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Genetic variability and population structure of Djallonke sheep in Ngaoundere (Adamawa-Cameroon)

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Abstract

The aim of this study is to contribute to a better knowledge of the genetic diversity of the indigenous Djallonke sheep in Ngaoundere (Cameroon). A total of 126 adult sheep (38 males and 88 females) were selected during the period from January to December 2020. Body measurements were taken using a measuring tape, a graduated measuring stick and a graduated ruler. Principal component analysis of 18 quantitative traits of genetic variability showed that the cumulative variances of the first 15 traits provided 98.12% evidence of the genetic variability observed in the study population. The analysis of discriminating factors revealed two genetic types; finally, the phylogenetic tree revealed that genetic type I is close to genetic type II. The present study should be complemented by a molecular characterisation in order to set up strategies for the conservation of local genetic resources of Djallonke sheep in Ngaoundere in particular and the sudano-guinean zone of Cameroon in general, which is their cradle.

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Introduction

With a population growth rate of 3% per year, cattle farming alone cannot meet the meat consumption needs of cameroonian populations, which amount to 46 kg of meat per capita per year (Ngandeu and Ngatchou, 2006). In order to meet the nutritional needs of the population and compensate for this soaring demand, Cameroon's action plan through the national development strategy document (MINEPAT, 2020) envisages developing the breeding of short-cycle species, particularly small ruminants, and ensuring the selection of animal breeds. In Cameroon, sheep are estimated at around 3 million head and have undeniable socio-economic importance (INS, 2015). Sheep rearing, in particular, is an important factor of social integration through the sacrifice of sheep during funeral ceremonies, for an inheritance, marriage dowry and especially for religious sacrifices (Ayantunde, 2008; Guingouain, 2017). The general traditional breeding method of the Djallonke breed favours anarchic crossbreeding and could constitute a real threat to the breed (Djogba *et al.*, 2019). The numbers of these ruminants tend to stabilise, or even decrease due to the reduction of their biotope in the face of growing demographic pressure and uncontrolled crossbreeding (Naves, 2009).

Thus, in view of the probable disappearance of this breed, conservation actions must be implemented. After a recent study on the morpho-biometric characterisation of Djallonke sheep in the outlying areas of Ngaoundere (Maliki *et al.*, 2022), the main objective of the present study is to contribute to a better knowledge of the genetic diversity of the indigenous Djallonke sheep in the peripheral areas of Ngaoundere (Cameroon). Specifically, to study the genetic variability, structuring and relationships between genetic types of the Djallonke sheep population in Ngaoundere.

Material and methods

Study area

A study on the genetic variability of Djallonke sheep in the urban and peri-urban areas of Ngaoundere was carried out from January to December 2020. This locality is located in the Adamawa region of Cameroon, at a northern latitude of 7°15'53.35'' and an eastern longitude of 13°32'53.44'', at an average altitude of 1,200 meters, with an average annual rainfall of 1,700 mm. The average annual temperature of the area is 22°C and the soil is basaltic with a pH of 5.4.

Animal material

Sampling: Depending on their availability, farmers were located using the snowball method. The farms were separated by at least one kilometer to reduce the risk of sampling related animals.

Selection of animals: For this study, 126 adult Djallonke sheep (38 males and 88 females) were selected and were randomly chosen regardless of sex from each of the flocks in the selected farms.

Collection of morpho-biometric data

Information on morpho-biometric traits was collected using a survey form adapted from FAO (2013). Body measurements were taken using a tape measure, a graduated measuring stick and a graduated ruler.

Data analysis

The biometric measurements were subjected to principal component analysis (PCA) in order to assess the cause of genetic variability in the studied Djallonke population. This made it possible to determine the linear relationship that exists between these different characteristics (FAO, 2013). Based on the body measurements, discriminant factor analysis (DFA) was used to identify the genetic types found within the studied population (FAO, 2013) in a bid to validate the purity of this breed. The different statistical analysis was carried out with the aid of the statistical tool SPSS 22.0.

Results

Genetic variability of Djallonke sheep in the peripheral areas of Ngaoundere (Adamawa-Cameroon)

The genetic variability of Djallonke sheep was assessed using principal component analysis of 18 quantitative traits of genetic variability (Table 1). The first 15 traits provide 98.1% evidence of the genetic variability observed in the study population.

Population structure of Djallonke sheep in the outlying areas of Ngaoundéré (Adamawa-Cameroon)

The population structure of Djallonke sheep in the study area was obtained through discriminant factor analysis (Table 2). This analysis revealed two genetic types (Type I and Type II). In general, genetic type I had significantly higher trait values than genetic type II with the exception of croup height which was significantly higher in genetic type II sheep.

Relationships between genetic types of the Djallonke sheep population in the peripheral areas of Ngaoundéré (Adamawa-Cameroon)

The relationship between genetic types was illustrated in Fig. 1. To confirm the population structure, the phylogenetic tree (Fig. 2) revealed that genetic type I is close to genetic type II.

Table 1. Contribution of the 18 principal components to the analysis of the variability observed in the Djallonke sheep.

Principal components (PC)	Measurements	Eigen values	Variance (%)	Cumulative variance (%)
PC1	Head length	10,646	56,032	56,032
PC2	Head width	1,333	7,014	63,046
PC3	Ear length	1,255	6,603	69,649
PC4	Length of horns	0,900	4,737	74,387
PC5	Neck circumference	0,830	4,367	78,753
PC6	Neck length	0,749	3,944	82,698
PC7	Body length	0,601	3,161	85,859
PC8	Height at back	0,530	2,791	88,649
PC9	Height at withers	0,501	2,636	91,286
PC10	Depth of the chest	0,382	2,013	93,298
PC11	Thoracic rim	0,302	1,592	94,890
PC12	Scapulo-ischial length	0,252	1,327	96,217
PC14	Croup height	0,195	1,026	97,243
PC15	Croup length	0,167	0,879	98,122
PC16	Tail length	0,123	0,649	98,771
PC17	Cannon circumference	0,056	0,296	100,000
PC18	Live weight	0,000	0,000	100,000

Discussion

Morphological variability can be considered as a good indicator of genetic variability and adaptive potential of the breed (Toro and Caballero, 2005; Esquivelzeta *et al.*, 2011). Thus, we were given the opportunity to use principal component analysis, discriminant factor analysis and phylogenetic tree to study the genetic variability of Djallonke sheep in the peripheral areas of Ngaoundere.

The genetic variability of Djallonke sheep was assessed using principal component analysis of 18 quantitative traits of genetic variability. The first 15 traits provide 98.1% evidence of the genetic variability observed in the study population. These results corroborate those of Baenyi *et al.* (2018) in the sudano-guinean zone of Cameroon which was 98.6% and Nsangou *et al.* (2022) which was 96.1% who worked on the goudali cattle of Banyo. This would imply that there is genetic variability.

Two genetic types were distinguished during the study through discriminant factor analysis. These results differ from those of Baenyi *et al.* (2018) and Méka *et al.* (2021) who found 3 genetic types in the sudano-guinean zone of Cameroon and Central Africa respectively. This difference would be due to the size of the study area which was relatively smaller in the present study. These results demonstrate a certain phenotypic heterogeneity in the Djallonke sheep population in the outlying areas of Ngaoundere; this would be due to the fact that there is a pronounced gene flow within the population, with anarchic crossing being one of the plausible reasons.

Table 2. Characteristics of the two genetic types in Djallonke sheep in the peripheral areas of Ngaoundere (Adamawa-Cameroon).

	TL	HB	TC	CH	BL	LW	HW	HL	DC	SIL	NL
Type I	28,32	53,02	64,82	60,37	44,49	24,94	59,24	21,74	29,41	50,08	27,59
Type II	27,55	52,74	64,71	64,71	44,04	24,86	59,16	21,64	30,26	50,29	27,36

TL: tail length; HB: height at back; TC: thoracic circumference; CH: CH: croup height; BL: body length; LW: live.

The dendrogram shows that the population is made up of two subgroups that seem to have a very large number of alleles in common and could have a common origin; this corroborates the studies of Dossa *et al.* (2007) in Benin who demonstrated that two goat ecotypes from the same agro-ecological zone are closely related, which probably explains why they have a common parental origin. In addition, the Djallonke breeds are practically the only breeds that adapt best in the sudano-guinean zone of which the study area is part.

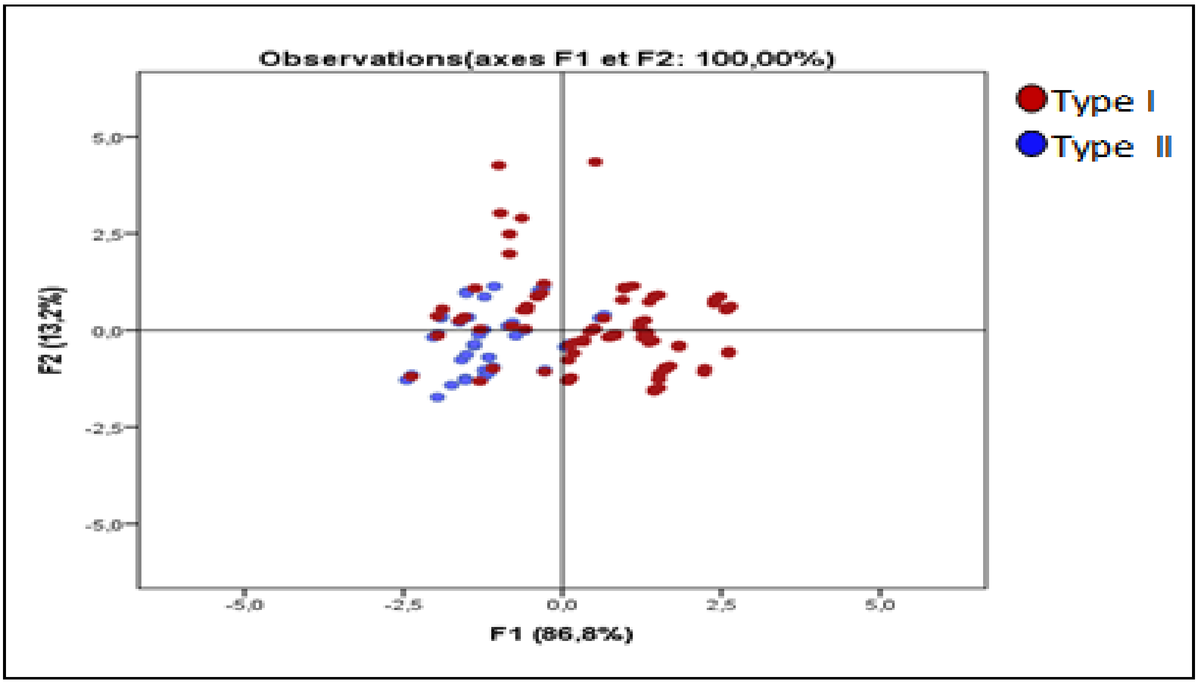

Fig. 1. Relationship between genetic type I and type II.

Conclusion

Finally, the trait measurements allowed us to study the genetic diversity that could exist in the sheep population of the Djallonke breed in the outskirts of the city of Ngaoundere. It was found that the cumulative variances of almost all the traits proved 98.12% of the genetic variability observed in the study population, two genetic types were revealed and the phylogenetic tree revealed that genetic type I is close to genetic type II. These results need to be complemented by molecular analyses carried out on a fine sampling of individuals that takes into account natural environmental and production differences to confirm our first results that were based on morpho-biometric characteristics.

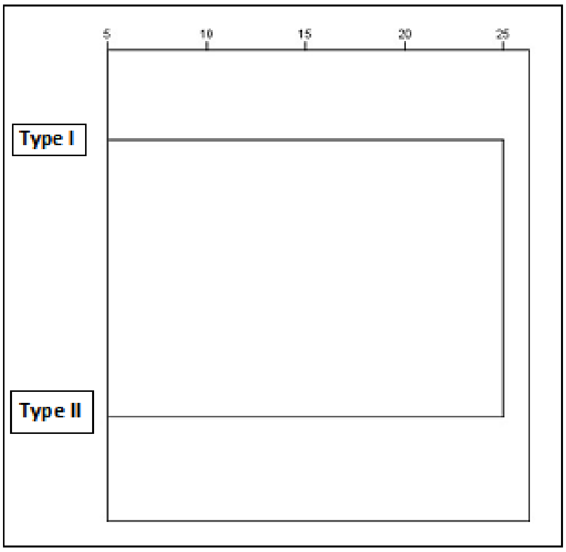

Fig. 2. Dendrogram of indigenous Djallonke sheep sub-populations in the outlying areas of Ngaoundere (Adamawa-Cameroon).

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