71.64 to 81.25 cm).

Table 7. Summary of stepwise selection of traits.

Step	Variables entered	Partial R^2	*F*-value	*P* > *F*	Wilk's Lambda	*P* < Lambda	Average Squared Canonical correlation	*P* > ASCC
1	HL	0.5056	409.11	***	0.494	***	0.505	***
2	EL	0.0138	5.57	**	0.487	***	0.512	***
3	WH	0.0065	2.59	**	0.484	***	0.515	***

***: $P < 0.001$; **: $P < 0.05$.
HL, hair length; EL, ear length; WH, wither height.

The coefficient of variation values of height at withers, heart girth and body length was similar to those found by Dossa, Wollny and Gauly (2007) and Pires *et al.* (2012). Traoré *et al.* (2008) cited higher values for the horns length, ear length and all other body measurements in Burkina Faso goats.

Principal components analysis

The graphical representation of the PCA allowed to first distinction goat subpopulations into two groups in the Jerid and Nefzawa areas. The exploitation of the multivariate techniques especially the principal components have been found useful for a quantitative measure of animal conformation which is desirable as it will enable reliable genetic parameters for these traits to be estimated and permits its inclusion in breeding programmes (Ibe, 1989; Mavule *et al.*, 2012; Silva *et al.*, 2013; Yakubu, 2013). The graphical representation of PCA observations permits distinguishing among genetic groupings/breeds of goats, from the most similar to the most dissimilar. It also facilitates preliminary visualization of the uniformity or lack of uniformity among individuals within each subpopulation, similar results were reported by Pires *et al.* (2012). Similar correlation values between same variables in the Jerid goats were mentioned by Nafti *et al.* (2009). Okpeku *et al.* (2011) reported greater values of correlations between the measurements which allowed him to conclude that two factors were extracted for each sex of the two breeds, although with varying degrees of factor loadings. Besides, La O-Arias *et al.* (2012) reported that body dimensions of Creole goats were grouped also into two components, the first component 17 of 22 variables, all of them negatively correlated with this component and explained 62.5 percent and the second component explained 12.69 percent of the total variance and was positively correlated.

Table 8. Standardized coefficients for the canonical discriminant function, the canonical correlation, the eigenvalue and the total variance percentage.

Traits	Discriminant variate		
	CAN1	CAN2	CAN3
Hair length	1.000	−0.076	0.115
Ear length	0.125	0.924	0.445
Wither height	−0.099	−0.662	0.798
Adjusted canonical correlation	0.784	0.228	0
Approximative standard error	0.011	0.027	0.028
Eigenvalue	1.599	0.567	0.041
Variance accounted for (%)	96.34	3.42	0.25
Cumulative variance (%)	96.34	99.75	100

Correspondence analysis of qualitative traits

In the correspondences analysis the most important factors that distinguish the four studied subpopulations were the hairs length and type in one hand and the genetic group in the other hand. Similar result was found by Lanari *et al.* (2003) when they reported that Neuquen Criollo breed could be characterized in two ecotypes: Short and long hair goats, a mixed type area and a crossbred area fulfil the type's distribution. Carneiro *et al.* (2010) cited that, in sheep, the most important factor that differentiate the animals measured and adult weight the most influenced by environment. While Dossa, Wollny and Gauly (2007) revealed clear differences between the vegetation zones, goats from the northernmost vegetation zone being more associated with presence of wattles, beard, drooping ear and absence of supernumerary teats whereas those from southernmost zones had erected ears and were mainly characterized by very high incidence of supernumerary teats. Amao *et al.* (2003) reported slight different results.

Discriminant analyses

The best discriminant function model used in this study included three morphological measurements (hair length, ear length and wither height). This demonstrates that taking measurements on this trait could be sufficient in differentiating between these four goat subpopulations than acquiring numerous other measurements on morphometric traits. Some of the discriminating variables obtained in the present study are similar to earlier findings (Herrera *et al.*, 1996; Dossa, Wollny and Gauly, 2007; Yakubu *et al.*, 2011; Dekhili, Bounechada and Mannalah, 2013; Yadav

Table 9. Mahalanobis distances between the studied subpopulations.

Subpopulation	Arbi Jerid	Arbi Nefzawa	Serti Jerid	Serti Nefzawa
Arbi Jerid	0			
Arbi Nefzawa	0.33	0		
Serti Jerid	6.38	6.10	0	
Serti Nefzawa	6.97	6.26	0.19	0

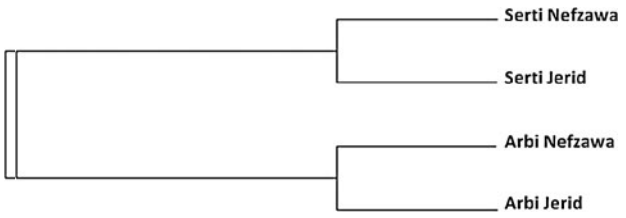

Figure 6. UPGMA tree based on pair-wise Mahalanobis distances of four goat subpopulations.

et al., 2013) in the morphostructural differentiation of sheep and goat breeds/populations. Some of the present discriminant variables are similar to those found by Dekhili, Bounechada and Mannalah (2013) working on Algerian goat population in Sétif area. Also Mahalanobis distances between Algerian populations were between 2.8 and 8.6 that are very close to our results.

The Mahalanobis distances differed between subpopulations. The highest distance between Arbi Jerid and Serti Nefzawa reflects differences in body size. Generally, such phenotypic divergence between breeds/populations might be partly associated with the differences in management practices, agro-climatic conditions and biophysical resources (Yadav *et al.*, 2013).

Conclusion

Tunisian oases goat subpopulations are a medium-sized animal. Its morphology corresponds to the milk-type animal although it is used for both milk and meat productions. The study establishes the structure and the degree of variability between the four subpopulations. The application of univariate and multivariate statistical methods enabled us to discriminate between the goat subpopulation using morphometric traits. Wither height, heart girth, ear length, hair length and wither height were all determinant in the discrimination between subpopulations in the oases areas of Tunisia. Additionally, the use of cluster analysis is successful in differentiating the populations into similar groups on the basis of morphological traits. The low Mahalanobis distance between Arbi Jerid and Arbi Nefzawa and between Serti Jerid and Serti Nefzawa at the morphological level could be attributed to the genetic exchange that has taken place between these goat subpopulations. This information will be the basis of further characterization, conservation and selection strategies in Tunisian goats.

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Animal Genetic Resources, 2014, 55, 39–46. © Food and Agriculture Organization of the United Nations, 2014
doi:10.1017/S2078633614000289

Maintenance of mtDNA diversity in Kalahari Red goat of South Africa imported to Nigeria

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Summary
Analysis of mitochondrial DNA (mtDNA) was carried out using 38 Kalahari Red (KR) goats randomly sampled from a flock imported into Nigeria in 2011 by the Federal University of Agriculture, Abeokuta, as an initial step to investigate the genetic structure of the breed, due to limited information on the breed. Apart from estimating genetic diversities, phylogenetic analysis to elucidate maternal lineages, relationship with wild goats as well as Tajima's D and Fu's F_s statistics were computed to test the departure from constant population size under the neutral model. The first hypervariable (HV1) region of mtDNA (481 bp) sequenced from 38 goats represented 11 haplotypes. Polymorphism of HV1 fragment was high, haplotype and nucleotide diversities were 0.869 ± 0.030 and 0.0299 ± 0.0067, respectively. Maximum-likelihood tree constructed with 11 haplotypes and 22 reference haplotypes representing six haplogroups worldwide revealed that five out of 11 haplotypes belong to haplogroup A, whereas six haplotypes belong to B. KR population clustered with *Capra aegagrus* as its wild ancestor. There was evidence of mitochondrial footprint that reflected past population decline based on positive and significant Fu's F_s estimate (6.283; $P < 0.01$). The mtDNA data did not however show that genetic variability of the breed has drastically reduced on account of population reduction. The information obtained is strategic to utilization and conservation of the population.

Keywords: *demographic history, Kalahari Red goat, lineages, mtDNA diversity*

Résumé
Analyse de l'ADN mitochondrial (ADNmt) a été réalisée à l'aide de 38 chèvres Kalahari rouge prélevés au hasard dans un troupeau importé au Nigéria en 2011 par l'Université fédérale de l'Agriculture, Abeokuta, dans un premier temps pour étudier la structure génétique de la race, en raison du peu de données sur la race. En dehors de l'estimation de la diversité génétique, l'analyse phylogénétique d'élucider des lignées maternelles et origine de la race ainsi que des statistiques D de Tajima et Fu F_s étaient calculés à tester le départ de la taille de la population constante sous le modèle neutre. La première région hypervariable (HV1) de l'ADN mitochondrial (481 bp) séquencée à partir de 38 chèvres représenté 11 haplotypes. Le polymorphisme du fragment HV1 était diversités haute, les haplotypes et les nucléotides respectivement 0.869 ± 0.030 et 0.0299 ± 0.0067. Arbre de maximum de vraisemblance construit avec des 11 haplotypes et 22 haplotypes de référence représentant les 6 haplogroupes dans le monde entier a révélé que 6 des 11 haplotypes appartiennent à haplogroupe A, tandis que 5 haplotypes appartiennent à la population de B. KR en cluster avec *Capra aegagrus* comme son ancêtre sauvage. Il y avait preuve de l'empreinte mitochondrial qui traduit devant le déclin de la population sur la base F_s estimation positive et significative de Fu (6.283; $P < 0.01$). Les données de l'ADN mitochondrial ne montrent pas cependant que la variabilité génétique de la race a drastiquement réduit en raison de la réduction de la population. L'information obtenue est stratégique pour l'utilisation et la conservation de la population.

Mots-clés: *diversité de l'ADN mitochondrial, lignées, origine, histoire démographique, chèvre de Kalahari rouge*

Resumen
Se realizó un análisis de ADN mitocondrial (ADNmt) con 38 cabras de raza Kalahari Roja elegidas al azar en un rebaño importado en Nigeria en 2011 por la Universidad Federal de Agricultura, en Abeokuta, como un primer paso para la investigación de la estructura genética de la raza, ya que es escasa la información que, sobre ella, existe. Además de estimar la diversidad genética, se llevó a cabo un análisis filogenético para determinar los linajes maternos y la relación con las cabras salvajes. Se calcularon también los estadísticos D de Tajima y F_s de Fu para evaluar la situación de partida bajo condiciones de neutralidad y estabilidad demográfica. La primera región hipervariable (HV1) del ADNmt (481 pares de bases) secuenciado en las 38 cabras presentó 11 haplotipos. El fragmento HV1 presentó un elevado polimorfismo, siendo la diversidad de haplotipos y de nucleótidos de 0.869 ± 0.030 y 0.0299 ± 0.0067, respectivamente. El árbol de máxima verosimilitud, construido con 11 haplotipos y 22 haplotipos de referencia, que representaban 6 haplogrupos de todo el mundo, mostró que 5 de los 11 haplotipos pertenecían al haplogrupo A, mientras que 6 haplotipos pertenecían al B. La población Kalahari Roja formó un conglomerado que tenía a *Capra aegagrus* como antepasado salvaje. Dado el valor positivo y significativo

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del estadístico F_s de Fu (6.283; $P < 0.01$), hubo indicios, en la información mitocondrial, de una disminución de la población en el pasado. La información del ADNmt no refleja sin embargo que se haya reducido drásticamente la variabilidad genética de la raza como consecuencia de la reducción de la población. La información obtenida resulta estratégica para la utilización y conservación de la población.

Palabras clave: *diversidad del ADNmt, linajes, origen, historia demográfica, cabra Kalahari Roja*

Submitted 10 February 2014; accepted 11 June 2014

Introduction

The Kalahari Red (KR) *goat* is native to South Africa. It was developed mainly for meat production (Kotze *et al.*, 2004; Simela and Merkel, 2008). There are two lines of KR goats; one line was developed from red-head Boer goats, whereas the other line was developed from unimproved indigenous goats (Campbell, 2003). There are further indications that the KR was a product of natural selection over a period of 20 years from unimproved indigenous goats kept by goat farmers in the Northern Cape Province and the Namibian part of the Kalahari Desert. The indigenous goats arrived in South Africa and Namibia along with the migrating tribes that traditionally kept goats (South African Indigenous Breeds. http://www.indigenousbreeds.co.za/indigenousbreeds/goat/kalahari). They feed on a vast variety of plants and are resistant to diseases and parasites and the need to be inoculated is far less than other breeds (Stonehaven, 2011). The breed has been well adapted to the arid and semi-arid savannah with good foraging and excellent mothering abilities, hence regarded as "minimum care/maximum profit" breed (Ramsay, Harris and Kotze, 2001). They are tall (54.05 cm) and long (69.8 cm) (Pieters *et al.*, 2009), which gives them excellent mobility. Their earthy (red) colour provides good camouflage that protects them from predators. Age at first breeding is 6 months, average birth weight is 2.5 kg and kids grow fast with mature buck weighing 115 kg while doe reach 75 kg (South African Indigenous Breeds. http://www.indigenousbreeds.co.za/indigenousbreeds/goat/kalahari). They are often used in cross-breeding to produce goats with uniform, solid, red colour and they have ability to kid three times in 2 years (Pieters *et al.,* 2009). According to Hauck (2014) (http://www.ramhbreeders.com/red), Australia has millions of feral goats that were seen as pests in the past but have brought in the KR goats because of its hardiness, earthen red colour and productivity. Currently, the Australian feral goats are being crossed with the KR goats by farmers to improve productiveness and hardiness which have greatly boosted the goat production industry, increasing the export of chevron to 82 percent. In the RAM H farm, according to the latter author, the purebred KR goat is more expensive than the other traditional breeds in Canada due to their limited supply and market demand. The erosion of KR with red Boar goats of South Africa, as noted by Kotze *et al.* (2004) is a major concern among livestock breeders; little empirical information is available with no comprehensive system of monitoring special characteristics.

The KR goat was imported into Nigeria in 2011 by the Federal University of Agriculture, Abeokuta, Nigeria (Figures 1 and 2). Evaluation of genetic diversity in the breed will further give insight about the prospect of achieving genetic progress from selection programmes and/or cross-breeding with other local goat populations. Genetic diversity studies based on microsatellite loci have been reported for the KR breed (Kotze *et al.*, 2004; Visser *et al.*, 2004). Microsatellite loci studied were polymorphic as indicated by moderate to high number of alleles per

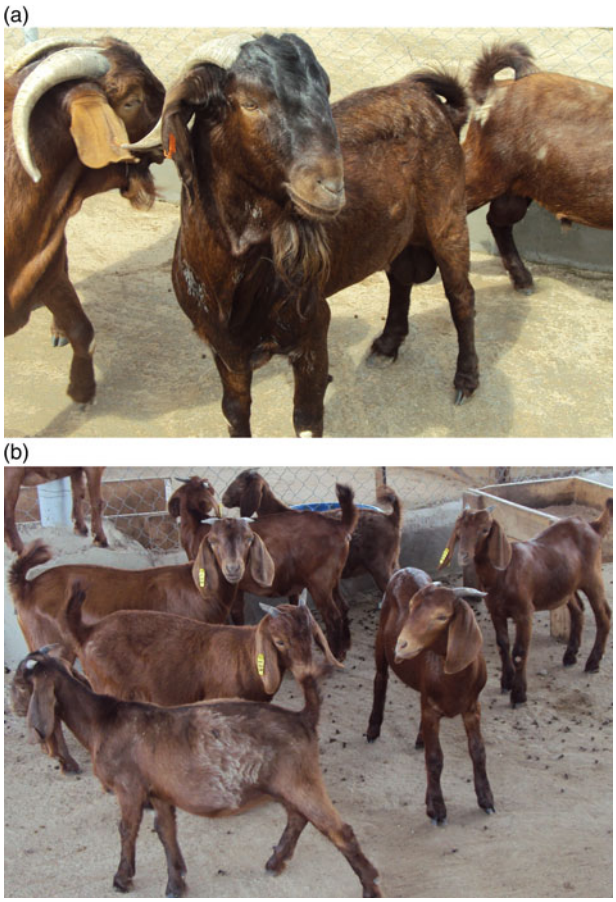

Figure 1. (a) KR bucks at the Federal University of Agriculture, Abeokuta. (b) KR weaners (females) born at the Federal University of Agriculture, Abeokuta.

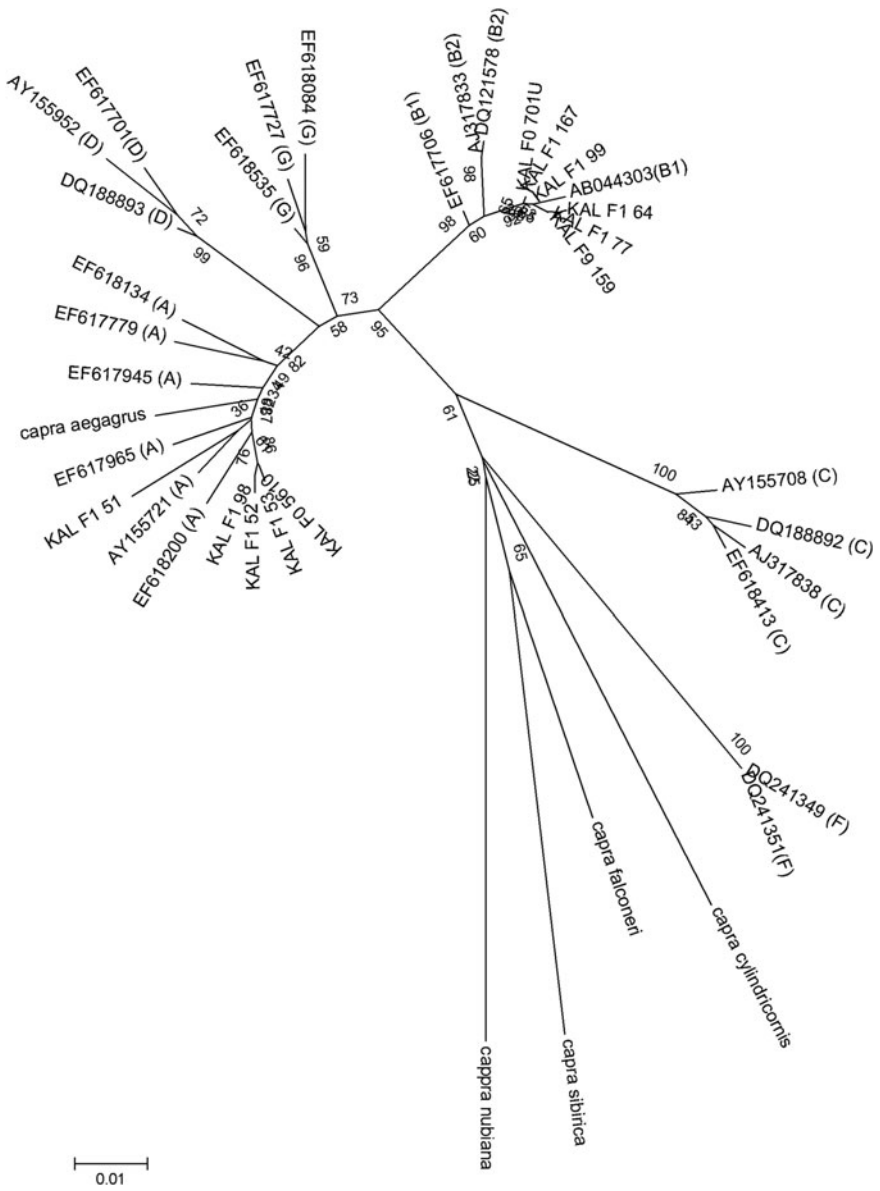

Figure 2. Tree topology obtained with ML phylogenetic method for 11 haplotypes and 22 reference haplotypes along with five sequences from wild goats included as out groups. Codes starting with two letters represent GeneBank Accession numbers of the 22 reference sequences. Other codes starting with KAL correspond to haplotypes belonging to the KR goat. Numbers at major clades represent bootstrap percentages computed after 1 000 replications.

locus and high polymorphism information content values. There is however paucity of information on analysis of mitochondrial DNA (mtDNA) marker-based genetic diversity of the breed under consideration. mtDNA is also favoured as a marker of choice because it is maternally inherited, has high mutation rate and copy number and lacks recombination unlike autosomal or X-chromosome-specific loci (Pereira, Carneiro and Asch, 2010). Many studies on different goat populations around the world have focused on analysis of the hypervariable (HV1) region of mitochondrial D-loop (Luikart *et al.*, 2001; Fan *et al.*, 2007; Naderi *et al.*, 2007, 2008; Wang *et al.*, 2008; Amills *et al.*, 2009; Groeneveld *et al.*, 2010; Han *et al.*, 2010; Benjelloun *et al.*, 2011; Cinar Kul and Okan, 2011; Zhao *et al.*, 2011; Martínez *et al.*, 2012; Lin *et al.*, 2013). Apart from very high haplotype diversities reported by most of the authors, the weak phylogeographic structure among different populations was also observed (Luikart *et al.*, 2001; Fan *et al.*, 2007; Naderi *et al.*, 2007, 2008; Amills *et al.*, 2009; Benjelloun *et al.*, 2011; Zhao *et al.*, 2011). Insignificant geographic structuring was mainly attributed to worldwide distribution of dominant A haplogroup, which included more than 90 percent of individuals among other haplogroups (B, B1, B2, C, D, F and G) reported (Naderi *et al.*, 2007). Owing to paucity of information on the KR breed, this study was designed to investigate the genetic diversity, maternal lineages and relationship with wild ancestors, as well as infer the demographic history of the population through analysis of mtDNA.

Materials and methods

Blood sample collection and DNA extraction

Blood samples were collected from 38 KR goats semi-intensively managed at the Federal University of Agriculture, Abeokuta (FUNAAB), Nigeria. Figure 1a and b represent Kalahari bucks and does, respectively, maintained at the farm. To represent the genetic diversity in breed, samples were randomly drawn from unrelated individuals of the parent stock imported from South Africa, excluding offsprings born at the farm of the University's Research Institute (Institute of Food Security, Environmental Resources and Agricultural Research (IFSERAR)). The blood samples were collected from the jugular vein of the goat directly onto Whatman FTA Classic cards (Whatman Bio Science, Maidstone, UK) and allowed them to dry for 1 h at room temperature and stored until DNA extraction was carried out using standard commercial kits according to manufacturer's instructions.

Polymerase chain reaction (PCR) amplification and sequencing

The HV1 region of mtDNA D-loop was amplified and sequenced in the STABVIDA laboratory, Portugal. The primers CAP-F (5′-CGTGTATGCAAGTACATTAC-3′) and CAP-R (5′-CTGATTAGTCATTAGTCCATC-3′) were used to amplify a 579-bp DNA fragment. The PCR-cycling protocol by Luikart *et al.* (2001) was adopted. A 481 bp segment of the PCR products was sequenced. PCR amplifications were conducted in a 25-µl volume containing 2.5 mM $MgCl_2$, 200 µM of each dNTP, 1 µM of each primer and 1 unit of AmpliTaq Gold Polymerase (Applied Biosystems). The PCR mixture underwent 35 cycles of 30 s at 95 °C, 30 s at 50 °C and 1 min at 72 °C. PCR products were purified using the Quaquick PCR columns (Qiagen). A 481-bp segment of the PCR products was sequenced using two "internal" primers CAP-FI (5′-TCCATATAACGCGGACATAC-3′) and CAP-RI (5′ATGGCCCTGAAGAAAGAAC-3′). All sequences were obtained for both DNA strands using the ABI PRISM Dye Terminator Cycle Sequencing Ready Reaction Kit (Applied Biosystems) in a 20-µl volume containing 40–50 ng of purified DNA and 3.2 pmol of primer. Sequencing reactions underwent 25 cycles of 30 s at 96 °C, 30 s at 58 °C and 4 min at 72 °C on a thermocycler (PE 2400, PE 9600 or PE 9700; Perkin–Elmer). Excess dye terminators were removed by spin-column purification. Sequencing reactions were electrophoresed for 6 h on an ABI 3700 PRISM DNA sequencer (Applied Biosystems) in a 5 percent Long Ranger gel (FMC). All sequences were deposited in the GenBank with accession numbers: KJ466263–KJ466273.

Data analyses

Genetic diversities and phylogenetic analyses were carried out using a 453 bp region shared by 38 mitochondrial sequences in the present study and 22 reference sequences retrieved from GeneBank (Naderi *et al.*, 2007) representing the diversity of six haplogroups (A, B, C, D, F and G) found worldwide. ChromasPro 1.7.5 (http://www.technelysium.com.au/ChromaSpro.html) was used for viewing and editing of the sequences. Multiple alignments of the sequences were performed using Clustal W in MEGA 5.2.2 (Tamura *et al.*, 2011). The polymorphisms in the analysed regions, nucleotide diversity (π) and haplotype diversity (h) were estimated using DnaSP v5.10.01 software (Librado and Rozas, 2009). Maximum-likelihood (ML) tree was created with MEGA 5.2.2 software (Tamura *et al.*, 2011) to classify the population into maternal lineages according to the reference sequences with accession numbers (AY155721), (EF618134), (EF617779), (EF618200), (EF617945), (EF617965), (ABO44303), (EF617706), (AJ317833), (DQ121578), (AY155708), (AJ317833), (EF618413), (DQ188892), (AY155992), (EF617701), (DQ188893), (DQ241349), (DQ241351), (EF618084), (EF618535) and (EF617727) (Naderi *et al.*, 2007). Reliability of the phylogenetic tree was assessed using bootstrap percentages computed after 1 000 replications. The D-loop region sequences of *Capra aegagrus* (EF989163) (Naderi *et al.*, 2008), *Capra caucasica* (AJ317875), *Capra sibirica* (AJ317874), *Capra cylindricornis* (AJ317870), *Capra nubiana* (AJ317871) and *Capra falconeri* (AJ317872) (Luikart *et al.*, 2001) were also included as out groups to ascertain relationship of KR with wild goats. Two different approaches were used to examine traces of population expansion. Fu's F_s statistic (Fu, 1997) as well as Tajima's D estimate were obtained with DnaSP v5.10.01 (Librado and Rozas, 2009). Mismatch distributions (pairwise sequence-difference distributions) for the population were also carried out to test departures from the null hypothesis of a constant population size under the neutral model.

Results and discussion

Sequence diversity

The HV1 sequences from the KR breed were highly polymorphic (Table 1). Most mutations were single nucleotide substitutions including 39 transitions and 39 transversions, with one insertion/deletion detected. The nucleotide changes identified from 38 sequences were grouped into 11 haplotypes (Table 2). The distribution of the haplotypes was such that two groups that were in majority were each represented by nine individuals, whereas other haplotypes had representation ranging from one to five individuals. Haplotype and nucleotide diversities were 0.869 ± 0.030 and 0.0299 ± 0.0067, respectively, which compared favourably with high estimates reported from several studies on different breeds of goats around the world (Luikart *et al.*, 2001; Naderi *et al.*, 2007; Wang *et al.*, 2008; Amills *et al.*, 2009; Benjelloun *et al.*, 2011; Cinar Kul and Okan, 2011; Zhao *et al.*, 2011). High genetic diversity may partly result from high mutation rate of the control region,

Table 1. Diversity indices, Fu's F_s and Tajima's D statistics of the KR goat imported into Nigeria.

	Estimate	Probability of significance
Diversity indices		
Sample size	38	
Number of sites analysed	453	
Number of polymorphic sites	39	
Number of haplotypes	11	
Haplotype diversity, $hd \pm sd$	0.869 ± 0.030	
Nucleotide diversity, $\pi \pm sd$	0.0299 ± 0.0067	
Number of transversions	0	
Number of transitions	39	
Number of substitutions	39	
Indels	1	
Population demographic indices		
Fu's F_s	6.283	$P < 0.01$
Tajima's D	1.62075	$P > 0.10$

multiple maternal wild ancestor (Naderi *et al.*, 2007) and capture of large part of the wild diversity during domestication (Benjelloun *et al.*, 2011). Consistent with the current observation, analysis of microsatellite-based genetic diversity of the KR goats similarly showed high genetic polymorphism in terms of high number of alleles and average heterozygosity (Kotze *et al.*, 2004; Visser *et al.*, 2004).

Maternal lineages and relationship of goats with wild ancestors

Tree topology (Figure 2) obtained with the ML phylogenetic method for the observed haplotypes (11) and 22 reference sequences (Naderi *et al.*, 2007) grouped the KR goat population into two distinct mtDNA lineages, A and B. Lineage A had five haplotypes, whereas lineage B had six haplotypes. Lineage A is widely reported in different studies around the world as predominant (Luikart *et al.*, 2001; Naderi *et al.*, 2007; Wang *et al.*, 2008; Han *et al.*, 2010; Benjelloun *et al.*, 2011; Zhao *et al.*, 2011; Martínez *et al.*, 2012; Lin *et al.*, 2013). According to Fan *et al.* (2007), lineage A was possibly derived from Tibetan founders and was further subject to domestication in Northern China, some of them were dispersed to Southern China, whereas others remained. The distribution to other locations has been attributed to human migration.

The B lineage, according to Luikart *et al.* (2001) is mostly found in whole Asia with very few individuals from Sub-Saharan Africa and one European goat from Greece. Since the KR goats were developed from two lines (red-head boar and "unimproved indigenous" goats) (Campbell, 2003), it is not surprising that haplogroups A and B were represented in the breed, thereby supporting the hypothesis of multiple maternal origins (Luikart *et al.*, 2001). The B lineage is likely to have arisen in Asia, according to the latter authors, while distribution to other locations has been attributed to human migration (Naderi *et al.*, 2007). Han *et al.*

Table 2. Mitochondrial HV1 sequence variations among the KR goats.

H	Base position																																						
	11	44	71	77	87	99	107	132	137	151	157	177	184	1941	211	214	229	233	238	239	240	241	244	245	246	247	256	270	274	275	283	291	301	304	306	309	330	337	414
1	A	G	T	C	A	A	G	T	A	C	C	G	G	T	T	T	T	T	T	T	T	C	C	C	G	G	A	C	T	T	G	G	C	T	T	C	C	C	C
2	G	.	C	.	.	.	A	.	.	.	T	A	A	C	.	C	C	.	.	C	C	T	T	T	A	.	G	T	C	C	A	A	T	C	.	T	.	.	.
3	G	.	C	.	.	.	A	.	.	.	T	A	A	C	C	C	C	.	.	C	C	T	T	T	A	.	G	T	C	C	A	A	T	C	.	T	.	.	.
4	.	.	.	T	G	G	A	.	.	T	.	.	.	.	.	.	.	.	C	.	.	.	T	.	.	A	.	.	.	.	A	.	.	.	C	T	T	T	T
5	.	A	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	T	.	.	.
6	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	A	.	.	.	.	.	.	.
7	G	.	C	.	.	.	A	C	G	.	T	A	A	C	.	C	C	C	.	C	C	T	T	T	A	.	G	T	C	C	A	A	T	C	.	T	.	.	.
8	G	.	C	.	.	.	A	C	.	.	T	A	A	C	C	C	C	C	.	C	C	T	T	T	A	.	G	T	C	C	A	A	T	C	.	T	.	.	.
9	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	T	.	.	.
10	G	.	C	.	.	.	A	C	.	.	T	A	A	C	.	C	C	C	.	C	C	T	T	T	A	.	G	T	C	C	.	A	T	C	.	T	.	.	.
11	G	.	C	.	.	.	A	C	.	.	T	.	A	C	.	C	C	C	.	C	C	T	T	T	A	.	G	T	C	C	A	A	T	C	.	T	.	.	.

H, represents haplotypes; Dot (.), represents the identical nucleotide with the type 1 sequence.

(2010) further suggested that lineage B, including B1 and B2 probably originated from China, thereby supporting the hypothesis that China may be one of the goat domestication centres. In another study by Lin *et al.* (2013), the frequency of lineage B was higher in mountain areas than in plain areas of Myanmar and Cambodia. In addition, morphological examinations by the latter authors revealed that the frequencies of the Roman profile and pendent ears were significantly higher in plain areas than in mountain areas and a significant correlation was observed between frequency of lineage B and these morphological traits, which are also typical characteristics of the KR breed under consideration. Bezoar-type goat with concave facial profile and prick ear in mountain area has high frequency of lineage B in Southeastern Asia, although the mitochondria lineages are definitely not responsible for the phenotypes (Lin *et al.*, 2012). Generally, haplogroups B, C, D, F and G were rare or absent (Luikart *et al.*, 2001; Naderi *et al.*, 2007; Amills *et al.*, 2009).

To determine the relationship of KR with wild goats, the ML phylogenetic tree (Figure 2) revealed that all goats from haplogroups A and B were identified on the same branch with *C. aegagrus* (EF989193), among the five wild ancestors considered. This shows that the KR goats possess ancient haplotypes similar to those of *C. aegagrus.* A review by Cinar Kul and Ertugrul (2011) attests to the fact that domestic goat (*Capra hircus*) originated from wild species (*C. aegagrus*, *C. caucasica*, *C. sibirica*, *C. cylindricornis*, *C. nubiana* and *C. falconeri*.

Demographic history of the population

Fu's Fs and Tajima's *D* estimates are provided in Table 1. Tajima's *D* value was positive and insignificant (1.621; $P > 0.10$), whereas Fu's F_s was positive and significant (6.283; $P < 0.01$). Fu's F_s statistic, which is based on the probability of having a number of alleles greater or equal to the observed number in a sample drawn from a stationary population (Fu, 1997), is considered to be more sensitive in detecting population expansion (Liao *et al.*, 2010). It is indicative from the significant and positive Fu's F_s value and the mismatch distribution (Figure 3) that KR population has experienced reduction in population size. This outcome is expected in view of the concern already noted among breeders that the KR goat is being eroded (Kotze *et al.*, 2004). Contrary to the mismatch distribution and significantly positive Fu's F_s observed for KR population, bell-shaped mismatch distributions reported for human population (Rogers *et al.*, 1996) and different goat breeds around the world (Luikart *et al.*, 2001; Zhao *et al.*, 2011), as well as significantly negative Fu' F_s value (Zhao *et al.*, 2011; Martínez *et al.*, 2012) are consistent with a demographic population expansion, such as would be expected for populations expanding after the domestication of relatively few founder-individuals (reviewed by Luikart *et al.*, 2001). According to Martínez *et al.* (2012), cryptic bottleneck genetic signatures might be relatively frequent in domestic species because population declines are usually smooth and sustained, rather than drastic and instantaneous, and also

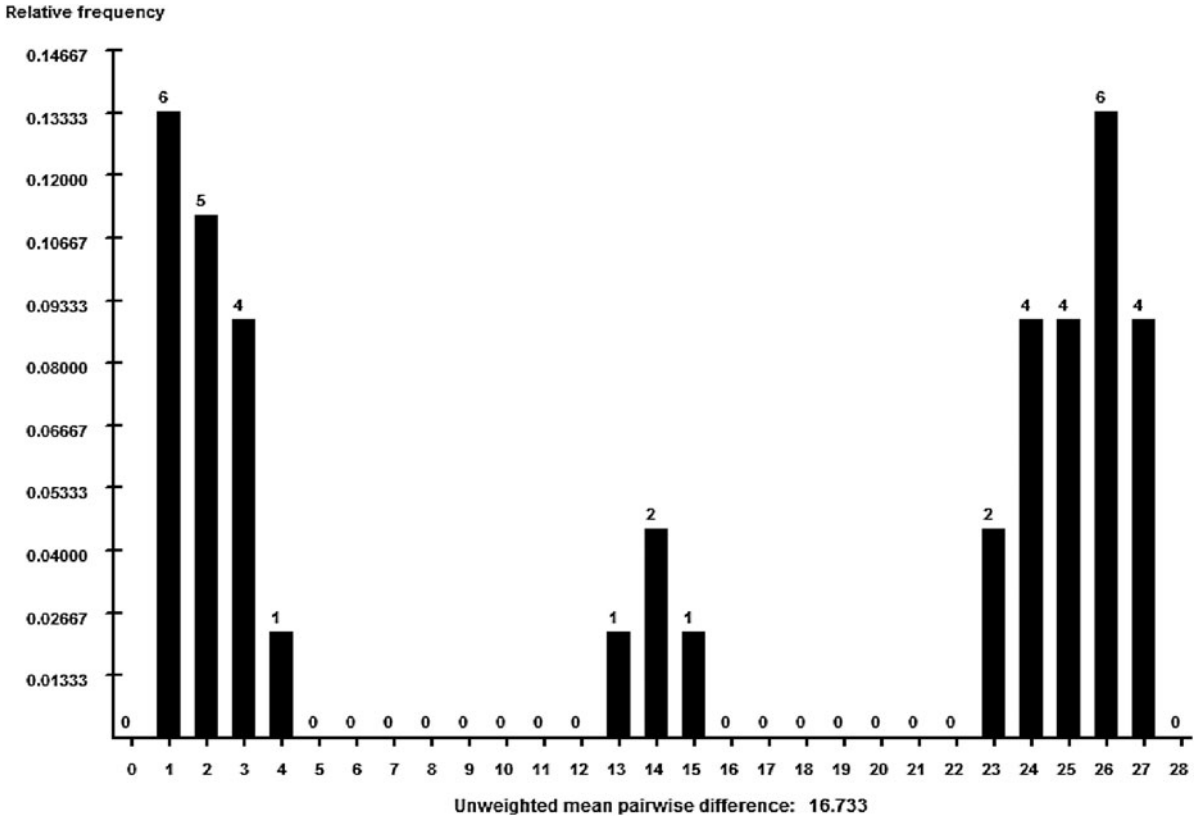

Figure 3. Mismatch distributions for mtDNA haplogroups in the KR goat.

because many concomitant factors, such as population subdivision, selection and migration, can alter their shape.

Conclusions

The genetic diversity of the KR goat population was high as revealed by the mtDNA analysis. Phylogenetic analysis revealed that the breed clustered with *C. aegagrus* as its wild ancestor and belongs to two mtDNA lineages (A and B), further supporting the possibility of multiple maternal origins. There is evidence of mitochondrial footprint that reflects past population decline based on positive and significant Fu's F_s estimate and the mismatch distribution. However, the mtDNA genetic variability of the KR breed has not been drastically reduced as a result of population decline. The information obtained will be useful in utilization and conservation of the KR population.

Acknowledgements

This study was partly funded by the research grant from Tertiary Education Trust Fund, an initiative of the Federal Government of Nigeria, through the Directorate of Grant Management of FUNAAB for which we are grateful. The authors are also grateful to the Management of the Institute of Food Security, Environmental Resources and Agricultural Research of FUNAAB for providing the experimental animals. We thank the Veterinary Officers, Security Officers and Technical Staff of the Institute for their immense assistance; the initiative of the former Vice-Chancellor of FUNAAB, Professor O.O. Balogun to import the Kalahari Red goat from South Africa to Nigeria; Biosciences Eastern and Central Africa (BecA-ILRI Hub) for supporting the Scientific Paper-writing Workshop that encouraged the writing of this paper; and Dr. Chris Beadle (CSIRO Ecosystem Sciences, Australia) for his constructive comments.

Statement of interest

None.

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Animal Genetic Resources, 2014, 55, 47–55. © Food and Agriculture Organization of the United Nations, 2014
doi:10.1017/S2078633614000307

Conservation of threatened goat breeds in India

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Summary
India is a rich repository of goat genetic resources having 23 well-recognized goat breeds. These breeds have evolved through natural selection and selective breeding by rearers for adaptation to specific agro-ecological conditions. As the indigenous goat breeds of India display great variation in adaptability, productivity, feed utilization, disease resistance, etc. so conservation for unique characteristics of indigenous breeds are of great importance. The recognized breeds of Indian goat population are facing a greater threat due to lack of enforcement of proper breeding policy, inadequate number of breeding bucks, indiscriminate crossbreeding and intermixing among breeds with local animals etc. Considering the current population size, declining rate of population, loss of habitat and introduction of other breeds in the area, the threatened goat breeds are Jamunapari, Beetal, Jakhrana and Surti in the northwestern region, Sangamneri, Osmanabadi, Malabari and Attappady Black in the southern region, Ganjam in the eastern region, and Chegu and Changthangi in the temperate Himalayan region. Furthermore, the positions of several breeds are more or less vulnerable in their breeding tracts. Now, efforts have been made to conserve the indigenous goat breeds for their unique characteristics in their home tracts through *in-situ* and *ex-situ* conservation in different agroclimatic regions of India.

Keywords: *conservation, goat, India, threatened breed*

Résumé
L'Inde est une riche réserve en ressources génétiques caprines avec 23 races de chèvre bien définies. Ces races ont évolué par sélection naturelle et l'élevage sélectif vers une adaptation à des conditions agro-écologiques spécifiques. Compte tenu du fait que les races caprines autochtones de l'Inde présentent une grande variation quant à son adaptabilité, sa productivité, son utilisation des aliments, sa résistance aux maladies, etc.…, la conservation des caractéristiques singulières des races autochtones revêt une grande importance. Les races reconnues de la population caprine indienne sont de plus en plus menacées à cause de la non-application de politiques d'élevage appropriées, le nombre inadéquat de boucs reproducteurs, le croisement sans discrimination des animaux autochtones avec des reproducteurs d'autres races, etc… Étant donnés la taille actuelle de la population, le décroissement de celle-ci, la perte d'habitat et l'introduction d'autres races dans la région, les races caprines menacées sont Jamunapari, Beetal, Jakhrana et Surti dans le Nord-Ouest, Sangamneri, Osmanabadi, Malabari et Attappady Noire au Sud, Ganjam dans la région Orientale et Chegu et Changthangi dans la région Tempérée de l'Himalaya. Par ailleurs, plusieurs races sont plus ou moins vulnérables dans leurs zones traditionnelles d'élevage. Actuellement des efforts se font, dans les différentes régions agro-climatiques de l'Inde, pour conserver, dans leurs régions d'origine, les races caprines autochtones, avec ses caractéristiques uniques, au moyen de la conservation in situ et ex situ.

Mots-clés: *conservation, race menacée, chèvre, Inde*

Resumen
La India es una rica reserva de recursos genéticos caprinos ya que atesora 23 razas de cabra bien definidas. Estas razas han evolucionado por selección natural y cría selectiva de los ganaderos hacia la adaptación a condiciones agroecológicas específicas. Dado que las razas caprinas autóctonas de la India muestran una gran variabilidad en cuanto a su capacidad de adaptación, su productividad, su aprovechamiento de los alimentos, su resistencia a enfermedades, etc…, la conservación de las características singulares de estas razas autóctonas resulta de una gran importancia. Las razas reconocidas de la población caprina india están cada vez más amenazadas debido a la no aplicación de políticas adecuadas de cría animal, un número inadecuado de machos reproductores, el cruzamiento indiscriminado y el mestizaje de los animales autóctonos con ejemplares de otras razas, etc… Teniendo en cuenta el tamaño actual de la población, el decrecimiento de la misma, la pérdida de hábitat y la introducción de otras razas en el área, las razas caprinas amenazadas son Jamunapari, Beetal, Jakhrana y Surti en la región Noroccidental, Sangamneri, Osmanabadi, Malabari y Negra Attappady en la región Meridional, Ganjam en la región Oriental y Chegu y Changthangi en la región Templada del Himalaya. Asimismo, varias razas se encuentran, en mayor o menor medida, en una situación de vulnerabilidad en sus lugares tradicionales de cría. En la actualidad, se están haciendo esfuerzos, en diferentes regiones agroclimáticas de la India, por conservar las razas caprinas autóctonas, con sus características únicas, en sus lugares de origen, mediante la conservación in situ y ex situ.

Palabras clave: *conservación, raza amenazada, cabra, India*

Submitted 31 October 2013; accepted 1 July 2014

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Introduction

India is one of the few countries in the world, which has contributed richly to the international livestock gene pool and improvement of animal production in the world. India possesses an enormous goat population numbering 125.46 million (FAO, 2010), which is the second highest in the world after China. As per the census report of the Department of Animal Husbandry, Dairying and Fisheries, Ministry of Agriculture, Government of India (2010), India is a rich repository of goat genetic resources having 23 well-recognized goat breeds and these breeds have evolved with respect to different geographical and climatic situation. These different breeds have specific importance in different agroclimatic zones and developed special adaptational features over the years to survive and simultaneously give sustained production under the agroclimatic conditions of their habitat. These breeds have generally been named after their place of origin and in some cases based on their prominent characteristics. Attempts have been made to characterize and register the breeds of goats in different regions, but so far only 23 breeds have been recognized, leaving about 75 percent of goat population being called as non-descript although they have certain unique characters.

Goats contribute greatly to the agrarian economy, especially in areas where crop and dairy farming are not economical, and play an important role in the livelihood of a large proportion of small and marginal farmers and landless labourers. However, intermixing of nearby breeds, introduction of exotic breeds and change in the farming system have resulted in decline in purebred population. Conservation of genetic resources in developing countries is far more complex, because, in a vast majority of the cases, information about available genetic resources, and need for and methods of conservation are not adequate. Determination of the status and characterization of indigenous goat genetic resources are essential for planning domestic animal diversity conservation plans (DAD-IS, 2010; FAO). Conservation of goat genetic resources, not only national but also an international issue, therefore, needs more attention to the present status of goat biodiversity and outlining the measures that are necessary if the goals of goat diversity conservation and self-reliance are to be combined.

Goat breeds and their distribution

There are 351 breeds of goats in the world, out of which 23 well-recognized breeds are found in India. The number, however, varies from 20 to 29 depending upon the reports available in the published literature. The vast genetic resources of goat breeds in the country mainly constitutes about 20–25 percent of the total goat population and remaining is non-descript having mixed features. The goat breeds with varying capacities to produce meat, milk and fibre have developed in India primarily through natural selection as well as by selective breeding or cross-breeding to diversified agroclimatic conditions based on their utility and production function (Table 1).

The goats are widely distributed all over the country in different agroclimatic regions (Figure 1) (2.4 percent of the total goat population in the temperate Himalayan region, 39.3 percent in the northwestern region, 32.1 percent in the eastern region and 26.2 percent in the southern region). The goat of the temperate Himalayan region grows fibres of good quality, where rainfall is low and possesses the finest quality of under coat called "Cashmere" or "Pashmina". The goat breeds found in north and northwestern regions are reasonably large in size and primarily of dairy type. In the southern and peninsular part of the country, goats of dual utility (meat and milk) are found. The highly prolific meat breeds are found in the eastern region of the country (Bhattacharyya and Khan, 1988).

Table 1. Distribution of goat breeds along with their utility in different regions of India.

Temperate Himalayan region (includes the states of Jammu and Kashmir, Himachal Pradesh and hilly areas of Uttar Pradesh)	Northwestern region (States of Haryana, Punjab, Rajasthan, Gujarat, Plains of Uttar Pradesh and north and western parts of Madhya Pradesh)	Southern region (States of Maharashtra, Karnataka, Kerala, Tamil Nadu, Andhra Pradesh and parts of Madhya Pradesh)	Eastern region (States of Bihar, West Bengal, Odisha and all the states in the eastern part of the country)
Gaddi (long hair, meat and pack animal)	Jamunapari (meat and milk)	Sangamneri (meat and hair)	Ganjam (meat)
Changthangi (fibre, meat and pack animal)	Marwari (meat and hair)	Osmanabadi (meat and milk)	Bengal goat (meat)
Chegu (fibre)	Zalawadi (meat and hair) Beetal (meat and milk) Kutchi (meat and milk) Sirohi (meat and milk) Barbari (Meat and milk) Mehsana (milk and meat) Surti (meat and milk) Jakhrana (milk and meat) Gohilwadi (meat and milk)	Kannai Adu (meat) Malabari (meat and milk) Attappady Black (meat) Konkan Kanyal (meat) Berari (meat)	

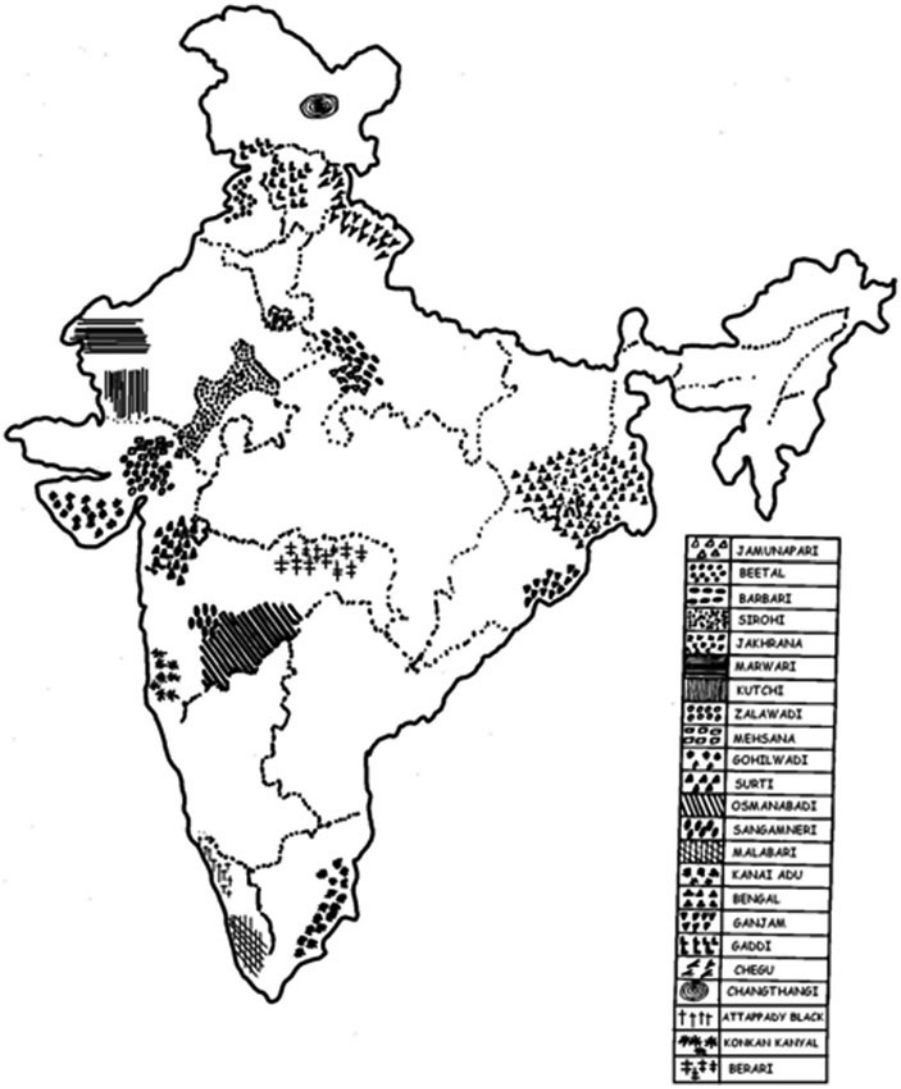

Figure 1. Distribution of goat breeds of India.

Marwari in the western dry region of Rajasthan, Kutchi in the Gujarat plains and Black Bengal in the lower gangetic plains of West Bengal are the important goat breeds for the purpose of meat production. The Jamunapari in the upper gangetic plane, Jakhrana in the central plateau and Osmanabadi in the western plateau and hill regions have been breeds of choice for higher milk production.

Moreover, there is no clear demarcation of the habitat of the breeds as most of the breeds have spread to contiguous areas by various means, which encompass migration, market dictation and economic compulsion, besides natural existence beyond the political boundaries. Thus, the breed boundary is obliterated. Similarly, the population size does not reflect the true picture as there is existence of non-descript animals in very large numbers in the habitat of most of the breeds due to genetic admixture. It is observed that there is regular migration of the goats of Western Rajasthan to the adjoining states during feed and fodder scarcity. In the process, they mix with the local goats resulting in indiscriminate crossing and loss of identity of the recognized breeds. There is no Breed Registration Society in India so far to ensure breed purity in goats and to provide identity to the enlisted animals.

As per the census report of the Department of Animal Husbandry, Dairying and Fisheries, Ministry of Agriculture, Government of India (2010), the current population of registered goat breeds of India is depicted in Table 2. However, these figures in Table 2, differ quite widely from those submitted by India to the FAO's Domestic Animal Diversity Information System (DAD-IS) online database (dad.fao.org) and other published reports. The Jakhrana, a breed found only in the Alwar region of Eastern Rajasthan, was considered to be endangered (population 8 000 in 2004 as on the DAD-IS website). However, as per the Livestock Census 2007 Reports, its population was 1.95 million. The Jamunapari breed was also considered endangered with a population of 5 000 in 2004, as per the DAD-IS database, but according to the Livestock Census 2007 Reports, its population was 1.05 million. The extremely small number of

Table 2. The habitat and population size of different goat breeds of India (Source: Official website http://dahd.nic.in/Default1.aspx).

Breed	Broad habitat	Population (in million)
Dual-purpose breeds (milk and meat)		
Barbari	Agra, Mathura, Etah and Aligarh districts in Uttar Pradesh	3.15
Beetal	Gurdaspur, Amritsar and Firozpur districts in Punjab	0.30
Gohilwadi	Bhavnagar, Amreli and Junagarh districts in Gujarat	0.32
Jakhrana	Jakhrana village in Alwar district of Rajasthan	1.95
Jamunapari	Chakarnagar Block in Etawah district of Uttar Pradesh	1.05
Kutchi	Kutch district in Gujarat	0.66
Malabari	Kozhikode, Kannur and Malappuram districts in Kerala	0.71
Marwari	Western Rajasthan	7.57
Mehsana	Mehsana and Banaskantha districts in Gujarat	0.59
Sirohi	Sirohi and Ajmer districts in Rajasthan	2.91
Surti	Surat and Vadodara districts in Gujarat	0.67
Zalawadi	Surendranagar and Rajkot districts in Gujarat	0.82
Meat breeds		
Black Bengal	West Bengal, Jharkhand, Odisha, Bihar and Assam	20.92
Gaddi	Chamba, Kangra, Kulu, Bilaspur, Kinnanaur and Lahul-Spiti districts in Himachal Pradesh	0.47
Ganjam	Ganjam district in Odisha	0.15
Kannai Adu	Ramanathpuram and Tirunelveli districts in Tamil Nadu	2.09
Osmanabadi	Osmanabad district in Maharashtra	1.55
Sangamneri	Ahmednagar district in Maharashtra	0.21
Konkan Kanyal	Konkan region of Maharashtra	–
Berari	Vidarbh region of Maharashtra	–
Attappady Black	Palakkad district of Kerala	0.007
Pashmina breeds		
Changthangi	Ladakh district in Jammu and Kashmir	0.21
Chegu	Uttarkashi, Chamoli and Pithoragarh districts in Uttaranchal	0.01

pure-bred Jamunapari animals remaining was also confirmed by the Animal Husbandry Department of Uttar Pradesh (Ahlawat, Gupta and Kumar, 2009). The Barbari breed population in 1987 according to DAD-IS was about 80 000 and, according to the 2007 census, it was 3.15 million. According to a survey done by NBAGR, the Beetal goat breed population in Punjab in 1997 was 20 800 (Pundir, 2010), whereas the 18th Livestock Census puts it was 0.30 million. The Sangamneri breed population, according to DAD-IS, was 40–60 000 in 1995, and the 2007 census reports it to be 0.21 million. With such huge discrepancies of population figures, it is more than likely that the breeds that need urgent efforts to boost their populations will be neglected (SA PPLPP, 2012).

Threatened goat breeds and its conservation

The modern goat breeds in India can be generally placed under two categories, i.e. endangered and vulnerable, although some of its wild predecessors that once existed in mountain ranges are already extinct. A breed is considered as *endangered*, when the effective population size is too small to prevent genetic loss through inbreeding leading to infertility and lack of survivability resulting in ultimate loss of the population (Bodo, 1989) According to Food and Agricultural Organization, a breed with a population size of 5 000 breeding females or less can be declared as endangered (FAO, 1995). On the other hand, a breed is vulnerable, when the population is rapidly declining numerically or its security is under threat (Maijala *et al.*, 1984; Quartermain, 1992). However, the need for conservation depends upon several factors, e.g. (i) the actual number of animals, (ii) the rate of decline in the population size, (iii) the closeness of relationship between individuals within the population, (iv) the sex ratio, (v) the geographical range and the rate of reduction of that range, (vi) special threats from introduced species, (vii) rapid changes in the environmental conditions including climate, (viii) predators, (ix) parasites, etc. (Henson, 1992).

The recognized breeds of Indian goat population are facing a greater threat of becoming endangered due to various reasons such as lack of proper breeding policy, inadequate number of breeding bucks, indiscriminate breeding and intermixing among breeds with local animals, etc. The other factors such as dispersed home tract of goat in two or more district/states, non-availability of breed-wise figures in the Indian Livestock Census Reports, migration of flocks, higher slaughter rate of fast-growing goats and the increase of ratio of non-descript to descript animals in different parts of home tract of recognized breeds makes it difficult to assess the exact population size of particular breed to plan for their improvement in population size or to declare as endangered one. A sound conservation programme of goat breeds that are adapted to high altitude, harsh environment and marginal agricultural regions has been perpetually neglected. They have not been adequately

maintained in their habitat for obtaining their maximum productivity. No attention has been given to valuable traits, such as fecundity, disease resistance, grazing habit, cheese quality, meat quality, skin characteristics, although these are crucial for the development programme of goats. Moreover, India is facing major environmental problems due to depletion in fallow land, increase in agricultural land, increase in human population, apathy for rangeland management and reservation of forests for wildlife protection, etc.

The purebred Jamunapari population has declined seriously and it is <8 500 in its habitat (Roy, Singh and Khan, 1982) due to various reasons such as shrinkage of grazing land, inadequate veterinary help, frequent selling of goats and labourer problems, etc. Beetal goat is drawing attention for conservation as the number is declining due to changing agricultural patterns in Punjab. Barbari is facing dilution in breed characteristics due to cross-breeding with Sirohi and Jamunapari breeds in its home tract. Owing to decrease in natural browse in their habitat, Surti and Jakhrana are decreasing in number. The Changthangi breed of the Ladakh region is the subject for special concern as they are declining both in number and in performance. More weightage on improvement of some breeds and extensive use of these breeds, such as Beetal, Barbari and Jamunapari could result in the elimination of other distinctive breeds by cross-breeding. Means for the conservation, multiplication and improvement of these breeds in the pattern of Open Nucleus Breeding Scheme (ONBS) were suggested (Acharya, Misra and Patil, 1982). Moreover, Devendra and Burns (1983) have also drawn attention for the conservation programme for specific goat populations in developing countries.

The need for conservation of distinct and well-adapted breeds has now lately been realized. It is apparent from the current population size, loss of habitat and introduction of other breeds in the area, the threatened breeds are Jamunapari, Beetal, Jakhrana and Surti in the northwestern region, Sangamneri, Osmanabadi, Malabari and Attappady Black in the southern region, Ganjam in the eastern region and Chegu and Changthangi in the temperate Himalayan region (Figure 2). The population of several breeds is more or less vulnerable except for Marwari and Black Bengal, who are at present in a rather comfortable position with respect to breed population, at large breeding tracts.

Necessity of conservation

The market competition created through introduction of exotic breeds, difficulties associated with low production potential of indigenous breeds and changes in the farming system have resulted in either steady decline in the number of purebred goats or dilution of the genetic material. The conservation of goat genetic resources is essential and is of paramount importance in recent times owing to their widespread destruction, overexploitation and degradation by mankind all over India. The conservation of animal genetic resources should now be a multidimensional activity, which has to encompass not only preservation and maintenance of existing breeds, but also their proper management and improvement. The overall aim is sustainable utilization, restoration and enhancement of

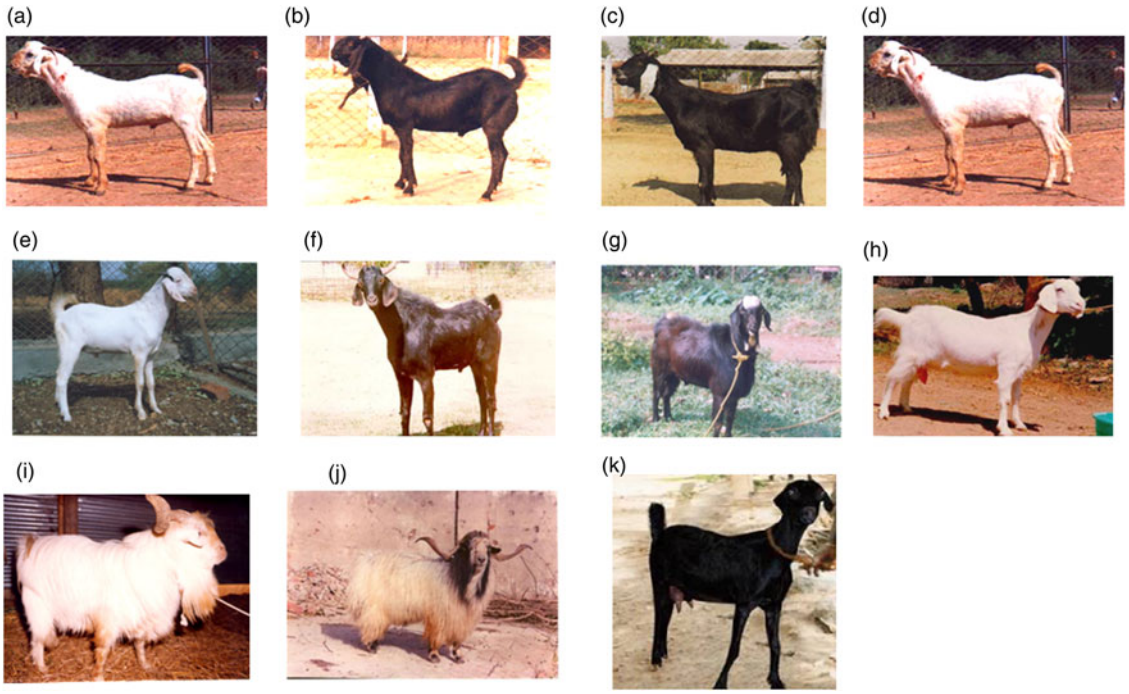

Figure 2. Threatened goat breeds of India (source: Roy, Roy and Mandal, 2009). (a) Jamunapari goat. (b) Beetal goat. (c) Jakhrana goat. (d) Surti goat. (e) Sangamneri goat. (f) Osmanabadi goat. (g) Ganjam goat. (h) Malabari goat. (i) Changthangi goat. (j) Chegu goat and (k) Attappady Black goat.

resources so as to meet the needs of mankind for the present as well as for the future generations.

There has been awareness for conservation of natural resources with various types of flora and fauna since a long time. However, the livestock species such as goat-gained attention only recently, when it was realized that the production-oriented propagation of goat through cross-breeding and upgrading did not work in the long term and this approach is eroding the existing genetic architecture of breeds and/or genetic variability in indigenous goat germplasm. Goats are fundamental and having close bondage to most agro-ecosystems in India and it is considered as the important genetic material for each production system. This material is critical for system resilience and flexibility and enables production and productivity to be increased. Food production will only be achieved and maintained by utilizing appropriate genetic resources. The type of genetic material required to meet these challenges must be determined by the nature of the production environment, which differs greatly within zones/regions. Climatic conditions, the type and availability of feed resources, including palatability and digestibility of feeds, fodders and grasses, disease stress, level of management and the kind and quality of products required must all be taken into consideration while taking up conservation programmes.

Generally two approaches, i.e. *ex situ* and *in situ* methods of conservation may be adopted for the goat breeds in India. Generally, embryos are considered to be the best material for *ex situ* conservation because they store all genetic material in a single entity, which can give rise to new progeny. Sperm and embryos of goats like other farm animal species can be frozen and subsequently used to produce a normal offspring. Moreover, cryogenic storage of DNA of different goat breeds may be done as an alternative approach for conservation of goat genetic resources in India.

Phenotypic characterization

The phenotypic characterization with respect to physical appearance, body growth and body measurements of most of the goat breeds viz. Jamunapari, Barbari, Jakhrana, Marwari, Sirohi, Zalawadi, Gohilwadi, Beetal, etc. was carried out by the Central Institute for Research on Goats (CIRG), Makhdoom, Mathura under the All India Coordinated Research Project (AICRP) on Goats and also by the National Bureau of Animal Genetic Resources (NBAGR), Karnal, Haryana, India. The detailed physical characterization of different goat breeds of India has been described by Roy, Roy and Mandal (2009).

Molecular genetic characterization

Molecular characterization of ten Indian goat breeds viz. Jamunapari, Barbari, Marwari, Sirohi, Jakhrana, Black Bengal, Pashmina, Osmanabadi, Kutchi and local goats has been completed at CIRG, Makhdoom, Mathura (Rout, Thangaraj and Mandal, 2004a; Rout *et al.*, 2008). Furthermore, attempts are being made to characterize these goat breeds genetically based on microsatellite markers linked to fecundity rate variability (Rout, Mandal and Roy, 2006). Microsatellite analysis of Jamunapari, Barbari, Black Bengal, Sirohi, Jakhrana, Marwari, Kutchi and Pashmina goats was carried out using three microsatellite markers, i.e. BM4621, OarAE101 and Oar HH56, which have been reported to be linked with the fecundity rate in cattle and sheep. At BM4621 locus, Jamunapari goats showed the highest number of alleles (15 alleles) and the highest heterozygosity was observed in Black Bengal, Barbari, Jamunapari and Jakhrana goats in BM4621 locus. About 12 alleles were observed for the locus OarAE101 in all the eight goat breeds, of which Barbari and Marwari showed ten alleles each. At this locus, the highest genetic variability was observed in Barbari, Marwari and Sirohi goats. The locus OarHH56 showed a total of 14 alleles in all the analysed samples, in which Jakhrana goats showed 12 alleles and the highest genetic variability was observed in Jakhrana, Sirohi and Pashmina goats in this locus. Thus BM4621 marker exhibited the highest gene diversity in Black Bengal, Barbari and Jamunapari goats as compared with other two markers indicating the best suitable marker for fecundity traits of Indian goat breeds.

Beside this, NBAGR, Karnal, Haryana also started molecular characterization work on different Indian goat breeds using microsatellite markers (Dixit *et al.*, 2008, 2010, 2011; Kumar *et al.*, 2009; Mishra *et al.*, 2012, 2013).

Conservation measures

Ex-situ conservation

Some preliminary work on *ex situ* conservation of goat genetic resources has already been started at CIRG, Makhdoom, Mathura, India. The breeds covered in this programme were mainly Jamunapari and Barbari goats. Cryogenic storage of DNA of different goat breeds is also initiated by CIRG, Makhdoom, Mathura and NBAGR, Karnal, Haryana.

In situ conservation

The *in situ* conservation of goats has been started by the CIRG, Mathura, Uttar Pradesh, India and has brought the success to CIRG in terms of farmers' participation and breed improvement at the farmers' level. For this purpose, flocks of Jamunapari, Barbari and Jakhrana goats are being maintained at the CIRG under the scientific management system for producing and supplying superior bucks for the breed improvement programme at farmers' flocks. Beside this, breed improvement and conservation programmes of different goat breeds under field condition were launched under the AICRP on Goats by establishing

several field units of different goat breeds of India (Swarup and Singh, 2011).

Under this *in situ* conservation programme, the most important Indian dairy goat breed, Jamunapari goats, received special attention. The breed improvement and conservation programme on Jamunapari goats in its home tract started functioning in 1993 in two villages of Chakarnagar block of Etawah district of Uttar Pradesh due to rapidly deteriorating state of Jamunapari goats in their home tract. The project was started with active support of farmers to restore the pride of the Jamunapari breed in its home tract. The goat population is a highly changing phenomenon due to frequent sale of animals. The selling pattern shows that the selling percentage of males has increased over the base year, whereas the sale of females has decreased. The increasing trend in body weight over the base populations observed in these two villages indicated the benefit of use of superior breeding bucks by villagers over the years. The average conception rate, kidding percentage, kidding rate and twinning percentage was 88, 77.4, 1.6 and 52.2 percent, respectively. The kidding rate and multiple birth rates are in increasing trend over the years. The multiple birth percentage had increased over the years, indicating selection of females having twin birth is preferred over single born kids. The fertility and viability are in increasing trend from the base population and the sex ratio is also maintained over the years. The effective population size has also increased from the base year and all these factors indicate that the conservation strategy is in desired direction and needs careful attention in future (Singh *et al.*, 2003; Rout *et al.*, 2004b).

Similarly, the other field-based units developed under AICRP on Goat Improvement programme were Rajasthan Agricultural University, Bikaner, Rajasthan; West Bengal University of Animal and Fishery Sciences, Kolkata, West Bengal; Odisha University of Agriculture and Technology, Bhubaneswar; Mahatma Phule Krishi Vidyapeeth, Rahuri, Maharashtra; Gujarat Agricultural University, Navsari, Gujarat; Livestock Research Station, Vallabhnagar, Udaipur, Rajasthan; Assam Agricultural University, Guhawati, Assam; Birsa Agricultural University, Ranchi, Jharkhand; Himachal Pradesh Krishi Viswavidyalaya, Palampur, Himachal Pradesh; Nimbkar Agricultural Research Institute, Phaltan, Maharastra; and Kerala Agricultural University, Mannuthy, Thrissur, Kerala for Marwari, Black Bengal, Ganjam, Sangamneri, Surti, Sirohi, Assam Hill, Black Bengal, Gaddi, Osmanabadi and Malabari goats, respectively (Swarup and Singh, 2011).

Furthermore, a programme for the conservation of the Beetal goat breed in Punjab was jointly implemented from 2005 to 2008 by the NBAGR with the Krishi Vigyan Kendra (KVK). This programme was operated by the Society for Creation of Heaven on Earth, an NGO working in Tepla, Ambala (Pundir, 2010). The objective of this programme was to reverse the declining trend in the population of Beetal goats since a survey conducted by NBAGR in 1997 showed the Beetal population is declining day by day. The programme was carried out in 92 farmers' flocks in 41 villages and the findings of this survey revealed that the Beetal goat rearing in Punjab is profitable and, as a result, many new farmers started rearing Beetal goats and population of this breed is now in increasing trend (Pundir, 2010).

Beside this, the Department of Animal Husbandry, Dairying and Fisheries, Ministry of Agriculture, GOI, had launched a programme for the conservation of threatened breeds of small ruminants (and rabbits, pigs, pack animals and equines), for which an outlay of Rs. 150 million was provided during the Tenth Plan (2002–2007). Its objective was to preserve the breeds of small ruminants, etc., which are on the verge of extinction by providing proper infrastructure and germplasm in association with State Governments and their undertakings, NGOs, professional bodies and institutes, private limited companies, etc. The Department intended to establish 18 units of small ruminants during the 10th Plan. However, funds were provided for the conservation of six goat breeds. The goat breeds were Terresa goat in the Andaman and Nicobar Islands, Malabari goat in Kerala, Sangamneri goat in Maharashtra, Black Bengal goat in Tripura and West Bengal, Jamunapari goat in Uttar Pradesh and the Long Haired goat in Nagaland. Of these, the Terresa and the Long Haired goat breeds are not registered. In the 11th Five Year Plan, Rs. 450 million was allotted for this programme. It was intended to support breeds with a declining population and an existing population of about 10 000 animals or less. Nucleus breeding units were to be supported along with strengthening of policy and institutional framework and linkages with research agencies. In the annual report of the Department for 2010–11, funding to the Government of Gujarat for a nucleus breeding unit of the Surti goat is also mentioned. However, no documented result is available on the impact of this project (SA PPLPP, 2012).

Discussion

Small ruminants play a vital role in the livelihood of small and marginal farmers, landless agricultural labourers in India. The strong association between people and goat is indicated by the fact that India ranks second in world's human as well as goat population. Goats are treated as part of rural family, sometimes particular buck and does are maintained till their death and only their offspring are sold for sustaining livelihood. Natural selection as well as selective breeding by the farmers leads to development of particular breeds, which can adapt well to a particular environment and produce well. So far, India has 23 recognized breeds of goats, but still more than 75 percent of goat population is categorized as non-descript. This is mainly

due to the fact that attempts have not been made so far to characterize these populations rather than lack of any distinct characters in many of the goats. The emphasis on "breeds" in the context of conservation or improvement programmes, needs to be reconsidered. Instead of emphasizing "breed purity", it is important to improve the existing adapted populations of various breed types in different parts of the country (SA PPLPP, 2012).

Overexploitation of a particular breed of goats for its unique character such as better meat quality leads to excessive/indiscriminate slaughter of younger ones even at early age, slaughter of breedable adults, insufficient numbers of breeding males leads to reduction in the population and possibility of becoming endangered. Flock migration, mixing up of different breeds in migratory flocks and indiscriminate cross-breeding lead to lack of uniqueness among the herd.

There is no better way to conserve an indigenous breed for future generations than to consistently keep the breed or population viable using an efficient, demand-driven, long-term breeding programme suitable to commercial and cultural needs of livestock owners (Phillipsson *et al.*, 2011). *In situ* conservation is, therefore, the most effective method of conservation, provided it is economically viable for livestock keepers. Smallholder livestock keepers should be supported to continue to maintain the breed. Well-implemented, small ruminant genetic improvement programmes delivering improved genotypes, together with other interventions such as improvements in health, nutrition and other aspects of livestock management, and establishing market linkages, have the potential to improve the income of the poorest of the poor rural households while contributing to the nation's food security.

Livestock genetic improvement programmes should be seen as investments because the effects of selection accumulate over time and will give benefits over all subsequent years without further intervention. Considering the constraints of lack of infrastructure, shortage of trained and experienced personnel, low level of literacy and awareness among livestock keepers in developing countries, even a benefit to cost ratio of 5 will make such improvement worthwhile. Small ruminant conservation and improvement programmes should, therefore, be seen as important parts of national and state policies, aimed at alleviating poverty and improving the food production of a country, region or locality and the income of livestock keepers. Funding agencies that support projects for "community development and livelihood promotion" should ensure that such projects have a livestock genetic improvement component, where appropriate. The duration of a genetic improvement programme – especially a selection programme – should be at least 10 years. At the end of 12–15 years, every effort should be made to make the programme self-sustainable. Funding and implementing agencies need to be aware that if they withdraw support half-way, the whole exercise would be meaningless. The extra investment due to the longer time period would be worthwhile because the gains due to genetic improvement are permanent and cumulative (SA PPLPP, 2012).

Steps are initiated by the Central and State Government agencies, non-governmental organizations to conserve certain breeds of goat as *in situ* as well as *ex situ* conditions. NBAGR and Central Institute of Research in Goats have made attempts in this line. Further financial support to the native rearers will help them to maintain the population without dilution.

Conclusion

The conservation of goat genetic resources in India helps maintain the uniqueness/traditional characteristics of indigenous goat breeds and biodiversity of this species. Among the various conservation approaches, the *in situ* conservation is the most effective method of conservation of goat genetic resources, provided it is economically viable for livestock keepers. Moreover, frozen semen and/or embryos of endangered or "at-risk" breeds should also be stored as *ex situ* conservation approach. Since reliable information on the actual numbers of different goat breeds in the country is not available, it is extremely difficult to identify breeds that are at the greatest risk of extinction. Mapping of well recognized/registered goat breeds and their present numbers must be undertaken urgently to identify the breeds that face the greatest risk of extinction. Furthermore, molecular genetic characterization of different breeds can also be helpful to characterize the relationships among the breeds and improvement programmes. The future of the goat in India lies in the appropriate approaches to conservation combining a number of integrally related components and effective action programmes approached holistically for successful conservation of goat genetic resources at the national level.

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Animal Genetic Resources, 2014, 55, 57–66. © Food and Agriculture Organization of the United Nations, 2014
doi:10.1017/S2078633614000344

Path analysis of the relationship between body weight and some linear characters in West African Dwarf sheep

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Summary

The usefulness of correlation analysis in life sciences is enhanced when the coefficient is partitioned into direct effects of one trait on the other and indirect effects caused by other characters which may be of importance in selection. A total of 417 mature (>22 months) West African Dwarf (WAD) sheep comprising of 201 rams and 216 ewes intensively reared were used for this study. Data were taken on body weight (BW) and 19 linear conformation traits. Linear body measurements considered were rump width (RW), rump length (RL), tail length (TL), wither height (WH),thorax depth (TD), shin circumference (SC), heart girth (HG), paunch girth (PG), rump height (RH), ear length (EL), fore-leg length (FLL), rear-leg length (RLL), body length (BL), shoulder width (SW), neck circumference (NC), head length (HL), head width (HW), horn length (HoL) and hock length (Hock). Descriptive statistics and path coefficients were computed. Correlation analysis was also explored to determine the degree of association among variables. Sexual dimorphism was observed in all traits considered ($p < 0.05$), except RL. Large coefficients of variation were obtained for BW, PG and NC relative to other traits considered. All linear traits had significantly positive ($p < 0.05$) correlations with BW in both sexes. The ranges of correlation between BW and all linear body parameters were, 0.227–0.726 and 0.183–0.878 in rams and ewes, respectively. The highest correlations with BW in rams and ewes were obtained for HG and NC, respectively. Significant path coefficients were obtained for HG and TD in rams while HG, FLL, PG, NC and RL had significant ($p < 0.05$) path coefficients in ewes. Though many predictor variables were considered in this study, it was concluded that HG contributed most to the coefficient of determination in both sexes. Moreover, all other predictor variables with similar ($p > 0.05$) path coefficients had high correlations with BW, their indirect effects were obtained mostly through HG.

Keywords: *path coefficient, phenotypic correlation, WAD sheep*

Résumé

L'utilité de l'analyse de corrélation en sciences de la vie est améliorée lorsque le coefficient est divisée en effets directs d'un trait sur les autres et les effets indirects causés par d'autres personnages qui peuvent être d'une importance dans la sélection. Un total de 417 matures (>22 mois) nains d'Afrique de l'Ouest (WAD) moutons comprenant 201 béliers et 216 brebis en élevage intensif ont été utilisés pour cette étude. Les données ont été prises sur le poids corporel (BW) et 19 caractères de conformation linéaires. Mensurations linéaires considérés étaient largeur croupe (RW), longueur croupe (RL), longueur de la queue (TL), Hauteur au garrot (WH), la profondeur du thorax (TD), tibia circonférence (SC), circonférence de coeur (HG), la circonférence panse (PG), hauteur croupe (RH), la longueur de l'oreille (EL), la longueur des antérieurs (FLL), longueur arrière-jambe (RLL), la longueur du corps (BL), la largeur des épaules (SW), circonférence du cou (NC), longueur de la tête (HL), la largeur de la tête (HW), longueur des cornes (HOL) et la longueur du jarret (Hock). Statistiques descriptives et coefficients de piste ont été calculés. L'analyse de corrélation a également été examinée pour déterminer le degré d'association entre les variables. Le dimorphisme sexuel a été observée chez tous les caractères considérés (p 0.05), à l'exception RL. Des coefficients de variation ont été obtenus pour BW, PG et NC par rapport à d'autres caractéristiques considérées comme. Tous les traits linéaires ont des corrélations positives significatives (p 0.05) avec BW chez les deux sexes. Les gammes de corrélation entre BW et tous les paramètres de corps linéaires étaient, de 0.227 à 0.726 et de 0.183 à 0.878 en béliers et brebis respectivement. Les plus fortes corrélations avec le poids corporel chez les béliers et brebis ont été obtenus pour HG et NC respectivement. Coefficients de chemin significatives ont été obtenues pour HG et TD dans béliers tout HG, FLL, PG, NC et RL ont significatifs ($p < 0.05$) des coefficients de chemin chez les brebis. Bien que de nombreuses variables prédictives ont été pris en compte dans cette étude, il a été conclu que HG le plus contribué à le coefficient de détermination dans les deux sexes. En outre, toutes les autres variables prédictives avec similaires ($p > 0.05$) coefficients de piste ont une forte corrélation avec BW, leurs effets indirects ont été obtenus principalement par HG.

Mots-clés: *coefficient de chemin, phénotypique corrélation, moutons WAD*

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Resumen
La utilidad de los análisis de correlación en ciencias de la vida se ve reforzada cuando el coeficiente se divide en los efectos directos de un rasgo sobre los demás e indirectos efectos causados por otros personajes que pueden ser de importancia en la selección. Un total de 417 maduras (>22 meses) West African Dwarf (WAD) ovejas que consta de 201 carneros y 216 ovejas cría intensiva se utilizaron para este estudio. Los datos se tomaron en el peso corporal (PC) y 19 rasgos de conformación lineal. Medidas corporales lineales considerados fueron anchura grupa (RW), longitud de la grupa (RL), longitud de la cola (TL), altura a la cruz (WH), profundidad del tórax (TD), la circunferencia de la pantorrilla (SC), perímetro torácico (HG), la circunferencia panza (PG), altura a la grupa (RH), longitud de la oreja (EL), longitud de la pata delantera (FLL), longitud trasera de la pierna (RLL), longitud del cuerpo (LC), anchura del hombro (SW), circunferencia del cuello (NC), longitud de la cabeza (HL), ancho de la cabeza (HW), longitud de los cuernos (HOL) y duración de la corva (Hock). Estadística descriptiva y coeficientes de trayectoria se calcularon. El análisis de correlación también fue explorado para determinar el grado de asociación entre las variables. El dimorfismo sexual se observó en todos los rasgos considerados (p 0.05), con excepción de RL. Las grandes coeficientes de variación fueron obtenidos para PN, PG y NC en relación con otros rasgos considerados. Todos los rasgos lineales tenían ($p < 0.05$) correlaciones significativamente positivas con BW en ambos sexos. Los rangos de correlación entre BW y todos los parámetros corporales lineales fueron, 0.227–0.726 y 0.183–0.878 de carneros y ovejas respectivamente. Las correlaciones más altas con el peso corporal en carneros y ovejas fueron obtenidos para HG y NC, respectivamente. Coeficientes de trayectoria significativas fueron obtenidas para HG y TD en los carneros mientras HG, FLL, PG, NC y RL tuvieron significativas (p 0.05) coeficientes de trayectoria en las ovejas. Aunque se consideraron muchas variables de predicción en este estudio, se concluyó que HG más contribuyó al coeficiente de determinación en ambos sexos. Por otra parte, todas las demás variables de predicción con ($p > 0.05$) coeficientes de trayectoria similares tenían altas correlaciones con BW, sus efectos indirectos fueron obtenidos principalmente a través de HG.

Palabras clave: *coeficiente de trayectoria, la correlación fenotípica, ovejas WAD*

Submitted 29 November 2013; accepted 28 August 2014

Introduction

Body weight of farm animals, a composite of different anatomical parts of the animal, has been predicted from linear body measurements using regression analysis (Latshaw and Bishop, 2001; Olawoyin, 2007; Raji, Igwebuike and Usman, 2009; Udeh, Isikwenu and Ukughere, 2011). The morphometric traits used for this purpose are carefully chosen based on their close association with one another and with body weight. The use of regression models does not only make on-farm determination of animal weight less tedious but also reduces the risk of hazards associated with the use of weighing scale especially in farm animals with large body size. Strong correlations between some linear body measurements and many production traits as well as qualities of carcasses in sheep have been documented (Otoikhian *et al.*, 2008; Abdel-Moneim, 2009).

Simple correlations between traits have commonly been used in the past; however, their suitability as a measure of degree of association between traits is enhanced when combined with path analysis. Yakubu and Mohammed (2012) opined that body measurements that are used to predict body weight may affect its determination directly and indirectly. Thus with the use of path analysis, the correlation coefficient between two characters is partitioned into direct (path coefficient) and indirect (effect exerted through other variables) portions. This provides an effective means of partitioning correlation coefficients into unidirectional path ways and alternate path ways, thus permitting a critical examination of specific factors that produce a given correlation; a standardized partial regression analysis that deals with a closed system of variables which are linearly related. Path analysis is very similar to multiple regression analysis, the critical difference between the two is that in the former the analytical model is built around specific causal relationships among linear measurements that determine body weight while the latter assumes a simpler causal relationship in which all linear measurements affect body weight. Even when predictor variables in multiple regressions have produced sufficiently high coefficient of determination (R^2) to justify the prediction of body weight, path analysis can provide guidelines about possible unmeasured predictor traits. The technique of path analysis in livestock experiments has been extensively used by Yakubu and Salako (2009); Ogah *et al.* (2011); Yakubu and Mohammed (2012). The objective of this study was to obtain a detailed relationship between body weight and some linear body measurements in West African Dwarf (WAD) sheep from Nigeria.

Materials and method

The study was carried out at the sheep unit of the teaching and research farm, University of Ibadan, Ibadan, Southwest Nigeria (Figure 1). Body weight and nineteen (19) linear measurements were taken from four hundred and seventeen (417) adult WAD sheep comprised of two hundred and one (201) rams, and two hundred and sixteen (216) ewes. Data were taken between August 2012 and May 2013. Although many of the sheep were purchased from pastoralists, they have been reared intensively in the teaching and research farm for a minimum of three months before measurements were

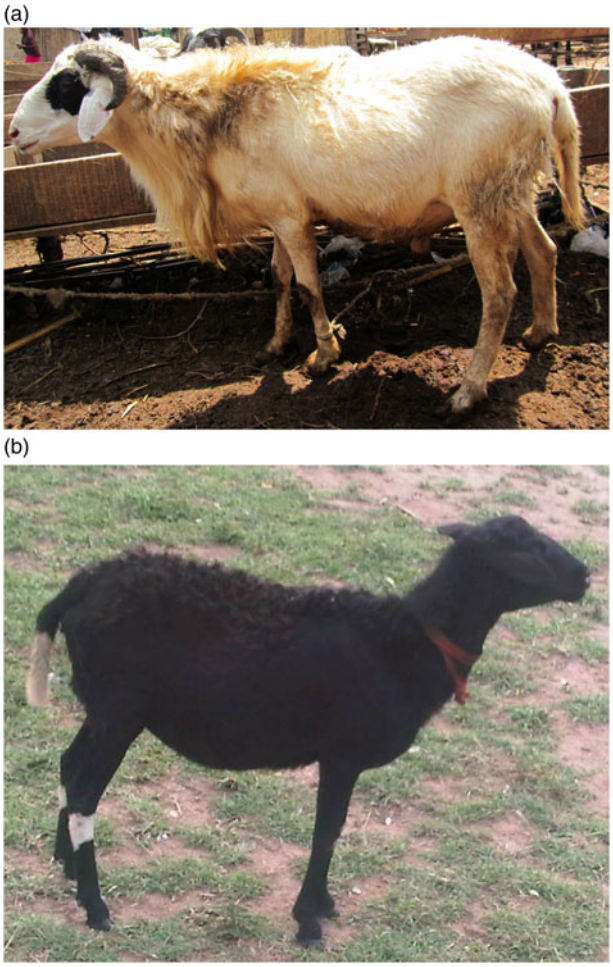

Figure 1. West African Dwarf (WAD) Ram (A) and Ewe (B), Teaching and Research Farm of University of Ibadan.

taken. Pregnant, lactating and sick animals were excluded from the study. Body measurements were taken when the animals were in standing position with head raised and weight on all four feet without body movement. Animals were restrained physically to limit movement. Measurements were taken in the morning before feed was supplied giving a minimum of 16 h between feeding and weighing. Linear characters were measured with a measuring tape. The methods used for the measurements are as described by FAO (2012). Anatomic reference points for the measurements are as described by Searle, McGraham and Donnelly (1989), and Salako and Ngere (2002). Linear body characters considered were rump width (RW), rump length (RL), tail length (TL), wither height (WH),thorax depth (TD), shin circumference (SC), heart girth (HG), paunch girth (PG), rump height (RH), ear length (EL), fore-leg length (FLL), rear-leg length (RLL), body length (BL), shoulder width (SW), neck circumference (NC), head length (HL), head width (HW), hock length (Hock) and horn length (HoL for rams alone).

Means, standard deviation (SD) and coefficient of variation (CV) were determined for live weight and linear body measurements. A *t*-test was used to check whether morphometric characters between the two sexes were significantly different. Pearson correlation coefficients were calculated to determine the degree of association between the variables. Data were checked for multicollinearity and singularity. Compound linear regression was also performed, where partial regression coefficients were standardized. The standardized linear regression coefficient (path coefficient) shows the direct effect of linear measurements (X) on live weight (Y).

$$\mathrm{PY}.X_{\mathrm{i}} = b_i \frac{\mathrm{SD}X_i}{\mathrm{SD}Y}$$

where PY.X_i, path coefficient from X_i to Y (i = HL, HW, HoL, EL, NC, HG, SW, TD, FLL, WH, Hock, BL, PG, RH, TL, RL, RLL, SC and RW); b_i, unstandardized or partial regression coefficient; SDX_i, standard deviation of linear measurements; SDY, standard deviation of live weight.

The indirect effects of X_i on Y through X_j were computed as

$$\mathrm{IEY}X_i = (rX_iX_jP)\,(\mathrm{PY}.X_j)$$

where IEYX_i, correlation coefficient between ith and jth linear measurements; PY.X_j, path coefficient that indicates the direct effect of jth linear measurement (exogenous variable) on live weight (endogenous variable).

The model for the multiple linear regression was

$$Y = a + b_1X_1 + b_2X_2 + \cdots + b_{19}X_{19}$$

Y, body weight (dependent variable); a, intercept; b, standardized regression coefficient; X, exogenous variable (HL, HW, HoL, EL, NC, HG, SW, TD, FLL, WH, Hock, BL, PG, RH, TL, RL, RLL, SW and SC).

The significance of each path coefficient in the model was tested by the *t*-test procedure according to the method of Yakubu and Mohammed (2012)

$$t_j = \frac{b_j - \beta_j}{\sqrt{\mathrm{var}(b_j)}} \sim t\alpha(n - p - 1); \quad j = 1,\ 2,\ \ldots,\ p$$

where var(b_j), the diagonal member of matrix S^2 (X′X)$^{-1}$; S^2, mean square of residual obtained from ANOVA.

Though partitioning of total coefficient of determination (R^2) into direct and combined effects of explanatory predictor variable is possible, the computation of combined effects will be ambiguous because of large number of predictor variables considered in this study. There are 171 combinations for 19 predictor variables ($^{19}C_2$). Thus, a

pooled combined effect was generated

$$R^2 \text{ resulting from direct effect} = P^2Y.X_1 + P^2Y.X_2 + P^2Y.X_3 + P^2Y.X_4 + P^2Y.X_5 + P^2Y.X_6 + P^2Y.X_7 + P^2Y.X_8 + P^2Y.X_9 + P^2Y.X_{10} + P^2Y.X_{11} + P^2Y.X_{12} + P^2Y.X_{13} + P^2Y.X_{14} + P^2Y.X_{15} + P^2Y.X_{16} + P^2Y.X_{17} + P^2Y.X_{18} + P^2Y.X_{19}$$

where, $P^2Y.X_1$, direct effects of predictor variables (HL, HW, HoL, EL, NC, HG, SW, TD, FLL, WH, Hock, BL, PG, RH, TL, RL, RLL, SW and SC) in contributing to the variation of Y (body weight). Data were analysed with SPSS 15.0 while computation of path coefficients was done manually.

Results and discussion

Descriptive statistics for body weight and linear body measurements

The difference in body weight means between rams and ewes was on average 5.91 kg (Table 1). The mean weight in this study was similar to the 15.28 kg found for rams and lower than the 15.90 kg for ewes reported by Yakubu (2010) for Yankasa lambs. There was significant sexual dimorphism in all traits considered ($p < 0.05$) except for length of rump. The means for linear body parameters in this study are similar to those reported by Yunusa, Salako and Oladejo (2013) for WAD sheep. The means of 58.35 ± 0.77 and 23.96 ± 0.31 cm obtained for paunch girth and neck circumference respectively are different from those of Yunusa, Salako and Oladejo (2013), and this may be explained by large environmental influences on these traits. Large coefficients of variation obtained for neck circumference (18.07 percent) and paunch girth (18.65 percent) may further suggest large environmental influence on these biometric traits (Table 2). Because of gut fill, the paunch girth of an animal depends on its feeding regime, and therefore is highly variable. Mane in the neck region, especially in WAD rams makes it a highly variable measure; there were large individual differences in the incidence and amount of mane. Thus, neck circumference in WAD rams is usually over estimated when mane is included. Although ewes do not have a mane, higher variability was obtained for them compared with rams. Height at wither obtained in this study for both sexes were lower than the 61.74 ± 0.29 cm reported by Salako and Ngere (2002) for mature WAD sheep, although the authors did not indicate sex of the animals. Mean wither height of 57.97 ± 0.60 cm obtained for WAD rams in this study was closer to the mean the previous author reported. They also reported mean body length 62.56 ± 0.37 cm for WAD sheep which is similar to what we obtained. The sheep were found to be longer than they are tall. Coefficients of variation of 48.67 and 52.03 percent were obtained for body weight of rams and ewes, respectively. The reason for the large coefficients

Table 1. Description of body weight and linear body measurements.

Traits	Ram (mean ± SE)	SD	CV	Ewe (mean ± SE)	SD	CV
Head length (cm)	18.71 ± 0.15[a]	2.21	11.81	15.76 ± 0.17[b]	2.44	15.48
Head width (cm)	12.31 ± 0.11[a]	1.54	12.51	10.22 ± 0.09[b]	1.31	12.82
Horn length (cm)	10.44 ± 0.42	6.05	57.95			
Ear length (cm)	11.71 ± 0.07[a]	1.01	8.63	11.05 ± 0.10[b]	1.44	13.03
Neck circumference (cm)	23.96 ± 0.31[a]	4.33	18.07	18.74 ± 0.25[b]	3.63	19.37
Hearth girth (cm)	57.97 ± 0.60[a]	8.44	14.56	47.44 ± 0.73[b]	10.75	22.66
Shoulder width (cm)	13.96 ± 0.14[a]	1.93	13.83	11.80 ± 0.12[b]	1.81	15.34
Thorax depth (cm)	17.20 ± 0.18[a]	2.59	15.06	14.53 ± 0.20[b]	2.89	19.89
Fore-leg length (cm)	38.65 ± 0.30[a]	4.28	11.07	34.04 ± 0.33[b]	4.82	14.16
Wither height (cm)	56.97 ± 0.56[a]	7.85	13.78	48.93 ± 0.50[b]	7.35	15.02
Hock length (cm)	25.00 ± 0.24[a]	3.38	13.52	22.16 ± 0.19[b]	2.82	12.73
Body length (cm)	61.70 ± 0.66[a]	9.41	15.25	50.75 ± 0.65[b]	9.55	18.82
Paunch girth (cm)	58.35 ± 0.77[a]	10.88	18.65	47.47 ± 0.78[b]	11.53	24.29
Rump height (cm)	58.78 ± 0.54[a]	7.72	13.13	49.58 ± 0.60[b]	8.88	17.93
Tail length (cm)	25.89 ± 0.34[a]	4.77	18.42	22.46 ± 0.30[b]	4.45	19.81
Rump length (cm)	11.70 ± 0.26	3.69	31.54	11.10 ± 0.51	7.54	67.92
Rear-leg length (cm)	41.97 ± 0.38[a]	5.42	12.91	37.11 ± 0.35[b]	5.18	13.96
Shin circumference (cm)	6.03 ± 0.04[a]	0.55	9.12	5.33 ± 0.03[b]	0.46	8.63
Rump width (cm)	9.33 ± 0.10[a]	1.36	14.58	8.25 ± 0.12[b]	1.71	20.73
Body weight (kg)	16.52 ± 0.57[a]	8.04	48.67	10.61 ± 0.38[b]	5.52	52.03

[ab]Means along same row with different superscripts are significantly different (P < 0.05).

Table 2. Direct and combined effects of the biometric traits.

Traits	Coefficient of determination (R^2)	
	Ram	Ewe
P^2LW.HL	0.03	0.01
P^2LW.HW	0.00	0.01
P^2LW.HoL	0.01	
P^2LW.EL	0.00	0.00
P^2LW.NC	0.00	0.03
P^2LW.HG	0.27	0.16
P^2LW.SW	0.05	0.01
P^2LW.TD	0.06	0.01
P^2LW.FLL	0.03	0.04
P^2LW.WH	0.00	0.09
P^2LW.Hock	0.00	0.00
P^2LW.BL	0.05	0.01
P^2LW.PG	0.00	0.04
P^2LW.RH	0.01	0.00
P^2LW.TL	0.00	0.01
P^2LW.RL	0.01	0.00
P^2LW.RLL	0.01	0.00
P^2LW.SC	0.00	0.01
P^2LW.RW	0.01	0.00
Total direct effect	0.54	0.41
Combined effects	0.03	0.43
Total	0.57	0.84

P^2, square of path coefficient; HL, head length; HW, head width; EL, ear length; NC, neck circumference; HG, heart girth; SW, shoulder width; TD, thorax depth; FLL, fore-leg length; WH, wither height; Hock, hock length; BL, body length; PG, paunch girth; RH, rump height; TL, tail length; RL, rump length; RLL, rear-leg length; SC, shin circumference; RW, rump width.

of variation is not clear. Body weight is the resultant of all component body parts; the large variability could have resulted from variability in gut fill since gut fill is a component of live weight. Within breed diversity has been reported for different breeds of sheep indigenous to Nigeria with the use of DNA markers (Agaviezor *et al.*, 2012a, 2012b; Yunusa, Salako and Oladejo, 2013), which suggest that many traits are still largely unselected for in these animals, thus confirming them as a valuable genetic resource.

Correlation between traits

Correlations among body weight and linear body measurements of WAD rams and ewes are presented in Table 3. There were significant correlations ($p < 0.05$) between all pairs of traits in rams. The range of correlations between body weight and all linear body measurements was 0.227–0.726 in rams. In ewes, rump length showed insignificant ($p > 0.05$) correlation with both hock length and paunch girth, indicated that these traits are not associated. The range of correlations between body weight and all linear body parameters was 0.183–0.878 in ewes. The highest and lowest correlations were obtained for heart girth and rump length with body weight, respectively, in both sexes. High correlation of heart girth with body weight has been documented (Searle, McGraham and Donnelly, 1989; Afolayan, Adeyinka and Lakpini, 2006; Yakubu, 2010). Afolayan, Adeyinka and Lakpini (2006) reported that heart girth accounted for 90 percent of total weight variance in Yankasa sheep. There was no multicollinearity between traits in both sexes since the pilot analysis indicated that the value of variance inflation factor (VIF) was less than 10 and the tolerance (T) value was greater than 0.1 in all cases (Gill, 1986; Pimentel *et al.*, 2007; Yakubu, 2010).

Path coefficient

Path coefficients of the linear body measurements (independent variable) of WAD rams are presented in Table 4. Path analysis permits the partitioning of correlation coefficients into component parts (Marjanovic-Jeromela *et al.*, 2008; Yakubu, 2010). The path coefficients reveal both positive and negative direct effects of linear traits on body weight. In the rams, the highest significant direct effect of linear traits on body weight as indicated by the *t*-test was exhibited by heart girth (0.52) followed by thorax depth (−0.24). Though other linear characters with insignificant ($p > 0.05$) direct effects had high correlations with body weight, their indirect effect through heart girth were generally positive and high in magnitude. The highest indirect effect was obtained for head length through heart girth (0.483) which explains 70.51 percent of the correlation coefficient for association between head length and body weight. The highest and lowest single effects were exerted by heart girth ($R^2 = 0.265$) and head width ($R^2 = 0.002$), respectively. Path analysis principle states that the sum of determination coefficients and determination error is equal to 1 (Wu *et al.*, 2008; Yakubu, 2010). In this study, the sum of determination coefficients of any predictor variable and combination of two predictor variables for rams $\sum d = 0.574$, thus the determination error ($1 - \sum d$) was 0.426. The pilot regression equation where all traits were considered in ram was:

$$\begin{aligned} BW = &- 22.20 + 0.19HL - 0.04HW + 0.11HoL \\ &+ 0.03EL.24NC + 0.52HG - 0.22SW \\ &- 0.24TD - 0.19FLL + 0.07WH - 0.06Hock \\ &+ 0.22BL + 0.05PG + 0.12RH - 0.06TL \\ &- 0.08RL + 0.09RLL + 0.06SC + 0.12RW \end{aligned}$$

Path coefficients of the linear body measurements (independent variables) in WAD ewes are presented in Table 5. Heart girth had the most significant ($p < 0.05$) direct effect on body weight followed by fore-leg length, paunch girth, neck circumference and rump length in decreasing order of magnitude. Similar to that obtained in rams, the highest indirect effects were obtained for all linear characters through their relationship with heart girth. Paunch girth exerted the highest indirect effect (0.36) through heart girth which explains 44.14 percent

Table 3. Simple correlation analysis of body weight and linear body measurements with ewes above the diagonal and rams below.

	HL	HW	HoL	EL	NC	HG	SW	TD	FLL	WH	Hock	BL	PG	RH	TL	RL	RLL	SC	RW	BW
HL		0.76		0.6	0.73	0.84	0.87	0.87	0.72	0.89	0.65	0.86	0.86	0.77	0.71	0.15	0.76	0.69	0.75	0.83
HW	0.87			0.5	0.55	0.64	0.74	0.79	0.47	0.67	0.47	0.76	0.7	0.6	0.55	0.14	0.51	0.48	0.52	0.61
HoL	0.78	0.71																		
EL	0.55	0.55	0.47		0.47	0.48	0.64	0.61	0.58	0.69	0.62	0.53	0.54	0.53	0.69	0.17	0.64	0.38	0.47	0.46
NC	0.86	0.81	0.8	0.4		0.7	0.74	0.7	0.65	0.76	0.51	0.73	0.74	0.6	0.58	0.12	0.61	0.71	0.71	0.76
HG	0.94	0.86	0.8	0.5	0.92		0.81	0.81	0.78	0.86	0.6	0.84	0.87	0.73	0.69	0.16	0.73	0.8	0.79	0.88
SW	0.9	0.82	0.71	0.5	0.79	0.86		0.86	0.69	0.85	0.65	0.82	0.84	0.77	0.67	0.16	0.68	0.63	0.7	0.77
TD	0.87	0.84	0.69	0.5	0.83	0.86	0.86		0.64	0.85	0.62	0.84	0.85	0.72	0.7	0.14	0.66	0.59	0.66	0.77
FLL	0.7	0.52	0.58	0.5	0.63	0.76	0.59	0.52		0.87	0.65	0.68	0.71	0.7	0.73	0.2	0.81	0.79	0.76	0.71
WH	0.8	0.72	0.69	0.5	0.73	0.81	0.73	0.74	0.68		0.73	0.84	0.86	0.81	0.8	0.18	0.84	0.76	0.79	0.84
Hock	0.58	0.49	0.44	0.4	0.47	0.58	0.54	0.49	0.58	0.55		0.59	0.63	0.63	0.76	0.13^{ns}	0.62	0.54	0.56	0.57
BL	0.92	0.85	0.77	0.5	0.86	0.91	0.87	0.84	0.67	0.76	0.56		0.84	0.7	0.64	0.19	0.67	0.68	0.74	0.82
PG	0.8	0.78	0.7	0.5	0.73	0.82	0.75	0.75	0.56	0.68	0.55	0.78		0.75	0.66	0.07^{ns}	0.68	0.7	0.73	0.84
RH	0.91	0.82	0.77	0.6	0.82	0.93	0.85	0.82	0.76	0.85	0.64	0.88	0.79		0.67	0.16	0.73	0.61	0.63	0.7
TL	0.78	0.71	0.68	0.6	0.67	0.78	0.7	0.67	0.75	0.71	0.6	0.76	0.66	0.82		0.18	0.7	0.63	0.6	0.66
RL	0.38	0.38	0.4	0.2	0.46	0.39	0.4	0.36	0.23	0.32	0.21	0.38	0.33	0.34	0.29		0.27	0.12	0.18	0.18
RLL	0.69	0.62	0.52	0.5	0.59	0.7	0.65	0.58	0.67	0.62	0.51	0.68	0.6	0.77	0.68	0.22		0.67	0.74	0.69
SC	0.5	0.42	0.39	0.3	0.59	0.61	0.42	0.46	0.65	0.5	0.36	0.5	0.43	0.53	0.54	0.21	0.44		0.75	0.75
RW	0.66	0.65	0.53	0.4	0.67	0.72	0.63	0.64	0.57	0.6	0.44	0.65	0.59	0.7	0.58	0.34	0.57	0.44		0.76
BW	0.69	0.63	0.62	0.4	0.67	0.73	0.59	0.59	0.54	0.61	0.39	0.68	0.61	0.69	0.56	0.23	0.55	0.44	0.56	

ns: non-significantly correlation.

HL, head length; HW, head width; HoL, horn length; EL, ear length; NC, neck circumference; HG, heart girth; SW, shoulder width; TD, thorax depth; FLL, fore-leg length; WH, wither height; Hock, hock length; BL, body length; PG, paunch girth; RH, rump height; TL, tail length; RL, rump length; RLL, rear-leg length; SC, shin circumference; RW, rump width; BW, body weight.

Table 4. Direct and indirect effect of linear body measurements on live weight of WAD rams.

Trait	*R*	Direct effect	Indirect effects																		Total indirect effects
			HL	HW	HoL	EL	NC	HG	SW	TD	FLL	WH	Hock	BL	PG	RH	TL	RL	RLL	SC	RW	
HL	0.69	0.19	–	−0.04	0.09	0.01	0.02	0.48	−0.20	−0.21	−0.13	0.05	−0.03	0.21	0.04	0.11	−0.05	−0.03	0.06	0.03	0.08	0.49
HW	0.63	−0.04	0.16	–	0.08	0.01	0.02	0.44	−0.18	−0.20	−0.10	0.05	−0.03	0.19	0.04	0.10	−0.04	−0.03	0.06	0.03	0.08	0.68
HoL	0.62	0.11	0.14	−0.03	–	0.01	0.02	0.41	−0.16	−0.17	−0.11	0.05	−0.03	0.17	0.03	0.09	−0.04	−0.03	0.05	0.02	0.06	0.48
EL	0.39	0.03	0.10	−0.02	0.05	–	0.01	0.27	−0.12	−0.12	−0.09	0.04	−0.03	0.11	0.02	0.07	−0.03	−0.01	0.04	0.02	0.05	0.36
NC	0.67	0.02	0.16	−0.03	0.09	0.01	–	0.47	−0.18	−0.20	−0.12	0.05	−0.03	0.19	0.04	0.10	−0.04	−0.04	0.05	0.04	0.08	0.64
HG	0.73	0.52*	0.17	−0.04	0.09	0.01	0.02	–	−0.19	−0.21	−0.14	0.05	−0.03	0.20	0.04	0.11	−0.05	−0.03	0.06	0.04	0.09	0.19
SW	0.59	−0.22	0.17	−0.03	0.08	0.01	0.02	0.44	–	−0.21	−0.11	0.05	−0.03	0.20	0.04	0.10	−0.04	−0.03	0.06	0.03	0.08	0.83
TD	0.59	−0.24*	0.16	−0.03	0.08	0.01	0.02	0.44	−0.19	–	−0.10	0.05	−0.03	0.19	0.04	0.10	−0.04	−0.03	0.05	0.03	0.08	0.83
FLL	0.54	−0.19	0.13	−0.02	0.07	0.01	0.02	0.39	−0.13	−0.12	–	0.05	−0.03	0.15	0.03	0.09	−0.04	−0.02	0.06	0.04	0.07	0.75
WH	0.61	0.07	0.15	−0.03	0.08	0.01	0.02	0.42	−0.16	−0.18	−0.13	–	−0.03	0.17	0.03	0.10	−0.04	−0.03	0.06	0.03	0.07	0.54
Hock	0.39	−0.06	0.11	−0.02	0.05	0.01	0.01	0.30	−0.12	−0.12	−0.11	0.04	–	0.13	0.03	0.07	−0.04	−0.02	0.05	0.02	0.05	0.44
BL	0.68	0.22	0.17	−0.04	0.09	0.01	0.02	0.47	−0.19	−0.20	−0.13	0.05	−0.03	–	0.04	0.10	−0.05	−0.03	0.06	0.03	0.08	0.45
PG	0.61	0.05	0.15	−0.03	0.08	0.01	0.02	0.42	−0.17	−0.18	−0.10	0.05	−0.03	0.18	–	0.09	−0.04	−0.03	0.06	0.03	0.07	0.58
RH	0.69	0.12	0.17	−0.03	0.09	0.02	0.02	0.48	−0.19	−0.20	−0.14	0.06	−0.04	0.20	0.04	–	−0.05	−0.03	0.07	0.03	0.08	0.58
TL	0.56	−0.06	0.15	−0.03	0.08	0.02	0.02	0.40	−0.16	−0.16	−0.14	0.05	−0.04	0.17	0.03	0.10	–	−0.02	0.06	0.03	0.07	0.63
RL	0.23	−0.08	0.07	−0.02	0.05	0.00	0.01	0.20	−0.09	−0.09	−0.04	0.02	−0.01	0.09	0.02	0.04	−0.02	–	0.02	0.01	0.04	0.30
RLL	0.55	0.09	0.13	−0.03	0.06	0.01	0.01	0.36	−0.15	−0.14	−0.12	0.04	−0.03	0.15	0.03	0.09	−0.04	−0.02	–	0.03	0.07	0.45
SC	0.44	0.06	0.09	−0.02	0.05	0.01	0.01	0.32	−0.09	−0.11	−0.12	0.03	−0.02	0.11	0.02	0.06	−0.03	−0.02	0.04	–	0.05	0.38
RW	0.56	0.12	0.12	−0.03	0.06	0.01	0.02	0.37	−0.14	−0.16	−0.11	0.04	−0.03	0.15	0.03	0.08	−0.03	−0.03	0.05	0.03	–	0.43

*: Path coefficient significant at 0.05; **: Path coefficient significant at 0.01.

r, correlation coefficient; HL, head length; HW, head width; HoL, horn length; EL, ear length; NC, neck circumference; HG, heart girth; SW, shoulder width; TD, thorax depth; FLL, fore-leg length; WH, wither height; Hock, hock length; BL, body length; PG, paunch girth; RH, rump height; TL, tail length; RL, rump length; RLL, rear-leg length; SC, shin circumference; RW, rump width.

Table 5. Direct and indirect effect of linear body measurements on live weight of WAD ewe.

Trait	*r*	Direct effects	Indirect effects																	Total
			HL	HW	EL	NC	HG	SW	TD	FLL	WH	Hock	BL	PG	RH	TL	RL	RLL	SC	RW	
HL	0.83	0.09	–	−0.05	−0.03	0.12	0.34	−0.06	−0.07	−0.14	0.26	−0.02	0.09	0.17	0.02	0.05	0.01	−0.03	0.05	0.03	0.74
HW	0.62	−0.07	0.07	–	−0.02	0.09	0.26	−0.05	−0.06	−0.09	0.2	−0.02	0.08	0.14	0.01	0.04	0.01	−0.02	0.03	0.02	0.69
EL	0.46	−0.05	0.05	−0.04	–	0.08	0.19	−0.05	−0.05	−0.12	0.2	−0.02	0.06	0.11	0.01	0.05	0.01	−0.03	0.03	0.02	0.50
NC	0.76	0.16*	0.06	−0.04	−0.02	–	0.28	−0.05	−0.05	−0.15	0.23	−0.02	0.08	0.14	0.01	0.04	0.01	−0.02	0.05	0.03	0.58
HG	0.88	0.40**	0.07	−0.05	−0.02	0.11	–	−0.06	−0.06	−0.15	0.26	−0.02	0.09	0.17	0.02	0.05	0.01	−0.03	0.06	0.03	0.48
SW	0.77	−0.07	0.07	−0.05	−0.03	0.12	0.33	–	−0.06	−0.14	0.25	−0.02	0.09	0.17	0.02	0.05	0.01	−0.03	0.043	0.03	0.85
TD	0.77	−0.08	0.07	−0.06	−0.03	0.12	0.32	−0.06	–	−0.13	0.25	−0.02	0.09	0.17	0.02	0.05	0.01	−0.03	0.04	0.03	0.84
FLL	0.71	−0.20*	0.06	−0.03	−0.03	0.12	0.31	−0.05	−0.05	–	0.26	−0.02	0.07	0.14	0.02	0.05	0.01	−0.03	0.06	0.03	0.92
WH	0.84	0.3	0.08	−0.05	−0.03	0.12	0.35	−0.06	−0.06	−0.17	–	−0.03	0.09	0.17	0.02	0.06	0.01	−0.03	0.05	0.03	0.55
Hock	0.57	−0.04	0.06	−0.03	−0.03	0.08	0.24	−0.05	−0.05	−0.13	0.22	–	0.06	0.12	0.01	0.06	0.01	−0.03	0.04	0.02	0.60
BL	0.82	0.11	0.07	−0.05	−0.02	0.12	0.34	−0.06	−0.06	−0.13	0.25	−0.02	–	0.17	0.02	0.05	0.01	−0.03	0.05	0.03	0.74
PG	0.84	0.20*	0.07	−0.05	−0.03	0.12	0.35	−0.06	−0.06	−0.14	0.26	−0.02	0.09	–	0.02	0.05	0.01	−0.03	0.05	0.03	0.66
RH	0.7	0.02	0.07	−0.04	−0.02	0.1	0.29	−0.06	−0.05	−0.14	0.24	−0.02	0.07	0.15	–	0.05	0.01	−0.03	0.04	0.03	0.69
TL	0.66	0.07	0.06	−0.04	−0.03	0.1	0.27	−0.05	−0.05	−0.14	0.24	−0.03	0.07	0.13	0.02	–	0.01	−0.03	0.04	0.03	0.60
RL	0.18	0.06*	0.01	−0.01	−0.01	0.02	0.06	−0.01	−0.01	−0.04	0.05	−0.01	0.02	0.02	0	0.01	–	−0.01	0.01	0.01	0.11
RLL	0.69	−0.04	0.07	−0.04	−0.03	0.1	0.29	−0.05	−0.05	−0.16	0.25	−0.02	0.07	0.13	0.02	0.05	0.02	–	0.05	0.03	0.73
SC	0.75	0.07	0.06	−0.03	−0.02	0.12	0.32	−0.05	−0.04	−0.16	0.23	−0.02	0.07	0.14	0.01	0.05	0.01	−0.03	–	0.03	0.69
RW	0.76	0.04	0.06	−0.04	−0.02	0.12	0.32	−0.05	−0.05	−0.15	0.23	−0.02	0.08	0.14	0.01	0.04	0.01	−0.03	0.05	–	0.70

r, correlation coefficient; HL, head length; HW, head width; EL, ear length; NC, neck circumference; HG, heart girth; SW, shoulder width; TD, thorax depth; FLL, fore-leg length; WH, wither height; Hock, hock length; BL, body length; PG, paunch girth; RH, rump height; TL, tail length; RL, rump length; RLL, rear-leg length; SC, shin circumference; RW, rump width.

of the correlation coefficient. The highest lone effect on body weight was exerted by heart girth ($R^2 = 0.160$).The determination error in ewes ($1 - \sum d$) was 0.159. The predictor variables in this study explain 84 and 57 percent of body weight in ewes and rams, respectively. High determination error in rams obtained in this study compared with ewes may be explained with two reasons, either there are some unmeasured linear traits in rams that explains the remaining 43 percent of body weight or linear body measurements are more useful in predicting body weight in ewes than rams. The pilot regression equation where all traits were considered in ewes was:

$$\begin{aligned} BW = &- 22.20 + 0.09HL - 0.07HW - 0.05EL \\ &+ 0.16NC + 0.40HG - 0.07SW - 0.08TD \\ &- 0.20FLL + 0.30WH - 0.04Hock + 0.11BL \\ &+ 0.20PG + 0.02RH + 0.07TL + 0.06RL \\ &- 0.04RLL + 0.75SC + 0.76RW \end{aligned}$$

Establishment of optimum multiple linear regression model

All predictor variables considered in rams except heart girth and thorax depth were statistically not significant ($p > 0.05$). This brought to light that these traits were not important in the estimation of body weight and were discarded. After the deletion of less important variables, the path coefficients of heart girth and thorax depth were 0.852 and −0.146, respectively, with R^2 of 0.533. The optimum regression model for WAD ram was $BW = -22.71 + 0.85HG - 0.15TD$.

Heart girth, neck circumference, fore-leg length, paunch girth and rump length were statistically significant in WAD ewes; the other predictor variables were discarded. The new path coefficients were 0.548, 0.228, −0.035, 0.219 and 0.059 for heart girth, neck circumference, fore-leg length, paunch girth and rump length, respectively. The optimum regression model for WAD ewes was $BW = -13.36 + 0.55HG + 0.23NC - 0.04FLL + 0.22PG + 0.06RL$ with R^2 of 0.824. Heart girth was the most important trait for prediction of body weight both in rams (0.85) and ewes (0.55).The use of path analysis to explain the relationship between morphometric traits and body weight of sheep had been reported (Yakubu, 2010). Although, the numbers of linear measurements considered in this study were more than what the author documented, however, heart girth was reported as the most important predictor variable with coefficients of 0.243 and 0.249 in male and female, respectively. The author further reported the highest indirect effects of both wither heights and body length on body weight, through their relationship with heart girth in both sexes. Lack of mane at the neck region in ewes may support the usefulness of neck circumference in the prediction equation. Ewes in this study have at least lambed once, the extension of abdominal region during gestation, which is not totally reversible, may support the significance of paunch girth in the optimal regression model.

Conclusion

All linear traits had significant correlation with body weight in both sexes. Heart girth had the highest correlations with body weight, both in rams and ewes. Although a large number of predictor variables were considered in this study, heart girth contributed the most to the coefficient of determination in both sexes. Predictor variables with insignificant path coefficients had high correlations with body weight; however, their indirect effects were obtained mostly via their relationship with heart girth.

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Animal Genetic Resources, 2014, 55, 67–76. © Food and Agriculture Organization of the United Nations, 2014
doi:10.1017/S2078633614000253

Fine-scale population structure analysis of seven local Swiss sheep breeds using genome-wide SNP data

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Summary
As part of the global sheep Hapmap project, 24 individuals from each of seven indigenous Swiss sheep breeds (Bundner Oberländer sheep (BOS), Engadine Red sheep (ERS), Swiss Black-Brown Mountain sheep (SBS), Swiss Mirror sheep (SMS), Swiss White Alpine (SWA) sheep, Valais Blacknose sheep (VBS) and Valais Red sheep (VRS)), were genotyped using Illumina's Ovine SNP50 BeadChip. In total, 167 animals were subjected to a detailed analysis for genetic diversity using 45 193 informative single nucleotide polymorphisms. The results of the phylogenetic analyses supported the known proximity between populations such as VBS and VRS or SMS and SWA. Average genomic relatedness within a breed was found to be 12 percent (BOS), 5 percent (ERS), 9 percent (SBS), 10 percent (SMS), 9 percent (SWA), 12 percent (VBS) and 20 percent (VRS). Furthermore, genomic relationships between breeds were found for single individuals from SWA and SMS, VRS and VBS as well as VRS and BOS. In addition, seven out of 40 indicated parent–offspring pairs could not be confirmed. These results were further supported by results from the genome-wide population cluster analysis. This study provides a better understanding of fine-scale population structures within and between Swiss sheep breeds. This relevant information will help to increase the conservation activities of the local Swiss sheep breeds.

Keywords: *dense marker data, genetic diversity, ovis aries*

Résumé
En el marco del proyecto internacional Hapmap Ovino, se genotiparon, con el chip Ovine SNP50 BeadChip de Illumina, 24 ejemplares de cada una de las siete razas ovinas autóctonas de Suiza (Oveja del Oberland de los Grisones (OG), Oveja Roja de Engadina (RE), Oveja Negra-marrón de Montaña (NM), Oveja Espejo (OE), Oveja Alpina Blanca (AB), Oveja de Hocico Negro del Valais (HN) y Oveja Pelirroja del Valais (PV)). En total, 167 animales fueron sometidos a un análisis minucioso de diversidad genética, para el cual se usaron 45 193 polimorfismos informativos de nucleótido simple. Los resultados de los análisis filogenéticos confirmaron la ya conocida cercanía entre ciertas poblaciones tales como la HN y la PV o la OE y la AB. El parentesco genómico medio intra-racial fue de 12 por ciento para la OG, de 5 por ciento para la RE, de 9 por ciento para la NM, de 10 por ciento para la OE, de 9 por ciento para la AB, de 12 por ciento para la HN y de 20 por ciento para la PV. Se detectó además parentesco genómico entre razas para ejemplares aislados de la AB y la OE, la PV y la HN y la PV y la OG. Por otro lado, no se pudieron confirmar 7 de las 40 parejas señaladas de progenitores-descendencia. Estos resultados fueron posteriormente respaldados por los resultados de un análisis de conglomerados del genoma completo de la población. Este estudio permite una mejor comprensión de la estructura a pequeña escala de las poblaciones intra- e inter- razas ovinas suizas. Con esta información, será posible llevar a cabo un mayor número de actividades para la conservación de las razas ovinas locales de Suiza.

Mots-clés: *diversité génétique, information de marqueurs denses, ovis aries*

Resumen
Dans le cadre du projet international Hapmap Ovins, 24 individus de chacune des sept races ovines autochtones de la Suisse (Mouton de l'Oberland Grison (OG), Mouton Roux d'Engadine (RE), Mouton de Montagne Noir-marron (MN), Mouton Miroir (MM), Mouton Alpin Blanc (AB), Mouton Nez-Noir du Valais (NN) et Mouton Roux du Valais (RV)) ont été génotypés en utilisant la puce Ovine SNP50 BeadChip d'Illumina. En tout, 167 animaux ont été soumis à une analyse minutieuse de diversité génétique, pour laquelle 45 193 polymorphismes nucléotidiques informatifs ont été utilisés. Les résultats des analyses phylogénétiques ont corroboré la proximité déjà connue entre certaines populations telles que NN et RV ou MM et AB. La parenté génomique moyenne intra-raciale a été de 12 pour cent pour le OG, de 5 pour cent pour le RE, de 9 pour cent pour le MN, de 10 pour cent pour le MM, de 9 pour cent pour le AB, de 12 pour cent pour le NN et de 20 pour cent pour le RV. En outre, des rapports génomiques interraciaux ont été décelés entre individus

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isolés des races AB et MM, RV et NN et RV et OG. Par ailleurs, 7 des 40 paires parents-descendants signalées n'ont pas pu être confirmées. Ces résultats ont été ultérieurement corroborés par les résultats d'une analyse de groupement de l'ensemble du génome de la population. Cette étude permet une meilleure compréhension de la structure à petite échelle des populations intra- et inter-races ovines suisses. Cette information servira à mener un plus grand nombre d'activités pour la conservation des races ovines locales de la Suisse.

Palabras clave: *diversidad genética, información de marcadores densos, ovis aries*

Submitted 7 March 2014; accepted 16 May 2014

Introduction

Switzerland has numerous indigenous and locally developed sheep breeds. These genetic resources with unique adaptive traits are assumed to respond best to the pressures of the local environment (Glowatzki-Mullis *et al.*, 2009). To understand variation within and between local sheep breeds, the regular analysis of available genetic diversity is advised. Pedigree-based analysis of different genetic diversity parameters has been conducted for four main breeds using a generic report for population management named POPREP (Groeneveld *et al.*, 2009): Swiss White Alpine (SWA), Swiss Black-Brown Mountain sheep (SBS), Valais Blacknose sheep (VBS) and Brown Headed Meat (Burren *et al.*, 2012). For the year 2008, almost 30 000 SWA lambs were produced by SWA, and, for the latter three breeds, about 10 000 lambs were born, according to herdbook records (Burren *et al.*, 2012). Due to the remarkable average inbreeding coefficient of 9.2 percent and an effective population size below 100 regular monitoring of the available genetic diversity was proposed for the VBS breed (Burren *et al.*, 2012), a local breed which is limited to one geographic region of Switzerland.

Beside the four main breeds under scrutiny, Glowatzki-Mullis *et al.* (2009) investigated the genetic diversity of Engadine Red sheep (ERS), Swiss Mirror sheep (SMS), Valais Red sheep (VRS), East Friesian and Skudden sheep using 44 microsatellites. Using the software program Structure (Pritchard *et al.*, 2000), the two local breeds (VRS and VBS), which originated in the same geographical area, could not be differentiated. In addition, genetic proximity between SWA and SMS was determined. These results were in line with the findings of an earlier study based on 31 microsatellites (Stahlberger-Saitbekova *et al.*, 2001).

Within the International Sheep Genomic Consortium (ISGC), a genome-wide single nucleotide polymorphism (SNP) panel was developed and tested based on genotypes from 2 819 sheep belonging to 74 breeds (Kijas *et al.*, 2012). Out of these, seven were local sheep breeds from Switzerland. Based on a principal component analysis (PCA), this study showed clear genetic divisions separating European, Asian and African sheep breeds. Even though: aspects of genetic diversity and fine-scale populations of local Swiss breeds are only sparsely covered by these authors. Therefore, the public available genotypes from 168 individuals of seven Swiss breeds (SWA, SBS, VBS, ERS, SMS, VRS and Bundner Oberländer sheep (BOS)) were isolated from the ISGC (Kijas *et al.*, 2012) and re-analysed with special focus on genetic diversity of local Swiss breeds. The primary goal of the current study was to investigate fine-scale population structures within and between Swiss sheep breeds using dense SNP data and applying network-based clustering methods. The results are compared with results from earlier studies based on microsatellites. Potential needs for genetic monitoring and conservation activities are underlined.

Material and methods

Data

The sheep breeds used in this study were previously described in detail by Kijas *et al.* (2012). During the trial, 24 individuals from each of the seven indigenous Swiss sheep breeds were genotyped using the Illumina Ovine SNP50 BeadChip (Kijas *et al.*, 2012). In the sheep HapMap project, it was subjected that a breed includes at least one parent–offspring pair, therefore some of the individuals included in the data sample are known relatives to each other (Kijas *et al.*, 2012) and these relationship were described in the data release. Totally, the analysed data set comprised 20 trios (i.e. genotyped individual and genotypes for both parents) (Table S1). Beside this information, no more pedigree information was available for genotyped individuals.

The data set was filtered using Plink-1.07 (Purcell *et al.*, 2007). Firstly, non-annotated SNPs or SNPs with missing positions were removed. Secondly, SNPs with a minor allele frequency below 0.05, with more than 10 percent missing genotypes per marker or per individual, or those deviating from Hardy–Weinberg equilibrium ($p = 0.0001$) were excluded. 45 193 SNPs (92 percent) from the initial available 49 034 SNPs passed the filtering procedure. Using quality filtered SNPs, the genome-wide proportions of shared alleles identical by descent (IBD) between all samples were calculated using Plink-1.07. The estimated genomic relationship (pi-hat) between two samples from the VRS breed was 100 percent (identical) and so one duplicate genotype was excluded from further

analysis. Due to restricted sample size, the genotypic information for 20 trios was not omitted from the final analysis. Finally, the genotypic information from a total of 167 individuals and 45 193 SNPs covering 26 ovine autosomes was considered for the population structure analysis.

Cluster analysis and genomic relationships

The program ADMIXTURE (Alexander, Novembre and Lange, 2009) was used to determine the optimal number of *k* clusters and for assigning individuals to their true clusters. The algorithms implemented in ADMIXTURE are considered to be computationally more efficient (Alexander, Novembre and Lange, 2009) than the algorithms implemented in the software STRUCTURE (Pritchard *et al.*, 2000) and can be easily applied on genome-wide data sets to infer individual ancestry. By adding the –cv flag, ADMIXTURE includes a cross-validation procedure that allows identification of the optimal value of *k* for which the model has best predictive accuracy (Alexander, Novembre and Lange, 2009). Within this analysis, –cv was set to 10, and the *k* with the lowest cross-validation error was used for the choice of the optimal number of clusters for the set of genotypes under investigation. The software DISTRUCT (Rosenberg, 2004) was used for the graphical presentation of each cluster assignment increasing *k* from 2 to 8.

Due to the availability of large numbers of SNPs, it was possible to calculate genome-wide IBD or identical by state (IBS) between samples using the PLINK-1.07 (Purcell *et al.*, 2007) option –genome. This option was used to estimate the genome-wide proportions of IBD (pi-hat) between individuals. The estimated proportions of IBD were graphically converted using the *R*-function levelplot of the package LATTICE (Sarkar, 2008).

Besides the model-based cluster analysis, we further investigated the population structure of sheep breeds using PCA and multi-dimensional scaling (MDS). PCA and MDS are non-parametric approaches, which utilize pairwise relationships between individuals for the final visualization of genome-wide population structures.

PCA identified the principal components that represented the population structure based on genetic correlations (shared ibs segments) between individuals, whereas MDS identified dimensions that explained observed genetic distance between individuals (Wang *et al.*, 2009). For MDS analysis, genome-wide pairwise ibs-distances between individuals were used in conjunction with the –mds-plot –cluster = 3 option in PLINK-1.07 (Purcell *et al.*, 2007). The MDS plot was created using the *R*-package SCATTERPLOT3D (Ligges and Mächler, 2003).

Finally, we used high definition network visualization for the available SNP genotypes to detect fine-scale population structures within and between sheep breeds (Neuditschko, Kathkar and Raadsma, 2012). The so-called NETVIEW approach (Neuditschko, Kathkar and Raadsma, 2012) consists of five distinct components: data preparation and editing, calculation of a genetic-relationship or genetic distance matrix among all individuals and samples, network construction, clustering of individuals within the population network and finally, the visualization of the clustering results using the software CYTOSCAPE (Shannon *et al.*, 2003). The number of nearest neighbours (*k*-NN) was set equal 10. For additional visualization of hierarchical population structures, the *R*-package PHYTOOLS (Revell, 2012) was applied. Thickness of lines connecting individuals was set in proportion to ibs-distances between individuals (i.e. ibs-distances >0.8 = thick line; ibs-distances <0.8 = thin line).

Phylogenetic analysis

To evaluate the general hierarchical population structure of the sheep breeds, pairwise F_{ST}-values were calculated among the seven sheep breeds from population allele frequencies across all 45 193 autosomal SNPs using the program package GENEPOP 4.1.4 (Rousset, 2008). For the graphical presentation of phylogenetic relationships between the seven breeds, the common applied neighbour-joining (NJ)-method was chosen, as implemented in the program SPLITSTREE4 (Huson and Bryant, 2006).

Derivation of linkage disequilibrium (LD) and estimation of effective population size (N_e)

PLINK-1.07 (Purcell *et al.*, 2007) was used to estimate pairwise LD between SNPs. r^2-values over all 26 autosomes were grouped according to their physical intermarker-distances, assuming a constant recombination rate, and were then averaged for distance bins of 50 kb. The smallest bin ranged from 0 to 50 kb and the largest from 1 950 to 2 000 kb, resulting in bins with a minimum average intermarker-distance of 25 kb up to a maximum of 1 975 kb. To derive estimates of recent effective population sizes (i.e. N_e five or ten generations ago) two 'maxi'-bins for pairs of SNPs with an average intermarker-distance of 4 975 and 9 975 kb, respectively, were created.

For the derivation of N_e, Sved's equation (Sved, 1971) was applied

$$E(r^2) = 1/(1 + 4N_e c).$$

In the case of restricted sample sizes, Weir and Hill (1980) proposed that the equation be completed using the term $(1/n)$. Thus, the equation was converted allowing for an estimation of N_e

$$E(r^2) = 1/(1 + 4N_e c) + 1/n,$$

where $E(r^2)$ is the expectation of the correlation between allele frequencies of two loci, n is 2* sampled animals, c is the genetic distance between loci in Morgan and N_e

is the effective population size. The genetic distance between SNPs (c) was approximated by setting 1 Mb equal to 0.01 Morgan. Applying this formula, N_e was estimated for $1/2c$ previous generations (Hayes *et al.*, 2003).

Results

Cluster analysis and genomic relationships

The graphical visualization of the results from cluster analysis of the 167 animals for k ranging from two to eight clusters is shown in Figure 1. The cross-validation error was assessed to define the optimal value for k for the different number of clusters (Supplementary Figure S2). The cross-validation error decreased to $k = 7$ and then increased again. Therefore, $k = 7$ was determined to be an optimal number of clusters for the analysis given in Figure 1.

The first principal component (PC1) explained 25 percent of the observed variation (Figure 2), the second (PC2) 8 percent and the third (PC3) 7 percent, respectively. The separation of the seven breeds was obvious by contrasting PC1 versus PC2 and PC2 versus PC3. The first component identified the separation of the Valais breeds (VBS and VRS) from the other breeds, whereas the second component showed the separation between SBS, ERS and BOS, as well as SMS and SWA. Using the third component, the separation between BOS and ERS became clearer, whereas the Valais breeds (VBS and VRS) and SMS had higher connection with SWA. The MDS plot is given in Supplementary Figure S1.

The visualization of the investigated network for the data is given in Figure 3. The thickness of the lines varies in proportion with the genetic distance and is used to visualize the individual relationships within and between populations. The node size varied in proportion to the numbers of edges per node, and illustrated how well each individual was connected within the population (Neuditschko, Kathkar and Raadsma, 2012).

Additionally, the network-based-cluster tree is given in Figure 4, where each breed is represented by the same colour as in Figure 3. At the base of the tree, the Valais breeds (VBS and VRS) were separated from the other five breeds. At the second level, all breeds were assigned into distinct clusters, except SMS and SWA individuals. At the third level substructures within BOS, ERS and the VBS breed became visible, while VRS, SBS and SMS reflect homogenous samples. Additionally, SWA and SMS were clustered according to the initial breed assignment into distinct groups, except two SMS individuals (SMS24 and SMS23). Substructure in SWA occurred at the fourth and the final level of the tree.

Genomic relationships within and between breeds are given in Figure 5. The average genomic relationships (within breeds) varied from 5 percent (ERS), 9 percent (SBS), 9 percent (SWA), 10 percent (SMS), 12 percent (BOS), 12 percent (VBS) to 20 percent (VRS). Some genomic relationships (>0 between populations) were found for two SMS individuals (SMS24 and SMS23) and SWA (light blue), for some VRS individuals with VBS (light green) and for one BOS individual with VRS. Estimated genomic relationships between the 20 offspring with their genotyped parents are given in Supplementary Table S1. For seven offspring genomic relationships below 0.35 with one parent were found.

Phylogenetic analysis

The NJ-tree (Supplementary Figure S3) represents the phylogenetic relationships for the seven Swiss sheep breeds based on F_{ST}-distances. VBS and VRS were found to be clearly distinct from other breeds. SWA and

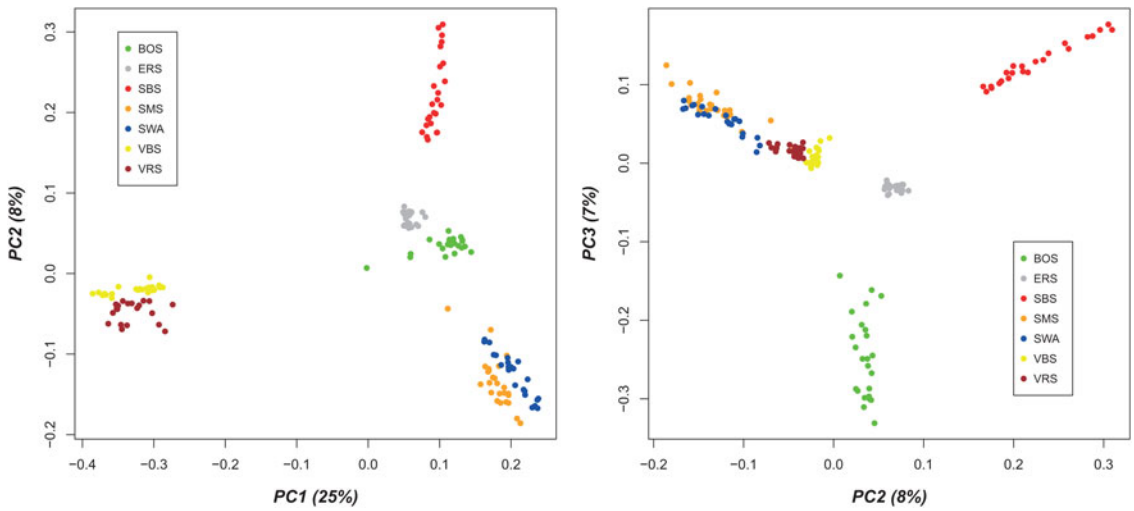

Figure 1. Results cluster analysis for $k = 2$–8. Based on the cross-validation $k = 7$ had the best fit and is therefore indicated in red.

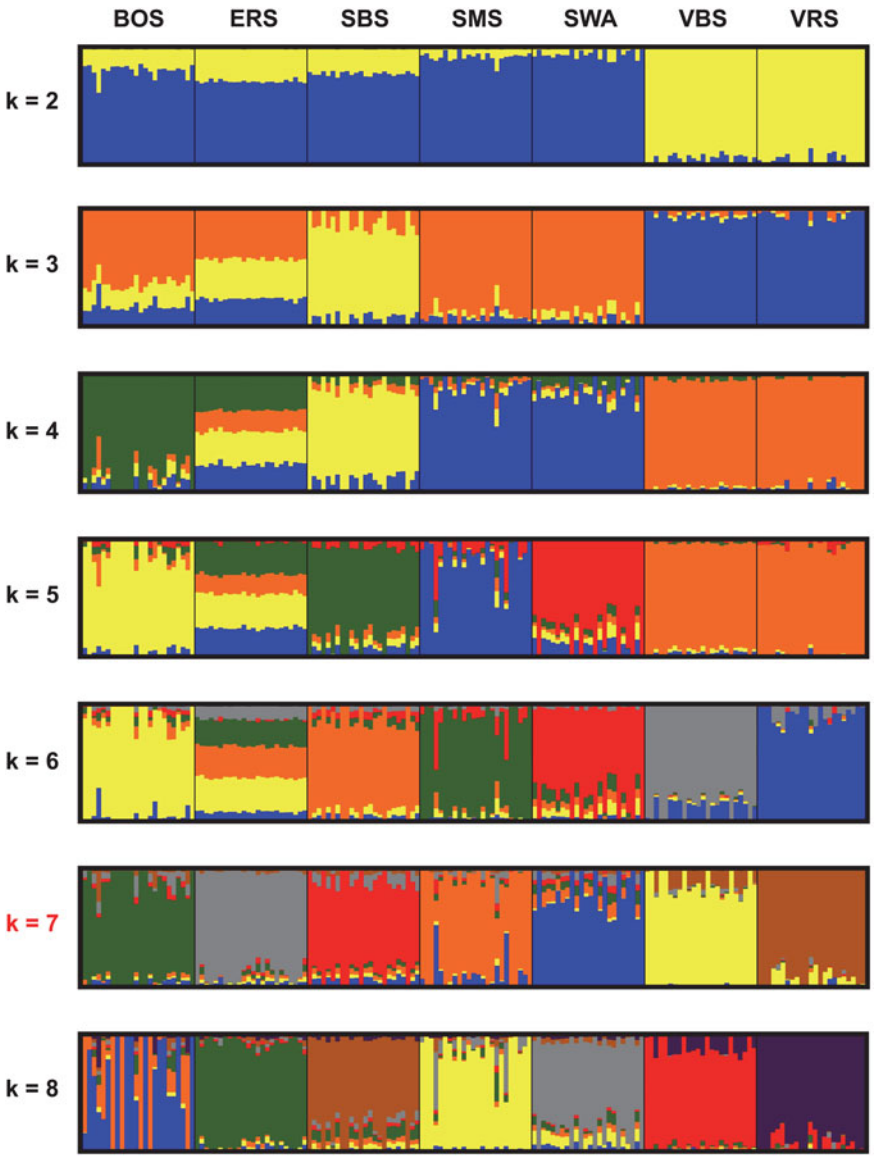

Figure 2. PCA for the seven breeds

SMS were also on a separate branch, but less far away from the other breeds. The shortest F_{ST}-distance was found between SBS and ERS breeds.

Marker-based estimation of effective population size

Estimates of pairwise LD between SNPs for different distance bins were used to derive effective population sizes for the seven Swiss sheep breeds investigated. The result for the development of N_e over the last 2 000 generations for all breeds is shown in Supplementary Figure S4, where the population sizes for all seven breeds showed a decreasing trend. Based on the two maxi bins, estimates for recent N_e (last five to ten generations) as 18–35 for SBS, 27–44 for VRS, 26–47 for BOS, 29–49 for SMS, 29–58 for VBS, 30–58 for ERS and 31–66 for SWA, respectively, were determined.

Discussion

Genetic diversity between breeds

Based on the PCA results (Figure 2) and the MDS plot (Supplementary Figure S1), the seven breeds can be clustered into five distinct groups with evidence of additional sub-structures. The three breeds, BOS, SBS and ERS, comprised distinct groups, whereby VBS/VRS and SMS/SWA individuals were not clearly separated from each other. The proximity between VBS/VRS and SMS/SWA was further supported by the Admixture and NetView analysis presented in Figures 1 and 4, while these two methods divide the individuals into seven respective breed groups. However, based on these results, it was assumed that the proximities within these two clusters are of different origin. VBS and VRS are local Swiss alpine breeds, which are geographically restricted to the canton of Valais. The differentiation of these two breeds from the other five breeds was supported by data

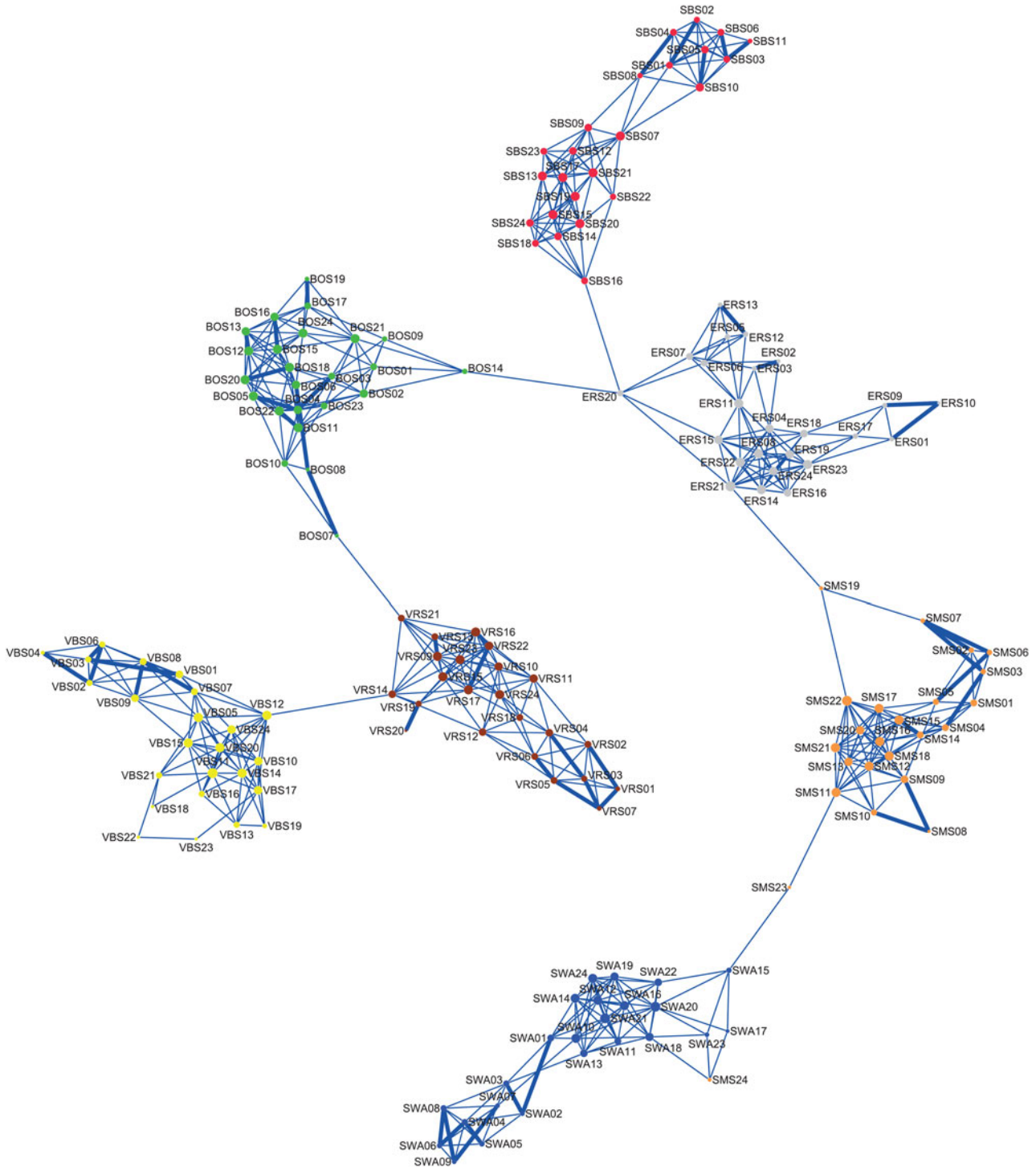

Figure 3. Organic NetView for the seven breeds (yellow: VBS, brown: VRS, green: BOS, red: SBS, grey: ERS, orange SMS and blue: SWA).

shown in Figure 1, i.e. from $k = 2$ to 5, the two breeds clustered together and are clearly distinct from all others. In Figure 4, VBS and VRS are separated from the other breeds at the base of the tree. Data illustrated in Figure S3 showed that the common branch connecting the two breeds with the other breeds is quite long. Therefore, it was assumed that the geographical differences for these two breeds compared with the other breeds is, genetically, rather old. The proximity between VRS and VBS was determined using 44 microsatellites (Glowatzki-Mullis *et al.*, 2009) and 31 microsatellites (Stahlberger-Saitbekova *et al.*, 2001). Based on PCA, Kijas *et al.* (2012) found the two Valais breeds to be genetically distinct from the other breeds. Based on their genetic uniqueness, a high potential for conservation is attributed to these two breeds.

Network visualization (Figure 3) showed that VRS21 was related to BOS07. This relationship was supported by four

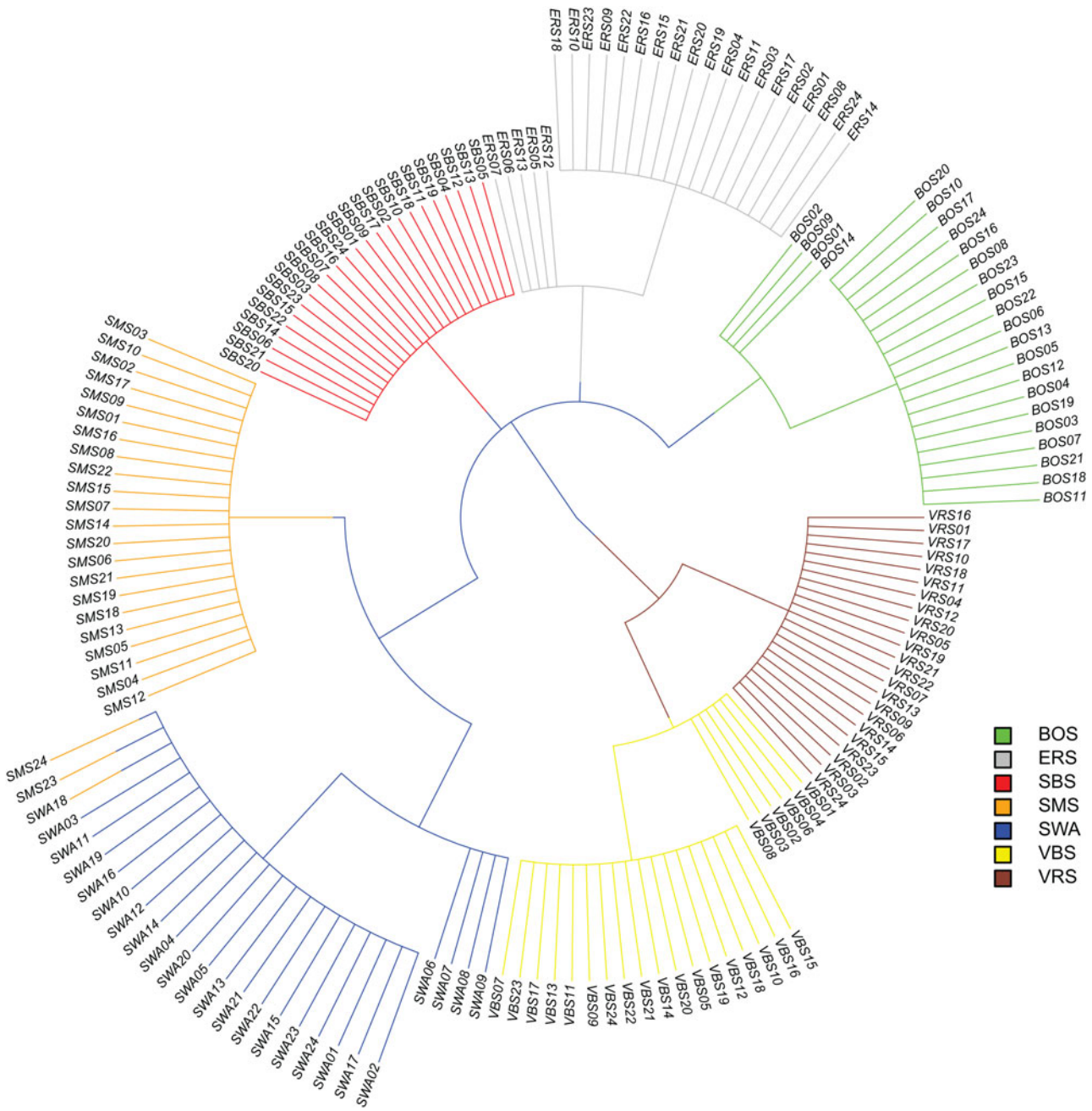

Figure 4. Network-based-cluster tree for the seven breeds (thick lines equal ibs-distances >0.8 and thin lines equal ibs-distances <0.8).

genomic relationships that were slightly greater than zero (0.0376, 0.0283, 0.0251 and 0.0247) between this VRS individual and two BOS individuals (Figure 5). This connection was thought to originate from breeding practices over the last 20 years. Four sheep breeds (BOS, ERS, SMS and VRS) were not officially annotated before 1999. In the year 1982, the foundation 'ProSpecieRara' was created to promote plant and livestock genetic resources (FOAG, 2007). The foundation collected remaining animals of these four sheep breeds and supported farms keeping such individuals. Therefore, it is possible that a certain exchange between these breeds happened by chance on farms with small herds of different breeds or before the collection of remaining individuals.

The similarity between SMS and SWA was supported by Glowatzki-Mullis *et al.* (2009), Stahlberger-Saitbekova *et al.* (2001) and Kijas *et al.* (2012). The SMS is a descendant of the ancient Grisons breed (FOAG, 2007) and, as stated previously, was not officially annotated until 1999. The main visual differentiation between SMS and SWA are the dark-haired patterns found in SMS animals around the mouth and the eyes (resembling spectacles). It is expected that crossbreeding with SWA – the most popular sheep breed in Switzerland – occurred in the recent past before the breeding programme for SMS started (Stahlberger-Saitbekova *et al.*, 2001; Glowatzki-Mullis *et al.*, 2009). The results from network-analysis (Figure 3) showed that one SMS individual (SMS23) fell between

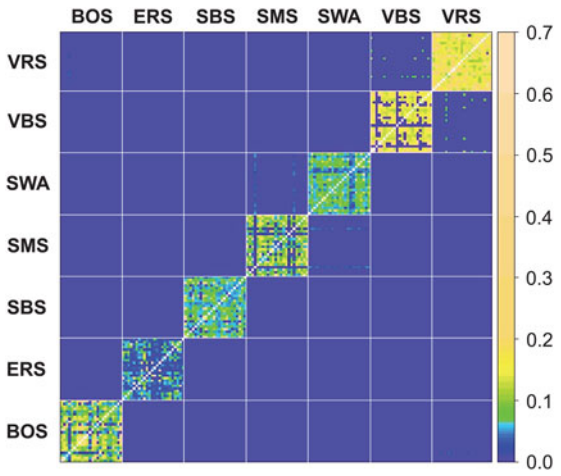

Figure 5. Genomic relationships within and between breeds (the colour scale for the levels of genomic relationships is given at the right end of the matrix).

the SMS and the SWA clusters and one individual from SMS (SMS24) lay in the SWA cluster, which is related to SMS. The first individual was assumed to be a crossbred with SWA, although for the second sheep, a wrong breed assignment of the sampled DNA could be an explanation. In Figure 4, these two individuals were grouped into the SWA cluster. In Figure 5, these two SMS individuals could be recognized, based on the genomic relationships. They were almost certainly not related to the majority of the other individuals from the SMS sample, but showed a certain relationship with many individuals of the SWA breed. Unfortunately, animal identities were not available and therefore the retrospective reconstruction of such connections based on herdbook-information was not possible.

The results for the ERS breed were also interesting. In the PCA plot (Figure 2) and the MDS plot (Supplementary Figure S1), the sample group for the ERS fell between all the other clusters. Based on the results from ADMIXTURE (Alexander, Novembre and Lange, 2009) for $k = 3$–6, the breed seemed to be a conglomerate of genetic resources from different origins (Figure 1). However, with $k = 7$, ERS became clearly distinguishable from the other clusters. The specific pattern of the ERS sample was not observed in a cluster analysis based on 41 microsatellites (Glowatzki-Mullis *et al.*, 2009). The network visualization allowed a more detailed understanding of connections between individuals of the ERS sample to individuals of the other breeds (Figure 3). One ERS individual fell outside the ERS cluster and had connections to individuals from the BOS and SBS breeds. Additionally, this individual was directly related to an ERS individual that was connected to an outlier of the SMS breed (Figure 3). According to the data shown in Supplementary Figure S3, the differentiation time was shortest between ERS and SBS, followed by BOS. However, no genomic relationships (>0) could be found between the 24 ERS individuals and those from the SBS and BOS samples. The origins of the ERS can be traced back to the Stone sheep of the Eastern Alps and the Bergamasca sheep (FOAG, 2007). In a recently published study, the genetic relationships between Italian sheep breeds and other European sheep breeds were derived using genome-wide SNP data (Ciani *et al.*, 2014). This study confirms the known proximity between ERS and the Bergamasca breed at molecular level as ERS clustered closest to this Italian breed in a NJ tree based on Reynolds-genetic distances. Hence, for the ERS breed it is concluded, that the consideration of samples from Swiss sheep breeds only, limits the understanding of its fine-scale population structures.

Genetic diversity within breeds

Average genomic relationships within breeds ranged from 5 percent (ERS) to 20 percent (VRS) (Figure 5). As previously stated, the VRS breed is historically restricted to a single region in the canton Valais. Furthermore, the actual population size of VRS is considerably small (about 1 000 herdbook individuals). With average genomic relationships of 12 percent, the VBS and BOS breeds showed the second highest average genomic relationships within breed. Based on pedigree information, an average inbreeding coefficient of 9.2 percent was found for the 10 000 VBS individuals born in the year 2008 (Burren *et al.*, 2012). For SBS, SMS and SWA breeds, the average genomic relationships ranged from 9 to 10 percent. The lowest average genomic relationships within the ERS sample was not surprising due to the known historic influences of different breeds mentioned above. The availability of dense SNP data allows the derivation of pairwise genomic relationships when pedigree information is missing (Hasler *et al.*, 2011). The genomic relationships of parent–offspring pairs for the 20 trio indicated in the initial file are given in Supplementary Table S1. For seven offspring, the estimated genomic relationships with one parent were found to be lower than 0.35. Due to the remarkable discrepancy of the realized genomic relationships from the expected relationships (eq. (0.5)) it assumed that the indication of six sires and one dam for these seven offspring is not correct. This finding was further supported by missing thick lines between these pairs in Figure 4.

NetView visualization demonstrated that the samples for all breeds showed a certain substructure (Figures 3 and 4). Reasons for this could include the sampling procedure (i.e. sampling related individuals from one herd) and crossbreeding. The substructure of the VBS and the SWA sample (Figures 3 and 4) is mainly a fact of the sampling of directly related animals (i.e. trio). The two main Swiss sheep breeds SWA and SBS are especially known to be influenced by other European sheep breeds. This result was supported by Kijas *et al.* (2012), where SWA, SBS and SMS were in an intermediate position in the PCA of European sheep breeds.

Estimates of ancestral and recent N_e for the seven sheep breeds based on SNP data are shown in Supplementary

Figure S4. The N_e showed a decreasing trend over the last 2 000 generations, with an increasingly steeper slope since about 700 generations ago. The highest historically effective population size was found for ERS and the lowest for SMS. For recent effective population sizes, the estimates varied from 18 (SBS) to 31 (SWA) five generations ago, to 35 (SBS) and 66 (SWA) ten generations ago. Generally, the differences for recent effective population sizes between breeds were rather small. However, as some of the investigated samples were influenced by admixture and restricted sample sizes, those estimates should be interpreted with caution (Corbin *et al.*, 2012).

Based on the genetic uniqueness of the VRS and the VBS breed and the high level of relatedness within those two breeds, the implementation of monitoring programmes to control genetic diversity in daily breeding practice is proposed. For the other breeds, regular monitoring of genetic diversity is advised.

Conclusions

Genomic relationships greater than zero were found for some individuals from different breeds. Thus having genome-wide SNP data available, it is possible to overcome the limitation of pedigree information and derive genomic relationships between breeds. The results related to general population structures are comparable with those from earlier studies based on microsatellites. However, dense SNP data used here in combination with network-theory allowed for a more detailed analysis of fine-scale population structures of seven Swiss sheep breeds. The two geographically separated breeds, VBS and VRS, are clearly distinct from the other Swiss sheep breeds and show remarkable genomic relationships within population. Therefore, the implementation of mechanisms to control genetic diversity is proposed for these breeds.

Acknowledgements

The Swiss Federal Office of Agriculture is acknowledged for the financial support of the costs for genotyping. Lucy Waldron is acknowledged for grateful support related to language editing.

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Animal Genetic Resources, 2014, 55, 77–86. © Food and Agriculture Organization of the United Nations, 2014
doi:10.1017/S2078633614000320

Nicobari pig: an indigenous pig germplasm of the Nicobar group of Islands, India

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Summary
The Andaman & Nicobar Islands are a group of 572 large and small islands & islets in the southeastern part of the Bay of Bengal. This preliminary study reports on husbandry practices and phenotypic characterization of indigenous Nicobari pig, in its home tract (Nicobar group of islands). A total of 377 families were surveyed in randomly selected villages on Car Nicobar, Nancowrie, Teressa, Katchal and Chowra islands. Results of the study revealed that Nicobari pigs were mostly semi feral in nature and reared under a free range system. Pigs were fed mainly with coconut and other locally available resources. The Nicobari pigs appeared short with long body. They showed high prolificacy with an average litter size of 8–10 numbers. These pigs were considered as a family asset among the Nicobari tribe. No commercial farms and slaughter was practiced by the tribes. It is concluded that the Nicobari pigs are considered as an indigenous pig breed/germplasm (*Sus scrofa Nicobaricus*) belonging to this island territory. Owing to its adaptation and performance under resource-driven island ecosystem, Nicobari pig warrants conservation and improvement. In addition, genetic characterization this pig using SNP would help to confirm their genetic distinctiveness and recognition as a new breed for conservation and sustainable utilization.

Keywords: *conservation, farming system, phenotypic charaterization, pig, Nicobari tribes India*

Résumé
Les îles Andaman-et-Nicobar sont un ensemble de 572 îles et îlots de différentes tailles situés dans la partie Sud-orientale du Golfe du Bengale. Cette étude préliminaire traite des pratiques d'élevage et de la caractérisation phénotypique du porc autochtone Nicobari dans son milieu d'origine (l'archipel des Nicobar). Un total de 377 familles a été enquêté dans différents villages choisis au hasard dans les îles Car Nicobar, Nancowry, Teressa, Katchal et Chowra. Les résultats de l'étude ont décelé que les porcs Nicobari se trouvaient pour la plupart dans un état semi-sauvage et étaient élevés en complète liberté. Les porcs étaient nourris principalement avec des noix de coco et avec d'autres ressources disponibles dans la zone. Les porcs Nicobari sont bas mais leur corps est long. Ils présentent une prolificité élevée avec une taille moyenne des portées de 8–10 porcelets. Ces porcs sont très prisés par les familles de la tribu Nicobari. Il n'existe pas de fermes commerciales et l'abattage est pratiqué directement par les tribus. Il peut donc être considéré que les porcs Nicobari constituent une race porcine autochtone o une ressource génétique (*Sus scrofa Nicobaricus*) appartenant à ce territoire insulaire. Compte tenu de son adaptation et de sa capacité à produire avec les ressources existantes dans l'écosystème des îles, le porc Nicobari ne pose pas de problèmes à sa conservation et à son amélioration. Par ailleurs, la caractérisation génétique de ces porcins en utilisant les polymorphismes nucléotidiques pourrait servir à confirmer leur singularité génétique et à obtenir leur reconnaissance comme une nouvelle race devant être conservée et exploitée de manière durable.

Mots-clés: *conservation, système d'élevage, caractérisation phénotypique, porc, tribus Nicobari de l'Inde*

Resumen
Las Islas Andamán y Nicobar son un conjunto de 572 islas e islotes de distintos tamaños situados en la parte Suroriental de la Bahía de Bengala. Este estudio preliminar aborda las prácticas de cría y la caracterización fenotípica del cerdo autóctono Nicobari, en su lugar de origen (el archipiélago Nicobar). Se encuestó a un total de 377 familias en pueblos elegidos al azar en las islas Car Nicobar, Nancowry, Teresa, Katchal y Chowra. Los resultados del estudio revelaron que los cerdos Nicobari se encontraban, la mayoría, en un estado semi-salvaje y que se criaban en condiciones de total libertad. Los cerdos eran alimentados principalmente con cocos y otros recursos disponibles en la zona. Los cerdos Nicobari alcanzan poca altura pero tienen un cuerpo largo. Presentan una elevada prolificidad con un tamaño medio de la camada de 8–10 lechones. Estos cerdos son de gran valía para las familias de la tribu Nicobari. No existen granjas comerciales y el sacrificio es realizado directamente por las tribus. Se puede por tanto considerar que los cerdos Nicobari constituyen una raza porcina autóctona o un recurso genético (*Sus scrofa Nicobaricus*) perteneciente a este territorio insular. Dadas su adaptación y su capacidad de producción con los recursos existentes en el ecosistema de las islas, el cerdo Nicobari ofrece garantías para su

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conservación y mejora. Asimismo, la caracterización genética de este cerdo usando polimorfismos de nucleótido simple podría servir para confirmar su singularidad genética y para obtener su reconocimiento como una nueva raza a conservar y a explotar de manera sostenible.

Palabras clave: *conservación, sistema de producción ganadera, caracterización fenotípica, cerdo, tribus Nicobari de la India*

Submitted 7 October 2013; accepted 7 July 2014

Introduction

India is one of the 12 mega-biodiversity centres in the world. The country is divided into ten biogeographical regions, where the islands and coast are considered one region. The Andaman and Nicobar group of islands are situated about 1 200 km from mainland India in the Bay of Bengal. They form an arched string of about 572 islands, islets and rocks stretching from Burma in the north to Sumatra in the south between 6° and 14° North latitudes and 92° and 94° East longitudes. They are summits of a submarine range of mountains connecting Arrakkan Yoma of Burma in the north and Pegungan Barrisan of Sumatra in the south enclosing the deep Andaman Sea between this archipelago and Malayan peninsula (Figure 1). Geographically these islands are separated into two groups, i.e. the Andaman group and Nicobar group, separated by a channel at 10°N. The total land area of all these islands amounts to only about 8 249 km^2, of which about 86 percent is covered by lush green tropical rain forests. These islands have a typical maritime climate and receive both southwest and northeast monsoons with an average rainfall of 3 100 mm distributed over 8 months (April–November). The natives of these islands represent primitive tribes, of which only the Nicobarese occur in large numbers (27 000) and other tribes include Onge, Jarawa, Sentinelese, Great Andamanese and Shompens. Other than tribes, the major population of the islands includes ex-convicts, settlers from various countries viz. Burma, Bangladesh, Sri Lanka and from various states of India viz. West Bengal, Tamil Nadu, Telangana, Seemandhra and Kerala (Ramakrishna, Ragunathan and Sivaperuman, 2010).

The geological isolation makes this group of islands unique and is endowed with rich floral and faunal biodiversity, which has not yet been fully studied. Efforts are currently underway to carry out inventories of the farm animal genetic resources of the islands. Deterioration of original breeds due to natural disasters, poor documentation and conservation measures, as well as non-systematic breeding has been a major threat to survival of indigenous domestic livestock breeds. Detailed information on their origin, distribution and breed characteristics warrant research.

Among the indigenous livestock germplasm, the pig occupies a major share among the tribes of Nicobar group of islands. Pigs are part of the community's traditions and culture, and these pigs constitute the chief source of protein (Tikader and Das, 1985). Boden Kloss (1903) reported

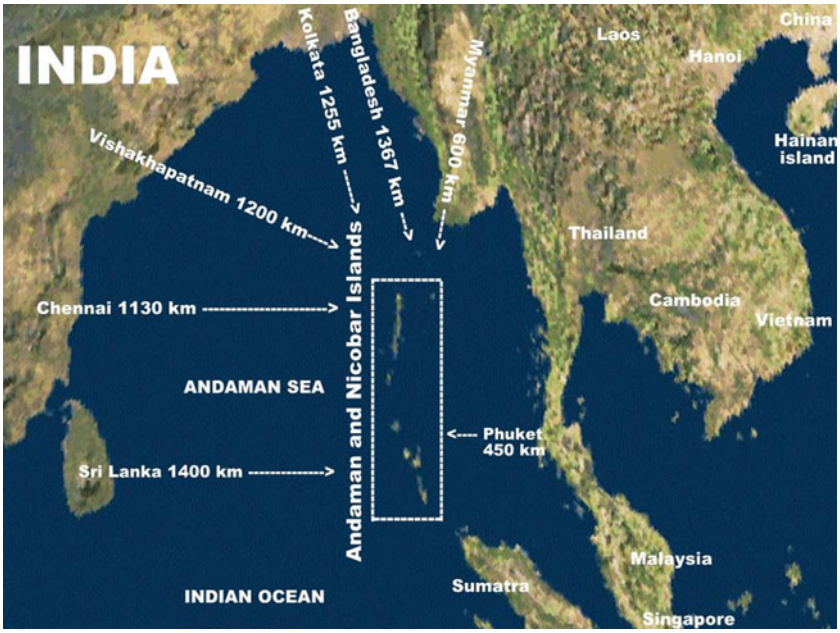

Figure 1. Location of Andaman and Nicobar Island and neighbouring countries.

that his team observed the track of pigs in various parts of the Southern group of islands viz. Car Nicobar, Kondul, Great Nicobar and Trinket. Nicobari pigs are believed to have an origin from *Sus scrofa*/*Sus cristatus* (Eurasian wild boar) and Nicobaricus as a region-specific subspecies and in recent times, they have generally been called the "*Nicobari pig*". These pigs have been present since time immemorial along with the primitive tribes of these islands, but have never been studied systematically. The lack of attention given to this pig is such that no-one has studied what types there are and what potential they might have, especially under typical tribal village conditions. Their valuable traits and performance viz. phenotypic characteristics, body conformation, ability to utilize waste, disease resistance and performance under a low-input production system remain largely unrecognized. This present paper presents preliminary report on phenotypic characterization and husbandry practices of *Nicobari pig*.

Materials and methods

Location, topography and climate of the study area

The islands are located between the 16° and 14° latitude, and 92° and 94° East longitudes.

These islands have a uniform tropical, warm and humid climate. The annual rainfall is 318 cm, but is irregular. It ranges from approximately 300 cm in the north to about 380 cm in the south. The major precipitation occurs during the southwest and northeast monsoons from April to November. These islands are subjected to cyclonic winds and gales, common with the change of monsoons and sudden depressions in the sea around. The maximum and the minimum temperatures are 30 and 23 °C, respectively. The mean relative humidity is about 78 percent, whereas mean wind speed is approximately 10.8 km/h. The Government of India declared the Nicobar Islands as an Aboriginal Tribal Reserve Area and these have become inaccessible to the common people. Those who wish to visit need a special tribal pass from the Andaman and Nicobar Administration to land on different islands.

Geographical distribution

The breeding tract of Nicobari pig is confined to Nicobar group of islands and it is reared by the Nicobari communities located in these islands and a small population of Nicobari pig are reared by Nicobari tribes on Little Andaman (Nicobari settlement area at Harminder Bay) Island (Jeyakumar and Sunder, 2009).

Communities of the breeding tract

The term "*Nicobarese*" refers to the community of indigenous tribal people from the Nicobar group of Islands, in general. Nicobari tribes belong to Mongloid origin, inhabitating large permanent villages mostly close to seashore and their population is around 27 000. The Nicobari tribes are spread over various islands of Nicobar group; however, they have territorial distinctions in terms of local dialect and socio cultural activities. Thus Nicobari tribes are fairly well divided into six groups viz. Car Nicobar, Chowra, Teressa with Bompooka, the Central group, the Southern group. The main occupation and source of income for their livelihood is coconut plantation-based horticulture and homestead farming. Fishing and pig rearing are major traditional farming activity to meet out their nutritional security.

Survey, collection of data and documentation of phenotypic characteristics

A total of 377 families were surveyed in randomly selected villages on Car Nicobar, Nancowrie, Teressa, Katchal and Chowra Islands. The necessary information on pig farming, population and characteristics was collected from tribal families as per the standard format developed for pigs by National Bureau of Animal Genetic Resources (NBAGR) through participatory conversation (interview). Permission from First Captain of a village is essential prior to survey in the tribal village. In general, most of the tribes were very reserved. Although the tribes spoke Hindi, it was difficult to understand what they were saying in Nicobari language and we used a Nicobari tribe as an interpreter to record information. Most of the time, the tribal people were in the forest or coconut plantations (from morning to evening) which were difficult to access. Frequently nobody could be found in the village and the principal investigator along with survey team went inside the forest to contact the tribes. Once the Sun begins to set, no outsiders were allowed to stay around the village. The Nicobari tribes did not know much information about the farming system and performance as the pigs were reared under free range system and they did not follow any systematic/scientific farming practices. In general, temperament (nervousness) of the male Nicobari pig was too much than the female pigs. At least ten people were needed to catch the pigs for slaughter. However, the female Nicobari pigs were very docile and could be controlled easily by the Nicobari tribal women. Therefore, the data were mostly based on the information provided by the tribes and as observed by the survey team. The phenotypic characteristics were recorded using measuring tape from the pigs available during the survey. General behaviour and appearance were recorded from a distance by direct observation and recorded using videos. Pigs squealed loudly when restrained and on hearing this other pigs scavenging nearby ran away. However, pigs which were roaming near the tribal household and confined under shelter were approached and caught with the help of tribes and phenotypic measurements were

Figure 2. Phenotypic measurements of Nicobari pigs of various age groups.

recorded (Figure 2) with photography. Phenotypic data viz. appearance (general appearance, coat, muzzle, eye lid and hoof colour, head, face, ear, eye, eye lid, snout, neck, shoulders, body, abdomen, legs, tail and activity) and body measurements (body height, length, chest girth, paunch girth, neck circumference, snout length, ear length, ear width, ear circumference, leg length and tail length) were recorded.

Results and discussion

Population trend of Nicobari pig in the breeding tract

The recent census data by the Department of Animal Husbandry and Veterinary Services on the pig population revealed that the post-tsunami, i.e. after 2004, status of the

Table 1. Pre- and post-tsunami Nicobari pig populations in Nicobar district (*Source*: Department of Animal Husbandry &Veterinary Service, Andaman and Nicobar Islands).

Island	Pre-tsunami (population as per the 17th Livestock Census – 2003)	Post-tsunami (population as per the 18th Livestock Census – 2007)	Percent variation
Car Nicobar Island	20 487	27 482	34.14
Chowra Island	4 245	2 048	−51.76
Teressa Island	10 154	3 089	−69.58
Katchal Island	3 917	939	−76.03
Nancowry Island	2 891	1 066	−63.13
Great Nicobar	1 990	699	−64.87
Overall population	43 684	35 323	−19.14

number of the Nicobari pig was highest in Car Nicobar followed by Teressa, Chowra, Nancowry and Katchal (Table 1). However, the population as per the 18th Livestock Census-2007 was minus 19 percent of the original population prior to tsunami, as most of the pig population was washed away. In Car Nicobar Island, there was less damage to the pig population and, the Southern group of the islands, particularly Nancowry, Teressa, Chowra and Katchal, were worst affected with a loss estimated to be 51–76 percent of total population based on the provisional 18th Livestock Census Report-2007, Office of the Senior Veterinary Officer, Nicobar District, Department of Animal Husbandry and Veterinary Services, Andaman and Nicobar Islands. This could be due to islands topography, force of tsunami waves and water ingression in the seashore and the population of pig caught in tsunami waves. In addition to loss during the tsunami, indiscriminate slaughter by tribes to meet the nutritional demand of the families, escape of pigs into the dense forest and death due to disease (swine fever) lead to the post-tsunami loss and slow progress in population growth.

The herd size (in numbers) of Nicobari pig per individual tribal family in Car Nicobar, Nancowry and Teressa ranged between 10 and 15 and was higher than on other islands. The overall herd size of the Nicobari pig was 12.46 for the 377 tribal families surveyed. The herd composition revealed that the adult female population ranged between 9 and 20 percent. The adult breeding populations were important to further propagate the germplasm and there was an immediate need to increase breedable population of female pigs in Nicobar group of islands.

Husbandry practices

The pigs were reared under a free-range system, roamed freely and might come to the residential area or remain in the forest. They were very active in the very early morning and late evening, moved in bands of 4 to 20 and ate an omnivorous diet (Tikader and Das, 1985). The pigs were mainly resting underneath the tribal's hut/shelter during day time (Figure 3). The Nicobari hut/shelters were in appropriate height above the ground level to protect the pigs from heavy rainfall. No separate pig sty or any housing pattern was constructed for the pigs. However, a separate enclosure/shelter for piglets were made using locally available material by all tribes. Sometimes pigs that had been caught in the forest, more ferocious pigs or pigs

Figure 3. Nicobari hut with shelter/resting place for pig below the hut.

Figure 4. Group feeding of Nicobari pig with coconut at Car Nicobar Islands in a traditional wooden feeder called "*naam*".

marked for slaughter were kept in a separate well-protected enclosure. The shelters were generally made of pieces of wooden planks, tree branches and the roofing was made using leaves/grasses. The shelters were made in different sizes depending on the population. These animals were largely vegetarian, although they were opportunists and mostly consumed a wide range of food of animal origin especially fish and fish waste. The tribes mainly fed the pigs in groups with coconut in the evening (Figure 4). Other than routine raw coconut feeding, the pigs are also fed with oil extracted coconut powder, Pandanus fruit (*Pandanus lerum*, locally called Kevri), Nicobari Alu (*Dioscorea alata*), tapioca (*Manihot esculenta*, locally called Malayal alu) and fish waste. In addition, the pigs are also given a small amount of kitchen waste by some tribes. Before feeding, each tribe summoned the pigs by raising peculiar sound either vocally or using an instrument or an object. The pigs, after hearing the sound, recognize their owners and go to their tribal hut/shelter. The Nicobari pig showed good rooting behaviour and fed on roots of wild palm. No feed (ration) was prepared separately for the pigs. The pigs were grown and fattened using locally available feed resources and without any concentrate ration. However, they may still lack a proper balanced nutrition (protein, energy and minerals, etc.). The feeding pattern for Nicobari pig was similar in all Nicobar groups of islands.

Table 2. Phenotypic characteristics (appearance) of Nicobari pig.

Body parts	Characteristics
General appearance	Short with compact body
Coat/skin colour	Black, brown, creamy-white, reddish-brown and black and brown mixed. Coarse hair with presence of mane
Muzzle colour	Light brown/pinky and strong
Hoof colour	Light brownish creamy-white or light black and white mixed
Head	Heavy, short (the profile of the face straight to broken, with an angle between forehead and nasal bone), large jowl
Ear	Short, coarse, erected upwards (no hanging ears), mostly attached close to the head/body
Eyes	small in size (mostly not visible easily due to deep lacrimal bone and muscle structure)
Eye lid	Small with brown or creamy white in colour
Snout	Medium to short with slight concave
Neck	Short, clean and heavy
Shoulders	Light, firm, free from coarseness, medium width and well laid on to body
Body	Medium length, slightly arched (downwards) at back, no uniform breadth/sides, well sprung ribs, strong and slightly wider loin and back; slightly broad hams, well-filled but not up to hocks
Abdomen/belly	Large, capacious/heavy and moderately pot-bellied
Legs	Short and strong (fast runner) well-set and square with the body; strong and smooth pastern; strong feet with/without wrinkles
Tail	Medium to long with tuft of hair in the tip of tail and hangs straight from base to hock
Temperament	Docile to ferocious

Table 3. Mean values (± SEM) of phenotypic parameters of adult male and female Nicobari pigs (>12 months of age).

	Adult Nicobari pig	
Physical characters	**Male ($n = 6$)**	**Female ($n = 6$)**
Body weight (kg)	63.67 ± 18.18	67.33 ± 17.01
Body height (cm)	56.51 ± 2.44	60.65 ± 2.68
Body length (cm)	84.89 ± 4.08	78.56 ± 2.77
Chest girth (cm)	84.45 ± 3.01	93.77 ± 3.87
Paunch girth (cm)	90.60 ± 3.76	85.42 ± 4.49
Neck circumference (cm)	78.10 ± 3.40	67.64 ± 3.86
Snout length (cm)	19.05 ± 0.56	18.97 ± 0.48
Ear length (cm)	13.28 ± 0.46	10.97 ± 0.39
Ear width (cm)	10.24 ± 0.22	8.83 ± 0.25
Ear circumference (cm)	17.45 ± 0.21	17.85 ± 0.36
Leg length (cm)	25.70 ± 0.48	28.75 ± 0.91
Tail length (cm)	19.25 ± 0.48	21.84 ± 1.48
Body temperature (°C)	99.58 ± 0.41	99.25 ± 0.31

Physical characteristics

Phenotypic appearance of Nicobari pigs and physical measurements of adult and piglet are presented in Tables 2–4. The male (Figure 5) and female Nicobari pig (Figure 6)

Table 4. Mean values (± SEM) of phenotypic parameters of male and female Nicobari piglets (2–3 months of age).

	Nicobari pig–piglet	
Physical characters	**Male ($n = 15$)**	**Female ($n = 8$)**
Body weight (kg)	10.09 ± 1.13	7.63 ± 0.98
Body height (cm)	38.22 ± 1.06	34.77 ± 0.94
Body length (cm)	43.00 ± 1.44	41.75 ± 1.78
Chest girth (cm)	45.72 ± 1.86	44.70 ± 1.18
Paunch girth (cm)	54.00 ± 1.62	49.93 ± 1.32
Neck circumference (cm)	43.10 ± 1.78	37.10 ± 0.98
Snout length (cm)	15.79 ± 0.44	14.75 ± 0.43
Ear length (cm)	7.21 ± 0.17	7.31 ± 0.39
Ear width (cm)	5.96 ± 0.10	5.91 ± 0.12
Ear circumference (cm)	11.27 ± 0.36	11.201 ± 0.56
Leg length (cm)	22.73 ± 0.78	25.73 ± 0.80
Tail length (cm)	13.71 ± 0.35	11.93 ± 0.39
Body temperature (°F)	99.76 ± 0.30	100.98 ± 0.42

Figure 5. Male Nicobari pig.

Figure 6. Female Nicobari pig.

Figure 7. Banded Nicobari piglet (left side).

was short with a long body. The pigs were sturdy and healthy in appearance. The skin colour of adult pig included shades of red-brown (5 percent), blackish grey (80 percent), brown and blackish brown (5 percent) and also with a faint black with a faint brownish wash on dorsal side (10 percent) which is similar to that observed by Tikader and Das (1985) and similar to the observation that the range of adult colours among the *Suidae* included shades of red brown, yellow-brown, black, grey, brown, blackish brown and fawn (Porter and Tebbit, 1993). In Car Nicobar, Teressa and Chowra Islands, piglets were occasionally born with stripes (dark reddish brown stripes/banding throughout the body) and the existence of striped pig (Figure 7) was indicative of primitive type or origin from wild pig group (Porter and Tebbit, 1993). John Nesfield, writing in *The Ark* in 1980 to describe the village pigs of Hindu India, remarked that the most of the young were striped at birth (Porter and Tebbit, 1993). Sometimes the undersides (belly) were cream or white and, in few pigs, the colouring extended over the whole body. The bristles were dense, coarse being black, brown or cream in colour. There was a marked bristle crest (mane) on the back of the pig extending from mid head/shoulder to base of the tail. There were no facial warts.

The snout of pigs varied from flat to concave. The uncastrated pigs were heavy with well grown tusks (upper and lower canine tooth), ferocious and tried to attack strange people which is similar to the observation of Tikader and Das (1985) that the Nicobari pigs were larger in size and its skull and teeth were distinctively larger than those of Andaman wild pig. These characters might indicate its wild origin. The muzzle, eyelid and hoof colours include fuscous (brownish-grey), brownish, creamy-white and the muzzle might also be pinkish/grey in colour. The most commonly observed feature was a slightly downward arch/curvature of the back (low back). The head was short with a strong slightly curved (downward) snout. Some of the pigs (10–20 percent) in the forest were observed with a long head and strong lengthy snout indicating wildness. Ears were short and erect. The neck was short with a very large jowl region. The leg was short and they were fast runners. The tail was generally medium to long and had no curl, extending beyond the hock (Figure 8). Porter and Tebbit (1993) stated in his book that, in India, it was claimed that all domesticated varieties, except Chinese, were the descendants of the Indian wild pig (*Sus scrofa cristatus* known as the jungle or Indian wild pig). The Nicobari pigs might be the descendants of the Eurasian wild Boar (*Sus scrofa*) since there was an extensive original range of pigs throughout Europe and Asia, and from which many regional sub species of *S. scrofa* evolved. In the context of domesticated pigs, the most interesting were also the most divergent of the sub-species: the European wild Boar (*Sus scrofa scrofa*) and South East Asia's Banded pig of Malaysia and Indonesia (*Sus scrofa vitatus)* and Indian Wild Boar or jungle pig (*Sus scrofa cristatus*). In this context, the *Sus scrofa nicobaricus*, which were available in Nicobar group of islands, the so called "*Nicobari Pig*" has been domesticated by the tribes over many centuries and up to present day. Considering the species *S. scrofa* as a whole, the natural habitat included dense forest, steppe lands, and a wide range of maritime climates to tropical rain forest (Porter and Tebbit, 1993),

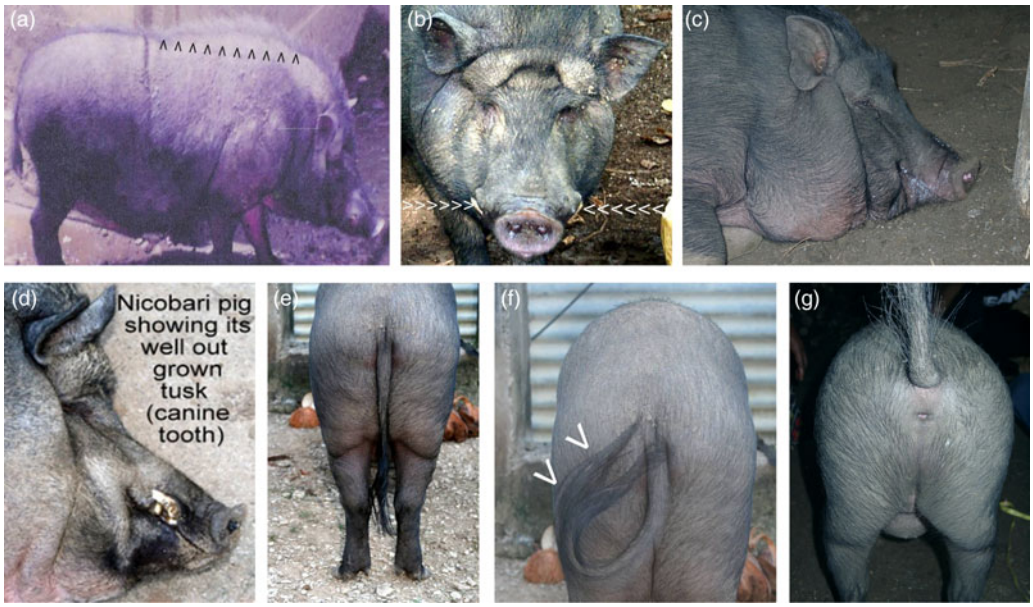

Figure 8. Photographs showing various phenotypic features viz. (a) crest of bristles, (b) head and face, (c) jowl, (d) tusk, (e) long tail, (f) tuft of hair in tail and (g) back portion of Nicobari pig.

which was similar to the present day Nicobri pig habitat. The process of domestication brings about morphological and behavioural changes in all species and it is possible to contemplate the evidence of origin from domestic animals. This was clearly evident from the morphological observation of Nicobari pig's appearance viz. varied coat colour, banded/striped coat, short to longer skull, shortening of face, mandible and lacrimal bone, shorter leg, the profile of the face was from straight to "broken" with an angle between muzzle and forehead, coarse bristle and a marked crest along the back, straight tail and pricked ears. These were important phenotypic characteristics suggestive of wild pig origin from which the Nicobari pig could be recognized as *S. scrofa nicobaricus*.

This is further confirmed by earlier reports of British/sea travellers who observed the existence of pigs as early as in the year 1846 along with tribal community when they passed through Car Nicobar, Teressa, Chowra and Nancowrie and Katchal Islands. In a paper on the "Nicobar Islands", in "The Geographical Magazine" in February, 1875 by F.A. de Roepstorff, it was written that the "Pig occupied the main stream among the tribes of Nicobar group of islands" (de Roepstorff, 1875). It was stated by many senior/aged tribesmen that the Nicobari pigs might exist on these islands for over thousands of years. Furthermore, he observed that the tribes were celebrating a feast in remembrance of a dead person and they slaughtered 24 large pigs. In the huts, they observed the slaughtered pigs, and the women were busy cutting them up. The faces and hands of all the people were smeared with pig's blood (http://andaman.org/NICOBAR/Book/Shompen/Shompen.htm). This century old observation clearly showed that the Nicobari pigs occupied the socio-cultural system of the tribes and as a major source of animal protein in their diet. Based on the geographical location of Nicobar group of islands, historical reports, phenotypic appearance and behaviour, the Nicobari pig may have genetic relatedness to pigs of South East Asian countries which could be further confirmed by molecular characterization.

Performance and breed utility

Pigs of both sexes roamed freely in the forest and breeding occurred inside the forest area through natural service and breeding data could not be obtained in detail. It was reported by the tribes that the sow in the last stage of gestation goes into the forest for farrowing. During survey, a farrowing nest (Figure 9) made by Nicobari pig was observed in the forest area and this shows the Nicobari pig's inherent behaviour for fashioning or building their nest. After a month, the sow, along with her 8–10 piglets

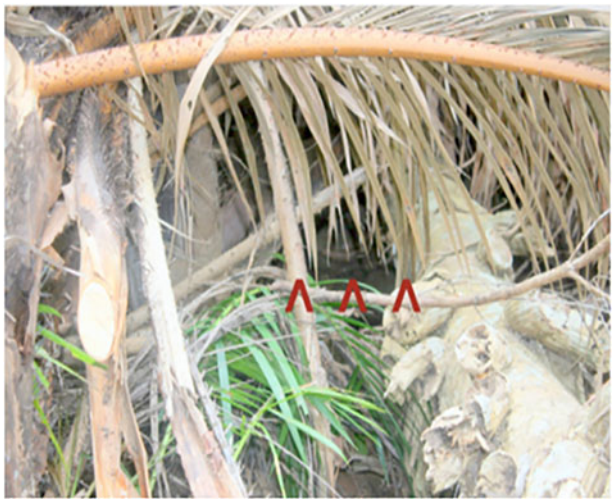

Figure 9. Recently farrowed pig in the farrowing nest.

Figure 10. Nicobari pig with its nine piglets.

Figure 11. Tribal youths carrying decorated Nicobari pig for marriage ceremony (Photo courtesy N. Ravishankar, CARI).

(Figure 10), comes to the tribal shelter and, therefore, litter size at birth and mortality were not known. However, based on interviews and observation, it was revealed that the mean ± SEM age at first farrowing (months), litter size (no.) farrowing interval (months) was 10.91 ± 0.85, 6.48 ± 0.31 and 8.06 ± 0.33, respectively. Teats were equally placed in sows and the number of teats ranged from five to six pairs indicating high mothering ability. The number of teats was an important trait for the mothering ability of sows (Pumfrey et *al*., 1980) and, in particular, teat number played a significant role when there are more piglets than number of teats (Hirooka *et al.*, 2001). Kim *et al.* (2005) concluded that 14 or more teat number compared to 11–13 teat numbers in gilts increased litter size at birth and at 21 day weaning. It was presumed that the Nicobari pig gave birth to more piglets, which needs to be confirmed by thorough monitoring under confined rearing. No specific weaning practices were followed and there was no information available about the pre or post-weaning mortality in pigs. This could be due to lack of postpartum care and attention on number of piglet delivered by a sow by the Nicobari tribe. Nicobari tribes practiced castration of their male pigs at 3–4 months of age with a belief that castrated pigs attain higher body weight and become docile. It was stated by the tribesmen that the piglets that show good health, body weight and active behaviour were not castrated and allowed go into the forest to give them the opportunity to become breeding males, which was similar to the practice followed by tribal people of Papua (former Dutch New Guinea) (http://www.papuaerfgoed.org).

Pigs are considered a family asset and reared mainly for pork consumption among the Nicobari tribes. During the pig festival (*Canahaun* in Nicobari language), which is celebrated after Christmas in January to Februry, Nicobari families select an adult swine from their stock, slaughter and distribute the carcass among their *Tuhet* which conists of 20–25 families. Pigs are also gifted (carried in a well-decorated manner) during the marriage ceremony (Figure 11) and slaughtered during various occasions such as the marriage ceremony, "*Fatya*" a function observed in fond remembrance of ancestors or recently dead person and during inter village *Mela* (local festival) on the island. No commercial system of pig rearing or sale of pork prevails among the Nicobari tribe. However, they exchange pigs between different islands during festivals and this significantly contributes to avoidance of inbreeding. This could be due to the fact that the tribes did not kill pigs regularly for meat consumption.

Pig slaughter

Pigs were slaughtered by direct cardiac puncture using a sharp-ended stick, which was passed through a small slit made just in front of the xiphoid of the sternum. Sometimes the tribesmen go for hunting pigs in the forest. Then, the entire pig was roasted on a fire for scalding (removing hair from a pig using scrapers) and cut off parts for consumption. The slaughter and processing procedure was done properly as per the standard procedure followed in the modern pig slaughter. Furthermore, it was reported that in Teressa Island, after consumption of the pork, the pig blood was smeared over the abdomen of the people present during slaughter believing that this practice improved their digestion. In Chowra Island, the pig blood is smeared all over the body for medicinal purposes. Since all parts of the pig were edible, it was presumed that dressing percentage could be approximately 70–80 percent which is similar to the report of Srivastava *et al.* (2002). Mostly, male/boars were preferred for slaughter. The average age (months) and live weight (kg) at slaughter was 12.76 ± 1.07 and 112.82 ± 14.26, respectively. It was stated by the tribesmen that the pig fat was smeared over the meat for long-term storage and consumption.

Conservation of indigenous Nicobari pig germplasm in its breeding tract

This unique indigenous pig germplasm is considered a sign of prosperity of Nicobari tribes on this island territory. The Nicobari pigs have adapted well to the island ecosystem over the centuries and perform well under the integrated resource-driven (plantation based) production system. The Nicobari pigs are under constant threat due to natural calamities (earthquake, tsunami), outbreak of disease (swine fever), predators (Reticulated pythons) and lack of scientific breeding and farming practices. As a part of conservation measure, the tribal people and school children were given awareness training on the importance of indigenous Nicobari pig germplasm and their conservation by the corresponding author and survey team in collaboration with staff of Department of Animal Husbandry and Veterinary services located at Car Nicobar Island. There is an urgent need to monitor the growth rate, molecular characterization studies for breed origin, identity, formulation of conservation strategies for the genetic improvement and conservation of this precious indigenous germplasm of India.

Conclusion

The phenotypic characters and farming system of *Nicobari pig* was documented for the first time and this study showed that the *Nicobari pigs* are indigenous to these islands and their existence was noted for many centuries. The Nicobari pigs were short in stature, with a long body and live with tribes under a free range system. Pigs were considered as a family asset by the Nicobari tribes. No commercial farms or sale of meat was practiced. The lack of interest in the indigenous pigs is such that there are only a few studies which have focused on characterization and performance under typical village conditions. Wild pigs could have an effect upon local domesticants and such species are of interest as they contribute significantly to sociocultural and livelihood of the tribes and the less privileged section of the society in many parts of the world. As in the case of the present day Nicobari pig, which could be descendants of *S. scrofus nicobaricus* (wild pig), the potentially valuable traits still remain largely unrecognized, such as adaptability, conformation, performance, the ability to utilize waste and their disease resistance under a tropical island ecosystem. Therefore, it is concluded that the Nicobari pigs could be a recognized indigenous pig breed/germplasm belonging to the Nicobar group of islands in India and this would attract academics, researchers and conservationists to pay special attention to it in future. This could lead to studies on conservation, as well as a detailed study on performance under existing tribal production system or under scientific management at an institutional level.

Acknowledgements

The authors are grateful to the INDIAN COUNCIL OF AGRICULTURAL RESEARCH Govt. of India, for providing necessary funding and facilities under the AP Cess project on “Conservation and characterization of Nicobari pig”. The first author thank specially Dr. R.B. Rai and R.N. Chatterjee for their initiatives, guidance and support. Thanks are also due to the Director, Central Agricultural Research Institute, Port Blair, Veterinary Officers and Para-veterinary staff of the Department of Animal Husbandry and Veterinary Services, Nicobari Tribes and Tribal Councils, A&N islands, and the project staff Dr T.P. Swapna, S.K. Jana, Dr T. Geetha, M. Gayathridevi and all the enumerators associated with the project.

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Animal Genetic Resources, 2014, 55, 87–91. © Food and Agriculture Organization of the United Nations, 2014
doi:10.1017/S2078633614000368

El cuy (*Cavia porcellus*): un recurso andino de interés agroalimentario
The guinea pig (*Cavia porcellus*): An Andean resource of interest as an agricultural food source

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Resumen

El cuy es un mamífero roedor originario de la Cordillera de los Andes de Colombia, Ecuador, Perú y Bolivia, donde ha mantenido una estrecha relación con el pueblo preincaico, ya sea como fuente de alimento alto en proteína y bajo en grasa o como animal asociado a tradiciones que se mantienen hasta la actualidad. La crianza del cuy se ha realizado de forma tradicional en pequeños espacios en las cocinas cerca de los fogones de la población rural de escasos recursos desde épocas ancestrales. Debido a la necesidad de buscar ingresos económicos para las familias campesinas, se ha introducido el sistema de producción comercial y con él, líneas/razas mejoradas que se han propagado en toda la Región Andina, absorbiendo casi por completo al cuy autóctono. Por otra parte, desde el siglo XVI de América el cuy ha tomado popularidad alrededor del mundo como animal de compañía, exhibición y experimentación. En el presente trabajo se realiza una revisión bibliográfica para recopilar y divulgar los principales aspectos que rodean al cuy y la población andina y de esta manera crear conciencia en la importancia de conservar los recursos zoogenéticos locales y como punto de partida para futuras investigaciones.

Palabras clave: *recursos zoogenéticos, conservación, carne, sistemas de producción, Latinoamérica*

Summary

The guinea pig is a rodent mammal native to Colombia, Ecuador, Peru and Bolivia in the Andes, where it has always had a close relationship with the pre-Inca people, either as a food source, high in protein and low in fat or as an animal associated with traditions maintained to the present day. Since ancient times, guinea pig breeding has traditionally been carried out in small spaces inside the kitchens of rural farming families, near the stove. To meet rural households' need for income, a commercial production system has been established and has introduced improved strains/breeds which have spread throughout the Andean region, almost completely absorbing the native guinea pig. On the other hand, since the sixteenth century the guinea pig has gained in popularity around the world as a pet, for exhibition purposes, or as a laboratory animal. In this paper, a literature review has been undertaken to compile and disclose the main issues concerning the guinea pig and the Andean population, with the aim of creating awareness of the importance of conserving local genetic resources and providing a starting point for future research.

Keywords: *zoogenetic resources, conservation, guinea pig meat, production systems, Latin America*

Résumé

Le cochon d'Inde est un mammifère rongeur originaire des Andes de la Colombie, l'Équateur, le Pérou et la Bolivie, où il a maintenu un lien étroit avec le peuple pré-incaïque, soit comme source d'une alimentation riche en protéines et pauvre en graisse ou comme animal lié à des traditions qui se conservent jusqu'à nos jours. Depuis les temps anciens, l'élevage du cochon d'Inde a été pratiqué dans des petits espaces de la cuisine, près des fourneaux, par une population rurale à ressources limitées. Dans le but d'accroître les revenus des familles paysannes, un système de production commerciale a été introduit et avec celui-ci des lignées/races améliorées qui se sont répandues dans toute la Région Andine jusqu'à presque absorber entièrement le cochon d'Inde autochtone. Par ailleurs, le cochon d'Inde est devenu populaire partout dans le Monde comme animal de compagnie, d'exhibition et d'expérimentation. Ce travail consiste en une revue de la littérature ayant pour but de compiler et de vulgariser les principaux aspects relatifs au cochon d'Inde et à la population andine pour ainsi sensibiliser à l'importance de conserver les ressources zoogénétiques locales et pour servir de point de départ à des recherches futures.

Mots-clés: *ressources zoogénétiques, conservation, viande, systèmes de production, Amérique Latine*

Presentado: 6 Enero 2014; aceptado: 8 Septiembre 2014

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Introducción

La primera evidencia arqueológica de la existencia del cuy *(Cavia porcellus*) fue encontrada en Perú y Colombia hace 9000 años, y el animal ha sido domesticado aproximadamente hace 4500–7000 años (Wing, 1986). Esta especie de roedor doméstico de la familia *Caviidae*, fue descrita por primera vez por Konrad von Gesner en 1554. El cuy se encuentra disperso en Colombia, Ecuador, Perú, Bolivia y una minoría en Guatemala y Cuba (Figura 1), donde son utilizados en la alimentación de la especie humana y proporcionan importantes ingresos económicos a las familias rurales por la venta de sus excedentes en el mercado local. En el Perú durante el año 2001 y el primer semestre del 2007 las exportaciones de carne congelada de cuy alcanzaron un valor acumulado de 306.864 dólares estadounidenses, monto muy importante entendiendo que provienen de un nuevo rubro de exportaciones de productos no tradicionales, lo cual motiva a los productores a ser mas competitivos (Gil, 2007). En los países andinos la mujer campesina es responsable de las tareas domésticas pero, al mismo tiempo, realiza un sinfín de actividades productivas en el campo. La crianza y el manejo del cuy es su dominio exclusivo (Archetti *et al.*, 1984).

La carne de cuy es un alimento de alto valor nutricional, que contribuye a la seguridad alimentaria rural y urbana, y que hoy en día es uno de los platos más exquisitos y apetecidos en diversos lugares del mundo (Figura 2) (Sánchez, 2004).

En los países Andinos existe una población más o menos estable de 35 millones de cuyes (Chauca, 1997). La

Figura 1. Ubicación geográfica del consumo de carne de cuy.

Figura 2. Canales de cuy deshuesado. (*Fuente*: Chauca, 2007: 227.)

mayor producción de esta especie se encuentra en el Perú, con 12.695.030 cuyes (INEI, 2012); en segundo lugar, el Ecuador, con 5.067.049 cuyes (INEC, 2002); Colombia en el tercer lugar, con 1.292.244 cuyes (ENA, 2007); y finalmente Bolivia, con 650.000 cuyes (MACA, 2004). El cuy gracias a su capacidad de roer es usado en el área agrícola para limpiar la cáscara blanda el fruto del Nogal de los Andes o 'tocte'; también en esta área se usa su estiércol incorporándolo al suelo como abono orgánico. En los países andinos el cuy está integrado profundamente en las tradiciones y los rituales, ya que se le atribuye poderes curativos para todo tipo de enfermedades.

Desde el siglo XVI, el cuy ha tomado popularidad alrededor de mundo como animal de exhibición, como una afectuosa mascota y como animal de experimentación. El propósito de esta revisión es recopilar y difundir información relevante sobre los estrechos lazos de esta especie con el pueblo andino en diferentes aspectos como: sistemas de producción, calidad de la carne, y usos en distintas áreas; y de esta manera valorar la importancia de conservar los recursos zoogenéticos locales e incorporar programas de conservación de los recursos zoogenéticos tan apreciados en la actualidad (FAO, 2009) (Figura 3).

Sistemas de producción

La producción de cuyes en general es una actividad ancestral rural de los Andes, aunque también se puede encontrar algunas explotaciones en la región costa y la amazonia, en donde predomina el sistema familiar-tradicional de producción de carne con bajas producciones destinadas al autoconsumo del cuy en ocasiones festivas como bautizos, grados, bodas, etc. (Usca, 1998). Las explotaciones tradicionales tienen índices productivos inferiores a 0,2; el promedio de crias por hembra al año es de 5,5. Los sistemas comerciales permiten lograr un índice productivo de 1 y un promedio de crias por hembra al año de 10,8 (FAO, s.f.). Estos índices se calculan relacionando la producción con los recursos empleados para obtener dicha producción, por ejemplo gazapos destetados por cuya y año.

Figura 3. Cuyes autóctonos del Ecuador.

Sistema familiar-tradicional

Es la más difundida en la región andina. Se caracteriza por desarrollarse sobre la base de insumos y mano de obra disponibles en el hogar. El cuidado de los animales lo realizan los hijos en edad escolar (10%), las amas de casa (73%) y los esposos (9%) (Zaldívar, 1990). La crianza tradicional se hace en las cocinas de las casas con un número promedio de 25 animales, compartiendo un mismo espacio, ya que el fuego y el humo ayudan a mantener una temperatura cálida y libre de insectos (Figura 4). En algunas comunidades indígenas aún se conserva la tradición de criar sus cuyes y conejos bajo las camas de los dueños. Debido a este particular sistema de producción, el proceso reproductivo no está controlado, y existen baja fertilidad y consanguinidad elevada; por otro lado, la alimentación de los animales es poco sistemática, y el control de enfermedades es esporádico y tardío, lo que provoca el 38% de mortalidad (Archetti *et al.*, 1984).

Dentro de la población campesina, es tradición en Ecuador regalar una pareja de cuyes a los recién casados. En la mayoría de los casos la mujer es la que asume la crianza de los cuyes, inclusive mucho antes de la invasión española; por ello, culturalmente la mujer tiene un conocimiento complejo que cubre casi todas las variables que entran en el proceso productivo. Otro aspecto que rodea

Figura 4. Cría de cuyes dentro de la cocina.

Figura 5. Sobada del cuy a un enfermo. Oleo de Pedro Anhuaman.

a este sistema es la 'sobada del cuy', practicada por los sobadores 'chamanes'; es simple pero está saturada de significados sociales y simbólicos (Figura 5). El sobador pide, por lo general, un cuy que viva con la familia del paciente. El tamaño y el color del animal varían de acuerdo con el tipo de paciente y con la práctica del sobador. El animal muere durante la ceremonia al ser frotado intensamente en el cuerpo del paciente. Luego de su muerte, el sobador observa los órganos del animal con el objetivo de encontrar la enfermedad que aqueja al cliente. La hipótesis que guía esta búsqueda es que el cuy 'absorbe' la enfermedad y permite de esta manera su identificación. Para muchos campesinos y sobadores esta 'absorción' es posible sólo si el cuy ha tenido una relación muy próxima con el enfermo (Barahona, 1982).

Sistema comercial

En la década de los 80, se inicia la crianza comercial a pequeña escala, donde se mejora y controla el manejo cavícola, ya que no se cría dentro de las casa, sino que se han construido galpones con pozas o jaulas y se clasifican los cuyes por tamaño y sexo; la alimentacion ya no se realiza con sobras de la comida de las familias y pastos fibrosos, han pasado a recibir forraje y pienso de buena calidad (Archetti *et al.*, 1984). En cuanto a la genética de los cuyes andinos, ha ido cambiando por la introducción de la línea comercial Perú, y posteriormente otras dos líneas (Inti y Andina), que se venían desarrollando en el Instituto Nacional de Investigaciones Agraria

Tabla 1. Valor nutricional de la carne de cuy comparada con otras especies cárnicas.

Especie animal	Humedad %	Proteína %	Grasa %	Minerales %	Carbohidratos %
Cuy	76.3	21.4	3.0	0.8	0.5
Ave	70.2	18.3	9.3	1.0	1.2
Vacuno	58.0	17.5	21.8	1.0	0.7
Ovino	50.6	16.4	31.1	1.0	0.9
Porcino	46.8	14.5	37.3	0.7	0.8

Fuente: Zumárraga, 2011.

(INIA) del Perú (Chauca, 2007: 227). Esto ha ocasionado que los cuyes comerciales absorbieran la genética autóctona de muchas comunidades que críaban cuyes mal denominados 'criollos', ya que ofrecían un animal para consumo 500 g más grande que el que se acostumbraba a criar tradicionalmente. Sin embargo, todavía se pueden encontrar animales nativos que se conservan en zonas rurales gracias a las tradiciones.

Figura 6. Cuyes de exhibición.

Propiedades nutritivas de la carne de cuy

Como alimento, la carne de cuy es saludable, altamente digestible y una valiosa fuente de proteínas, superior a otros productos cárnicos (Tabla 1). Es baja en contenidos de colesterol (65 mg/100 g) y sodio, y contiene vitaminas especialmente del complejo B (15 mg/100 g) (Crespo, 2012). Además hay la presencia de ácidos grasos linoleico y linolénico, esenciales para el ser humano; cabe resaltar que el nivel de dichos ácidos grasos es bajísimo o casi inexistente en otras carnes, y son precursores de la conformación del acido graso araquidónico (AA) y acido graso docosahexaenoico (DHA). Estas sustancias AA y DHA son vitales para el desarrollo de las neuronas (especialmente cerebrales) y membranas celulares (protección contra agentes externos), y forman el cuerpo de los espermatozoides; además están especialmente recomendados para mujeres embarazadas y niños (Zoetecnocampo, s.f.). El rendimiento promedio en carne de cuyes enteros es de 65%. El 35% restante involucra las vísceras (26,5%), pelos (5,5%) y sangre (3,0%) (FAO, 2000).

Otros usos

Desde el siglo XVI el cuy se ha convertido en una popular mascota alrededor del mundo, hasta formar asociaciones para realizar exhibiciones muy competitivas como: la American Cavy Breeders Association en los Estados Unidos y Canadá; el British Cavy Council en el Reino Unido; asociaciones en Australia (Australian National Cavy Council) y Nueva Zelanda (New Zealand Cavy Club). Cada club publica su propia norma de juzgamiento (Figura 6).

En España, específicamente en las Islas Canarias, se obtuvo información de forma oral que los cuyes, denominados en este lugar 'cobayas', eran usados como animales de protección para gallinas, en contra de las ratas en los establos.

El cuy como animal de experimentación, es utilizado en la empresa farmacéutica en pruebas de valoración de tintes para el cabello, ya que su pelo posee características estructurales similares a las del ser humano. En la investigación, en varios países se está utilizando la sangre de cuy para el tratamiento de algunas clases de tumores o neoplasias, ya que ésta presenta una enzima que han denominado como alfa asparaginasa.

Figura 7. Nogal de los Andes.(*Fuente*: http://dioskonyv.bionuss.eu/04-06/1.htm)

Tabla 2. Cantidad, calidad y valor del estiércol de cuy comparado con otras especies.

Especie	Tonelads/ año	N Kg/t	N Kg. por año	Valor del estiércol en función del N Producido USD (2007)
Cerdo	35.55	04.50	159.55	92.53
Cuy	29.02	15.08	437.62	253.81
Vaca	26.66	05.04	134.36	77.92
Caballo	17.77	06.20	110.17	63.89
Oveja	13.33	12.60	167.96	97.41
Gallino	10.00	14.20	142.00	82.36

Nota: N (Nitrogeno)
Fuente: Aliaga *et al.,* 2009.

En el área agrícola, los campesinos de la Sierra ecuatoriana durante los meses de julio, agosto y septiembre cosechan el fruto del Nogal de los Andes (*Juglans neotropica)*, conocido como 'tocte' (Figura 7), cuyos frutos son colocados en el cuyero para que los cuyes roan su cáscara blanda, dejando el fruto con su cáscara dura y limpia para comercializarlo (Pazmiño, 2005). Además la producción de estiércol del cuy es la más alta en cantidad y calidad en comparación a otras especies (Tabla 2), cuya incorporación al suelo mejora la textura y la proliferación de microorganismos, lo cual permite un cultivo limpio, libre de agroquímicos y residuos nocivos para la salud humana (Aliaga *et al*., 2009: 484).

Conclusión

El cuy gira en torno a las tradiciones ancestrales de los pueblos andinos. Debemos consolidar la importancia de conservar las características autóctonas de estos animales para sus distintos usos como hemos visto en este artículo, mediante la identificación y caracterización de los cuyes autóctonos de los Andes, para así mejorar los diferentes sistemas de producción existentes con cuyes de mejor calidad cárnica, aprovechando su rusticidad y resistencia a enfermedades, características invalorables de los animales autóctonos.

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Animal Genetic Resources, 2014, 55, 93–99. © Food and Agriculture Organization of the United Nations, 2014
doi:10.1017/S2078633614000290

Egg quality traits of local Ghanaian chickens and influence of storage period

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Summary
Egg quality traits of local Ghanaian chickens from two agro-ecological zones were measured and compared with those of an imported breed, SASSO T44 chickens from the day of lay to a period of 21 days in storage. On the average SASSO T44 chickens had significantly ($P < 0.05$) higher egg weight, shell weight, albumen height (AH), albumen weight, yolk weight, albumen ratio and Haugh units (HU). Eggs of the local chicken ecotypes had significantly ($P < 0.05$) higher yolk ratios than the SASSO T44 birds with chickens from the forest zone being superior ($P < 0.05$) to those from the savannah in AH. Fluctuations in egg quality traits during the 3-week study period were similar in the three ecotypes studied. Conversion of AH to HU narrowed the gap in egg quality performance between local and SASSO T44 chickens. There was a negative effect of storage time on egg quality irrespective of the chicken ecotype. It was recommended that chicken eggs should be kept at temperatures cooler than ambient temperatures to minimize deterioration of their quality.

Keywords: *albumen height, ·albumen ratio, ·Haugh unit, ·storage time, yolk ratio*

Résumé
Se midieron los parámetros de calidad de huevo en gallinas autóctonas ghanesas de dos zonas agroecológicas, para después compararlos con los de una raza importada, gallinas SASSO T44, desde el día de la puesta hasta los 21 días de almacenamiento. De media, las gallinas SASSO T44 presentaron ($P < 0.05$) mayor peso de huevo, mayor peso de la cáscara, mayor peso y altura del albumen, mayor peso de la yema, mayor proporción de albumen y más unidades Haugh. Los huevos de los ecotipos de gallina autóctona presentaron ($P < 0.05$) mayor proporción de yema que los de las aves SASSO T44, siendo la altura del albumen mayor ($P < 0.05$) en las gallinas de la zona de selva que en las de la sabana. Las variaciones en los parámetros de calidad de huevo a largo de las tres semanas del periodo de estudio fueron similares en los tres ecotipos considerados. La conversión de la altura del albumen a unidades Haugh redujo las diferencias en calidad de huevo entre las gallinas autóctonas y las SASSO T44. Se dio un efecto negativo del tiempo de almacenamiento sobre la calidad de los huevos, independientemente del ecotipo de ave considerado. Se recomendó que los huevos de gallina fueran guardados a temperaturas menores que la temperatura ambiental para minimizar el deterioro de su calidad.

Mots-clés: *unité Haugh, proportion de jaune, hauteur d'albumen, proportion d'albumen*

Resumen
Les paramètres de qualité de l'œuf ont été mesurés chez des poules autochtones ghanéennes de deux zones agro-écologiques et ont été comparés à ceux d'une race importée (SASSO T44), du jour de la ponte aux 21 jours de stockage. En moyenne, les poules SASSO T44 ont présenté ($P < 0.05$) des œufs plus lourds, un poids de la coquille plus élevé, un poids et une hauteur d'albumen plus grands, un poids du jaune plus élevé, une proportion d'albumen plus grande et un plus grand nombre d'unités Haugh. La proportion de jaune a été plus grande ($P < 0.05$) dans les œufs des poules autochtones que dans ceux des poules SASSO T44, avec la hauteur d'albumen étant plus grande ($P < 0.05$) chez les poules de la forêt que chez celles de la savane. Les variations dans la qualité de l'œuf au cours des trois semaines de durée de l'étude ont été similaires chez les trois écotypes étudiés. La conversion de la hauteur de l'albumen en unités Haugh a réduit les différences en qualité d'œuf entre les poules autochtones et les SASSO T44. Un effet négatif du temps de stockage sur la qualité de l'œuf a été décelé, indépendamment de l'écotype de poule considéré. Il a été recommandé de garder les œufs à une température inférieure à la température ambiante afin de minimiser leur perte de qualité.

Palabras clave: *unidad Haugh, proporción de yema, altura de albumen, proporción de albumen*

Submitted 3 February 2014; accepted 1 July 2014

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Introduction

The hen's egg consists of yolk (30–33 percent), albumen (approximately 60 percent) and shell (9–12 percent; Ahmadi and Rahimi, 2011). Egg quality refers to its inherent properties that determine its excellence and

acceptability to the consumer (Singh, Cheng and Silversides, 2009). Even under the most favourable conditions, egg quality is relatively unstable, as the interior quality of the egg deteriorates from the time it is laid to the time it is consumed. Quality changes may render eggs useless for food before they reach the consumer. Egg quality and composition also change in accordance with level of production and age of layer. The proportion of yolk increases with age while the proportions of albumen and shell thickness decrease (Akbar *et al.*, 1983; Fletcher *et al.*, 1983).

Genetic differences in egg shell formation characteristics exist between species, and between breeds, strains and families within species (Buss, 1982). Albumen quality is a standard measure of egg quality that is most often measured as the height of the inner thick albumen. Albumen height (AH) can give a measure of the freshness of the egg because the height of the inner thick albumen decreases in the logarithmic scale with storage time (Silversides and Scott, 2001). The major influences on AH are the strain and age of the hen laying the egg and storage time and conditions (Williams, 1992). Eggs increase in weight over a production, while egg shell thickness and strength usually decreases (Anderson *et al.*, 2004). The trend in egg consumption is moving from shell egg consumption towards egg products, leading to a greater focus on the internal egg composition (Hartmann *et al.*, 2002). Production of good quality eggs should thus contribute to the economic fortunes of the poultry farmer but in Ghana little work has been done on egg quality characteristics of chickens. Characterization of egg quality traits however constitutes and important step in the development of sustainable breeding programme for local avian genetic resources. The objective of the present study therefore was to assess the effect of storage on the quality characteristics of local chicken eggs and compare them with those of SASSO T44 chickens.

Materials and methods

Egg quality parameters of local chickens from the Forest and Savannah zones of Ghana and SASSO T44 chickens (a strain of the *Label Rouge* from France) kept at the Livestock and Poultry Research Centre (LIPREC), University of Ghana were measured. 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 128–1709 mm distributed bimodally. 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 1500 h ranges between 58 and 83.7 percent and is slightly lower at 0900 h.

Management of the experimental chickens has been described by Osei-Amponsah, Kayang and Naazie (2012). A total of 140 eggs were collected from the two local ecotypes – forest (98) and savannah chicken (52) and 107 eggs from the control population (SASSO T44). Eggs were collected and stored from 0 to 21 days at room temperature (27 °C) and a relative humidity (60 percent) and stored at the Animal Biotechnology Laboratory of the Department of Animal Science, University of Ghana, Legon. Egg quality characteristics were measured at 3-day intervals over the study period of 21 days. Eggs were weighed individually at day of collection and on the day of taking measurements. Egg quality traits evaluated were egg weight (EW), AH, albumen weight (AW), yolk weight (YW) and Haugh unit (HU). Eggs were collected and weighed using an electronic beam balance (OHAUS, 2006). Egg length and width were measured with the aid of a pair of vernier callipers calibrated in mm. Eggs were later carefully opened and content poured into a tripod micrometer (Froning and Fank, 1958) to determine the maximum AH at its widest part at a position half-way between the yolk and the outer margin. The yolk and albumen were carefully separated and weighed separately using the beam balance to determine their respective weights. Albumen, yolk and shell ratios were determined as their weights relative to egg weight. In order to correct for the difference in egg weight, the AH was converted into HUs (Haugh, 1937). HUs were calculated for individual eggs using the formula:

$$\mathrm{HU} = 100 \log(H - 1.7\, W^{0.37} + 7.57),$$

where HU is the Haugh unit; H is the height of the albumen (mm); and W is the weight of the egg (g).

Analysis-of-variance (ANOVA) procedures were used to isolate the effect of ecotype on egg quality characteristics while variations in egg quality characteristics of the experimental chicken were depicted in line graphs using the software SPSS (SPSS, 2007).

Results

Eggs of the French SASSO T44 chickens were significantly ($P < 0.05$) heavier with heavier shells and yolks compared with those of local chickens with the forest birds being superior to the Savannah ecotypes (Table 1). The SASSO T44 chickens were superior ($P < 0.05$) to the local chicken ecotypes in most of the internal egg quality traits except yolk ratio (Table 2). Within the local ecotypes eggs from chicken from the Forest zone were heavier than eggs from their Savannah counterparts. Irrespective of ecotype, there is a general reduction in EW with storage time (Figure 1).

The trend in AW and YW were similar for local chicken ecotypes and SASSO T44 chicken studied (Figures 2 and 3) with more erratic fluctuations in AW than YW. AW of the SASSO T44 chicken was higher than those of the local ecotype during the entire storage period (Figure 2). The local chicken ecotype eggs had similar albumen ratios to SASSO T44 (Figure 4) but their yolk ratios were higher than the control population at every storage period

Table 1. Means and standard errors of external quality traits of experimental chickens.

Genotype	Egg weight (g)	Shell ratio	Shell weight (g)	Yolk weight (g)
Forest	$43.43^{b} \pm 0.44$	$0.11^{b} \pm 0.001$	$4.68^{b} \pm 0.06$	$15.67^{b} \pm 0.21$
Savannah	$40.16^{c} \pm 0.72$	$0.11^{b} \pm 0.001$	$4.35^{c} \pm 0.09$	$15.13^{b} \pm 0.31$
SASSO T44	$55.2^{a} \pm 0.58$	$0.10^{a} \pm 0.001$	$5.38^{a} \pm 0.05$	$17.18^{a} \pm 0.23$

Within columns means followed by different superscripts are significantly ($P < 0.05$) different.

Table 2. Means and standard errors of internal egg quality traits of experimental chickens.

Genotype	Albumen height mm	Albumen weight g	Albumen ratio	Haugh unit	Yolk ratio
Forest	$3.17^{b} \pm 0.10$	$26.12^{b} \pm 0.72$	$0.60^{b} \pm 0.015$	$67.34^{b} \pm 0.85$	$0.36^{b} \pm 0.01$
Savannah	$2.89^{c} \pm 0.13$	$23.59^{b} \pm 1.00$	$0.59^{b} \pm 0.022$	$64.97^{b} \pm 1.20$	$0.38^{a} \pm 0.01$
SASSO T44	$3.84^{a} \pm 0.12$	$36.61^{a} \pm 0.88$	$0.66^{a} \pm 0.01$	$72.43^{a} \pm 0.89$	$0.31^{c} \pm 0.01$

Within columns means followed by different superscripts are significantly ($P < 0.05$) different.

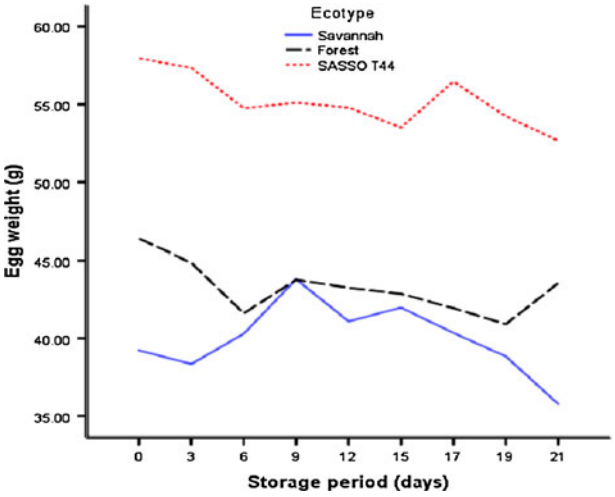

Figure 1. Variations in egg weight of experimental chickens during storage.

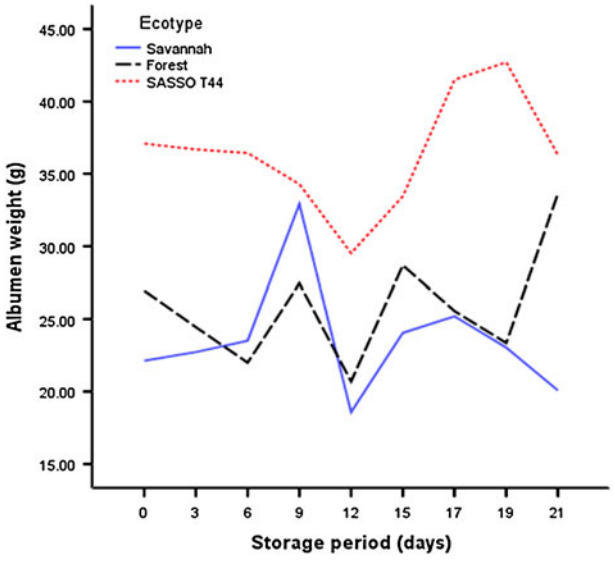

Figure 2. Variations in albumen weight of experimental chickens during storage

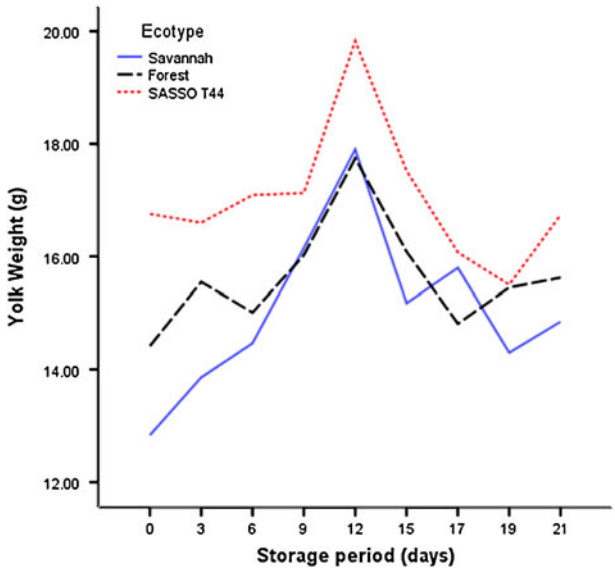

Figure 3. Variations in yolk weight of experimental chickens during storage

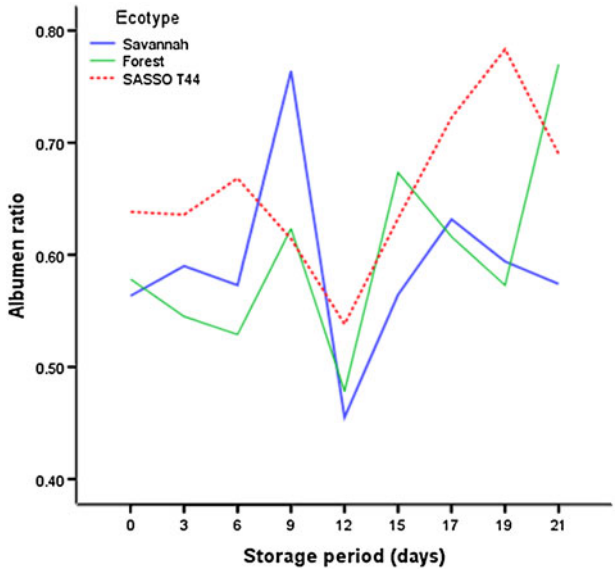

Figure 4. Variations in albumen ratio of experimental chickens during storage

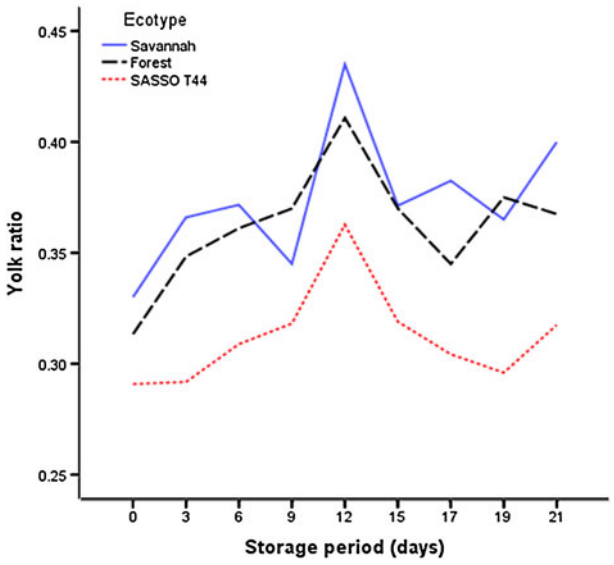

Figure 5. Variations in yolk ratio of experimental chickens during storage

(Figure 5). Fluctuations in YW and yolk ratio followed a similar pattern as shown in Figures 3 and 5.

Correlation co-efficients between the egg quality traits indicated highly significant ($P < 0.01$) correlations between EW and AW, shell weight, AH and HU (Table 3). However, the correlation between EW and shell ratio and yolk ratio were negative. Table 3 also shows a highly significant ($P < 0.01$) negative correlation was recorded between AW and yolk ratio as well as between yolk ratio and AH and HU. A highly significant ($P < 0.01$) positive correlation was also recorded between AH and HU. The trend in AH and HUs were observed to be similar as shown in Figures 6 and 7 but conversion to HUs narrowed the gap in egg quality of local and SASSO T44 chicken. Variations in shell ratio by storage periods followed a specific pattern in all the experimental groups with the local chickens having a higher shell ratio at every point (Figure 8).

Discussion

The superiority of the SASSO T44 in most of the egg quality traits is to be expected as it has relatively larger eggs and most of the quality traits are positively correlated to egg size. This is in line with other findings of Islam and Dutta (2010) as well as Moula *et al.* (2013). The significantly ($P < 0.05$) higher shell ratios of the local chickens indicates a possible relatively stronger shells compared with those of SASSO T44 chickens. This is an advantage as egg shells need to be strong enough to remain intact throughout the chain from the time that the egg is laid until it is used by the consumer and to keep the contents of the egg safe from microbial contamination (Jacob, Miles and Mather, 2000). Scott and Silversides (2000) found that eggs from ISA-Brown hens were heavier than those from ISA-White hens and had more shell and albumen, but less YW and AW. The superiority of the forest chickens over the savannah chickens within the local chicken ecotypes could be attributed to genotype as all experimental animals were raised on-station. Fayeye *et al.* (2005) evaluated thirteen internal and external egg traits of 30 eggs of *Fulani*-ecotype chickens and the indices of internal egg quality indicated that the *Fulani*-ecotype chicken is highly desirable producing eggs with good shell thickness which could be genetically exploited to reduce losses due to cracked eggs. SASSO T44 is a strain developed from the Franch *Label Rouge* and has been selected over the years as a larger breed for meat production resulting in relatively bigger eggs of its hens. EW influences the weight of components of eggs especially egg albumen and yolk (Tadesse *et al.*, 2013). Furthermore, egg size increases with increasing hen age but the increase in weight is not accompanied by a proportional increase in shell weight, so that the ratio of shell weight to EW (percentage shell) decreases (Ahmadi and Rahimi, 2011).

SASSO T44 chickens were superior in most of the internal quality traits particularly AH which is also highly significantly ($P < 0.01$) correlated to HU. While heavier YWs were recorded in the control population (SASSO T44 chickens), the yolk ratios were higher in the local ecotypes due to a relatively higher AW in the control population. Furthermore, the relatively higher ($P < 0.05$) yolk ratios of local chicken eggs which is in line with findings of Moula *et al.* (2013) may indicate their relative higher

Table 3. Phenotypic correlation co-efficients between egg quality traits local and SASSO T44 chickens.

	EW	YW	AW	SW	SR	AR	YR	AH	HU
EW	1.00	0.44**	0.71**	0.73**	−0.51**	0.21**	−0.68**	0.43**	0.40**
YW		1.00	0.17*	0.50**	−0.12**	−0.26**	0.32**	−0.06	−0.07
AW			1.00	0.40**	−0.50**	0.83**	−0.85**	0.24**	0.22**
SW				1.00	0.18**	0.003	−0.41**	0.32**	0.28**
SR					1.00	−0.31**	0.48**	−0.23**	−0.23**
AR						1.00	−0.98**	0.02	0.02
YR							1.00	−0.56**	−0.54**
AH								1.00	0.99**
HU									1.00

** – Highly significant ($P < 0.01$); * – Significant ($P < 0.05$).
EW, egg weight; YW, yolk weight; AW, albumen weight; SW, shell weight; SR, shell ratio; AR, albumen ratio; YR, yolk ratio; AH, albumen height; HU, Haugh unit.

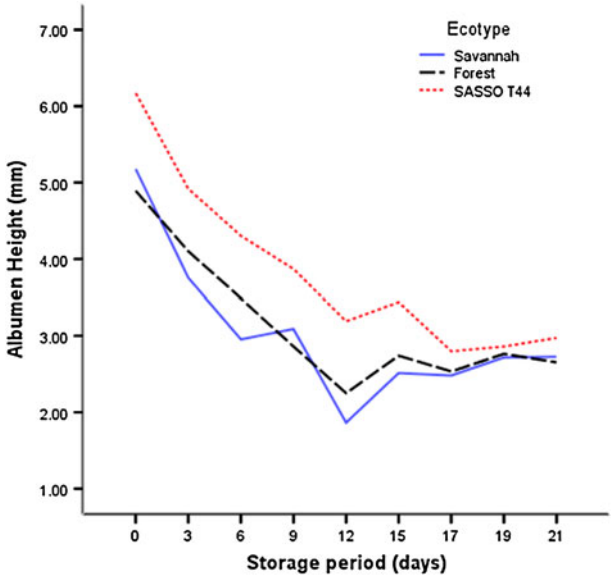

Figure 6. Variations in albumen height of experimental chickens during storage

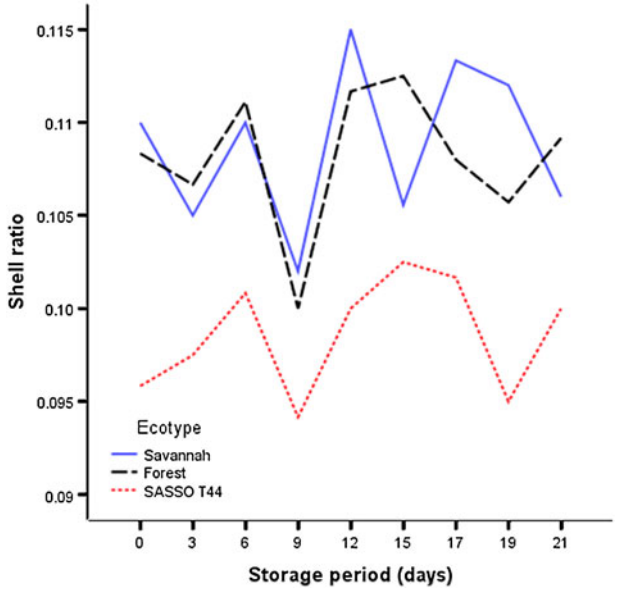

Figure 8. Variations in shell ratio of eggs of experimental chickens during storage

yolk richness. Local breeds adapted to less industrial production systems have the potential to offer more flavour products for increasingly health-conscious consumers (Moula *et al.*, 2009) and high egg quality traits for local chickens of Nigeria have also been reported by Momoh, Ani and Ugwuowo (2010).

Average EW, AH, shell weight and shell ratio obtained in the present study for the local ecotypes were lower than those of Chatterjee *et al.* (2007) who reported average EW of 48.5 g and AH of 6.77 mm for the indigenous *Nicobari* chicken of India. However, values of the average AW, albumen ratio, YWs and yolk ratio reported for the three ecotypes in the present study were higher than those reported by Chatterjee *et al.* (2007). Monira, Salahuddin and Miah (2003) also reported relatively higher EWs for White Leghorn, Barred Plymouth Rock, Rhode Island Red and White Rock than those recorded in the present study. The difference in the results can be attributed to genetic differences of the chicken strains involved as the White Leghorn has been selected for improved egg production performance. External and internal egg quality traits have genetic basis and can also be affected by non-genetic factors (Alsobayel and Albadry, 2011).

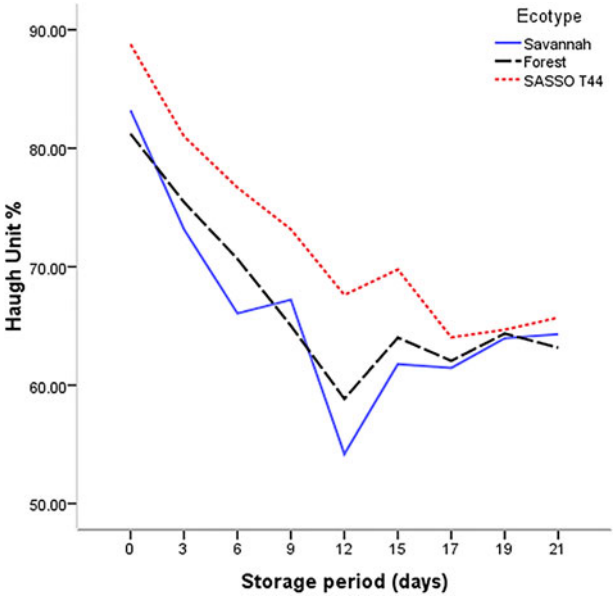

Figure 7. Variations in Haugh unit of experimental chickens during storage

HU of 45.81, 54.2, 45.81 and 58.68, respectively for White Leghorn, Barred Plymouth Rock, Rhode Island Red and White Rock (Monira, Salahuddin and Miah, 2003) are lower than those obtained in the present study. With the exception of AH values of egg quality traits of local Ghanaian ecotypes were higher than those reported for Ethiopian indigenous chickens (Mogesse, 2007) while HUs are comparable between Ghanaian and Ethiopian chicken ecotypes. Our results for shell, albumen and YW are comparable with those obtained by Vij, Tantia and Vijh (2006). Average AH and HU reported for Fayoumi chickens and its crosses naked neck and Rhode Island Red chickens raised under semi-scavenging conditions in Bangladesh were slightly better than those obtained in the present study (Zaman Sørensen and Howlider, 2004). Furthermore, Varguez-Montero *et al.* 2012 found a significant effect of housing system on egg quality of Rhode Island Red hens. With the exception of the AH and HU egg quality characteristics obtained for local and SASSO T44 chicken are higher than those reported for the Fulani-ecotype chicken (Fayeye *et al.*, 2005).

The effect of storage period on egg quality traits of the experimental chickens revealed some interesting results.

In general, EW declined with increasing storage period due to loss of carbon dioxide (CO_2). There were fluctuations in AW of eggs of all the experimental chicken indicating biological reactions within the egg. Irrespective of ecotype, YW increased till the 12th day and fell indicating due to deterioration of the previtelline membrane which surrounds the yolk. Albumen ratio levels fluctuated with storage time and getting to the lowest level on day 12 in all the ecotypes studied. This can be attributed to loss of CO_2 through the shell causing the albumen to become more transparent and increasingly watery in storage (Benton and Brake, 2000). The trend in the yolk ratio was also similar to YW peaking around day 12 of the study period. This can be explained by the negative correlation between AW and yolk ratio. AH as expected decreased consistently up to day 12 and then stabilized. The fluctuations in the HU followed closely that of AH. This is consistent with the findings of Silversides and Scott (2001). In general, the albumen quality of eggs decline with increasing storage time and poor storage conditions. During storage the thick albumen becomes thinner allowing greater movement of the yolk (Jacob, Miles and Mather, 2000). EW, AH and yolk height, HU, albumen and yolk indices decrease with increase in storage time (Tabidi, 2011) and poor storage can result in deterioration in its quality and consequently loss and waste of eggs (Raji *et al.*, 2009; Khan *et al.*, 2013).

Room storage condition (ambient temperature) could be responsible for the relatively lower HUs obtained in the present study. Egg handling and storage practices have a significant impact on the quality of eggs reaching the consumer. Albumen quality is a standard measure of egg quality and it is influenced by genetic and environmental factors. The AH of eggs is at a maximum when the eggs are laid and decreases with increasing storage time (Jin *et al.*, 2011).

Irrespective of ecotype, the HU declined sharply with increasing storage time. All the three ecotypes had very high HU values when the eggs were fresh but egg quality reduced significantly after 2 weeks of storage. This is in line with the findings of other researchers (Alsobayel and Albadry, 2011; Tabidi, 2011). HU is affected by many factors such as the storage time, temperature, age of hen, strain of bird, nutrition, disease, supplements, artificial exposure to ammonia, induced moult and medication (Ahmadi and Rahimi, 2011). Poor storage conditions present nutritional challenges in many areas of the world where eggs are stored without refrigeration due to economic or energy constraints. For instance, eggs stored in the layer house have been reported to have poorer albumen quality than those stored in the cooler conditions (Miles and Henry, 2004). Increasing storage time also had a detrimental effect on albumen quality. Quality declined more rapidly in eggs stored at ambient temperature than in cooler temperatures (Miles and Henry, 2004). The present study confirms that eggs stored at ambient temperatures and humidity lower than 70 percent will lose 10–15 HU in a few days from the point of lay (Ahmadi and Rahimi, 2011).

Conclusions

Local chicken eggs have relatively stronger shells and yolk ratios compared with SASSO T44. However, the egg quality of local chickens is lower than SASSO T44 due to the negative correlation between yolk ratio and AH, the main determinant of egg quality. Within the local chicken population, birds from the forest zone were superior in AH but the two local ecotypes did not differ significantly in HUs. Egg quality traits deteriorated under room temperature storage conditions. Deterioration of egg quality of chicken eggs could be minimized by storing at cooler temperatures and at a higher relative humidity or where not possible utilizing the eggs within a week of lay.

Acknowledgements

Appreciation is expressed to the DURAS Project for permission to use data and the University of Ghana Graduate Fellowship programme for award of fellowship to R. Osei-Amponsah. The Carnegie – funded University of Ghana "Next Generation of Academics in Africa" Project for the Write-Shop held in June, 2013 facilitated the preparation of the manuscript for publication and the authors are grateful to the co-ordinator, mentors and all participants for their valuable inputs.

Statement of interest

The authors declare no conflict of interest.

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Animal Genetic Resources, 2014, 55, 101–113. © Food and Agriculture Organization of the United Nations, 2014
doi:10.1017/S2078633614000319

Phenotypic characterization of indigenous chicken populations in Southeastern Oromia Regional State of Ethiopia

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Summary

The objective of this study was to characterize the native chickens reared in three agro-ecological zones of Southeastern Oromia Regional State of Ethiopia. Data on visual appraisal and linear body measurements were obtained from a total of 600 matured local chickens of both sexes drawn from 240 households. The results indicated that the average flock size, age at first egg of hens and eggs produced per clutch were 11.9 heads, 6.2 months and 15.4 eggs, respectively. The majority of the male chicken possessed snake head shape (60.7 percent) and most of them had rose combs (57.9 percent), red feather plumage (46.1 percent), yellow shanks (86.3 percent), red earlobes (84.2 percent) and yellow skin (56.8 percent). Majority of the hens possessed single combs (43.5 percent), red earlobes (77.3 percent), yellow shanks (44.4 percent), yellowish brown feather (27.4 percent) followed by red (24.2 percent) and black (21.2 percent). The cocks were generally heavier (1.39 kg) than the hens (1.22 kg). The average values for breast angle (degrees), body length, body width, shank length, shank circumference, keel bone length, wing span, comb length and beak length of the cocks were 45.9, 24.1, 24.9, 7.43, 3.86, 9.63, 7.99, 4.86 and 1.91 cm, respectively. The corresponding values for the hens were 40.2, 22.7, 23.8, 7.43, 3.46, 8.95, 7.40, 2.47 and 1.71. The values for wing span, comb length, beak length, body weight, breast angle and keel bone length differed ($P < 0.05$) across the agro-ecologies. The best predictor for assessing the body weight of hens was breast angle and body length, whereas in the cocks it was best estimated using breast angle and shank circumference values. The present study suggests that indigenous chickens in the study area possess useful economic traits that could be improved through systematic breeding for enhanced productivity under scavenging production systems.

Keywords: *agro-ecological zones, indigenous chickens, linear body measurements, phenotypic characterization, Southeastern Ethiopia*

Résumé

L'objectif de cette étude a été de caractériser les poules indigènes élevées dans trois zones agro-écologiques de l'État Régional d'Oromia, au Sud-est de l'Éthiopie. Différentes données ont été collectées par observation et par mesures corporelles linéaires sur un total de 600 volailles locales adultes des deux sexes provenant de 240 foyers. Les résultats ont indiqué que la taille des groupes, l'âge des poules au premier œuf et les œufs pondus par couvée ont été en moyenne de 11,9 têtes, 6,2 mois et 15,4 œufs, respectivement. La plupart des mâles avaient une tête en forme de serpent (60,7 pour cent), une crête en rose (57,9 pour cent), un plumage de couleur rouge (46,1 pour cent), les tarses jaunes (86,3 pour cent), les oreillons rouges (84,2 pour cent) et la peau jaune (56,8 pour cent). La plupart des poules possédaient une crête simple (43,5 pour cent), des oreillons rouges (77,3 pour cent), des tarses jaunes (44,4 pour cent) et un plumage marron jaunâtre (27,4 pour cent), rouge (24,2 pour cent) ou noir (21,2 pour cent). En général, les coqs ont été plus lourds que les poules (1,39 versus 1,22 kg). Chez les coqs, les valeurs moyennes d'inclinaison de la poitrine (angle en degrés), de la longueur du corps, de la largeur du corps, de la longueur des tarses, de la circonférence des tarses, de la longueur du bréchet, de la longueur de l'aile, de la longueur de la crête et de la longueur du bec ont été de 45,9, 24,1, 24,9, 7,43, 3,86, 9,63, 7,99, 4,86 et 1,91 cm, respectivement. Les valeurs correspondantes pour les poules ont été de 40,2, 22,7, 23,8, 7,43, 3,46, 8,95, 7,40, 2,47 et 1,71, respectivement. Des différences significatives ($p < 0.05$) ont été décelées entre les zones agro-écologiques pour la longueur de l'aile, la longueur de la crête, la longueur du bec, le poids corporel, l'inclinaison de la poitrine et la longueur du bréchet. Les meilleurs prédicteurs pour estimer le poids corporel des poules ont été l'inclinaison de la poitrine et la longueur du corps alors que les variables qui ont prédit le mieux le poids des coqs ont été l'inclinaison de la poitrine et la circonférence des tarses. La présente étude suggère que les poules autochtones du territoire étudié possèdent des caractères d'intérêt économique qui pourraient être améliorés au moyen d'une sélection systématique cherchant à optimiser la productivité sous des systèmes d'obtention de la nourriture par picorage.

Mots-clés: *zones agro-écologiques, poules autochtones, mesures corporelles linéaires, caractérisation phénotypique, Sud-est de l'Éthiopie*

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Resumen
El objetivo de este estudio fue caracterizar las gallinas nativas criadas en tres zonas agroecológicas del sudoriental Estado Regional de Oromía en Etiopía. Se recogieron diferentes datos por observación y por medidas corporales lineales sobre un total de 600 aves locales maduras, de ambos sexos, tomadas de 240 hogares. Los resultados indicaron que, de media, el tamaño de los grupos, la edad de las gallinas al primer huevo y los huevos puestos por nidada fueron respectivamente de 11,9 cabezas, 6,2 meses y 15,4 huevos. La mayoría de los machos presentaron cabeza con forma de serpiente (60,7 por ciento), cresta en rosa (57,9 por ciento), plumaje rojo (46,1 por ciento), tarsos amarillos (86,3 por ciento), orejillas rojas (84,2 por ciento) y piel amarilla (56,8 por ciento). La mayoría de las gallinas presentaron cresta sencilla (43,5 por ciento), orejillas rojas (77,3 por ciento), tarsos amarillos (44,4 por ciento) y plumaje marrón amarillento (27,4 por ciento), rojo (24,2 por ciento) o negro (21,2 por ciento). Por lo general, los gallos fueron más pesados que las gallinas (1,39 versus 1,22 kg). En los gallos, los valores medios de inclinación de la pechuga (ángulo en grados), longitud corporal, anchura corporal, longitud de los tarsos, circunferencia de los tarsos, longitud de la quilla, longitud del ala, longitud de la cresta y longitud del pico fueron respectivamente de 45,9, 24,1, 24,9, 7,43, 3,86, 9,63, 7,99, 4,86 y 1,91 cm. Los valores correspondientes para las gallinas fueron de 40,2, 22,7, 23,8, 7,43, 3,46, 8,95, 7,40, 2,47 y 1,71, respectivamente. Los valores de longitud del ala, longitud de la cresta, longitud del pico, peso corporal, inclinación de la pechuga y longitud de la quilla difirieron ($p < 0.05$) entre las zonas agroecológicas. Los mejores predictores para determinar el peso corporal de las gallinas fueron la inclinación de la pechuga y la longitud corporal mientras que las variables que mejor predijeron el peso de los gallos fueron la inclinación de la pechuga y la circunferencia de los tarsos. El presente estudio sugiere que las gallinas autóctonas del área estudiada poseen características de interés económico que podrían ser mejoradas a través de una selección sistemática encaminada a optimizar la productividad bajo sistemas de alimentación por picoteo de desperdicios.

Palabras clave: *zonas agroecológicas, gallinas autóctonas, medidas corporales lineales, caracterización fenotípica, Sudeste de Etiopía*

Submitted 23 January 2014; accepted 14 July 2014

Introduction

The importance of village poultry production in the national economy of developing countries and its role in improving the nutritional status and incomes of many small farmers and landless communities has been recognized by various scholars and rural development agencies for the past few decades (Melesse, Maak and Von Lengerken, 2005; Moges, Melesse and Dessie, 2010; Melesse and Negesse, 2011). According to CSA (2012), the chicken population of Ethiopia was estimated to be about 44.9 million heads; of which 96.5 percent are indigenous chickens indicating the significance of local chickens as potential genetic resource of the country. According to CSA (2012), the Oromia region contributes 36.4 percent of the total chicken population in the country. Even within the Oromia region majority of the chickens are found in the Arsi zone followed by the East Harerghe zone.

Indigenous chickens in Ethiopia are distributed across different agro-ecologies managed under the traditional scavenging management system indicating that they are important avian resources reared as a source of animal protein and income to many of the rural populations (Moges, Melesse and Dessie, 2010). Furthermore, their widespread distribution indicates their diverse adaptive potential to the prevailing environment, diseases and other stresses. Most of the indigenous chickens have evolved through adaptation to various agro-climatic conditions. As perceived by Egahi *et al.* (2010) the indigenous chickens possess genes and special adaptations not found in other improved modern breeds.

Melesse and Negesse (2011) reported that identification and characterization of the chicken genetic resources generally requires information on their adaptation to a specific environment, possession of unique traits of current or future economic value and socio-cultural importance, which are crucial inputs to decisions on conservation and utilization. Variations in major morphological traits such as outline and feather contours, shank and ear-lobe colours, and comb types are common among indigenous chicken populations. These morphometric traits provide basis for grouping the native chickens according to their phenotypic and morphological appearances. However, as the chickens are mostly selected (naturally or by their keepers) for their adaptive traits the native chickens are quite poor in egg production performance, have longer age at maturity and extended broodiness (Moges, Melesse and Dessie, 2010).

Lack of sufficient information is one of the major hindrances in the chicken improvement programmes of the country (Duguma, 2009; Dana *et al.*, 2010; Melesse and Negesse, 2011). The phenotypic diversity of the local chicken resources in Ethiopia in general and in Arsi Zone of Oromia region in particular is yet to be studied in detail. Thus, the present study was conducted to characterize the native chickens reared in Tiyo, Hetossa and Dodota Woredas of Arsi zone representing high-, mid- and lowland agro-ecological zones, respectively.

Materials and methods

Description of the study areas

The study was conducted in three adjacent Woredas (Tiyo, Hetossa and Dodota) of Arsi zone, Oromia Regional State of Ethiopia. The woredas are located between 7°49′ N and 8°30′N latitudes, and 38°57′E and 39°38′E longitudes. Arsi zone is one of the 17 zones of Oromia Administrative Region situated in Southeastern Ethiopia. According to AZADO (2011), the Arsi administrative zone contains the three major agro-ecological zones of high-, mid- and lowland at a proportion of 43.4, 27.5 and 29.1 percent, respectively. The respective altitudinal ranges for high-, mid- and lowland are <1 500, 1 500–2 500 and >2 500 m a.s.l., respectively (Table 1).

For this study, three districts such as Tiyo, Hetossa and Dodota were purposely selected representing the three agro-ecological zones (Table 1). The Tiyo district has an estimated total land area of 638 km^2 classified into 36 percent plain, 43 percent mountainous and 21 percent hilly/gorgy physical land forms, which represents the highland agro-ecological zone in the present study. The Hetossa district has an estimated total land area of 1 216 km^2 classified into 65 percent plain, 20 percent mountain and 15 percent hill and gorge physical landscapes, which represents the midland agro-ecology. The Dodota district has an estimated total land area of 469 km^2 comprising a physical landform of 75 percent plain, 20 percent mountain and 5 percent hill and gorge and represents the lowland agro-ecological zone.

Sampling and data collection procedures

The field survey design and data collection procedure of this study were performed according to the FAO's exploratory characterization approach (FAO, 2012). With the help of experts from the Agriculture of Arsi Zone, four rural Farmers' Kebeles (FKs) with the least chance of exotic chicken distribution outreach were purposively selected from each of the three agro-ecological zones, which have been already described herein. Then, 20 households who possess a minimum of five adult chickens of indigenous ecotypes per household were randomly chosen from each FKs. Accordingly, a total of 240 households (20 households × 4 FKs × 3 agro-ecologies) were used in the present study. Households possessing exotic chicken or their crosses in the neighbourhood were purposely excluded in the study. Closely adjoining households were also skipped to avoid the risk of sampling chickens sharing the same cock.

Table 1. Ecological and demographic characteristics of the studied agro-ecological zones.

Description	Agro-ecological zones		
	Highland	Midland	Lowland
Altitude (m a.s.l.)	>2 500	1 500–2 500	<1 500
Annual rainfall (mm)	980–1 370	640–1 149	540–870
Mean annual temperature (°C)	9–26	11–27	13–32
Human population	86 727	124 179	63 302
Average family size	6	7	5
Number of chickens	58 610	57 538	23 762
Ecology	Tepid cool to cold sub-moist	Humid to sub-moist	Warm sub-humid

Source: AZADO (2011).

A structured questionnaire was designed to collect data on flock characteristics, flock composition and management practices. The interviews were conducted at farmers' houses with the assistance of agricultural extension officers. Moreover, phenotypic characterization of both qualitative and quantitative traits of local chicken populations was conducted on 600 matured chickens whose ages were approximately 36 weeks and above. This age was chosen by considering the slow maturation process of indigenous chickens to reach their adult stage and was determined by the "recalling method" of the interviewed farmers.

Qualitative phenotypic data were collected based on feather morphology, feather distribution and patterns, plumage colour, shank colour, earlobe colour, skin colour, comb and head types following the FAO's checklist for phenotypic characterization of chickens (FAO, 2012). Descriptions of comb types were based on the illustrations presented by Somes (2003), Ensminger (1992) and Roberts (1997).

Quantitative data on body weight, body width (the circumference of the breast region), body length (the distance from the insertion of the neck to the tail) and shank length (length of the shank from the top of the flexed hock joint to the bottom of the footpad) and shank circumference, comb length, wattle length, keel bone length, breast angle and body weight were collected from both sex groups following the FAO's descriptor for chicken genetic resources (FAO, 2012). Shank length was measured using mathematical divider and corresponding the equivalent reading by putting it on a graduated ruler. Comb, wattle and keel lengths were measured using the same instrument and converted into readings of a graduated ruler. Folded wing span, body length and body girth were measured using a tailor's graduated tape. Live body weight was measured in kilogram using a "CAMRY" hanging scale. Breast angle was measured using a goniometer with two movable arms.

Statistical analysis

Preliminary data analysis (homogeneity test, normality test and screening of outliers) was employed before conducting the main data analysis. Discrete measurements on the qualitative morphological traits of the investigated animals were analysed using the frequency procedure of

Chi-square (χ^2) test. Body weight and quantitative linear body measurements were analysed using the Generalized Linear Model procedures (SPSS, 2007). Agro-ecological zones were fitted as fixed independent variables, whereas quantitative measurements were fitted as dependent variables. Means were compared using Duncan's Multiple Range Test procedure and values were considered significant at $P < 0.05$. Stepwise regression procedure was used to regress body weight for both sexes to determine the best-fitting regression equations for the prediction of live body weight. Regression equations were calculated and the adjusted coefficient of determination (R^2_{adj}) was used to establish the accuracy of the equations.

Results

Flock dynamics and productivity of indigenous chickens

The survey results indicated that the average flock size per household in high-, mid- and lowland agro-ecological zones was 10.3, 14.1 and 11.2, respectively (Table 2). The largest proportion of chicken population was thus reported from midland agro-ecological zone, which is significantly higher than others. The average number of cocks and hens were significantly higher for midland than high- and lowland agro-ecological zones.

Significant difference ($P < 0.05$) was also observed in age at first egg among the studied agro-ecological zones. Accordingly, the age at first egg was longer for chicken in the lowland, followed by those of high- and midland agro-ecological zones (Table 3). Comparably the highest number of eggs per clutch was found in the highland, whereas it was lower for low- and midlands. The hatchability and survivability rates of chicks were similar among agro-ecological zones.

Phenotypic characterization

Qualitative morphometrical traits

The results of the present study indicated that the majority of the observed chickens (67.2 percent) were female chickens, whereas the rest (32.8 percent) were male birds. About 55, 58 and 61 percent of the male chicken in the high-, mid- and lowlands, respectively, possessed rose combs (Figure 1). Most hens were characterized by having single and pea combs with similar proportions (Table 4). Walnut and double comb types were the least. Snake head shape was the most prominent type among both the sexes irrespective of the agro-ecological zones. The colour of the shank in cocks was predominantly yellow with the average value of about 86 percent in all agro-ecological zones. The female chickens reared in the midland were characterized by having both yellow and green shanks with similar values, whereas those in lowland possessed shanks with yellow colour followed by green and differed significantly from others. Most of the highland female birds had grey shanks (46.3 percent) followed by yellow (36.8 percent). Earlobes with a red colour were the main characteristics of studied indigenous chickens. However, about 45 percent of male birds in the highland had a black earlobe. The predominant eye colour in both male and female chickens in the three agro-ecological zones was blue black and differs significantly from other eye colours (Table 4). The main colour of the skin of both sexes was observed to be yellow followed by blue black across all agro-ecological zones.

The plumage colour of the indigenous chickens in the study areas were classified into body feather, colours of their feathers of the breast, neck and back regions. The predominant body feather colour of the hens reared in the high- and midlands was yellowish brown (Wosera) followed by black (Tikur) and red (Kei), while that of the lowlands was red followed by yellowish brown plumage (Figures 1 and 2). Hens with white (Netch) body feather were observed in both high- and lowland agro-ecological zones.

As shown in Table 5 and Figures 1, the dominant body feather colour of the cocks was red (Kei) followed by yellowish brown (Woera) tipped with other colours. The study also indicated that the cocks reared in all agro-ecological zones had red breast feather, which was closely followed by black colour, while the hens were distinguished by multicoloured breast feathers followed by red and black colours. The dominant feather colour around the neck of the cock's was red in all agro-ecological zones, whereas that of the hens was mainly brown combined with multicolour patterns. Cocks with red back feather were dominant across all agro-ecological zones. Hens reared in the all agro-ecologies mainly possessed brown back feather mixed with other colours followed by red and black (Table 5).

Quantitative morphological traits

As presented in Table 6, the body weight of cocks was similar across agro-ecological zones and was generally higher than that of hens. Hens reared in the highland were heavier ($P < 0.05$) than those reared in the midland. The results for average body length and width, shank length and circumference and body shank length ratio for both groups of chicken were comparable across all the three agro-ecological zones. The values pertaining to the keel bone length for the hens reared also differed ($P < 0.05$) across the agro-ecologies with the least value being observed in the highlands, whereas it did not vary between the hens reared in the other two agro-ecologies (Table 6).

The wing span differed ($P < 0.05$) in cocks reared across the high- and midland agro-ecologies, whereas the values observed in the lowland was intermediate between the two (Table 6). The results pertaining to comb length of both sex groups and wattle length for the cocks differed ($P < 0.05$) between the high- and midland agro-ecologies. However, the values from the lowland agro-ecology were intermediate between the two extremes. Similarly, the

Table 2. Flock compositions of households in the studied agro-ecological zones of Southeastern Ethiopia (mean ± SE).

Flock composition	Highland	Midland	Lowland	Overall mean ($N = 240$)
Hens	4.11 ± 0.71^{b}	5.02 ± 0.02^{a}	3.96 ± 0.77^{b}	4.37 ± 0.55
Cocks	1.40 ± 0.33^{b}	2.49 ± 0.92^{a}	1.25 ± 1.23^{b}	1.71 ± 0.62
Cockerels	0.79 ± 0.03^{a}	0.14 ± 0.01^{b}	0.29 ± 0.02^{b}	0.74 ± 0.02
Pullets	1.00 ± 0.04^{b}	1.62 ± 0.06^{a}	1.31 ± 0.04^{ab}	1.31 ± 0.03
Chicks	2.95 ± 0.09^{b}	4.85 ± 0.13^{a}	4.40 ± 0.60^{a}	4.07 ± 0.36
Total	10.3 ± 0.96^{b}	14.1 ± 0.87^{a}	11.2 ± 1.02^{b}	11.9 ± 0.97

[a,b,c]Means across a raw with different superscript letters are significantly ($P < 0.05$) different.
SE, standard error of the mean.

magnitudes for the beak length and breast angle differed ($P < 0.05$) for the hens reared between all the three agro-ecologies.

Prediction of body weight from linear body measurement traits

As shown in Table 7, positive correlations ($P < 0.01$) were observed among all studied linear body measurement traits. However, the associations of wing span with other traits were variable and insignificant. High correlations were observed between body weight and all linear body measurements for both sexes. The associations of body width with body length as well as breast angle with body weight were numerically higher than other parameters. In cocks, the correlation values of live body weight with those of breast angle, shank circumference and body length were comparatively higher than those of other values. Higher correlation values of body weight with breast angle, shank length, body width and length were also observed in female chickens.

As presented in Table 8, the best predictors (R^2_{adj}) of body weight of cocks in all agro-ecological zones were found to be breast angle and shank circumference. The best estimators for assessing the body weight in hens reared in the high- and lowland areas were breast angle, body depth and body length, whereas in the midland it can be estimated using breast angle alone.

Discussion

Flock size and productivity

The results indicated that the sex ratio (female to male) were more skewed towards the former, which is explainable since farmers need to regularly replace their breeding stocks. The values for the numbers of chicken per household in the present study find similarity with the observations of Mekonnen (2007) for Southern Ethiopia and Hunduma *et al.* (2010) for the Rift Valley region of Oromia, Ethiopia. However, the values reported in various regions of Ethiopia by Halima *et al.* (2007), Dana *et al.* (2010) and Melesse and Negesse (2011) are lower than those observed in the current study. Higher values for the numbers of chickens reared per household were reported by Dessie *et al.* (2003) and Moges, Melesse and Dessie (2010) from the central parts of Ethiopia and in Northwestern Ethiopia, respectively. The flock size variations reported in various parts of the country might be due to the occurrence of diseases, presence of predators, availability of feed resources as well as the economic status of the owners who regularly sell chickens to meet their immediate financial requirements.

The average age at maturity of the hens reared in the low- and highland agro-ecologies in the present study are in accordance with the observations of Dessie *et al.* (2003), Kugonza, Kyarisiima and Lisa (2008) and Iqbal and Pampori (2008) who reported about 6–7 months. The average age of maturity in the midland agro-ecology finds similarity with the observations of Mengesha, Tamir and Dessie (2008) from northeastern part of Ethiopia who indicated that the maturity of the chickens was 5.4 months. The reason for delayed age of sexual maturity of those chickens reared in the low- and highland agro-ecologies could be attributed to lack of supplementary feeds and exposure of chickens to excessive high and low ambient temperatures, which are characteristics of both two agro-ecologies.

Table 3. Performance of indigenous chickens in high-, mid- and lowland agro-ecological zones of Southeastern Ethiopia (mean ± SD).

Parameters	Highland	Midland	Lowland	Overall mean ($N = 240$)
Age at first egg (months)	6.12 ± 0.92^{b}	5.48 ± 1.02^{c}	6.90 ± 1.12^{a}	6.17 ± 1.17
Egg number per clutch	15.8 ± 2.70	15.3 ± 1.99	15.1 ± 2.25	15.4 ± 2.34
Eggs incubated per hen	12.0 ± 1.61	11.7 ± 1.34	11.6 ± 1.50	11.8 ± 1.53
Hatchability (%)	80.7 ± 9.40	82.0 ± 9.70	81.8 ± 8.80	81.5 ± 9.28
Survivability (%)	63.3 ± 14.5	60.8 ± 18.6	64.0 ± 14.6	62.7 ± 16.0

[a,b,c]indicated values among rows for traits significantly differ at $\chi^2 < 0.05$.
SD, standard deviation.

Figure 1. Basic plumage colours of indigenous chicken populations in Southeastern Oromia, Ethiopia. *Upper left*: Cock with red (Kei) plumage; *Upper right:* White (Netch) feathered hen with rose comb; *Lower left*: Tikur (Black plumage) hen with single comb and black shank; *Lower right*: Wosera (yellowish brown) hen with single comb and yellow shank.

The present finding pertaining to the clutch size, egg production per clutch per hen, number of eggs incubated and number of chicks hatched differed from the results of Worku, Melesse and Teklegiorgis (2012) and Melesse, Worku and Teklegiorgis (2013), who reported significant differences in the traits among the chickens reared in the northwest region of Ethiopia. This could be explained by the management differences practiced by households in different regions such as provision of supplementary feeding, housing, control of parasitic diseases, etc. The average numbers of eggs per hen as obtained from the present study find similarity with the observations of Mandal, Khandekar and Khandekar (2006) from India. The results of studies by Aganga *et al.* (2000) from Botswana however indicated that the numbers of egg produced by the native chickens were lower than those observed in the present study. The results also indicated that the average numbers of eggs incubated by a hen in the study areas are higher than those reported by Yakubu (2010). The figures are, however, comparable with the observations of Pedersen (2002) who reported that the average number of egg incubated per individual hen was 10.6 with average hatchability rate of 73 percent. The figures observed in the present study are however lower than those of Ssewannyana *et al.* (2008) who reported higher hatchability percentage (87 percent) among native chickens of Uganda. Hatchability of eggs from the scavenging local chicken could be affected by a number of factors including age of the hen and the mating cock, type of nesting used, season and number of eggs incubated by the hen.

Qualitative morphometric traits

The present study indicated that majority of the female chicken possessed single comb, which is in accordance with the findings of several studies from other developing countries (Egahi *et al.*, 2010; Faruque *et al.*, 2010; Apuno, Mbap and Ibrahim, 2011; Guni and Katule, 2013). The findings of Melesse and Negesse (2011) indicated that 55 percent of the chickens in Southern Ethiopia were characterized by single comb followed by rose (28.5 percent) and pea (15.2 percent) combs. Single and rose combs were reported to be the most prominent types in local chicken of Bure district of Amhara region, Ethiopia (Moges, Melesse and Dessie, 2010). The fact that single combed chickens were predominant followed by those possessing rose and pea combs are also in good agreement with the observations of Ikeobi *et al.* (2001), and Daikwo, Okpe and Ocheja (2011) for indigenous chickens of Nigeria. Studies by Badubi, Rakereng and Marumo (2006) indicated that 90 percent of the indigenous chickens in Botswana were single combed, whereas very low proportion of rose (4.9 percent) and pea (1 percent) combs were observed.

Badubi, Rakereng and Marumo (2006) reported that the indigenous chickens of Tanzania were mostly single combed as was also observed by Bhuiyan, Bhuiyan and Deb (2006) among the indigenous chickens of Bangladesh. The higher values observed for the single comb type suggests a selection advantage and greater adaptability to the production environments in which they have been reared for many decades. Combs are important structures for heat loss in

Table 4. Percentage values of some qualitative traits of indigenous chicken in high-, mid- and lowland agro-ecological zones of Southeastern Ethiopia ($N = 600$).

Qualitative traits	Highland		Midland		Lowland	
	Cock ($n = 64$)	Hen ($n = 136$)	Cock ($n = 74$)	Hen ($n = 126$)	Cock ($n = 59$)	Hen ($n = 141$)
Comb type						
Rose	54.7^{b}(35)	10.3^{a}(14)	58.1^{b}(43)	6.3^{a}(8)	61.0^{b}(36)	14.9^{a}(21)
Pea	9.30^{a}(6)	37.0^{b}(50)	13.5^{a}(10)	50.8^{b}(64)	8.40^{a}(5)	41.8^{b}(59)
Walnut/strawberry	3.10^{a}(2)	6.00^{b}(8)	2.70(2)	NR	3.40(2)	1.40(2)
Single	31.3^{a}(20)	46.0^{b}(63)	24.3^{a}(18)	42.8^{b}(54)	25.4^{a}(15)	41.8^{b}(59)
V shape/double	1.60^{b}(1)	0.70^{a}(1)	1.30(1)	NR	1.70(1)	NR
Head shape						
Snake	67.2(43)	75.7(103)	60.8(45)	69.8(88)	54.2(32)	68.1(96)
Flat	32.8(21)	NR	39.2^{b}(29)	0.80^{a}(1)	44.1^{b}(26)	2.10^{a}(3)
Crested	NR	24.3(33)	NR	29.4(37)	1.70^{a}(1)	29.8^{b}(42)
Shank colour						
Yellow	86.0^{b}(55)	36.8^{a}(50)	86.5^{b}(64)	44.4^{a}(56)	86.4^{b}(51)	52.0^{a}(73)
Black	1.60^{a}(1)	10.3^{b}(14)	1.30^{a}(1)	12.0^{b}(15)	1.70^{a}(1)	9.20^{b}(13)
Green	-NR	0.70(1)	12.2^{a}(9)	43.6^{b}(55)	12.0^{a}(7)	39.0^{b}(55)
Grey	12.5^{a}(8)	46.3^{b}(63)	NR	NR	NR	NR
White	NR	6.10(8)	NR	NR	NR	NR
Earlobe colour						
Red	54.7 (35)	69.8(95)	100^{b}(74)	77.0^{a}(97)	98.3^{b}(58)	85^{a}(120)
White	NR	NR	NR	18.2(23)	1.70^{a}(1)	10.0^{b}(14)
Black	45.3^{b}(29)	22.0^{a}(30)	NR	NR	NR	NR
Other	NR	8.10(11)	NR	5.01(6)	NR	5.02(7)
Eye colour						
Black	12.5^{a}(16)	22.1^{b}(30)	35.0(26)	31.0(39)	31.0(18)	35.0(49)
Blue black	68.7(44)	70.0(95)	55.4(41)	55.5(70)	56.0(33)	54.0(76)
Dark brown	6.20(4)	8.01(11)	9.40(7)	13.4(17)	13.5(8)	11.4(16)
Skin colour						
Yellow	55.0(35)	66.2(90)	51.0(38)	59.3(85)	64.4(38)	67.0(94)
Blue black	26.0(17)	22.0(3)	38.0(28)	33.3(42)	25.4(15)	23(32)
White	19.0(12)	12.0(16)	11.0(8)	7.35(9)	10.1(6)	10.0(15)

[a,b,c]Different superscripts within row indicate significant different percentages at $p < 0.05$.
NR, not reported; values in parenthesis indicate number of observations.

birds (Van Kampen, 1974) and since the tropical climate is predominantly characterized by high ambient temperature, large combs would provide an efficient means of heat dissipation through the process of vasodilatation. Although not reported separately for both sex groups, all of the above reports are in close agreement with the findings of the present study for hens, whereas only those reports for indigenous chicken in Ethiopia wherein rose combs are most prominent agrees with the present finding for the male chicken.

The results of the shank colour in the present study are in line with the findings of Melesse and Negesse (2011) who reported that about 53 percent of the chicken populations in Southern Ethiopia had a yellow shank. The results also indicated that above 80 percent of cocks had yellow shank, which is consistent with the reports of Guni and Katule (2013). It is evidenced that the shank colour is mainly affected by the plane of nutrition mainly feed sources containing carotene. Most scavenging chickens are apparently dependent on naturally available feed resources, which are mainly composed of kitchen and household wastes with sporadic supplementation of low-quality grains. The results as observed in the study suggest that cocks might have better access to feed resources as they can compete better than hens.

Eye colour to a large extent depends on the pigmentation (carotenoid pigments and blood supply) of a number of structures within the eye (Crawford, 1990). In the present study, above 55 percent of the studied chickens were characterized by blue black eye colour and is consistent with the findings of Apuno, Mbap and Ibrahim (2011) who reported eye colours of dark brown (37.9 percent), light brown (28.8 percent) and dark red (28.6 percent) for indigenous chickens of Nigeria. On the other hand, Mancha (2004) and Guni and Katule (2013) reported orange eye colour as most common among the indigenous chickens of Nigeria and Tanzania, respectively. Similar findings were also reported by Ssewannyana *et al.* (2008) for Ugandan local chickens. The eye colour values obtained from the present study however could not be compared among Ethiopian chicken populations due to lack of literature pertaining to the trait. The results as observed for the earlobe colour are not in agreement with the observations of Duguma (2006) and Egahi *et al.* (2010) from western and eastern parts of Ethiopia and Nigeria, respectively. The fact that earlobe colour is

Figure 2. Combination of various plumage colours in local chickens of Southeastern Oromia, Ethiopia. *Upper left*: Gebsima (greyish plumage) cock with rose comb and red ear lobe; *Upper right*: Reddish brown chickens; *Lower left*: Amorima (black and white mixtures) hen with pea comb and light green shank; *Lower right*: Ambesma (multi-coloured plumage) naked neck chicken.

a breed-specific trait, the observed variations across regions could suggest the existence of local chickens with specific genetic backgrounds. Breeds of the Mediterranean Class (Leghorn) for instance possess white earlobes while most other chicken breeds are characterized by having red earlobes.

Substantial amount of phenotypic diversity for various traits in the indigenous chicken genetic resources of Ethiopia is expected because of diverse agro-climates, ethnic groups, socio-economic, religious and cultural differentiations. In the present study, highly diverse plumage manifestations were observed among the local chickens of the study region. It can vary between different age classes, sexes and season. Studies on the traditional poultry production systems as was also observed in the present study have indicated that farmers prefer to raise birds with different plumage colours for various purposes such as for egg production, meat production, healing ceremony and cultural purposes (Dana *et al.*, 2010; Melesse and Negesse, 2011) indicating selection for each of these attributes.

Red, yellowish brown with mixed colour patterns and black plumages were the dominant plumages as observed in the study area and are similar to those observations reported by Worku, Melesse and Teklegiorgis (2012) and Moges (2008), from Western Amhara Region of Ethiopia. The results as obtained by Halima *et al.* (2007) however indicated that the chickens of Northwestern Ethiopia had predominantly white colour of feathers. Studies by Kibret (2008) indicated that chickens in the Fogera district of Northwestern Ethiopia had mostly white and red colour feathering. The occurrence of several plumage colours observed in the local chicken population of Ethiopia in general might be the result of uncontrolled breeding of local chickens with exotic chickens in the rural areas under free range management system. Moreover, preference of the people in the study area (for socio cultural reasons) towards red and brown plumages might have accounted for the largest occurrence of these feather colours (Moges, Melesse and Dessie, 2010; Melesse and Negesse, 2011).

Quantitative traits

The average live weight values for both sexes in the current study are comparable with those reported by Fayeye *et al.* (2006), Dana *et al.* (2010) and Apuno, Mbap and Ibrahim (2011). The results as obtained by Melesse and Negesse (2011) for average live weight of the cocks reared in Southern Ethiopia are comparable with the present findings. However, the values of hens as reported by the same authors were higher than those observed in the present study. These variations for the trait could be attributed to the genetic background of local chickens and the quality and quantity of the available scavengable feed resources in different regions. Sexual dimorphism as was observed for live weight with cocks weighing higher than the hens are in accordance with the reports of Halima *et al.* (2007) and Dana *et al.* (2010).

The average body width and length values of the native chickens as were observed in this study are comparable with those of Fayeye *et al.* (2006) but the values were lower than those reported by Daikwo, Okpe and Ocheja

Table 5. Percentage values of some feather colour variables of indigenous chicken reared in high-, mid- and lowland agro-ecological zones of Southeastern Ethiopia ($N = 600$).

Plumage	Highland		Midland		Lowland	
	Cock (n = 64)	Hen (n = 136)	Cock (n = 74)	Hen (n = 126)	Cock (n = 59)	Hen (n = 141)
Feather colour						
Netch	7.82[a](5)	14.0[b](19)	6.73(5)	8.10(10)	7.20[a](4)	15.6[b](22)
Tikur	7.80[a](5)	21.3[b](29)	12.2[a](9)	24.0[b](30)	13.5(8)	18.2(25)
Kei	42.2[b](27)	19.1[a](26)	45.1[b](33)	25.2[a](32)	51.1[b](30)	28.3[a](39)
Wosera	23.4(15)	29.4(40)	20.3(15)	27.3(34)	20.3(12)	25.5(36)
Gebsima	14.1[b](9)	6.62[a](9)	13.5[b](10)	5.54[a](7)	5.12(3)	9.22(13)
Reddish brown	NR	8.80(12)	NR	9.52(12)	NR	4.34(6)
Multicoloured	4.71[b](3)	0.73[a](1)	2.74[b](2)	0.73[a](1)	3.44(2)	NR
Breast feather colour						
Black	21.8(14)	22.1(30)	28.4(21)	24.6(31)	25.4(15)	18.0(25)
Red	43.7[b](28)	22.3[a](30)	38.2(28)	25.3(31)	46.0(27)	28.0(39)
White	9.32(6)	12.5(17)	12.0(9)	8.01(10)	12.1(7)	16.0(22)
Multicoloured	25.0[a](16)	43.0[b] (59)	22.0[a](16)	43.0[b](54)	17.0[a](10)	39.0[b](55)
Neck feather colour						
White	8.01(5)	14.0(19)	6.71(5)	11.1(14)	8.40(5)	16.3(23)
Black	12.5(8)	18.4(25)	16.2(12)	25.0(31)	20.3(12)	18.4(26)
Red	41.0[b](26)	17.6(24)	42.0[b](31)	22.2[a](28)	51.0[b](30)	29.0[a](41)
Greyish	11.0[b](7)	3.02[a](4)	12.2[b](9)	0.71[a](1)	5.10(3)	3.50(5)
Brown with other colours	26.6(17)	38.2(52)	22.0(16)	33.2(42)	15.2(9)	28.4(40)
Reddish brown	1.60[a](1)	9.0[b](12)	1.31[a](1)	8.11[b](10)	NR	4.30(6)
Back feather colour						
White	6.20[a](4)	14.0[b](19)	6.71(5)	9.51(12)	6.82[a](4)	15.6[b](22)
Black	11.0[a](7)	21.3[b](29)	17.6(13)	25.4(32)	17.0(10)	18.0(25)
Red	50.0[b](32)	20.0[a](27)	46.0[b](34)	25.0[a](31)	51.0[b](30)	27.0[a](38)
Greyish	11.0[b](7)	6.61[a](9)	9.40[b](7)	3.11[a](4)	7.03(4)	8.50(12)
Reddish brown	1.60[a](1)	8.02[b](11)	NR	9.0(11)	NR	3.50(5)
Multiple colours	20.3[a](13)	30.1[b](41)	20.3(15)	29.5(36)	19.0[a](11)	28.0[b](39)

[a,b,c]Different superscripts within row and agro-ecological zone indicate significant different percentages at $p < 0.05$.
NR = not reported; values in parenthesis indicate the number of observations
Kei, feather with red colour; Tikur, feather with black colour; Netch, feather with white colour; Wosera, yellowish brown feather containing mixtures of yellow, red and white colours with variable proportions; Gebsima, greyish feather containing mixtures of white and black with varying shades of multi-colours

(2011) for native chickens of Nigeria. The study also indicated higher values for the two traits as compared with those reported by Youssao *et al.* (2010) for native hens and cocks reared in Benin. Body width is an indicator of fleshing, which would be used for selecting chickens suitable for meat production.

The values pertaining to the breast angle could not be compared due to lack of available literature for the trait among the chickens reared in Ethiopia. The wing span values obtained from the present study was lower than those reported by Halima *et al.* (2007) for local chickens of Northwestern Ethiopia.

The average values of shank length in cocks are lower than those reported by Halima *et al.* (2007) in Northwestern Ethiopia and Melesse and Negesse (2011) for those reared in Southern Ethiopia. The shank length values as reported by Badubi, Rakereng and Marumo (2006) from Botswana and Daikwo, Okpe and Ocheja (2011) from Nigeria were however within the range of the present findings. Shank circumference values in the present study are consistent with those of Mulyono, Sartika and Nugraha (2009) reported for Wareng–Tangerang Indonesian local chickens; but higher than those reported by Halima *et al.* (2007) for Northwestern Ethiopia. The body weight to shank length ratio is an indicator of degree of fleshing in relation to body size and the heavier the bird the higher would be the ratio (Renema *et al.*, 2007).

Sexual dimorphism was observed for the most traits with cocks having higher values when compared with the hens. Sexual dimorphisms for various morphological traits have also been reported in local chickens (Msoffe *et al.*, 2004; Fayeye *et al.*, 2006; Halima *et al.*, 2007; Dana *et al.,* 2010; Youssao *et al.*, 2010), in the Muscovy duck (Raji, Igwebuike and Usman, 2009; Yakubu, 2011) and in the turkey (Ogah, 2011). Owens and Hartley (1997) were of the opinion that sexual dimorphism in size is associated with high levels of social polygamy, a sort of intra-sexual competition described by traditional classifications of social mating systems. Baeza *et al.* (2001) observed that sexual dimorphism is attributable to the normal between sex differential hormonal actions, which invariably leads to differential growth rates. Another possible explanation for the appearance of sex-related differences is the strong selection of females for high quality males or competition among males for limited

Table 6. Linear body measurements of male and female indigenous chicken populations in the high-, mid- and lowland agro-ecological zones of Southeastern Ethiopia (mean ± SE).

Morphological traits (cm)	Sex	Highland ($n = 200$)	Midland ($n = 200$)	Lowland ($n = 200$)
Body weight (kg)	Male	1.40 ± 0.02	1.37 ± 0.02	1.40 ± 0.02
	Female	1.24 ± 0.01[a]	1.20 ± 0.01[b]	1.23 ± 0.01[ab]
Body length	Male	24.0 ± 0.15	24.2 ± 0.12	24.1 ± 0.15
	Female	22.6 ± 0.13	22.8 ± 0.09	22.6 ± 0.12
Body width	Male	25.2 ± 0.21	25.4 ± 0.11	24.2 ± 0.14
	Female	23.7 ± 0.15	24.0 ± 0.10	23.7 ± 0.11
Shank length	Male	7.50 ± 0.70	7.37 ± 0.06	7.41 ± 0.06
	Female	6.52 ± 0.33	6.52 ± 0.02	6.55 ± 0.03
Shank circumference	Male	3.92 ± 0.03	3.83 ± 0.03	3.82 ± 0.03
	Female	3.50 ± 0.02[a]	3.42 ± 0.02[b]	3.46 ± 0.02[ab]
Body density*	Male	18.8 ± 0.24	18.6 ± 0.21	18.6 ± 0.21
	Female	18.8 ± 0.21	18.7 ± 0.13	19.0 ± 0.15
Breast angle (degrees)	Male	46.4 ± 0.55	45.6 ± 0.51	45.8 ± 0.60
	Female	41.1 ± 0.41[a]	39.6 ± 0.33[b]	39.8 ± 0.35[b]
Keel bone length	Male	9.51 ± 0.73	9.67 ± 0.05	9.70 ± 0.80
	Female	8.82 ± 0.05[b]	9.02 ± 0.05[a]	9.02 ± 0.05[a]
Wing span	Male	8.17 ± 0 0.08[a]	7.85 ± 0.07[b]	7.94 ± 0.09[ab]
	Female	7.35 ± 0.04	7.42 ± 0.04	7.42 ± 0.04
Comb length	Male	5.32 ± 0.24[a]	4.42 ± 0.17[b]	4.85 ± 0.21[ab]
	Female	2.59 ± 0.07[a]	2.39 ± 0.05[b]	2.44 ± 0.06[ab]
Wattle length	Male	3.31 ± 0.08[a]	3.03 ± 0.08[b]	3.22 ± 0.09[ab]
	Female	0.92 ± 0.03	0.83 ± 0.04	0.96 ± 0.06
Beak length	Male	1.92 ± 0.02	1.93 ± 0.02	1.87 ± 0.02
	Female	1.75 ± 0.02[a]	1.68 ± 0.01[b]	1.69 ± 0.01[ab]

[a,b]Means within a row with different superscript letters are significantly different ($P < 0.05$).
*Body weight/shank length; SE, standard error of the mean.

access to females, which leads to fixation of larger body size and other secondary sexual characters in males (McCracken, Paton and Afton, 2000). According to Remes and Szekeley (2010), difference in sizes of males and females is perceived as a key evolutionary feature that is related to ecology, behaviour and life histories of organisms.

Prediction of live weight from linear body measurements

In the present study, high correlations were observed between body weight and all linear body measurements for both sexes and are in agreement with the findings Apuno, Mbap and Ibrahim (2011). Body weight is a trait of economic importance to livestock farmers, and therefore, selection for body weight in order to improve productivity in indigenous chickens is increasing (Peters *et al.*, 2007). In animal breeding, predicting body weight from linear measurements is a common practice (Ogah *et al.*, 2009). The positive and significant correlations between body weight with breast angle, body length, body width, breast angle and shank circumferences suggest that selection for any of these linear body parameters will cause direct improvement in body weight. Moreover, the significant correlations observed in the present study indicate that in the absence of some measuring facilities, measuring one of these easily measurable traits could enable

Table 7. Correlation coefficients of linear body measurement traits for local cocks (upper diagonal, $N = 197$) and hens (lower diagonal, $N = 403$).

	LBW	BDL	BDW	BRA	SHL	SHC	KBL	WSP
LBW	1	0.556**	0.473**	0.854**	0.293**	0.655**	0.415**	0.457**
BDL	0.550**	1	0.898**	0.462**	0.354**	0.332**	0.767**	−0.099
BDW	0.562**	0.922**	1	0.501**	0.445**	0.265**	0.772**	−0.115
BRA	0.816**	0.598**	0.565**	1	0.214**	0.549**	0.467**	0.359**
SHL	0.618**	0.386**	0.332**	0.521**	1	0.477**	0.380**	0.278**
SHC	0.284**	0.294**	0.312**	0.206**	0.276**	1	0.217**	0.473**
KBL	0.483**	0.632**	0.679**	0.372**	0.327**	0.090*	1	−0.183*
WSP	0.216**	0.047	0.030	0.148**	0.097*	−0.043	0.088*	1

*$P < 0.05$; **$P < 0.01$.
LBW, live body weight; BDL, body length; BDW, body width; BRA, breast angle; SHL, shank length; SHC, shank circumference; KBL, keel bone length; WSP, wing span.

Table 8. Stepwise multiple regression equations for estimation of body weight of cocks and hens reared in different agro-ecologies by fitting linear body weight measurements.

Sex	Agro-ecological zones	R^2_{adj}	Fitted stepwise multiple regression equations
Cocks	Highland	0.707	−0.090 + 0.032(BRA)
		0.772	−0.560 + 0.025(BRA) + 0.203(SHC)
	Midland	0.768	−0.131 + 0.027(BRA)
		0.808	−0.235 + 0.023(BRA) + 0.14(SHC)
	Lowland	0.730	−0.086 + 0.029(BRA)
		0.766	−0.207 + 0.024(BRA) + 0.131(SHC)
	Overall	0.728	−0.090 + 0.032(BRA)
		0.776	−0.560 + 0.025(BRA) + 0.203(SHC)
Hens	Highland	0.746	−0.039 + 0.029(BRA)
		0.796	−0.376 + 0.024(BRA) + 0.028(BDL)
	Midland	0.580	−0.409 + 0.02(BRA)
	Lowland	0.629	−0.342 + 0.022(BRA)
		0.666	−0.010 + 0.019(BRA) + 0.02(BDW)
	Overall	0.665	−0.24 + 0.025(BRA)
		0.702	−0.102 + 0.022(BRA) + 0.02(BDL)

BRA = breast angle; SHC = shank circumference; BDL = body length; BDW = body width.

predicting the values for the correlated traits without additional cost and time.

Regression analysis is frequently used in animal research to describe quantitative relationships between a response variable such as body weight and one or more explanatory variables including linear body measurements, particularly when there is no access to weighing equipment. The high and significant correlation coefficients between body weight and linear body measurements for both sex groups suggest that either of these variables or their combination could provide a good estimate for predicting live body weight of the studied indigenous chickens. Breast angle had the highest correlation coefficient values with body weight in both sexes followed by shank length and circumference, body length and width suggesting the suitability of these variables in predicting body weight of local chickens under scavenging production system.

As shown in Table 8, breast angle was the primary variable to explain most of the variations followed by shank circumference (in cocks), shank length (in hens), body length and body width. However, it would be worthwhile to note that under field conditions it becomes difficult to take multiple measurements on individual animals as catching the bird would be a problem and hence becomes impractical.

Conclusions

Female chickens were characterized by having single and pea combs, while males had rose combs. The main body feather colour in hens was yellowish brown followed by red, whereas males were characterized by red followed by yellowish brown. The colour of the shank in cocks was predominantly yellow, while in females it varied considerably between agro-ecological zones. The predominant eye colour in both sexes was blue black in all agro-ecological zones. The average values of body length and width, shank length and body shank length ratio for both groups of chicken were comparable across all the three agro-ecological zones. The authors recommend an in-depth assessment of the local chickens using the FAO's confirmatory characterization approach (preferably on-station comparison) to identify suitable chicken ecotypes for defined production purposes. We further recommend similar evaluation practices through FAO's exploratory characterization approach in the adjoining districts of the study area to obtain comprehensive information on qualitative and quantitative phenotypic characteristics of indigenous chicken populations.

Acknowledgements

This research project was financially supported jointly by Adama Science and Technology University and the Ethiopian Ministry of Education for which the authors are highly grateful. The Alexander von Humboldt Foundation is highly appreciated for awarding a research fellowship for the corresponding author during the preparation of this manuscript. The authors express their sincerely gratitude to all participating farmers in giving access to their chickens for visual appraisal and quantitative measurements.

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Animal Genetic Resources, 2014, 55, 115–124. © Food and Agriculture Organization of the United Nations, 2014
doi:10.1017/S2078633614000356

Morphological features of indigenous chicken ecotype populations of Kenya

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Summary
This study characterized indigenous chicken (IC) ecotypes morphologically. Five IC ecotypes studied were Kakamega (KK), Siaya (BN), West Pokot (WP), Narok (NR) and Bomet (BM). Data on morphological features were collected from 1 580 chickens and 151 for zoometric measurements. Descriptive statistics, non-parametric and *F* tests were used in analysis. A non-parametric Kruskal–Wallis, Binomial test and Mann–Whitney *U* test was used to evaluate whether the ecotype have effects on the qualitative morphological variables. Zoometric measurements was analysed with the PROC GLM of SAS. Results revealed that, black, black-white striped, brown and red body plumage colours were significantly different ($P < 0.05$) between the ecotypes. Feather morphology (%) were not significantly different ($P > 0.05$). Distribution of body feathers (%), comb types (%) and zoometric measurements were significantly different ($P < 0.05$). Eye colours varied significantly ($P < 0.001$) within the ecotypes unlike between the populations. In conclusion, IC ecotypes studied are heterogeneous population with huge variability in morphological features.

Keywords: *ecotype, indigenous chicken, morphological features*

Résumé
Cette étude a cherché à caractériser d'un point de vue morphologique des écotypes de poule autochtone. Les cinq écotypes étudiés ont été Kakamega (KK), Siaya (BN), Pokot Occidental (PO), Narok (NR) et Bomet (BM). L'information concernant les traits morphologiques a été obtenue sur 1 580 volailles alors que les mesures zoométriques ont été prises sur 151. Les données ont été analysées avec de la statistique descriptive, des tests non-paramétriques et le test F. Un test non-paramétrique Kruskal-Wallis, un test Binomial et un test Mann-Whitney U ont été utilisés pour évaluer si l'écotype avait un effet sur les variables morphologiques qualitatives. Les mesures zoométriques ont été analysées avec la procédure GLM du logiciel SAS. Les résultats ont révélé que la couleur du plumage corporel (noir, barré noir-blanc, marron et rouge) différait significativement ($P < 0.05$) entre les écotypes. Par contre, aucune différence significative ($P > 0.05$) n'a été décelée pour la morphologie des plumes. La distribution des plumes du corps (en pourcentage), les types de crête (en pourcentage) et les mesures zoométriques ont aussi présenté des différences significatives ($P < 0.05$). La couleur des yeux a varié de manière significative ($P < 0.001$) au sein des écotypes mais pas entre les populations. En conclusion, les écotypes autochtones de poule étudiés constituent une population hétérogène ayant une énorme variabilité dans les caractères morphologiques.

Mots-clés: *écotype, poule autochtone, traits morphologiques*

Resumen
Este estudio llevó a cabo una caracterización morfológica de ecotipos autóctonos de gallina. Los cinco ecotipos estudiados fueron Kakamega (KK), Siaya (BN), Pokot Occidental (PO), Narok (NR) y Bomet (BM). La información sobre los rasgos morfológicos se tomó de 1 580 aves mientras que se usaron 151 para las medidas zoométricas. Los datos fueron analizados con estadística descriptiva, tests no paramétricos y el test F. Se usaron un test no paramétrico Kruskal-Wallis, un test Binomial y un test Mann-Whitney U para evaluar si el ecotipo tenía efecto sobre las variables morfológicas cualitativas. Las medidas zoométricas se analizaron con el PROC GLM de SAS. Los resultados mostraron que el color del plumaje corporal (negro, barrado negro-blanco, marrón y rojo) difería significativamente ($P < 0.05$) entre los ecotipos. Por el contrario, no se dieron diferencias significativas ($P > 0.05$) para la morfología de las plumas. La distribución de las plumas del cuerpo (en porcentaje), los tipos de cresta (en porcentaje) y las medidas zoométricas también difirieron significativamente ($P < 0.05$). El color de los ojos varió de manera significativa ($P < 0.001$) dentro de los ecotipos pero no entre las poblaciones. En conclusión, los ecotipos de gallina autóctona estudiados constituían una población heterogénea con una amplia variabilidad en los caracteres morfológicos.

Palabras claves: *ecotipo, gallina autóctona, rasgos morfológicos*

Submitted 28 May 2014; accepted 28 August 2014

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Introduction

Indigenous chicken (IC) genetic resources are a heterogeneous population which exhibit vast phenotypic variability (FAO, 2012) without standard phenotypic characteristics. They vary in body sizes, comb types, colours (plumage, eye, skin, shank and earlobe colours), outline and feather contours (Teketel, 1986; Ndirangu *et al.*, 1991; Dana *et al.*, 2010; Kingori, Wachira, A.M. & Tuitoek, 2010; Cabarles *et al.*, 2012). Distinct phenotypic variations among IC in different regions (ecotypes) have been documented in some countries. In Uganda, Ssewanyana *et al.* (2003b) reported a wide phenotypic variability in plumage, shank, eye, earlobe, comb, skin, feathers, feather distribution, body size, comb type, wattle and earlobe sizes among IC population found in the Soroti, Mbale, Jinja, Masaka, Sembabule and Mbarara districts. Similarly, large variations in plumage colours, comb types, skin colours, shank colours, eye colours, earlobe colours and body positions among Ethiopian IC ecotypes (Tilili, Horro, Jarso, Tepi, Gelila, Debre-Elias, Melo-Hamusit, Gassay/Farta, Guangua and Mecha ecotypes) have been reported (Tadelle *et al.*, 2003a; Halima, 2007; Bogale, 2008; Dana *et al.*, 2010; Abera and Tegene, 2011). In Kenya, morphological variations of IC population have been reported by Ndirangu *et al.* (1991), Maina (2000), Njenga (2005) and Nyaga (2007). However, IC morphological characterization studies in Kenya were not based on the ecosystems and information of IC distributed in the specific regions of the country is presently limited. Each agro-ecological zone is anticipated to host chicken exhibiting different morphological characteristics. Therefore, there is a need to distinctively characterize morphologically IC populations in each agro-ecological zone.

The objective of this study was to characterize IC ecotypes morphologically. Information generated is crucial inputs to IC genetic improvement activities, future development of chicken breeds utilizing IC genetic resources and provide foundation for decision-making on conservation interventions needed.

Materials and methods

Study sites

The study was carried out in five administrative counties in Kenya; Bomet, Narok, Kakamega, Siaya and West Pokot counties. Counties were selected based on their geographical distances, ecological characteristics, coverage of the past chicken improvement programmes (distribution of exotic birds) and the socio-economic roles of IC (Okeno, 2012). In these counties, most rural households keep IC in rural households (MOLD, 2010; Okeno, 2012) and have wide variation in temperatures, annual rainfall and altitude.

Study population

Kakamega (KK), Siaya (BN), West Pokot (WP), Narok (NR) and Bomet (BM) ecotypes were studied. Indigenous chicken ecotypes were named according to the county of origin.

Sampling and data collection

Three divisions and three locations within each division in each county were randomly sampled. The households in the villages with highest number of IC in each location were recorded. Simple random sampling procedure was used to select households for interviews by randomly picking names of the households from the list. A pretested structured questionnaire was used to gather information. The main features in the questionnaire related to chicken morphological characteristics and flock size per morphological characteristics. Data were collected from free ranging IC through direct observations. Data on morphological features (qualitative data) collected included feather morphology, feather distribution (body and head), body plumage colours, skin colours, earlobe colours, comb types, eye colours, shank colours. Zoometric measurements collected were body weight (BW) and shank length (SL). Measurements were taken in centimetres using a tape measure for SL and a digital weighing scale for BW. Only mature chicken (older than 8 months of age) were considered for morphological characterization.

Data were collected based on Cuesta (2008), Francesch *et al.* (2011), Cabarles *et al.* (2012) and FAO (2012). A total of 98, 122, 99, 96 and 87 IC farmers were interviewed in BN, KK, BM, NR and WP counties, respectively. Qualitative traits data were collected from a total of 1 580 IC from BN (285), KK (415), BM (287), NR (282) and WP (311). Zoometric measurements data were collected from 151 IC from BN (31), KK (32), BM (29), NR (28) and WP (31).

Statistical analysis

Descriptive statistics were generated using frequency procedures and cross-tabulation using SPSS (SPSS, 2011). A non-parametric Kruskal–Wallis test was used to evaluate whether the ecotype have effects on the qualitative morphological variables (Dana *et al.*, 2010; Cabarles *et al.*, 2012). Variables with overall significant test based on Kruskal–Wallis test were followed-up with a Mann–Whitney *U* test to examine unique pairs. A Binomial test was used to analyse the significance of the differences in feather morphology (normal or frizzle), head feather distribution (crested or normal) and skin colour (white or yellow). The PROC GLM of SAS (SAS, 2008) was used for analysis of variance for BW and SL. A model that accounted for the fixed-effects of ecotype, sex and interaction between ecotype and sex was fitted. The age of

the bird was not included in the model because only adults, 8 months or older were sampled. Least-squares means were separated using least significant difference (LSD) option. The linear model fitted was:

$$Y_{ijk} = \mu + a_i + b_j + (ab)_{ij} + \varepsilon_{ijk},$$

where Y_{ijk} is the response expected in the dependent variable, μ is the mean of the population, a_i is the effect of ecotype (i = KK, BN, BM, NR and WP), b_j is the effect of sex (j = male or female), $(ab)_{ij}$ is the effect of interaction between ecotype and sex and ε_{ijk} is the random error.

Results and discussion

Body plumage colours

Body plumage colours are presented in Table 1 and Figure 1. Among the body plumage colours, percentages of black, black-white striped, brown and red were significantly different ($P < 0.05$) between the ecotypes. BM, NR and WP ecotypes was dominated by black body plumaged chicken. BN ecotype had predominantly brown body plumage, whereas KK were dominated by black and white. Body plumage colouration play a role in survival success of IC raised under scavenging system characterized by frequent attack from predators. Indigenous chicken susceptibility levels to predators depend on the camouflaging ability to their numerous local habitats. Differences in camouflaging ability and reaction response to predator attack might have led to diverse frequencies in body plumage colouration. Farmers have colour preferences which influence body plumage colour frequencies among the ecotypes. In Ethiopia, plumage colours frequencies have been affected by farmer's preferences (Dana *et al.*, 2010). Conversely, IC challenges under scavenging environment such as interaction with feather degradation bacteria, which degrade feather pigments might have contributed to the observed varied frequencies of the body plumage colours. According to Goldstein *et al.* (2004), adaption to microbial infections especially from bacteria which degrades feather pigments results in different feather colours. Additionally, different plumage colours may be due to the adaptive significance in the thermoregulation (Hill and McGraw, 2006; Protas and Patel, 2008) under tropical conditions.

Distribution of body and head feathers

Body feather distributions in the different body plumaged chickens within each ecotype are presented in Table 2 and Figure 2. Body feathers were distributed normally across the ecotypes (61–69 percent) except in KK population. KK population was composed of normal (31 percent), naked-neck (31 percent) and crested (35 percent) chicken.

Distribution (%) of head feathers (crested or normal) for the different body plumage colours within the populations are presented in Table 3. Distribution of head feathers were significantly different ($P < 0.05$) between the different body plumage colours within each population. Normal head-feathered-type chickens were dominant over crested in all the body plumage colours in BN, BM and WP populations.

Feather distribution is of vital importance in IC because of their physiological roles especially on thermoregulation. Different ecotypes might have evolved in feather arrangement to allow them to adapt and radiate in their respective habitats. In hot environments such as KK where IC are reared under the scavenging system, naked-neck chicken may have been suitable because it allows better heat dissipation than other genotypes. Low percentages of the naked (Na) neck genotype in other counties except KK may be due to farmers' selection preferences and cultural issues.

Table 1. Body plumage of five ecotype populations (percentage of chickens within the population).

Body plumage colour	BM (%)	NR (%)	BN (%)	KK (%)	WP (%)	N (%)
Black	22.9^{c}	23.8^{bc}	14.2^{a}	19.0^{b}	22.5^{ab}	321(20)*
Black-white striped	9.3^{b}	9.1^{a}	14.2^{a}	9.2^{a}	10.3^{a}	163(10)*
Black-white spotted	11.5	14.5	9.5	10.8	11.9	183(12)
Brown	13.6^{a}	8.4^{ab}	20.0^{a}	7.5^{b}	11.9^{b}	187(12)*
Red	9.0^{a}	12.3^{ab}	5.5^{a}	15.2^{b}	10.0^{b}	171(11)*
Red-brown spotted	9	7.3	12.7	7.5	11.6	150(9)
Red-brown	11.1	6.9	6.2	5.5	5.5	110(7)
Grey	4.3	2.8	4.7	6.7	5.8	79(5)
White	8.2	14.5	12.7	18.6	9	206(13)
Other colours	1.1	0.4	0.3	0	1.6	10(1)
N	287	282	285	415	311	1580

BM, Bomet ecotype; KK, Kakamega ecotype; BN, Siaya ecotype; NR, Narok ecotype.
N, figures within each column of body plumage; %, percent of total N within a population; N (%), figures and their percentage of each body plumage.
Note: Asterisks in last column indicate significant differences between ecotypes (columns) at the 5 percent (*) probability levels, based on the Kruskal–Wallis test.
[abc]Means in a row with one or more letter superscripts in common are not significantly different ($P \geq 0.05$) based on the Mann–Whitney U test.

Figure 1. Body plumage colours of indigenous chicken ecotypes.

Feather morphology

Feather morphologies (normal or frizzle feathers) are presented in Table 2 and Figure 3. Two types of feather morphology were observed with normal feathered chickens being the majority. Statistical analysis revealed that feather morphology between the ecotypes was not significantly different ($P > 0.05$). Frizzle feathered chickens with the genes known to affect the structure of the feathers and enable heat dissipation constituted less than 10 percent. Frizzled chickens are crucial for cultural and traditional activities through their roles in rituals and sacrifices (Ojo, 2002) and may have contributed higher demand hence low frequency observed in the study. For instance in KK county, frizzled IC are used for cultural purposes such as protection from witchcraft and payment of dowry. Conversely, frizzle feathering gene (F) is lethal when homozygous (Fayeye and Oketoyin, 2006) which may explain the low frequency in adult frizzle chicken in this study. Since homozygous F gene is lethal, farmers who may be aware of the condition may have done cross-breeding with other genotypes to conserve the allele.

Variations in shank and skin colours

Shank colours (white, yellow, green and black) with their respective percentages within each ecotype are presented in Table 2 and Figure 4. Results showed that majority of BM, NR, KK and WP population had yellow shank. White shanks contributed almost half (49 percent) of the BN population followed by yellow (39 percent). Skin colours (white or yellow) for the different ecotypes are presented in Table 2. Occurrences of white and yellow skin were significantly different ($P < 0.001$) within an ecotype but similar ($P > 0.05$) between the ecotypes. White skin was common in NR (52 percent), BN (62 percent) and WP (58 percent) population compared with yellow. KK population recorded equal (50 percent) in both white and yellow skin colours.

Skin and shank colours are used as indicators of chicken health (nutritional and immune status), foraging efficiency and sexual attractiveness (Blount *et al.*, 2003; Blas *et al.*, 2006; Eriksson *et al.*, 2008). Different skin colours observed in this study were in the range reported for Ethiopian IC where 52 and 48 percent had yellow and white skin, respectively (Dana *et al.*, 2010). Colour diversity originates from the diet depending on the presence or absence of Oxycarotenoids (Seemann, 2000). Significant differences in shank and skin colours within the populations could be as a result of diet found in their local habitat, variation of genes from the ancestral lineages and the effect of consumer preference. Genetically, shank colour is controlled by three genes; dermal melanin (id+), inhibition of dermal melanin (Id), black extension factor (E) and autosomal white (W+) genes located in the Z sex

Table 2. Morphology and distribution of feathers, comb types and colours (skin, shank and eye) of five IC ecotypes.

		BM (%)	NR (%)	BN (%)	KK (%)	WP (%)	χ^2
Feather morphology		**	**	**	**	**	5.6
	Normal	100	100	100	91	96	
	Frizzle	0	0	0	9	4	
Skin colour		**	**	**	**	**	6.4
	White	46	52	62	50	58	
	Yellow	54	48	38	50	42	
Body feather distribution		**	**	**	**	**	15.6**
	Normal	69	77	61	31	69	
	Naked neck	17	9	6	31	13	
	Feathered shank	7	1	22	3	11	
	Muff and bearded	0	4	0	0	0	
	Crest	7	9	11	35	7	
Shank colour		**	**	**	**	**	12.8*
	White	21	28	49	21	34	
	Yellow	75	38	39	53	39	
	Green	0	19	6	13	9	
	Black	4	15	6	13	18	
Comb type		**	**	**	**	**	9.8*
	Single	83	100	100	100	96	
	Pea	4	0	0	0	0	
	Rose	0	0	0	0	4	
	Cushion	13	0	0	0	0	
Eye colour		**	**	**	**	**	1.6
	Orange	87	63	89	92	76	
	Brown	9	16	0	0	16	
	Red	4	11	0	0	0	
	Pearl	0	11	11	8	8	
N		287	282	285	415	311	

BM, Bomet ecotype; KK, Kakamega ecotype; BN, Siaya ecotype; NR, Narok ecotype.
N, figures within each column; %, percent of total N within a population. Note: Asterisks indicate significant differences between rows at the 5 percent (*) and 1 percent (**) probability levels, based on the Binomial test for feather morphology and skin colour and the Cochran test for distribution of body feathers, comb types, shank and ear lobe colours.
χ^2, the χ^2 values in last column with "*" (5 percent) or "**" (1 percent) denote significant differences between columns (ecotypes) based on the Kruskal–Wallis test.

Figure 2. Body feather distribution of indigenous chicken ecotypes.

Table 3. Distribution of head feathers (crested or normal) within ecotype populations (percentage of chickens within each population).

Body plumage colour	Head feathers	BN (%)	KK (%)	BM (%)	NR (%)	WP (%)	χ^2
		**	**	**	**	**	
Black	Crested	1.1	5.9	1.4	0.4	1.1	7.7
	Normal	13.1	13.1	21.5	23.4	21.4	7.7
Black-white stripes	Crested	2.1	3.9	0.1	0.6	0.9	21.5**
	Normal	12.1	5.3	9.2	8.5	9.4	21.5**
Black-white spotted	Crested	1.1	2.1	0.4	0.7	1.0	2.9
	Normal	8.4	8.7	11.1	13.8	10.9	2.9
Brown	Crested	3.4	3.9	0.2	4.2	1.1	16.1**
	Normal	16.6	3.6	13.4	4.2	10.8	16.1**
Red	Crested	0.9	5.6	0.5	0.4	0.3	6.3
	Normal	4.6	9.6	8.5	11.9	9.7	6.3
Grey	Crested	0.3	2.4	0.8	0.5	0.3	5.5
	Normal	4.4	4.3	3.5	2.3	5.5	5.5
White	Crested	1.7	5.5	0.1	0.7	0.8	3.3
	Normal	11	13.1	8.1	13.8	8.2	3.3
Red-brown spotted	Crested	0.3	3	0.3	0.6	0.5	10.6*
	Normal	12.4	4.5	8.7	6.7	11.1	10.6*
Red-brown	Crested	0.1	2.7	2.8	0.6	0.8	7.6
	Normal	6.1	2.8	8.3	6.3	4.7	7.6
Others	Crested	0.0	0.0	0.4	0.0	0.2	2.3
	Normal	0.3	0	0.7	0.4	1.3	2.3
N		285	415	287	282	311	

BM, Bomet ecotype; KK, Kakamega ecotype; BN, Siaya ecotype; NR, Narok ecotype.
N, figures within each column; %, percent of total N within a population.
Note: Asterisks indicate significant differences between rows at the 5 percent (*) and 1 percent (**) probability levels, based on the Binomial test for head feathers (crested or normal); χ^2, the χ^2 values in last column with "*" (5 percent) and 1 percent (**) denote significant differences between columns (ecotypes) based on the Kruskal–Wallis test.

Figure 3. Feather morphology of indigenous chicken ecotypes.

chromosome (Smyth, 1990). White skin alleles are presumed to originate from red jungle fowl (*Gallus gallus*), whereas yellow skin is from hybridization of grey jungle fowl (*Gallus sonneratii*), Ceylon jungle fowl (*Gallus lafayettii*) and red jungle fowl (Eriksson *et al.*, 2008; Cabarles *et al.*, 2012) and might be the reasons for the different colours in IC population studied.

Comb types

Comb types (single, pea, rose and cushion) within and between the ecotypes with their respective percentages are presented in Table 2 and Figure 5. Comb types varied significantly ($P < 0.001$) within and between the ecotypes and could be associated with the variation in prevailing climatic conditions in their rearing environments and the effect of comb genes (Somes, 1990b; Duguma, 2006). All the ecotypes were dominated by single comb (above 83 percent) and in agreement with the reports by Egahi *et al.* (2010) and Apuno, Mbap and Ibrahim (2011) on Nigerian IC and contrary to those reported in Ethiopia by Dana *et al.* (2010). Comb is important in scavenging IC as it acts a cooling mechanism under hot tropical conditions because chickens cannot sweat. Single comb in IC

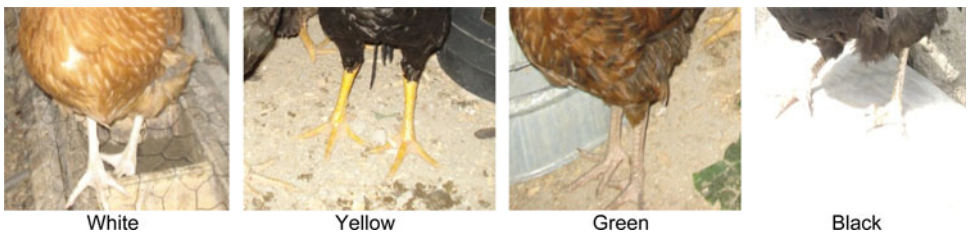

Figure 4. Shank colours of indigenous chicken ecotypes.

Figure 5. Comb types of indigenous chicken ecotypes.

helps in losing body heat up to 40 percent under prevailing environmental temperature of 80°F and below (Nesheim Austic and Card 1979).

Eye colours

Eye colours (orange, brown, red and pearl) for the different ecotypes are presented in Table 2. The widely distributed eye colour among the population was orange (>62 percent), whereas brown, red and pearl were below 17 percent. Eye colours within an ecotype varied significantly ($P < 0.001$) but not between ecotypes ($P > 0.05$). Within ecotypes diversities in eye colour could be attributed to genes of an individual, which affects blood supply and melanin levels, environmental effect in terms of availability of carotenoids and interaction of blood supply, melanin and carotenoids (Smyth, 1990; Stoddard and Prum, 2011; McCartney *et al.*, 2014). Variation in colour is as a result of pigmentation of a number of structures within the eye (iris, retina, uveal tract and ciliary) due to sex-linked

Table 4. Earlobe colours within different body plumage colours for each IC ecotype.

Body plumage colour	Earlobe colour	BN	KK	BM	NR	WP	χ^2
		**	**	**	**	**	
Black	White	2.8	6.8	6.2	3.4	6.4	17.8**
	Red/pink	5.3	8.9	12.7	10.0	12.4	
	Black	6.1	3.3	4.0	10.4	3.7	
Black-white stripes	White	3.9	3.8	2.8	3.2	3.3	4.1
	Red/pink	7.6	4.7	6.5	4.3	6.0	
	Black	2.7	0.7	0.0	1.6	1.0	
Black-white spotted	White	2.3	3.3	2.9	6.1	3.3	1.6
	Red/pink	6.2	6.6	7.9	4.5	7.6	
	Black	1.0	0.9	0.7	3.9	1.0	
Brown	White	4.4	2.8	3.6	2.2	1.8	11.4
	Red/pink	11.2	4.7	7.6	4.2	10.0	
	Black	4.4	0.0	2.4	2.0	0.0	
Red	White	0.7	6.5	1.7	1.1	1.3	15.8**
	Red/pink	2.9	7.5	6.9	10.7	8.5	
	Black	1.9	1.2	0.4	0.5	0.2	
Red-brown spotted	White	2.2	2.6	2.7	2.3	2.9	1.7
	Red/pink	9.4	4.4	6.2	4.2	8.4	
	Black	1.1	0.5	0.1	0.8	0.3	
Red-brown	White	1.8	1.8	2.8	0.0	1.3	2.6
	Red/pink	3.6	2.8	6.5	6.9	4.2	
	Black	0.8	0.9	1.8	0.0	0.0	
Grey	White	1.9	1.5	1.8	0.6	2.0	2.1
	Red/pink	2.5	4.7	2.5	1.7	3.7	
	Black	0.3	0.5	0.0	0.5	0.1	
White	White	4.6	7.1	1.6	7.3	3.6	5.4
	Red/pink	7.3	11.5	6.4	6.8	5.0	
	Black	0.8	0.0	0.2	0.4	0.4	
Other	White	0.3	0.0	0.0	0.0	0.0	1.3
	Red/pink	0.0	0.0	1.1	0.0	1.3	
	Black	0.0	0.0	0.0	0.4	0.3	
N		285	415	287	282	311	

BM, Bomet ecotype; KK, Kakamega ecotype; BN, Siaya ecotype; NR, Narok ecotype.
N, figures within each column; %, percent of total N within a population. Note: Asterisks indicate significant differences between rows at the 5 percent (*) and 1 percent (**) probability levels, based on the Cochran test.
χ^2, the χ^2 values in last column with "*" (5 percent) or "**" (1 percent) denote significant differences between columns (ecotypes) based on the Kruskal–Wallis test.

Figure 6. Earlobe colours of indigenous chicken ecotypes.

dermal melanin genes (id^+ and id^M) and its correlation with other genes expressing colours to other parts (Smyth, 1990; Cabarles *et al.*, 2012) of the chicken body.

Earlobe colours

Table 4 and Figure 6 present the earlobe colours (white, red/pink and black). Generally, earlobe colours were significantly different ($P < 0.05$) within the populations. Red/pink earlobe was common in the populations. White earlobes were common in black-white spotted and white chicken. Earlobe pigmentation has a role in thermoregulation by absorbing or radiating solar radiation from chicken body (Stettenheim, 2000; Egahi *et al.*, 2010). Differences in earlobe colours observed in this studied may be due to adaptability of IC ecotypes to their local habitats and differences in ancestral lineages. Ancestral lineages of white ear lobe are bankiva, murghi and gallus, and of red ear lobe are jabouillei and spadecius and their hybridization (Nishida *et al.*, 2000; Ohta *et al.*, 2000).

SL and BW

Variations in SL and BW for the different ecotypes are shown in Table 5. SL between ecotypes were significantly different ($P < 0.05$). Ecotypes with SL not significantly different ($P > 0.05$) were BM, KK, NR and WP as well as BN, KK and WP in another group. The longest shank was recorded in NR ecotype followed by BM, WP, KK and BN. SL can be used as a predictive live BW in IC particularly where weighing scales are not readily available, as is the case in most smallholder African rural farmers and meat markets (Mani, Abdullah and Von Kaufmann, 1991; Nesamvumi *et al.*, 2000; Kabir *et al.*, 2006). SLs in chicken in this study were generally longer than Ethiopian (Dana *et al.,* 2010) and Nigerian IC (Apuno, Mbap and Ibrahim, 2011) but in the range with some Tanzanian ecotypes (Msoffe *et al.,* 2001). NR ecotypes with longer shanks are found in a relatively dry region with flat terrain and chicken may need to cover long distance in search of food.

Table 6. Least-squares means ± standard error of BW of mature female and male chicken under on-farm condition. Measurements were taken after 1 day of starving.

Ecotype	Female	Male
BM	1081.06 ± 71.08^{c}	1328.12 ± 97.34^{b}
BN	1321.66 ± 79.47^{a}	1445.00 ± 104.06^{ab}
NR	1247.50 ± 79.47^{ab}	1643.57 ± 104.06^{ab}
KK	1162.64 ± 66.77^{bc}	1442.77 ± 91.77^{ab}
WP	1108.12 ± 68.83^{bc}	1776.66 ± 91.77^{a}

BM, Bomet ecotype; KK, Kakamega ecotype; BN, Siaya ecotype; NR, Narok ecotype.
[abc]Means in a column with one or more letter superscripts in common are not significantly different ($P \geq 0.05$) based on LSD.

BW were significantly different between the ecotypes ($P < 0.05$). On average, adults weighed 1 367, 1 259, 1 167, 1 393 and 1 348 g for BN, KK, BM, NR and WP, respectively (Table 5). BW for NR was not significantly different ($P > 0.05$) from BN, KK and WP. Significant difference ($P < 0.05$) between sexes with cocks being heavier than hens was recorded (Table 6). WP (heaviest) and BM (lightest) males were significantly different ($P < 0.05$). Females from BM and BN were the lightest and heaviest, respectively. Narok, KK and WP females were not significantly different ($P > 0.05$), whereas BM hens were similar to KK and WP hens. The significant differences in average BW could be attributed to genetic make-up, feed availability and age of the birds (the precise age of birds were unknown due to lack records under on-farm).

Conclusion

Indigenous chicken ecotypes studied are heterogeneous population with large variability in morphological features. Black body plumage, normal feathers, single comb, white skin, orange eye colour and red/pink earlobes were the predominant morphological features.

Table 5. Least-squares means ± standard error of zoometric measurements of mature chicken under on-farm condition. Measurements were taken after 1 day of starving.

	BM	BN	KK	NK	WP
N	29	31	32	28	31
BW	1167.41 ± 69.56^{b}	1367.45 ± 72.00^{a}	1259.91 ± 58.65^{ab}	1393.80 ± 76.96^{a}	1348.81 ± 66.00^{ab}
SL	10.92 ± 0.32^{a}	9.79 ± 0.35^{b}	10.29 ± 0.31^{ab}	11.08 ± 0.34^{a}	10.43 ± 0.32^{ab}

BM, Bomet ecotype; KK, Kakamega ecotype; BN, Siaya ecotype; NR, Narok ecotype; N, number of chicken per ecotype; BW, Body weight; SL, shank length.
[abc]Means in a row with one or more letter superscripts in common are not significantly different ($P \geq 0.05$) based on LSD.

Acknowledgments

The authors are grateful to the Wageningen University, The Netherlands, Koepon foundation and Indigenous Chicken Improvement Programme (InCIP) for funding. We sincerely thank the farmers who participated in the project.

Conflict of interest

None.

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Animal Genetic Resources, 2014, 55, 125–135. © Food and Agriculture Organization of the United Nations, 2014
doi:10.1017/S2078633614000332

The past, present and future genetic improvement of indigenous chicken of Kenya

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Summary
Genetic improvement of farm animals encompasses both mating and selection for desired traits and indigenous chicken genetic resources are no exception. In Kenya, previous attempts to genetically improve indigenous chicken involved cross-breeding scheme by utilizing cockerels and pullets of exotic breeds with the local indigenous chicken. This scheme was complimented with farmer training on good management practices and vaccination for disease control. The scheme was partially successful with improved performance in the crossbreds that declined with subsequent generations. Failure of the programme to meet stakeholder's expectation led to its' termination. The current attempt through the Smallholder Indigenous Chicken Improvement Programme has initiated an holistic and comprehensive approach to analysing the entire indigenous chicken actors and avert the causes of previous failures. The programme has genetically and phenotypically characterized the chicken; established reference/base population collected from different ecotypes/counties, established the breeding goals and designed breeding programmes that best suit the Kenyan stakeholders. The on-station research has reported variation on production traits, determined heritability estimate on growth. Current and ongoing research is focused on molecular characterization, selection for improved immune response, carcass quality, eggs production, growth and adaptation traits. The research is also concerned with conservation of these genetic resources.

Keywords: *indigenous chicken, Kenya, genetic improvement, genotypes, breeding programmes*

Résumé
Lorsque l'on cherche à améliorer les caractères des animaux d'élevage, il faut envisager aussi bien les accouplements que la sélection génétique et en cela les ressources génétiques avicoles autochtones ne font pas exception. Au Kenya, les tentatives passées d'amélioration génétique des poules autochtones consistaient à croiser de jeunes mâles et femelles de races exotiques avec des coqs et des poules indigènes. Ce programme était complété par des formations aux éleveurs en bonnes pratiques de gestion et vaccination pour le contrôle des maladies. Ce système a joui d'un certain succès en raison de l'amélioration des performances que l'on atteignait sur les animaux croisés. Cependant, les résultats se détérioraient dans les générations suivantes. La non réponse aux attentes des acteurs impliqués conduisit à l'abandon de ce programme.

Actuellement, le Programme pour l'Amélioration des Poules Autochtones des Petits Éleveurs, suivant une approche holiste et intégratrice, prétend prendre en considération tous les acteurs impliqués dans l'élevage des poules autochtones afin d'éviter des échecs comme ceux survenus dans le passé. Le programme a caractérisé les poules aussi bien du point de vue génétique que phénotypique, a créé une population de référence constituée de poules de différents écotypes et départements, a fixé les objectifs de la sélection et a conçu les schémas de sélection qui satisfont le plus les parties prenantes kényanes. La recherche menée à la station a décelé une certaine variabilité dans les caractères productifs et a permis d'estimer l'héritabilité de la croissance. La recherche présente et future s'oriente vers la caractérisation moléculaire et la sélection pour l'amélioration de la réponse immunitaire, la qualité de la carcasse, la production d'œufs, la croissance et les caractéristiques d'adaptation. La recherche vise de même à conserver ces ressources génétiques.

Mots-clés: *poules autochtones, Kenya, amélioration génétique, génotypes, programmes de sélection*

Resumen
Cuando se desea mejorar cierto carácter en los animales de granja se debe prestar atención tanto a los apareamientos como a la selección genética y en ello los recursos genéticos avícolas autóctonos no son una excepción. En Kenia, los intentos pasados por mejorar la genética de las gallinas autóctonas consistieron en el cruzamiento de machos y hembras jóvenes de razas exóticas con gallos y gallinas autóctonos. Este esquema se completaba con la formación de los ganaderos en buenas prácticas de manejo y vacunación para la prevención de enfermedades. Este esquema resultó en cierto modo exitoso por la mejora de los rendimientos productivos que se alcanzaba en los animales cruzados. Sin embargo, los rendimientos empeoraban en las generaciones siguientes. La no satisfacción de las expectativas de las partes interesadas hizo que se acabase abandonando este programa.

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En la actualidad, el Programa para la Mejora de las Gallinas Autóctonas de los Pequeños Propietarios pretende, con la adopción de un enfoque holístico e integrador, tener en cuenta a todos los agentes implicados en la cría de las gallinas autóctonas para así evitar que se repitan fracasos como los anteriores. El programa ha caracterizado las gallinas tanto desde un punto de vista genético como fenotípico, ha establecido una población base de referencia formada por aves de diferentes ecotipos y provincias, ha marcado los objetivos de la mejora y ha diseñado los esquemas de selección que, en mayor medida, satisfacen a los agentes keniatas implicados. La investigación llevada a cabo en la estación ha sacado a la luz la existencia de cierta variabilidad en los caracteres productivos y ha permitido estimar la heredabilidad del crecimiento. La investigación presente y futura va encaminada a la caracterización molecular y a la selección para la mejora de la respuesta inmune, la calidad de la canal, la producción de huevos, el crecimiento y las características de adaptación. La investigación busca asimismo la conservación de estos recursos genéticos.

Palabras clave: *gallinas autóctonas, Kenia, mejora genética, genotipos, programas de selección*

Submitted 11 December 2013; accepted 14 July 2014

Introduction

Domestication of chicken

Chicken are believed to be the most popular poultry species worldwide and are believed to have descended from the four species of the jungle fowl: the red jungle fowl (*Gallus gallus*), the grey jungle fowl (*Gallus sonnerati*), the Ceylon jungle fowl (*Gallus lafayettei*) and the green jungle fowl (*Gallus varius*) (Dana, Van der Waaij and Van Arendok, 2011). It is still an open question whether the modern chicken were domesticated from one or all of these species. Cumulative data from the geographic range of the species (Crawford, 1990), archaeological discoveries (West and Zhou, 1988), protein polymorphisms and morphological characteristics (Moiseyeva *et al.*, 2003), suggested that domestic chickens were derived from the red jungle fowl. The studies that utilized four species of genus *Gallus* (*G. gallus*, *G. varius*, *G. lafayettei* and *G. sonnerati*), three subspecies of *G. gallus* (*G. g. gallus*, *G. g. spadiceus* and *G. g. bankiva*), nine domestic breeds of chicken from South Asia, South East Asia, Japan and Europe, (Akishinonomiya *et al.*, 1994, 1996) on their 400 base pairs of mt DNA D-loop region, presented results which suggested that domestic chickens are derived from a single continental population of *G. g. gallus*. However, other subspecies of the red jungle fowl are believed to be modern ancestor of current chicken (Liu *et al.*, 2006). Genetic integration of species in the genus Gallus has been demonstrated as well. This suggests that several species might have contributed to origin of modern chicken (Nishibori *et al.*, 2005). Eriksson *et al.* (2008) by examining the origins of skin colour variations in domestic chickens, revealed that although the white skin allele in modern chickens is derived from the red jungle fowl, the most likely origin of the yellow skin gene is the grey jungle fowl (*G. sonnerati*). Contrary to Crawford (1990), Liu *et al.* (2006) using maternal DNA found evidence suggesting that origin of indigenous chicken was centred around South and South East Asia. This was in agreement with previous studies by Akishinonomiya *et al.* (1994, 1996).

Introduction of chicken to Africa and Kenya

The route and dates by which chicken entered the African continent remain poorly understood. It is suggested that chickens were first introduced into Africa via Egypt from South-western Asia via the middle-east (Magothe *et al.*, 2012). According to Blench and MacDonald (2000), archaeological evidence and other representations indicate occasional presence of chickens in Egypt in the period between 1425 and1123 BC (Dana, Van der Waaij and Van Arendok, 2011). During that time, the chickens were thought to have been kept for cockfighting sports. Around 650 BC and beyond there was change of chicken utility from recreational to cultural and spiritual usage; it is thought that chickens were used to tell the time of day and for sacrifices before planting or harvesting (Maina, 2000) and subsequently introduced as source of food. At around 500 BC, human migration to the South led to the spread of chickens to Central Africa (Magothe *et al.*, 2012). Chicken are believed to have entered Kenya through different routes. Migration of the Bantu people from Central Africa eventually led to the arrival of chickens in Western Kenya at around 100 BC. Migration of the Paranilotics from the North at around 50 AD and the Nilotics along the Nile valley later on is also thought to have brought more chickens (Maina, 2000). The early Greco-Roman east-coast trade is hypothesized to have brought the Asiatic and game chickens along the Kenyan coast at around 100 AD (Blench and MacDonald, 2000) and eventually reaching Eastern Kenya probably at around 200 AD (Maina, 2000).The long span of period is thought to have caused the change of relative importance of chicken.

The modern world breeds of chickens can be grouped into four evolutionary lineages: (a) egg-type chickens of Mediterranean origin; (b) game chickens of Asiatic origin; (c) meat-type chickens of Asiatic origin and (d) true Bantams of various descents (Moiseyeva *et al.*, 2003). Trade with several empires may have introduced the Asiantic types into present Kenya, while migration from the north may possibly have brought more of the

Table 1. Population and distribution of indigenous chicken in Kenya.

Geographical regions (Provinces)	Population
Rift Valley	6 667 262
Nyanza	5 605 478
Western	4 144 351
Eastern	4 107 618
Central	3 039 786
Coast	1 599 696
North Eastern	422 899
Nairobi	279 397
Total	25 866 487

Source: Kenya National Beaurea of Statistics, 2010.

Mediterranean and the Bantams types. Selection, mutations and random drifts over time may have resulted in the modifications and subsequent development of the various chicken eco- and genotypes presently available in various climatic regions in Kenya.

The primary reasons for domesticating animals in Africa were their cultural, ritual and social values. Their role as source of food came much later with the expansion of human population (Clutton-Brock, 1993). The conflict between archaeological findings to date on one hand and the apparently deep embedding of chicken in many African cultures, as well as the linguistic and ethnographic evidences on the other hand, suggest presence of chicken in Africa at much earlier dates (Williamson, 2000). Hence, it is possible that chicken were present in Africa well before the earliest date yet attested by archaeological findings.

Kenyan indigenous chicken genetic resources and population

Population, distribution and classification of indigenous chicken

The Kenyan chicken population is estimated to be 32 million, with approximately 80 percent being classified indigenous and 20 percent as commercial layers and broilers (KNBS, 2010). Other poultry types such as turkey, duck, pigeon, ostrich, guinea fowl and quail are becoming increasingly important.

The indigenous chickens of Kenya consist of various unimproved, non-selected sub-populations of heterogeneous features such as plumage colour, comb and wattle types, earlobes and body sizes. They are evenly distributed across the country as presented in Table 1, with exception of Nairobi (which is small and mainly urban) and North Eastern (which is majorly an arid area with nomadic lifestyle) provinces. This distribution is attributed to rural human population, environmental conditions and availability of feed resources. Most of farmers in these regions practice crop production which is the major feed source for the indigenous chicken. Okeno, Kahi and Peters (2012) observed that the number of indigenous chicken per household were high in crop production regions, but declined gradually from high agricultural potential regions to semi-arid and further in arid regions.

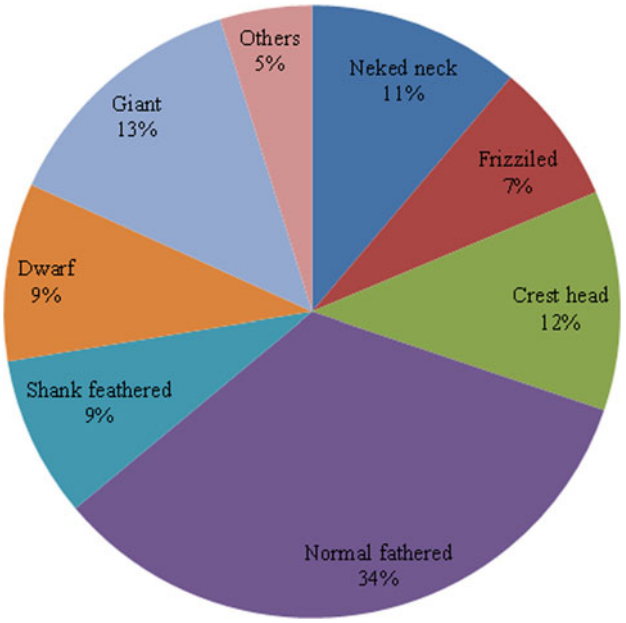

Figure 1. Population structure and distribution of different Kenyan indigenous chicken genotypes. Source: Okeno et al., 2011.

The Kenyan indigenous chicken as in most other developing countries in the tropics have not yet been classified to breeds, but commonly named according to regions of placements or ecotypes or phenotypic expression of major genes. For instance different ecotypes such as Bondo, Bomet and Narok, Kakamega, West Pokot, Lamu and Taita-Taveta have been studied and named based on the regions where they are found in Kenya (Okeno, Kahi and Peters, 2012). On the other hand the Kenyan indigenous chicken have been grouped as naked-neck, frizzled-feathered, shanked feathered, normal-feathered, dwarf, giant, rumples and crested head (Magothe, Muhuyi and Kahi, 2010; Okeno, Kahi and Peters, 2012) based on their phenotypic expression of major genes. The relationship between phenotypes and genotypes in chicken is well known as these phenotypes are a result of genes with major effects (Falconer, 1989). Although the exact population of both genotypes and ecotypes for the Kenyan indigenous chicken are not well documented, the study by Okeno, Kahi and Peters (2011) could give an insight on the population structure for different genotypes and ecotypes. In that study, the populations of different indigenous chicken genotypes were sampled from six counties (Kakamega, Bondo, Bomet, Turkana, Narok and West Pokot) in different climatic conditions. In the pooled data, they demonstrated the population structure for different genotypes within the farmers' households as presented in Figure 1.They also demonstrated that although the population is dominated by normal-feathered birds, the other genotypes are well represented in all the counties.

The genetic diversity of the Kenyan indigenous chicken could have been as a result of their dispersal from putative centres of domestication to different regions with diverse environmental conditions and people of different cultural orientations (Mwacharo *et al.*, 2013). Other factors that may have played a role in the genetic differentiation include founder effects, natural and human selection, mutation and genetic drift (Dana, 2011). Although, both genetic, nutritional and disease resistance studies have been carried out on different genotypes (Magothe, Muhuyi and Kahi, 2010) and ecotypes (Kaingu *et al.*, 2010; Kingori, Wachira and Tuitoek, 2010; Ngeno *et al.*, 2013) of indigenous chicken and further studies are still ongoing under Indigenous Chicken Improvement Program (InCIP – http://incip.org/) under Kenyan conditions, their classification have not been published in the Domestic Animal Diversity Information System (DAD_IS) website (http://dad.fao.org/) except Naked-neck and frizzled-feathered.

Adaptation characteristics of different ecotype and genotypes of indigenous chicken

The indigenous chicken have a number of adaptive traits and genes such as naked-necks and frizzle feathers, black bones and meat, which have special utility in the hot and humid tropics (Horst, 1989). In Kenya for instance, the naked-neck, frizzle, dwarf and rump-less genotypes are mostly found in Western and Coastal regions which are characterized by warm and humid climatic conditions and Eastern and Northern parts which are hot and dry (Olwande *et al.*, 2010; Okeno, Kahi and Peters, 2012). This could be explained by the fact that these genotypes are known to be tolerant to high ambient temperatures and other environmental stresses associated with such areas (Horst, 1988). In high altitude areas such as Mount Kenya and the highlands East and West of Rift Valley, which are characterized by cool and wet climatic conditions, normal-feathered, crested head, feathered shank and bearded genotypes are predominant (Njega, 2005). This could be explained by the fact that these genotypes have well-covered bodies with feathers which insulate and protect them against body heat loss. There is, however, ample evidence that some of these genotypes in most of these regions are endangered and on the verge of becoming extinct (Maina, 2000).

The expression of the genotypes in specific zones shows that there are a number of genes with major effects on the phenotype that seem to be of special interest for chicken keeping in smallholder systems (FAO, 2010). These adaptive genes can be split into three categories; feather-reducing genes, genes that reduce body size and genes that control plumage colour (FAO, 2010).The feathered chickens/genotypes are predominant in cold climates, their body is well covered with feathers and this helps in insulation and protection against losing body heat. On the contrary, warm and hot climate is dominated by naked-necks or frizzle feathers a feature that allows better heat dissipation from the skin. The naked-neck genotype is characterized by featherless skin on the neck, on the breast and on ventral part of the thigh. This expression is caused by an incomplete dominant gene termed Na (Mérat, 1986). The homozygous dominant Na/Na chickens have no feathers on 30–40 percent of the body surface and the heterozygote Na/na chickens have no feather cover on 20–30 percent of the body surface. Moreover, the heterozygotes have a tuft of several dozen feathers on the front of the neck (Crawford, 1976). The frizzled genotype is caused by a single incomplete dominant gene F. In homozygotes, the shafts of all feathers are extremely recurved (i.e. fletched arrow feathers) and the barbs are curled. In the heterozygote, only the contour feathers are recurved. These birds are not able to fly, and the feathers are easily broken off by crowding. The homozygotes, in particular, may look bare. There are modifying genes that make the extent of curling less extreme (Hutt, 1949).

Genotypes possessing the naked-neck and frizzle genes, either singly or in combination are associated with increased growth rates, superior body weights, better feed conversion, higher egg production and disease tolerance in tropical environments (Islam and Nishibori, 2009; Magothe, Muhuyi and Kahi, 2010). These genotypes and *Kuchi* genotype (found in the coastal region of Kenya and Tanzania (Msoffe *et al.*, 2002) would be ideal for meat production in warm and humid areas. The *Kuchi* genotype has game chicken characteristics and would thus be better able to evade or fight off predators (Magothe *et al.*, 2012). The dwarf genotype has better feed efficiency and mass egg production. They have a lower feed intake due to reduced body size and produce more eggs and could thus be utilized for cross-breeding purposes thus employing mating as a breeding tool.

Maina (2000) characterized indigenous chicken based on morphology and feather colours, and reported wide variations in these features. They reported the crested genotype to be more distinct than others while the naked-neck and feathered shank were more genetically close to one another. There exists many morphological clades of indigenous chicken (Okeno, Kahi and Peters, 2012) and evidenced adaptive, biological, reproductive and production traits variations (Kingori, Wachira and Tuitoek, 2010). Despite these observed variations, molecular characterization using 30 microsatellite markers, concluded that the Kenyan indigenous chicken can be grouped into four genetic clades; Coastal, Central, Western and Northern Kenya groups (Figure 2) (Mwacharo *et al.*, 2007). Recent studies by the same authors using 30 autosomal microsatellite markers on genomic DNA revealed two major gene pools/groups. They included Eastern (Kilifi, Taita-Taveta, Muranga, Kitui, Meru, Marsabit) and Western (Kisii, Nandi, HomaBay, Kakamega) Kenya (Mwacharo *et al.*, 2013).This study also revealed population admixture between the two gene pools (Figure 3) with east to west genetic cline of gene pool two. In tandem to that study, Ngeno *et al.* (in press), while studying genetic diversity and MHC region variability in indigenous chicken in

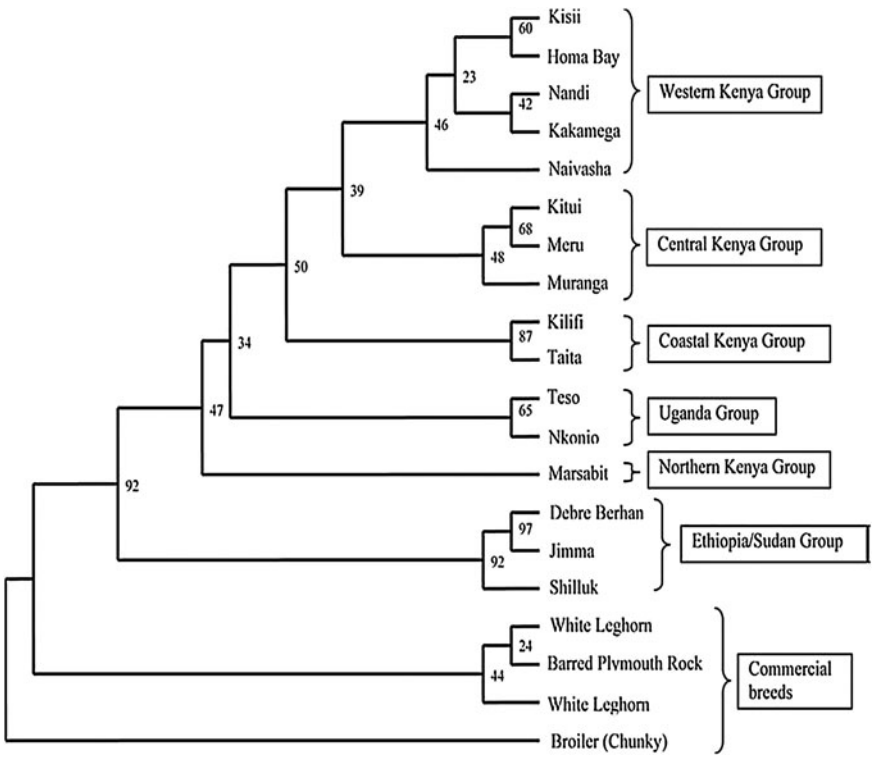

Figure 2. Dendrogram showing phylogenetic relationships within and between Kenyan and other indigenous chicken sampled from Ethiopia, Uganda and Sudan. The numbers at each interior node is the bootstrap value from 1000 re-samplings of loci with replacement (Mwacharo et al., 2007).

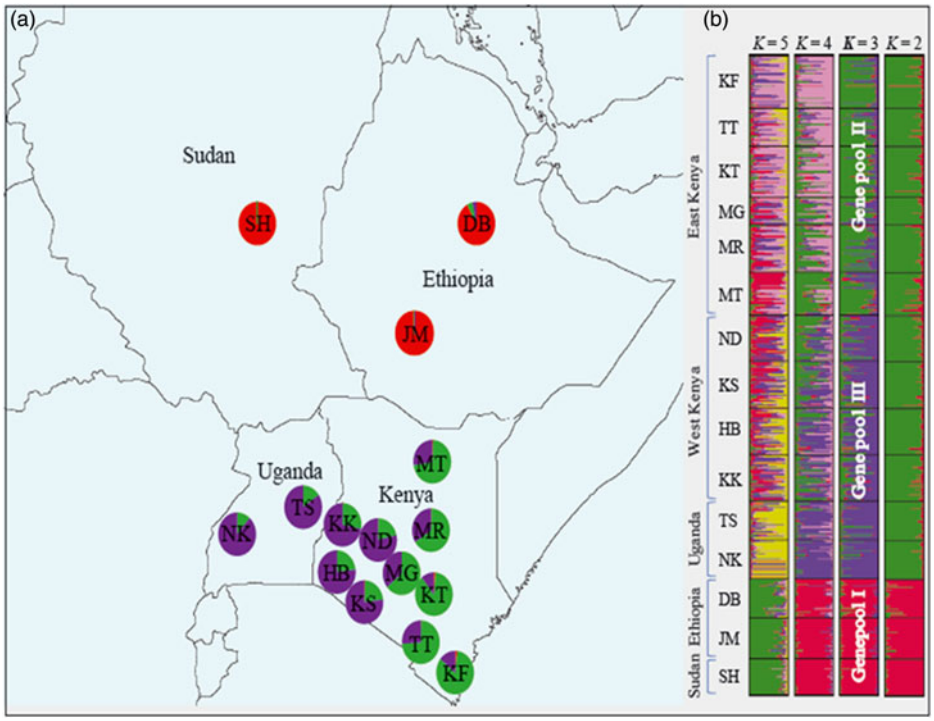

Figure 3. (a) Geographic distribution of village chickens. The shaded area in each pie is proportional to the number of individuals in each population observed for each gene pool. (Population abbreviations: East of Kenya: KF, Kilifi; TT, Taita; KT, Kitui; MG, Muranga; MR, Meru; MT, Marsabit; West of Kenya: KS, Kisii; ND, Nandi; HB, Homa Bay; KK, Kakamega; Ethiopia: DB, DebreBerhan; JM, Jimma; Sudan: SH, Shilluk; Uganda: TS, Teso; NK, Nkonjo). Colour codes: Red, Gene pool I; Green, Gene pool II: Purple, Gene pool III. (b) Bayesian analysis of population structure of East African village chickens. Individuals (represented by single vertical lines) are assigned to three distinct gene pools based on clustering result at K = 3. Color codes: Red, Gene pool I; Green, Gene pool II; Purple, Gene pool III. (Mwacharo et al., 2013).

Kenya, reported that the indigenous chicken host 46 polymorphic MHC marker LEI0258 alleles. The Cluster analysis in that study indicated a clear ecotype subdivision into two to three genetically distinct groups. Two main population clusters indicated by ΔK and PCoA are Lamu (one cluster) and populations from Kakamega, West Pokot, Turkana, Bomet, Narok and Siaya as a second cluster. An extra group (third cluster) was from Taita-Taveta. It is worth noting that although the two studies reported equal gene pool numbers, the sampling sites were different. Ngeno *et al.* (in press) sampled from localities that were never reached by the cockerels exchange programme (Wainaina 1994). Besides, Mwacharo *et al.* (2013) did not sample from Lamu a distinct cluster realized in Ngeno's study.

Contributions of indigenous chicken to rural households

Village chickens make substantial contributions to household food security throughout the developing world. Indigenous chicken serves as an investment and source of security for households in addition to their use as sources of meat and eggs for consumption and of income (Muchadeyi *et al.*, 2007a, 2007b). Indigenous chicken are alternative source of animal protein due to the fact that they can be slaughtered and consumed as a single meal hence do not require storage facilities. Their demand is ever increasing and thus marketing is easy thus providing source of income to resource-poor rural families (Bett *et al.*, 2012a, 2012b). They are also a means of investment in low-input farming systems in the tropics (Dana, Van der Waaij and Van Arendok, 2011; Okeno, Kahi and Peters, 2012). Besides rural households, these low-input, low-output poultry-husbandry systems are an integral component of the livelihoods of most of peri-urban, and some urban households in most parts of the developing world (Magothe *et al.*, 2012). A review by Guèye (2000) indicated that an average family flock of five adult chickens (two males and three females) enabled women in Central Tanzania to generate an additional income equivalent to 10 percent of the average annual income. In the Niger Delta, family poultry husbandry contributes 35 percent of the income of household women, which represents about 25 percent of Nigerian minimum wage and 50 percent of the per capita income. Experiences in many other developing countries have shown that village poultry can be used as an effective means of empowering women and as a tool for poverty alleviation (Kitalyi, 1998). Besides economic considerations, the chickens are useful in a number of social, cultural and spiritual activities such as entertainments, gifts, funeral rights and spiritual cleansing (Njega, 2005). In some parts of the country, cock fighting is an exciting and popular entertainment for rural folk (Maina, 2000; Okeno, Kahi and Peters, 2011).Other uses include disposal of kitchen leftovers, manure production, being biological clocks for telling time of day especially in rural areas and a means of controlling insect.

Conservation and utilization of indigenous chicken in Kenya

Having recognized the enormous roles played by indigenous chicken to the resource-poor rural households, the Kenya Government through National Poultry Development Programme (NPDP);initiated InCIP in 1974 (Wainaina, 1994; Magothe *et al.*, 2012). The aim of the project was to increase the smallholder farmers' income and protein intake through commercialization of indigenous chicken production. The program was implemented by importation of exotic breeds such as Rhode Island Red, White Leghorn, Black Australop and Light Sussex which were to be crossed with indigenous chicken. The idea was that famers were to be supplied with exotic pullets and cockerels in exchange for indigenous chicken cocks. The program was also supported by management practices such as massive vaccination of indigenous chicken for Newcastle disease and training of farmers and field officers on management of the improved stock. Although, the resultant genotypes had improved productivity, the program was terminated in 1993 as the subsequent crosses were not adapted to the harsh environmental conditions among other reasons (Magothe *et al.*, 2012). This unplanned and poorly organized cross-breeding strategy was also a danger to indigenous chicken genetic diversity and conservation.

Having learnt from mistakes done under NPDP (Magothe *et al.*, 2012), the Kenya Government and World Bank initiated a second improvement program in 2006.This was introduced under the umbrella InCIP (http://incip.org/) which was a collaborative project between the Ministry of Livestock Development, Egerton University, and Kenya Agricultural Research Institute. The main objective of this program was to undertake comprehensive analysis of indigenous chicken actors for the purpose of understanding the sub-sector and build human capacity in different fields in sub-sector. Such undertaking was found to be critical as it would provide insight in to the existing situations in terms of strengths, weaknesses, dynamics and complexities, which are important in formulating solutions. Currently the indigenous chicken actors in Kenya has been analysed (Bett *et al.*, 2012a, 2012b), the indigenous chicken sub-sector characterized, breeding objectives and management strategies defined and within indigenous chicken genotype and ecotype selection programme initiated (Ngeno, 2011; Magothe *et al.*, 2012; Okeno, Kahi and Peters, 2013).The InCIP programme activities are presently, mainly funded by European Union through African Union and have expanded its activities to other African countries such as Malawi in collaboration with Lilongwe University of Agriculture and Natural Resources. In Malawi the main aim of InCIP is to establishing local breeding programme for improvement and conservation of Malawian indigenous chicken which are also under threat due to indiscriminate cross-breeding with Black Australorp breed (Safalaoh, 2001). Previously, the

Malawi Government introduced the Smallholder Poultry Improvement Programme (SPIP) in the 1950s with the objective to increase egg and meat production of indigenous chicken through cross-breeding with the Black Australorp (Safalaoh, 2001). Although the project has been running for more than 50 years, very few studies have been conducted to evaluate cross-breeding as a strategy to improve productivity of the indigenous chickens. The same scenario was realized in Kenyan case with no performance record taken to assess the magnitude, benefit and extend of genetic dilution of the indigenous chicken.

In 2012, the Kenyan Government and stakeholders in the poultry sector formulated Poultry Development Bill 2012 (http://www.parliament.go.ke/plone/archive/archive-10th *Parliament/bills*). This bill has a lot of input emanating from InCIP activities and findings. Some of the key issues the bill addresses include characterization, conservation and development of indigenous poultry breeds, feed resources and disease control, marketing and capacity building. When passed to law the bill will regulate indiscriminate cross-breeding and replacement of indigenous chicken with exotic which is not only a threat to genetic diversity, but could also lead to extinction of some of the uniquely adapted indigenous chicken genotypes and ecotypes.

Utilization of cross-breeding programme has been practiced and benefit noted (Safalaoh, 2001). However for its ultimate success a clear strategy has to be adhered to. Amongst them, is training of farmers on proper guidelines on how to conduct the cross-breeding. For instance because the exotic hens do not sit on their eggs, the farmers should be encouraged to buy exotic cocks which can then be crossed with local hens (Okeno, Kahi and Peters, 2013). Where local cocks are crossed with exotic hens, the fertilized eggs from the exotic hens should be placed under local brooding hens for natural incubation. Alternatively, the eggs can be placed, in artificial incubators if the facility is presented. Rather than leaving the task of cross-breeding to the farmers, InCIP could be encouraged to carry out the cross-breeding themselves so that the farmers are actually sold the cross-breeds as a terminal product. This would require identification and selection of the local breeds with the best performance in terms of desired traits (Okeno, Kahi and Peters, 2013). The cross-breeds could combine the characteristics of improved productivity from the exotic breeds and adaptability and stress tolerance to the local harsh conditions from the local chicken and should be able to survive in the prevailing harsh village conditions better than the exotic breeds.

Past attempts to genetically improve indigenous chickens of Kenya

The demand and popularity of indigenous chicken genetic resources has been increasing since time immemorial (Okeno, Kahi and Peters, 2012).Market trends in Kenya, see consumers shifting interest from the dominant hybrid layer eggs and broiler meat towards what is conceived as a healthier diet of free-range or indigenous eggs/chicken. According to Magothe *et al.* (2012), from 1984 to 2004, indigenous chicken population increased by more than 75 percent and their egg and meat products increased by more than 34 and 79 percent, respectively. The observed increase was attributed to an increase in the human population and hence a corresponding demand for indigenous chicken products. In recent study to assess the demand and price dynamics of indigenous chicken products in Kenya (Bett, Peters and Bokelman, 2011), there is evidence of escalating indigenous chicken products prices and the consumers' willingness to pay more as compared with other poultry products . The observed increase in demand of indigenous chicken products by consumers has caused farmers, Research Institute, Universities, Government and Non-governmental organizations, to engage in attempts to improve their productivity. For instance, since 2006 in the forefront is the Smallholder InCIP at Egerton University that has established breeding and multiplication centre and initiated a number of activities to improve the indigenous performance (www.incip.org).

Previously, poor quality and inadequate feed resources, health care, marketing, housing and lack of breeding stock have been identified as constraints towards improved performance of indigenous chicken in developing countries (Gondwe and Wollony, 2007; Kingori, Wachira and Tuitoek, 2010; Okeno, Kahi and Peters, 2011). To address nutritional constraints in Kenya, attempts have focused on models to supplement feeding at different times and stages of growth and production, determining protein and energy requirement levels (Chemjor, 1998; Kingori, Wachira and Tuitoek, 2010). Although, these interventions increased productivity under on-station (Kingori, Wachira and Tuitoek, 2010), their adoption and sustainability under on-farm conditions was low due to high unavailability of feed resources, high cost of formulated feeds and low genetic potential of indigenous chicken for growth and egg production.

The past genetic improvement programmes for increasing chicken productivity in developing countries mainly focused on use of imported temperate breeds (Dana, Van der Waaij and Van Arendok, 2011). Many exotic breeds of chicken (White and brown Leghorns, Rhode Island Red, New Hampshire, Cornish, Australorp, Light Sussex etc.) were introduced over the years. The other approach to improve productivity of the village poultry production was based on use of cross-bred animals. This involved crossing of unselected local chicken to different levels of exotic blood. In Ethiopia for instance, evaluations of cross-bred chicken at the DebreZeit Agricultural Research Centre indicated that 62.5 percent white leghorn crosses showed superior performance to the locals as well as pure white leghorns in terms of egg production (DZARC, 1991, 2007). In a cross-breeding programme at Assela, Brannang and Persson (1990) also compared

different York × local crosses. Their results indicated that egg production declined with increasing level of exotic inheritance (above 50 percent). Increasing the level of exotic blood also resulted in loss of broody behaviour, a trait of considerable economic value under village systems. Although the cross-breeding programmes produced successful results under experiment stations almost all of them were discontinued decades ago for various reasons (Dana, 2011).

In the 1970s and 1980s the Ministry of Agriculture in Kenya and Ethiopia, respectively, initiated a cockerel distribution scheme. This involved importation and distribution of cockerels to be used as breeding males in villages. In Ethiopia, the scheme failed because farmers were unwilling to remove their local cocks and the exotic cocks failed to adapt in the village environments (Dana, Van der Waaij and Van Arendok, 2011).

In Kenya, the genetic improvement was started through a cross-breeding scheme by the National Poultry Development Programme (NPDP); unlike Ethiopia, the programme utilized crossing between cockerels and pullets of exotic breeds with the local indigenous chicken. The initiative termed cockerel exchange programme started in 1976 initially in 12 districts and by 1980 another additional 9 districts were included. Later more districts were recruited into the programme and by 1993, 26 out of 54 districts were involved in the programme (FAO, 2007a, 2007b). A hybrid cock was exchanged for the local cock and then all the local cocks were killed. For the pullet exchange, a farmer was required to keep 10–15 pullets. Farmers' training on poultry management and vaccination for disease control was also undertaken as components. The programme witnessed improved performance in the crossbreds but declined with subsequent generations (Okeno, Kahi and Peters, 2012). Failure of the programme to meet stakeholders' expectation led to its termination in 1994 (FAO, 2007a, 2007b). The factors attributed to its failure included poor planning and understanding of the indigenous chicken sub-sector with respect to production environment, needs of actors (i.e. farmers, marketers and consumers), lack of clear breeding objectives and lack of sustainable breeding programme to supply constant pure-line breeding stock (Ndegwa *et al.*, 2012).

Current genetic improvement of Indigenous chicken in Kenya

Since 2006 another collaborative programme called the Smallholder InCIP was initiated with the view of holistic and comprehensive approach to analysing the entire indigenous chicken production actors and avert the causes of previous failures. The InCIP mandate is to characterize the indigenous chicken production system, develop clear breeding objectives accounting for all players in the sectors, design appropriate selection and mating schemes for modern dissemination of superior genetic resources. It is therefore true that InCIP has in mind the fundamental questions common to a breeder namely; "which are the best indigenous chicken among and between the populations and how can they be genetically improved?"

In addressing these questions, InCIP initiated basic but prudent methodologies. First, eggs and live birds were collected from various Agro-ecological regions or ecotypes namely; Kakamega, Bondo, Narok, West Pokot, Bomet, Taita-Taveta, Lamu, Egerton and Mwingi. These ecotypes are currently on-station at Egerton University Poultry Research and Breeding (PRB) facility for multiplication, performance recording and selection. It is upon the performance records that selection and mating are based. In line with the project objectives several studies have been conducted and findings disseminated. Ngeno (2011) reported variations on body weights among the ecotypes, and further estimated heritabilities and genetic correlations. A similar study by Magothe, Muhuyi and Kahi (2010) showed that the naked-neck, frizzle and crested-head genotypes do influence body weights and growth patterns. Magothe, Muhuyi and Kahi (2010) noted that the crested-head genotype had a slower growth rate and were lighter compared with the normal-feather genotype when subjected to the same level of management. Growth rate and egg production being inversely correlated, the authors speculated that the crested-head genotype could be a superior egg producer. This hypothesis is currently being tested on-station at Egerton University. Several studies done outside Kenya on general or morphological characterization, production and reproduction performances of available indigenous chicken genotypes did not vary from Kenyan situation (Okeno, Kahi and Peters, 2010).

In determining where to go, a study by Okeno, Kahi and Peters (2011) determined the selection criteria by farmers and traits of economic importance preferred by the farmers. In that study, the authors reported that farmers prefer selection based on growth rate, large body size, high egg production, hatchability and good mothering ability. They also indicated that normal feathered, crest-head, necked-neck and giant (i.e. big body size) genotypes were the most predominant genotypes (Figure 1). To define breeding objectives among farmers, marketers and consumers, the study identified egg number, growth rate, body size, fertility, disease resistance, meat quality, egg size, egg shell colour, broodiness and mothering ability to be traits of economic importance (Okeno, Kahi and Peters, 2012). However, all these traits cannot be included in the breeding objectives and some are negatively correlated, this therefore calls for critical decisions to be made on which trait to account for in the breeding objective. In a simulation study Okeno, Kahi and Peters (2013) demonstrated that improving IC for growth and therefore meat production would result to better genetic gains and economic returns. Based on this finding the selection for indigenous chicken at the PRB has been focused on growth.

Future genetic improvement strategies

The future genetic improvement practices will be done at PRB, Egerton University and are based on the previous findings of Okeno, Kahi and Peters (2013) and principles of genetic improvement of livestock. The InCIP noble course is anchored on Millennium Development Goals (UNDP, 2013) through Kenya Vision 2030 (www.vision2030.go.ke) for eradication of extreme poverty and hunger and improved food security in Kenya respectively. In plan are a plethora of integrated quantitative and molecular research projects to be formulated and implemented. To improve disease resistance, InCIP intends to first determine genetic variation among the indigenous chicken ecotypes and genotypes using both innate (natural antibodies, compliment) and adaptive immunity (interleukins, specific antibodies after vaccine challenge).If variation exists, the birds will be divergently selected for low and high immune response for subsequent generations. Individual performance will be recorded and pedigree data established. This will assist in estimating genetic parameters. Breeding for enhanced immunity is sustainable (Parmentier *et al.*, 2004; Okeno, Kahi and Peters, 2010), will save the farmer their money for antimicrobial drugs and eradicate the consumers' food safety concerns. Such study will give insight in the biological mechanism of immunity for genetic control of a plethora of ever increasing pathogens of birds and compliment vaccination strategy as a disease prevention measure (Parmentier *et al.*, 2004; Khobondo, 2012). Following Okeno, Kahi and Peters (2012), recommendation based on traits preferred by farmers, there is already on-station selection for improved production and reproduction traits for subsequent estimation of genetic parameters and variance components for the economically important traits. Such selection programmes will cause change in input requirements, e.g. feed intake for maintenance and production requirements of the birds. Since feed costs account for over 70 percent of the cost of production (Kingori, Wachira and Tuitoek, 2010), InCIP considers avenues to reduce costs of production besides increasing revenues. This makes feed efficiency (a measure of how much saleable product is produced for each unit of feed consumed and can be expressed as either gross feed efficiency or net feed efficiency) a trait of economic importance that should be included in breeding objective alongside production traits due to its direct influence on production costs. The aim of incorporating feed efficiency study is to carry out an analysis of net feed efficiency within the indigenous chicken flock in Kenya. In the proposed study, variance components, genetic and phenotypic parameters for net feed efficiency traits and growth characteristics will be estimated and the genetic and phenotypic parameters obtained. The results from this study will provide information required for breeding programmes aimed at improving efficiency in the production of indigenous chicken.

To achieve these goals InCIP team will employ basic breeding tools of mating and selection on-station. Pure-line ecotypes will be selected generation after generation based on economic traits (Okeno, Kahi and Peters, 2012) at nucleus tier, multiplied at the second tier for ultimate cross-breeding/mating at the commercial tier. The resulting hybrid will then be sold to farmers. It is with no doubt there are morphological and production variations amongst the different ecotypes and genotypes (Magothe, Muhuyi and Kahi, 2010; Ngeno, 2011), this calls for molecular characterization using microsatellite and single nucleotide polymorphism (SNPs) to decipher the witnessed differences.

InCIP will employ the safest conservation method by continuous breeding involving sufficient numbers of birds to avoid inbreeding and genetic drift (FAO, 2007a, 2007b). InCIP propose to train farmers to optimally utilize the indigenous chicken that match with their environment and production system. For instance, in hot and cold ecozones/regions, InCIP will advocate for rearing of adaptive genotypes that best suits the environment. Where management is enhanced, with high input availability, high producing meat and egg pure lines will be encouraged. This may be complimented with cross-breeding with exotic breeds. In addition, InCIP plans to use cryoconservation method. Cryoconservation of avian sperms, ova and embryo has been successful in France (Blesbois, 2007; Blesbois *et al.*, 2008). For traits with low heritability, InCIP will employ genome wide association studies to build a consensus prediction formula for genomic breeding value estimation in the nucleus scheme. This will lower generational interval and could be economical in long run.

Conclusions

There have been several attempts to improve indigenous chicken production and address constraints in their production in Kenya. These attempts had minimal success due to, among others, lack of a holistic approach in solving the constraints and dissemination of inappropriate technologies given the production circumstances and market dynamics. This review has highlighted the various past attempts, discussed current improvement strategies and suggested possible future directions to improve the indigenous chicken productivity which could improve the livelihood of the rural households in line with Kenya vision 2030. Current studies have suggested potential for improvement of indigenous chicken production in Kenya given the available genetic and physical resources and have recommended a holistic approach/strategy that increases productivity. Future research entails modern studies that will improve traits of economic importance using quantitative genetics and genomics. Besides, the current improvement programme entails conservation strategies and cross-breeding principles.

Acknowledgement

We acknowledge the Indigenous Chicken Improvement Programme for the provision of facilities. The programme is funded by the European Union through the African Union.

Statement of interest

No conflict of interest.

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Edited by K. Kume West Print Published in 2013, pp. 71

doi:10.1017/S207863361400040X

The booklet results from a project on the evaluation of the current status of Busha cattle with the purpose to provide information for developing a regional breeding programme. The project was supported by the European Regional Focal Point for Animal Genetic Resources (ERFP). Busha cattle exists in the Balkans since Neolithic times and it is said to be well adapted to harsh environmental conditions. Nowadays the population is highly fragmented into small strains scattered throughout the various Balkan countries. Fragmentation is one of the reasons why the breed is in high danger of extinction. The main part of the book describes the current status of the populations in Albania, Bosnia and Herzegovina, Croatia, Greece, Kosovo, Macedonia, Montenegro and Serbia provided by several authors. Some authors include in their description of the situation a subchapter on the farmers' view on this old breed revealing a growing interest in the breed especially in relation with agro-tourism and organic production. Countries policies and institutional capacity as well as the need for developing a regional conservation programme are discussed. A brief chapter deals with the ERFP project and its outputs.

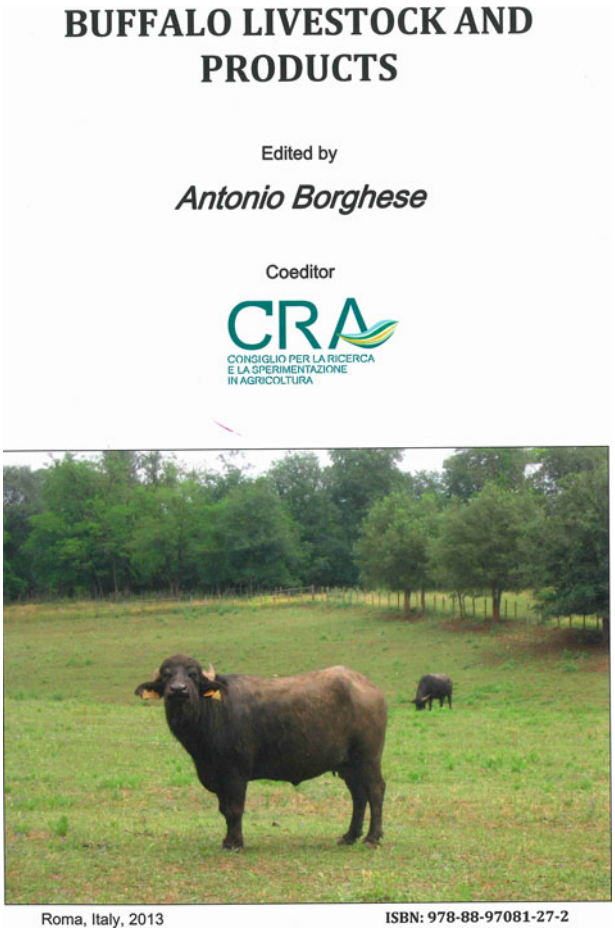
Recent Publication

Buffalo livestock and products

Edited by A. Borghese CRA – Council for Research in Agriculture Published in 2013, pp. 511.
ISBN 978-88-97081-27-2
Similar version available at http://umvp.kormany.hu/download/3/40/60000/BUFFALO%20LIVESTOCK%20AND%20PRODUCTS.pdf

doi:10.1017/S2078633614000411

This book provides a comprehensive update of the book "Buffalo Production and Research" published in 2005. Several senior researchers devoted to the development and promotion of buffalos contributed to it. The editor dedicates it to the presidents and members of the International Buffalo Federation, who organized every three years the World Buffalo Congresses from his foundation in Egypt on 1985 onwards. Four chapters offer a good overview on buffalo populations almost all over the world, their management and products and recent technological developments including suggestions for their use for a sustainable management of buffalos. The last chapter describes international organisations dealing with management and development of buffalos and provides the interested reader with names and even contact addresses.



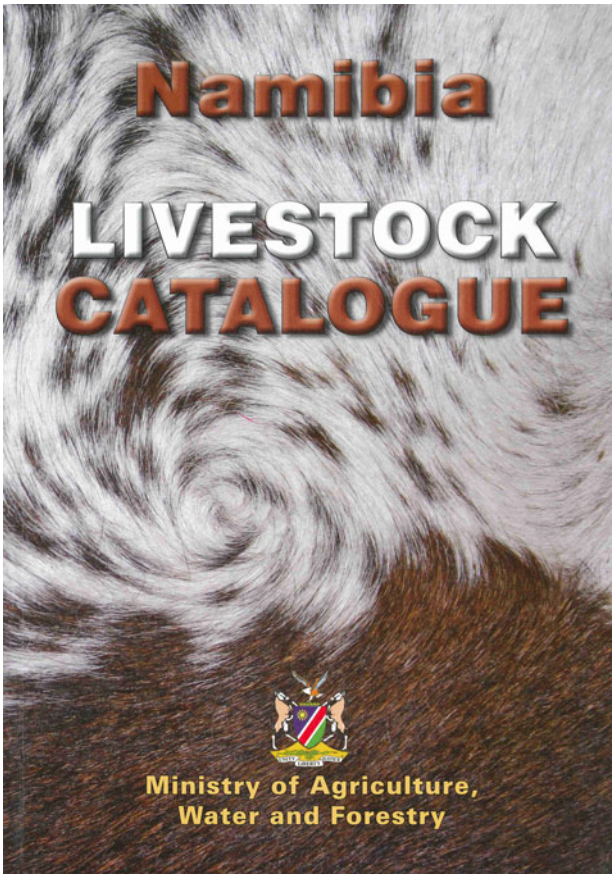
Animal Genetic Resources, 2014, 55, 141.

Recent Publication

Namibia. Livestock catalogue

Ministry of Agriculture, Water and Forest. Windhoek, Namibia.
Published in 2013, pp. 176.
ISBN 978-99945-0-067-3

doi:10.1017/S2078633614000423



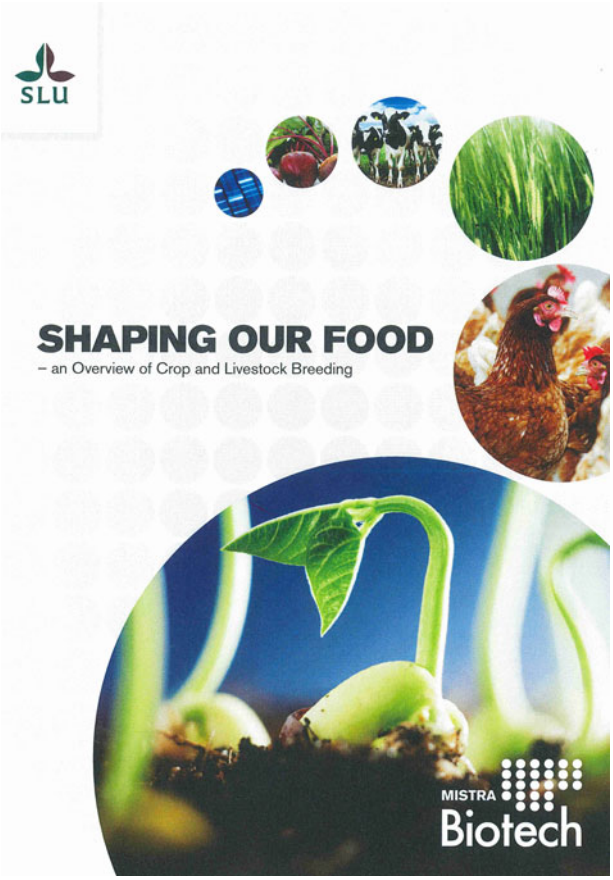
Namibia, being rated as having the driest climate in sub-Saharan Africa, is predominantly a livestock farming country. Livestock production accounts for 70% of the total agricultural output. Namibian farmers keep various livestock species and within these there is a wide range of well-adapted breeds and ecotypes, some of them of economic importance, but relatively unknown. Against this background the Ministry of Agriculture, Water and Forestry has launched the Namibia Livestock Catalogue to inform farmers about the different livestock breeds in Namibia, their origins, characteristics and their adaptability. The catalogue is a synopsis of breeds found in Namibia, and can be used as a guideline in livestock production. It is intended to inform and educate about the production and the adaptability of such breeds in the Namibian environment. The catalogue is supposed to assist aspiring livestock farmers to make informed decisions when selecting livestock breeds. Breeds belonging to the following species are presented: cattle, horses, donkeys, sheep, goats, pigs and poultry. For each breed three sections are provided on origin, characteristics and some strategic information. The later yields information such as on the breed type, frame size, occurrence in Namibia, puberty and performance related to beef or dairy traits, allowing the farmers to choose the right breed. The breed descriptions are accompanied by high quality photographs.

Recent Publications

Shaping our food – an overview of crop and livestock breeding

Edited by A. Lehrman Swedish University of Agricultural Sciences (SLU), Uppsala, Sweden Published in 2014, pp. 176
ISBN 978-91-637-5757-0
Available at http://tr.anpdm.com/track?t=c&mid=11856281&uid=603295709&&&http%3A%2F%2Fwww.slu.se%2Fshapingourfood%2Fen

doi:10.1017/S2078633614000435



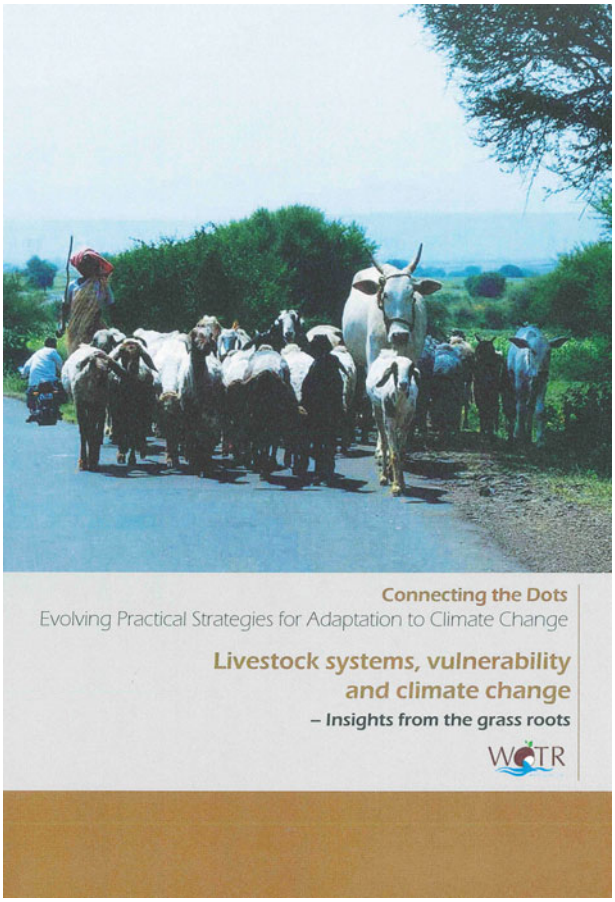
Although the breeding of plants and livestock have shaped more or less everything we eat, few people know about the scientific achievements and the tedious work that results in the food we see on our plates every day. With this book the authors wish to give an overview of the background of domestication and breeding, from the beginning of farming more than 10,000 years ago to the molecular work of today. They present the basics of the structures and functions of genes, describe why and how different breeding methods are applied to crops and livestock, and give some insight into legislation surrounding the use of biotechnology in breeding in the EU and in Sweden. Further an overview of different products produced through genetic modification, a summary of the economic impact of such crops, and some ethical issues related to breeding in general and to genetic modification in particular are provided.

Recent Publication

Livestock systems, vulnerability and climate change – Insights from the grass roots

K. Bhavana Rao and Ramkumar Bendapudi Watershed Organisation Trust. Published in 2013, pp. 20.
ISBN 978-81-86748-37-4 Available at http://wotr.org/system/files/Position_Papers/WOTR-Livestock%20Position%20Paper.pdf

doi:10.1017/S2078633614000447



Climate change is already happening, and its effects, especially on rural communities in India, are particularly adverse. There is a need to highlight key issues and understand the practical challenges that must be addressed, if India is to build the capacities of its rural communities to robustly adapt to climate change and realize the National and State Action Plans on Climate Change. Since the last four years, the Watershed Organisation Trust (WOTR) has been implementing a large-scale integrated project on climate change adaptation in rural Maharashtra, Andhra Pradesh, and Madhya Pradesh, in collaboration with several partners. This project has catalyzed insights, lessons, and experiences from multiple stakeholders which are presented in several position papers. The paper 'Livestock systems, vulnerability, and climate change – Insights from the grass roots' attempts to explore indications of vulnerability at the grass roots. It attempts to see the impact of the logic of using crossbreeding and sedenterisation as a means of poverty alleviation/higher economic returns for livestock keepers and the rural poor. The booklet addresses the following questions: Have the poor really benefitted economically or is their vulnerability even increased, especially in the context of climate change? The paper urges the need to clear certain areas of prejudice against indigenous cattle, small ruminants, and poultry breeds, and proposes special policy measures for livestock production in dryland regions of India in the context of climate change. Key messages are presented in a clear and easy understandable way.

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CONTENTS

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