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# Preservation of Genetic Diversity of the Asian Native Goats

Takeshi Honda<sup>1,\*</sup>, Mayu Shibano<sup>1</sup>, Hirokazu Matsumoto<sup>2</sup>, Shinji Sasazaki<sup>3</sup>, Kenji Oyama<sup>1</sup>, Hideyuki Mannen<sup>3</sup>

<sup>1</sup>Food Resources Education and Research Center, Graduate School of Agricultural Science, Kobe University, Hyogo, Japan

<sup>2</sup>Laboratory of Animal Genetics, Department of Animal Science, School of Agriculture, Tokai University, Kumamoto, Japan

<sup>3</sup>Laboratory of Animal Breeding and Genetics, Graduate School of Agricultural Science, Kobe University, Kobe, Japan

## Email address:

takhonda@diamond.kobe-u.ac.jp (T. Honda)

\*Corresponding author

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**Abstract:** Using single nucleotide polymorphisms (SNPs), the relative importance of 10 subpopulations of Asian native goats in preserving genetic diversity was investigated. Analysis of prioritizing by removal of subpopulations identified the subpopulations of Mongolia (MGL), Myanmar (MYA), Cambodian plains (CAM\_P), India (IND), and Philippine (PHI) as genetically important subpopulations because their removal resulted in a 6.38% reduction of expected heterozygosity. The removal of the remaining five subpopulations resulted in a 1.45% increase. Likewise, analysis using the core set method identified five subpopulations (MGL, MYA, CAM\_P, IND, and PHI) as genetically important subpopulations. Among these five subpopulations, the IND was most important because of low molecular coancestry within itself and between the other subpopulations. The subpopulations of Cambodian mountainous (CAM\_M) and Vietnam (VIE) were also considered to be important in this analysis. Based on these two investigations, we concluded that MGL, MYA, CAM\_P, IND, and PHI are essential, and that CAM\_M and VIE are worth preserving.

**Keywords:** *Capra Hircus*, Single Nucleotide Polymorphism, Molecular Coancestry, Expected Heterozygosity, Core Set Method

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## 1. Introduction

Goats are raised all over the world, and more than 65% of these goats are in developing countries. The production of meat, milk, and hide is very important and supports the lives of people in those countries. Although Asia has rich native goat resources, these animals have been crossed with imported profitable breeds, and face the risk of extinction [1]. Therefore, proposing a specific preservation scheme for native goat genetic resources in Asia is an urgent task.

Recently, the origin, phylogeny, and genetic diversity of Asian native goats were studied using various molecular genetic techniques ([2], [3], [4]). However, genetically important subpopulations for preserving the genetic variability of Asian native goats have not yet been identified. Prioritizing subpopulations is an essential task because both human and economic resources for the preservation schemes are usually limited, and should be

conducted before the establishment of the preservation scheme. In this study, we identified genetically important goat subpopulations among 10 subpopulations from Asia (Mongolia (MGL), Laos (LAO), Myanmar (MYA), Cambodian mountainous (CAM\_M), Cambodian plains (CAM\_P), Vietnam (VIE), Bhutan (BHU), Bangladesh (BAN), India (IND), and Philippine (PHI)), using 65 single nucleotide polymorphism (SNP) markers developed by Lin et al. [3].

## 2. Materials and Methods

### 2.1. Animals

Thirty animals were sampled from each subpopulation except for IND, from which 20 animals were sampled. Genomic DNA was extracted from blood according to the standard phenol and chloroform method.

## 2.2. SNP Detection

For detailed information about the process of detection of SNP markers, see Lin *et al.* [3].

## 2.3. Population Genetic Analysis

Caballero & Toro [5] proposed a method for genetically prioritizing the subpopulations, in which the change (decrease or increase) of expected heterozygosity [6] is examined when one or more subpopulations are assumed to be removed from the whole population. Assuming an equal subpopulation size and letting  $f_{ij}$  be the molecular coancestry between subpopulations  $i$  and  $j$ , average molecular coancestry of the whole population ( $\bar{f}$ ) can be decomposed into

$$\bar{f} = \bar{f} - \bar{D}, \quad (1)$$

where  $\bar{f}$  is the average of within-subpopulation coancestry ( $f_{ii}$ ) and  $\bar{D}$  is the average of Nei's minimum distance ([7]:  $D_{ij} = (f_{ii} + f_{jj})/2 - f_{ij}$ ) among all the subpopulations. Equation (1) indicates that the average molecular coancestry of the whole population ( $\bar{f}$ ) depends on the within-subpopulation component ( $\bar{f}$ ) and averaged distance among the subpopulations ( $\bar{D}$ ). Thus, the total genetic diversity of the whole population ( $GD_T$ ) expressed as expected heterozygosity is also decomposed as

$$GD_T = 1 - \bar{f} = (1 - \bar{f}) + \bar{D} = GD_{WS} + GD_{BS},$$

implying that the total genetic diversity of the whole population is partially ascribed to within-diversity components of each subpopulation ( $GD_{WS}$ ) and to between-diversity components among all the pairs of subpopulations ( $GD_{BS}$ ).

In a second investigation for prioritizing the 10 subpopulations, optimal genetic contributions of subpopulations for maximizing the genetic diversity of a hypothetical gamete pool were calculated. This calculation was conducted using the core set method of Eding *et al.* [8], which was originally proposed for ranking animal breeds regarding conservation of genetic diversity within a livestock species. The similar technique is used in many situations

nowadays (e.g. [9]). Suppose  $g_i$  gametes are sampled from subpopulation  $i$  to obtain a hypothetical gamete pool with  $g_T$  total gametes, so that the genetic contribution of subpopulation  $i$  is  $c_i = g_i/g_T$  and

$$\sum_{i=1}^n c_i = 1. \quad (2)$$

Letting  $f_{ij}$  be the molecular coancestry between subpopulations  $i$  and  $j$ , and  $F = [f_{ij}]$  be the molecular coancestry matrix of all the subpopulations, the expected molecular coancestry of the hypothetical gamete pool is

$$\bar{f}_c = c'Fc,$$

where  $c$  is a column vector of  $c_i$ . Thus, maximization of genetic diversity of the hypothetical gamete pool ( $1 - \bar{f}_c$ ) is equivalent to the problem of finding optimal  $c$  ( $c_{opt}$ ) such that  $\bar{f}_c$  is minimized under the restriction of Eq. (2). This problem can be solved by applying the Lagrange multiplier method, and the optimal contribution of each subpopulation is obtained as

$$c_{opt} = \frac{F^{-1}1}{1'F^{-1}1},$$

where  $1$  is a unit vector (for detailed derivation, see Eding *et al.* [8]).

All the computations were conducted using our original Fortran programs.

## 3. Results

Genetic diversity and its proportional changes according to the removal of subpopulations are provided in Table 1. The genetic diversity of the whole population ( $GD_T$ ) was 0.388, and it was decomposed into 0.331 for the within-diversity component ( $GD_{WS}$ ) and 0.057 for the between-diversity component ( $GD_{BS}$ ). Removal of MGL, MYA, CAM\_P, IND, and PHI was accompanied by the reduction of  $GD_T$ , indicating that these five subpopulations are genetically more important than the remaining five subpopulations for preserving genetic diversity.

**Table 1.** Total genetic diversity of the whole population ( $GD_T$ ), within-subpopulation component ( $GD_{WS}$ ), and between-subpopulation component ( $GD_{BS}$ ), according to the removal of subpopulations and their proportional changes in percentages.

Removed subpopulation				Changes (%)		
	$GD_{WS}$	$GD_{BS}$	$GD_T$	$GD_{WS}$	$GD_{BS}$	$GD_T$
None <sup>a</sup>	0.331	0.057	0.388	-	-	-
MGL	0.329	0.056	0.385	-0.55	-0.29	-0.84
LAO	0.331	0.059	0.390	0.00	0.40	0.40
MYA	0.327	0.061	0.388	-1.17	1.06	-0.11
CAM_M	0.341	0.049	0.389	2.43	-2.11	0.32
CAM_P	0.329	0.058	0.387	-0.54	0.32	-0.22
VIE	0.333	0.056	0.389	0.50	-0.38	0.12
BHU	0.328	0.060	0.388	-0.79	0.79	0.00
BAN	0.331	0.059	0.390	-0.11	0.54	0.44
IND	0.328	0.054	0.382	-0.84	-0.76	-1.59
PHI	0.335	0.052	0.387	1.06	-1.40	-0.34
MGL+MYA+CAM_P+IND+PHI	0.317	0.047	0.363	-3.67	-2.72	-6.38
LAO+CAM_M+VIE+BHU+BAN	0.345	0.049	0.394	3.67	-2.21	1.45

<sup>a</sup>Genetic diversity of the whole population without any removal of subpopulations.

The reduction of  $GD_T$  caused by the simultaneous removal of the previous five subpopulations (MGL, MYA, CAM\_P, IND, and PHI) (6.38%) was substantially larger than the sum of individual effects (3.10%). In addition, removal of the remaining five subpopulations (LAO, CAM\_M, VIE, BHU, and BAN) increased  $GD_T$  (1.45%), indicating that all five subpopulations (MGL, MYA, CAM\_P, IND, and PHI) are necessary for preserving genetic diversity of Asian native goats.

**Table 2.** Average molecular coancestries within and among the 10 subpopulations.

	MGL	LAO	MYA	CAM M	CAM P	VIE	BHU	BAN	IND	PHI
MGL	0.650									
LAO	0.595	0.669								
MYA	0.597	0.619	0.628							
CAM_M	0.559	0.646	0.624	0.754						
CAM_P	0.586	0.619	0.612	0.633	0.650					
VIE	0.594	0.658	0.612	0.642	0.604	0.686				
BHU	0.615	0.612	0.611	0.602	0.604	0.603	0.641			
BAN	0.611	0.620	0.621	0.620	0.611	0.610	0.638	0.665		
IND	0.613	0.572	0.587	0.540	0.588	0.567	0.598	0.600	0.640	
PHI	0.587	0.602	0.598	0.619	0.595	0.600	0.609	0.618	0.577	0.706

Optimal genetic contributions of each subpopulation obtained by the core set method are presented in Table 3. The maximum possible genetic diversity was estimated to be 0.398. The subpopulations with positive contributions were the five subpopulations that were found to be genetically important in the previous analysis (MGL, MYA, CAM\_P, IND, and PHI), as well as CAM\_M and VIE.

**Table 3.** Genetic contributions of each subpopulation ( $c_i$ ) obtained using the core set method.

Subpopulation	$c_i$
MGL	0.104
LAO	0.000
MYA	0.089
CAM_M	0.132
CAM_P	0.055
VIE	0.109
BHU	0.000
BAN	0.000
IND	0.410
PHI	0.101

## 4. Discussion

Recalling that expected heterozygosity on the biallelic loci reduces at the rate of  $1-1/2N_e$  [10], where  $N_e$  is the effective population size, and that standard effective population sizes of livestock breeds are around 100 [11], even a 0.5% change of heterozygosity resulting from removal of the subpopulation is not negligible. Among the five subpopulations that were found to be genetically important in the first analysis (MGL, MYA, CAM\_P, IND, and PHI), the effect of MGL and IND were relatively large, and reductions were observed in both components of  $GD_{WS}$  and  $GD_{BS}$ . These two subpopulations are geographically separated from the other subpopulations of Southeast Asia and are the oldest subpopulations of domestic goats introduced by nomadic tribes on the Silk Road [12].

Table 2 lists the average molecular coancestries within and among the 10 subpopulations. Molecular coancestries within each subpopulation were higher than those between the other subpopulations. Specifically, molecular coancestries within CAM\_M and PHI were extremely high, indicating that these two subpopulations were affected by the larger amount of genetic drift. MGL and IND have relatively low coancestries between the other subpopulations.

Removal of CAM\_M substantially reduced  $GD_{BS}$ ; however, it greatly increased  $GD_{WS}$  and inflated  $GD_T$  as a consequence (i.e., frequencies of two alleles in each locus became equalized). This is because CAM\_M has relatively large genetic distance from the other subpopulations, but also has quite small within-variability (cf. [3]). Steep mountain paths might limit the introgression of new genetic variants. A large reduction of  $GD_{BS}$  was also observed when PHI was removed. Geographical effect would be responsible for this reduction, i.e., PHI is an isolated island subpopulation.

In the core set analysis, the contribution of IND was fairly large, indicating that this subpopulation is predominantly important. Molecular coancestry of this subpopulation was the second lowest, and coancestries between the other subpopulations were relatively low (Table 2). India has rich goat resources; consumption of beef and pork is prohibited by Hinduism and Muslimism so goats are an important protein source [12]. The neighbor-joining tree constructed by Lin et al. [3] formed two clusters (cluster A MGL, BHU, BAN, and IND; cluster B LAO and VIE), and the remaining four subpopulations were independently distributed. MGL and IND were selected as non-zero contributors from cluster A, and VIE was selected from cluster B. This might be why BHU, BAN, and LAO could not contribute to the hypothetical gamete pool (i.e., why these subpopulations were not recognized as genetically important subpopulations).

## 5. Conclusion

Based on the analysis in this study, we concluded that the subpopulations MGL, MYA, CAM\_P, IND, and PHI are primarily important for preserving the genetic diversity of Asian native goats, and that if the preservation resources remain, CAM\_M and VIE are worth preserving. Compared to previous studies that uncovered origin, phylogeny, and genetic

diversity of many livestock species in Asia using various molecular genetic techniques, this rare study provides a specific and systematic preservation scheme. In addition to neutral molecular variation, adaptive traits possessed by each subpopulation should also be taken into account in future study, as suggested by Wellmann *et al.* [13], and deriving the economic values of each subpopulation and designing breeding schemes is essential [14].

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