GENETIC DIVERSITY OF DOMESTIC GOATS FROM CENTRAL LAOS

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SUMMARY

Maintaining genetic diversity and variation in livestock populations is critical for allowing natural and artificial selection genetic improvement well as for avoiding inbreeding. The Laotian government and farmers are concerned that there has been a decrease in genetic diversity and an increase in inbreeding among native goats in their village-based smallholder system. The objective of this study was to investigate the genetic diversity of Lao native goats in a small-scale farming system in central Laos using genotype data. The results showed that there was a close genetic relationship between Lao native goats with Chinese goat breeds and a low to moderate genetic differentiation among goat populations in Central Laos ranging from 0.0112 to 0.0427. This goat population had close to zero inbreeding coefficients (-0.093 to 0.052).

INTRODUCTION

In developing countries, local livestock breeds are crucial for the welfare of rural communities producing a wide range of products and requiring low levels of management and health care. The genetic diversity of goat populations has been studied in Asia (Tarekegn *et al.* 2019; Hermes *et al.* 2020), Africa (Nandolo *et al.* 2019; Tarekegn *et al.* 2019), Europe (Oget *et al.* 2019; Danchin-Burge *et al.* 2012) and Oceania (Brito *et al.* 2017). These studies used genetic indexes such as genetic differentiation (F_{ST}) and inbreeding coefficient (F_{IS}) to describe population characteristics and history. French goat breeds are genetically very well described with an average F_{ST} and F_{IS} of 0.092 and 0.0213 respectively, between breeds and regions in France (Oget *et al.* 2019). However, the genetic diversity of goats in other Asian countries like the Lao People's Democratic Republic (Laos) has not been investigated, and detailed information about this population would benefit its management and production. In Laos, almost all goat production comes from smallholder systems with 2 to 5 goats per household (Windsor *et al.* 2018). Goat production is an essential source of income for household incomes and in recent years, Lao's goat population has significantly increased due to the high demand of goat meat to export to neighbouring Vietnam (Stür and Gray 2014). The objective of this study was to identify the genetic diversity of Lao's native goats and assess levels of inbreeding.

MATERIALS AND METHODS

Sample collection and genotyping. During the period from February to April 2022, a total of 420 ear-notch samples were collected in the Savannakhet province of Laos. These samples were obtained from 140 households situated in seven villages located in Phin, Songkhone, and Sepon districts (Figure 1). The samples were then genotyped using the goat 50K Illumina BeadChip at GenomNZ in New Zealand.

Reference population. To assess the diversity at a Asian level, a reference dataset comprising genotype information from 1132 goats, including 185 indigenous goats from Mongolia (Mukhina *et*

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al. 2022), 237 local Russian goats (Deniskova *et al.* 2021), 193 Chinese goats (Berihulay *et al.* 2019), 416 Pakistan goats, 16 Iranian goats and 85 goats from Turkey (Colli *et al.* 2018).

Quality control. A quality control assessment of genomic data was performed in PLINK v1.9 (Purcell *et al.* 2007). SNPs on the sex chromosomes, unmapped location, minor allele frequency (MAF) lower than 0.05, call rate lower than 90% and a deviation from Hardy-Weinberg equilibrium of $p < 10^{-6}$ were excluded from the analysis. Individuals with more than 10% missing SNPs were also excluded. After quality control, 419 genotyped goats with 42666 SNPs remained in the analysis. The Laos goat dataset was merged with the reference population which, after quality control included 43429 autosomal SNPs and 1546 individuals.

Genetic diversity and inbreeding analysis. A principal component analysis (PCA) was performed in PLINK and visualized with the R package "ggplot2". Pairwise genetic differentiation (F_{ST}; Weir and Cockerham 1984) and inbreeding coefficient (F_{IS}; Wright 1965) as well as expected and observed heterozygosity for each population were calculated in R using the "hierfstat" package (Goudet 2015).

Figure 1. Geographical location of goat samples used in this study

RESULTS AND DISCUSSION

The principal component analysis of the combined Laos and reference population showed clear differentiation between indigenous Lao goats and other Asian breeds (Figure 2A). The first principal component (PC1) accounted for 35.36% of the total variation and separated Lao native goats and Chinese breeds from other Asian breeds. The PCA for Lao goats suggested that genetic structure exists within this population with goats in Sepon clearly differentiated from those in the Phin and Songkhone districts in the PC1 and PC2, which accounted for 12.64% and 8.75% of the total variation, respectively (Figure 2B).
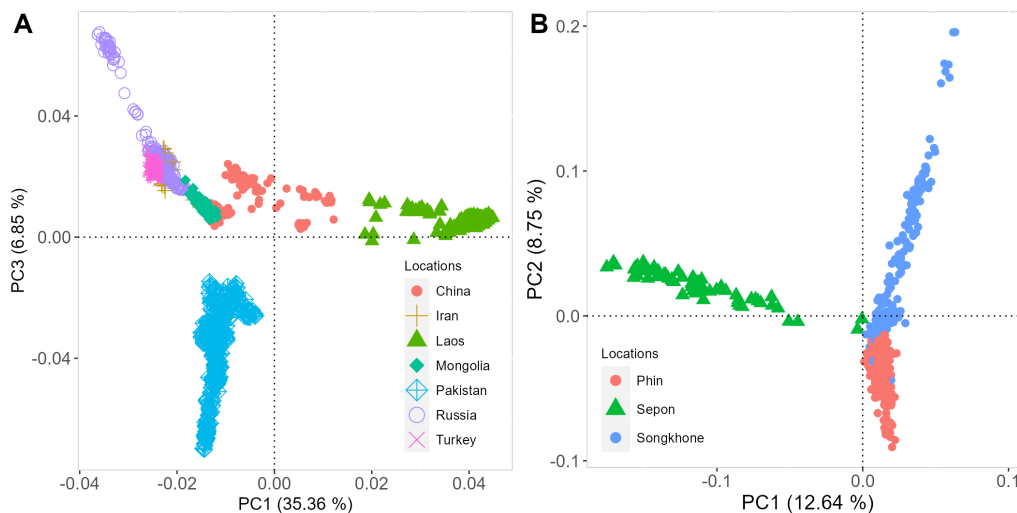

Figure 2. Principal component analysis for (A) Lao goats and Asian goat breeds, and (B) goat populations from different districts in Laos

Table 1. Pairwise FST values for goats from different Asian countries

	China	Iran	Laos	Mongolia	Pakistan	Russia
Iran	0.0408	-				
Laos	0.0481	0.0731	-			
Mongolia	0.0135	0.0327	0.0512	-		
Pakistan	0.0351	0.0433	0.0507	0.0291	-	
Russia	0.0295	0.0195	0.0614	0.0197	0.0371	-
Turkey	0.0385	0.0201	0.0703	0.0292	0.0418	0.0143

The average pairwise F_{ST} values between breeds in seven Asian countries were 0.0418, and ranged from 0.0135 to 0.0731 (Table 1), indicating a low to moderate genetic differentiation among these populations. The Mongolian and Chinese goat breeds showed the lowest level of differentiation (0.0135), while the highest level of differentiation (0.0731) was observed between Laos and Pakistan goat breeds. Results from the pairwise F_{ST} between Lao goats and other goat breeds from Asia confirmed the PCA results as there was a low genetic difference between Laos and Chinese goat breeds (F_{ST} = 0.0481), and there were moderate genetic differences between Lao goat breeds with other goat breeds in Asia (F_{ST} > 0.05).

In this study, the F_{ST} for Laos was 0.0223 and ranging from 0.0211 to 0.0815 which is slightly higher than the F_{ST} reported in Mongolia (0.009 to 0.035; Mukhina *et al.* 2022), but lower than F_{ST} in Russia (0.06 to 0.11; Deniskova *et al.* 2021) and Chinese goat population (0.02 to 0.16; Berihulay *et al.* 2019).

Table 2. Pairwise fixation index (F$_{ST}$) among districts in Laos

	Phin	Sepon
Sepon	0.0404	-
Songkhone	0.0112	0.0427

Genetic differentiation among goats from three districts in Central Laos revealed low genetic differentiation with greater differentiation between Sepon and Phin and Songkhone districts than between Phin and Songkhone (Table 2). This was supported by the PCA results that showed a gene flow between goats in Phin and Songkhone districts. Berihulay *et al.* (2019) described that genetic differentiation between two populations could be explained by natural geographic isolation. Phin and Songkhone were not located far from each other and they both have access to the main road, known as Route 13. The farmers in these two districts were able to easily trade goats between each other's locations in Xathamua town which is located almost halfway between the two districts and is close to the Savannakhet province centre. On the other hand, Sepon is more culturally isolated, being of a more distinct ethnic and linguistic group (Mong Kong), which may reduce the trade with other two districts. Additionally, Sepon is closer to the Vietnam border and it is easier for farmers to trade goats with Vietnamese dealers.

Overall, the observed heterozygosity values were less than the expected heterozygosity, except in Sepon (Table 3). The Ho and He in three Lao districts were lower than those in any Asian country. The average value of Ho and He in Asia were 0.3655 and 0.3956, respectively. The average Ho and

He in three districts in Laos were very similar, varying from 0.288 to 0.299 (Ho), and from 0.264 to 0.308 (He), respectively.

Table 3. Genetic diversity indices for goats from seven Asian countries and three districts in Laos. Ho: observed heterozygosity, He: expected heterozygosity, F_{IS}: inbreeding coefficient

	Asian country							Districts in Laos		
	China	**Iran**	**Mongolia**	**Pakistan**	**Russia**	**Turkey**	**Laos**	**Phin**	**Sepon**	**Song**
Ho	0.3672	0.343	0.4006	0.3379	0.409	0.408	0.292	0.299	0.288	0.2888
He	0.4023	0.419	0.4071	0.3831	0.434	0.421	0.303	0.308	0.264	0.3046
F_{IS}	0.0873	0.181	0.0158	0.118	0.056	0.03	0.037	0.028	-0.093	0.052

In general, F_{IS} were close to zero with positive F_{IS} values for Laos population (F_{IS}=0.0367), Phin (0.0283) and Songkhone (0.052), while a negative value was observed for Sepon (-0.093) indicating low outbreeding depression in this district. Similarly, low F_{IS} was found in Mongolian goat breeds, ranging from -0.013 to 0.025 (Mukhina *et al.* 2022) and it varied from -0.014 to 0.062 in the Chinese goat breeds (Berihulay *et al.* 2019). Those values were close to zero, indicating low levels of inbreeding in Lao natives. However, additional genomic analysis can assess the levels of relatedness between individuals and give insights into the history of Laos populations.

CONCLUSION

The results of Lao native goats revealed a closer genetic relationship with Chinese goat breeds than with other Asian goat breeds. Low to moderate genetic differentiation within Lao native goats was found, especially between Sepon and other locations. Inbreeding coefficients were close to zero being negative in Sepon and low but positive in Phin and Songkhone districts. These findings are not consistent with inbreeding depression being a major cause of small body size and low productivity in Lao native goats. Further analyses such as run of homozygosity are needed to identify levels of homozygosity in genomic regions.

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