

On Phylogenetic Relationships Among Native Goat Populations Along the Middle and Lower Yellow River Valley

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ABSTRACT : This paper is based on the 9 goat colonies along the middle and lower Yellow River valley and 7 local goat colonies in the Northeast, Tibet and the Yangtze valley. After collecting the same data about the 22 goat colonies in China and other countries, it establishes and composes the matrix of fuzzy similarity relation describing the genetic similarities of different colonies. It also clusters 38 colonies according to their phylogenetic relationship. The establishment of the matrix and the cluster are effected in terms of the frequency of 18 loci and 43 allelomorphs in blood enzyme and other protein variations. The study proves that the middle Yellow River valley is one of the taming and disseminating centers of domestic goats in the South and East of Central Asia. Compared with other goat populations in this vast area, the native goat populations in the west of Mongolian Plateau, the Qinghai-Tibet Plateau and the middle Yellow River valley share the same origin. The colonies in the lower Yellow River valley and those in the middle valley, however, are relatively remote in their phylogenetic relationship. The native goat colonies in the southeast of Central Asia can be classified into two genetic groups: "East Asia" and "South Asia" and the colonies in Southeast Asia belong to either group. (*Asian-Aus. J. Anim. Sci.* 2000. Vol. 13, No. 2 : 137-148)

Key Words : Phylogenetic Relationship, Native Goat Colonies, The Yellow River Valley

INTRODUCTION

The phylogenetic classification of domestic animal populations is one of the bases for determining the scope of a breed, estimating the possibility of the potential distribution of special gene resources in a specific population, judging the possibility of identical gene (or gene groups), controlling similar body shapes in different populations, analysing the population characteristic of genetic coadaptation, predicting the heterosis, and devising the breeding strategy (Chang et al, 1995). There are 135.92 million goats in China (China Agri. Ministry, 1996). The number of goats in the middle and lower Yellow River valley accounts for 35% in the whole country; they include many breeds with local characteristics such as Zhongwei Goat, Inner Mongolia Cashmere Goat, Jining Grey Goat, etc. It is the aim of this paper to examine the systematic relationship of the native goat populations in this area, to provide a basis for the development of

goat husbandry in this area and other part of China, and to supplement an important link for the research into goat phylogenetic systems in the world.

MATERIALS AND METHODS

Materials, sampling methods & size of samples

This paper investigates the 9 goat colonies in the middle and lower Yellow River valley below Heishanxia of Gansu Province and makes a contrast between these 9 colonies and the 7 colonies in the northeast, Tibet and the Yangtze River valley. The 33 loci that control the enzyme type and other protein variation have been tested. The sampling of all the populations was in central area of the native haunt except Liaoning Cashmere Goat, which was in a main area of colonization.

In each and every population all the male goats, female goats and wethers that were 2 years old and above are included. We tried to avoid sampling two (or more) individuals that have traceable phylogenetic relationship. Table 1 indicates the sampling methods, the size of samples and the place of sampling of the various populations. Figure 1 marks the geographical distribution of the sampling locations. Figure 2 gives a snapshot of its morphological characters.

Collection and treatment of blood samples

8-10 ml of blood is taken from the cervical vein and put into a centrifugal tube with antiagglutinin. The blood serum is separated by centrifugation (800 cycles/minute, 5-10 minutes) and transferred to a capped test tube. After 5 ml of 0.9% NaCl is added,

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Received January 28, 1999; Accepted May 4, 1999

Table 1. The sampling method and place

Population and name abbreviation	Size of population (thou.)	Sampling method and size of sample	Sampling location
Inner Mongolia Cashmere Goat in Alashan AMR	600	RCS 2 clusters, 84 Head	Zahanbrug-village of Xilingolo-township, Yuejing-village
Zhongwei goat ZHW	200	SRCS 2 systems, 2 clusters, 80 Head	Zhongwei Goat Ranch in Xiangshan-township, Zhongwei county, Ningxia, Shanghai-village of Xianggandalai-township, Alashan Left Banner
West Ziwuling Native ZWX	720	RCS 2 clusters, 80 Head	Taie-township, Heshui County, Chengguan-township, Huachi County, Gansu Province
East Ziwuling Native ZWD	480	SRS 83 Head	Zhidan County, Ansia County, Ganquan County, Shaanxi Province
Luling Black Goat LLH	300	SRCS 2 systems, 4 clusters, 82 Head	Chengnan-township, Shuidi-township, Xi County, Chengguan-town, Luocheng-town, Shilou County, Shanxi Province
Taihang Goat TAH	2480	RCS 2 clusters, 72 Head	Sujazhuang-township, Pingshan County, Huosui-township, Wuan-city, Hebei Province
Funiou Goat FUN	200	RCS 2 clusters, 64 Head	Xiayu-township, Loning County, Shizimiao-township, Lancuan County, Henan Province
Jining Grey goat JNQ	800	SRCS 2 systems, 3 clusters, 75 Head	Weian-town, Liangditou-township, Wulou-township, Cao County, Shandong Province
Wadi White Goat WDB	60	SRS 72 Head	Hekou-district, Dongying-city, Chenzhuang-town, Lijing County, Shandong Province
Yangtze River Delta White Goat CSB	3180	SRCS 2 systems, 4 clusters, 70 Head	Silaiqiao Island of Yangzhong-city, Jiangshu Province, Huqiao-township, Fengxian County, Shanghai Municipality
Chengdu Grey Goat CDM	70	RCS 3 clusters, 42 Head	Yuelaizhen-township, Danfeng-township, Jinxing-township, Deyi County, Sicuan Province
Shaannan White Goat SNB	556	SRCS 2 systems, 7 clusters, 92 Head	Guyuan-village, Lianhua-village, outskirts of Xixiang County, Danfeng County, Shaanxi Province
Liaoning Cashmere Goat LNR	156	RCS 3 clusters, 79 Head	Liaoning Cashmere Goat Ranch in Ganquan County, Hezhung-township, Meiquan-village, Ganquan County, Shaanxi Province
Yadong Goat YAD	0.2	RCS 5 clusters, 45 Head	Upper Yangdong-township, Duina-township, Yadong County, Tibet
Nileamu Goat NLM	0.5	RCS 5 clusters, 28 Head	Congdui-township, Nielamu County, Tibet
Tibet Plateau Goat ZGY	5100	RCS 6 clusters, 45 Head	Jiangre-township, Jiangzi County, Tibet

RCS : random cluster sampling, SRCS : stratified random cluster sampling; SRS : simple random sampling in typical colony.

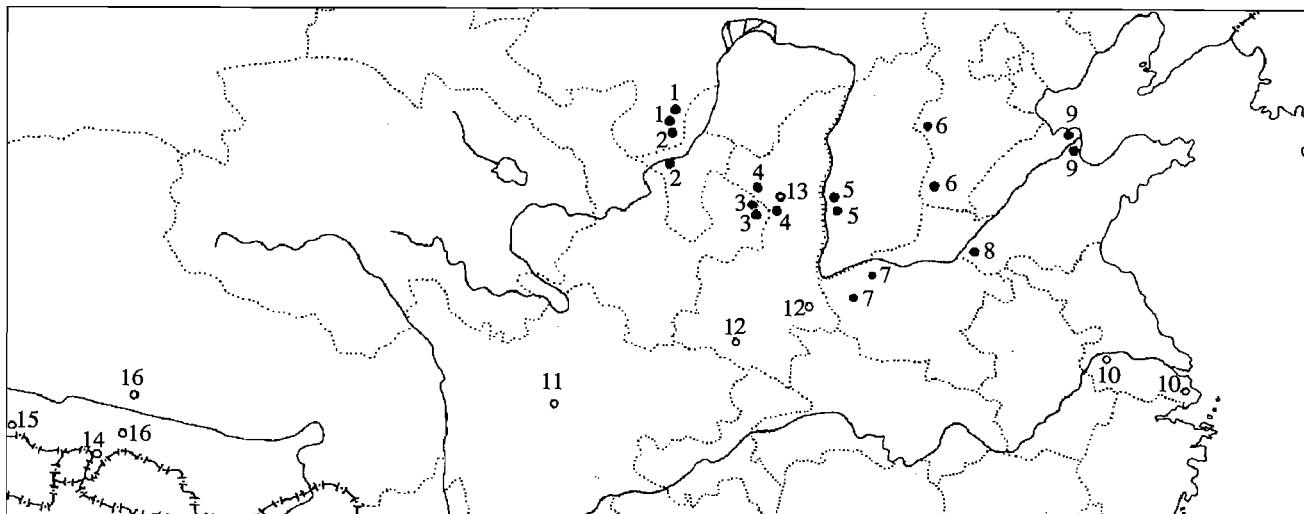


Figure 1. Geographical distribution of the sampling locations

● The population as object ○ The population as background

1. AMR; 2. ZHW; 3. ZWX; 4. ZWD; 5. LLH; 6. TAN; 7. FUN; 8. JNQ;
 9. WDB; 10. CSB; 11. CDM; 12. SNB; 13. LNR; 14. YAD; 15. NLM; 16. ZGY



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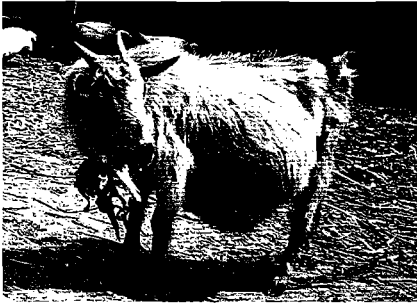
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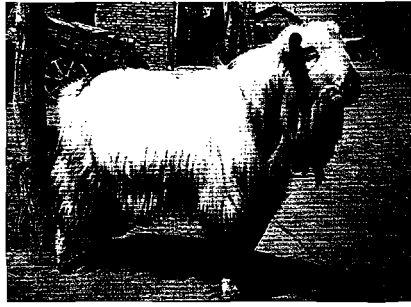
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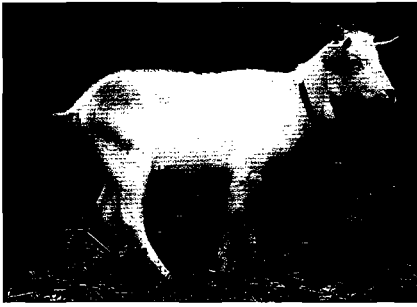
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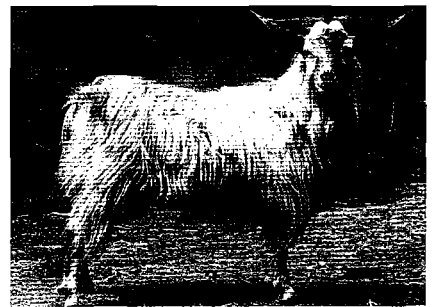
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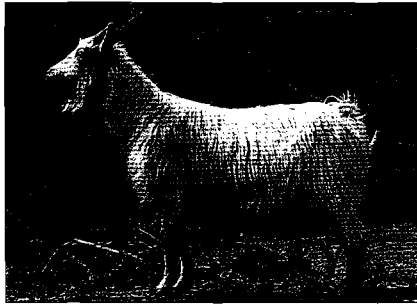
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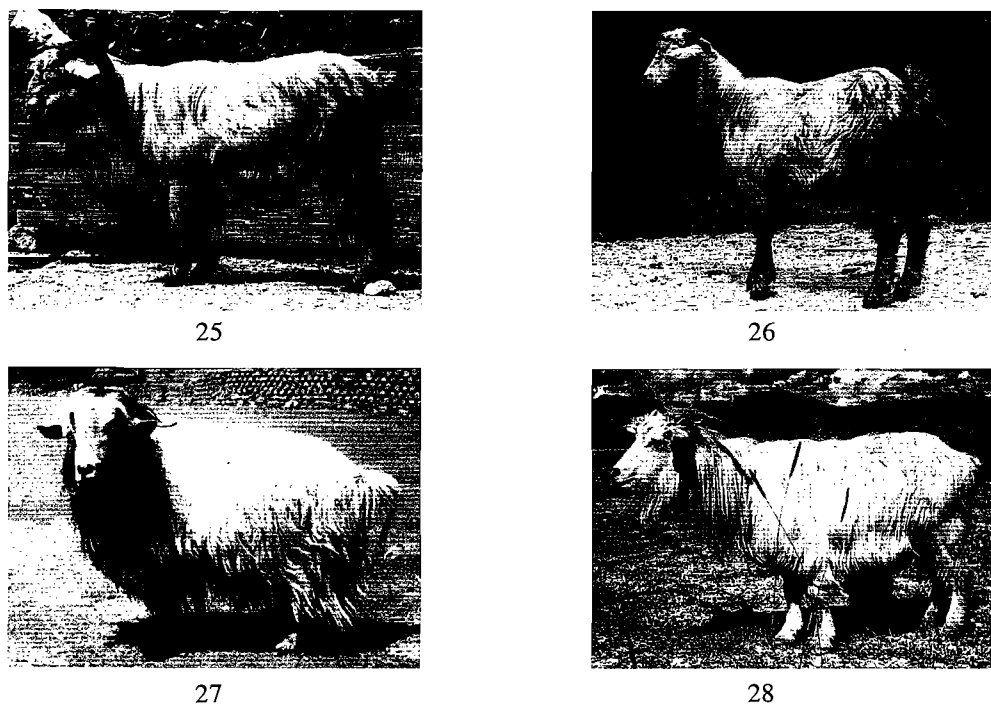


Figure 2. The photos of native goat

- | | |
|---|--|
| 1, 2. Inner Mongolia Cashmere Goat in Alashan (♂, ♀); | 3, 4. Zhongwei Goat (♂, ♀); |
| 5, 6. Ziwuling Native (♂, ♀); | 7, 8. Lüling Black Goat (♂, ♀); |
| 9, 10. Taihang Goat (♂, ♀); | 11, 12. Funiou Goat (♂, ♀); |
| 13. Jining Grey Goat (♀); | 14. Wadi White Goat (♂); |
| 15, 16. Yangtze River Delta White Goat (♂, ♀); | 17, 18. Chengdu Grey Goat (♂, ♀); |
| 19, 20. Shannan White Goat (♂, ♀); | 21, 22. Liaoning Cashmere Goat (♂, ♀); |
| 23, 24. Yadong Goat (♂, ♀); | 25, 26. Nielamu Goat (♂, ♀); |
| 27, 28. Tibet Plateau Goat (♂, ♀); | |

the remaining blood plasma in the washing tube is centrifuged two to three times (800 cycles/minute, 5-10 minutes). After the last centrifugation, the upper layer of blood plasma is drawn and injected into another capped test tube. After numbering, the tube is kept in a refrigerator (below -20°C).

Multiloci electrophoresis

Starch gel electrophoresis is used to determine the variations of the 33 loci in encoded hemoglobin- α II (Hb- α II), hemoglobin- β (Hb- β), plasma albumin (Alb), plasma transferrin (Tf), plasma haptoglobin (Hp), plasma slow- α_2 (α_2), plasma non-specific esterase (Es), plasma ceruloplasmin (Cp), plasma Leucine aminopeptidase (Lap), plasma prealbumin-1 (PA-1), plasma prealbumin-2 (PA-2), plasma prealbumin-3 (PA-3), plasma alkaline phosphatase (Alp), plasma amylase (Amy), cell esterase D (Es-D), cell 6-phosphogluconate dehydrogenase (6 PGD), cell phosphohexose isomerase (PHI), cell malate dehydrogenase (MDH), cell NADH-diaphorase (Dia), cell acid phosphatase (ACP), cell tetrazolium oxidase (To), cell

lactate dehydrogenase-A (LDH-A), cell lactate dehydrogenase-B (LDH-B), cell esterase-1 (CEs-1), cell esterase-2 (CEs-2), cell adenylate kinase (AK), cell catalase (Cat), cell peptidase-B (Pep-B), cell isocitrate dehydrogenase (IDH), cell glutamic-oxaloacetic transaminase (GOT), cell phosphoglucomutase (PGM), cell glucose-6-phosphate dehydrogenase (G6PD) and cell glyoxalase-1 (GO-1). The types of the variations are determined according to the standards universally accepted in the countries neighboring China. Electrophoretic method and variational patterns in each locus are those described minutely by Sun (Sun et al., 1998) and Liu (Liu et al., 1998).

Statistical analysis

The frequency and variance of genes are estimated according to sample structure and sample size of the populations (Chang et al., 1989). The following two formulae are used to calculate the reliability that ensures the estimate does not deviate from the true value more than 0.5 times and the relative deviation when the reliability reaches 0.9545.

$$\beta = \int_0^{\lambda} \frac{2e^{-\frac{\lambda^2}{2}}}{\sqrt{2\pi}} d\lambda ; \quad \eta = 2[V(P^{\frac{1}{2}})] \cdot P^{-1}$$

In the above formula, P and $V_{(P)}$ stand for gene frequency and gene variance, respectively; λ is the standardized deviation of the estimate and is suitable for the first formula when its standardized deviation is

$$\lambda = 0.5P \div [V_{(P)}]^{\frac{1}{2}}$$

Phylogenetic relationship cluster :

According to the frequency of the genetic loci 9 in each population, the following formula is used to describe the fuzzy consistency relationship matrix of the similarity between populations and to compose the fuzzy similarity relation. Thus population cluster is achieved.

$$\mu_{R(x,y)} = \frac{1}{2} \ln(J_{x,y} / \sqrt{J_x \cdot J_y}) + 1$$

In the above formula, J_x , J_y and J_{xy} stand respectively for population X, population Y and the probability average among loci of the same alleles acquired at random from the first two populations; $\mu_{R(x,y)}$ stands for the membership function under the fuzzy consistency relation R between X and Y populations.

Quotation of source materials

In the above phylogenetic relationship clusters, the frequency distribution of 33 loci in 22 colonies are shown in table 2. These data are reported by other researchers with the same techniques.

The 18 loci which have been fixed in 22 colonies were excluded from table 2.

RESULTS

Frequency distribution of blood enzyme and other protein loci

Of the 33 loci tested, 9 have polymorphism. Table 3 shows the estimates of gene frequencies, the reliability of the estimate not deviating more than 0.5 times and the reliability reaching 0.9545 (relative deviation). It is seen from table 3 that the reliability of the estimate of 203 non-fixed gene frequencies on 9 loci in 16 colonies not deviating more than 0.5 times approaches 100% (0.9999~1.0000) most of the time. When the reliability reaches 95.45%, most of the relative deviations are below 0.20. The lowest reliability of the genes with their frequency above 0.10 is $\beta=0.9025$ (Yadong Goat, Tfb). Therefore, the

estimates of gene frequency among 16 colonies are, on the whole, accurate and reliable and may serve as a basis for the analysis of phylogenetic relationships. If the 22 populations in table 2 are also considered, it is found that 18 loci have polymorphisms and there are altogether 43 alleles.

Phylogenetic clusters

Figure 3 shows the phylogenetic relationship among 38 populations, the base of which is the fuzzy similarity matrix.

As far as the 9 colonies in the middle and lower Yellow River valley are concerned, the colonies on the two sides of Ziwuling Mountain Chain first of all cluster on $\mu_{R37}(x,y) \geq 0.9990$ secondly Taihang Goat and Funiou Goat cluster on the level value of 0.9989; thirdly Zhongwei Goat and Inner Mongolia Cashmere Goat cluster on the level value of 0.9988. The colonies in the middle Yellow River valley except Luliang Black Goat all cluster on the level value of $\mu_{R37}(x,y) \geq 0.9982$. However, the cluster of Zhongwei and Alashan colonies on the upper part of the middle Yellow River valley with the 4 colonies along middle and lower Jing and Wei River valleys is the last of these clusters. The Jining Grey Goat and the Wadi White Goat colonies along the lower Yellow River valley cluster on the level value of 0.9987; the two do not cluster with the 6 colonies in the middle valley until the level value comes to 0.9971. The genetic division of the 8 colonies in the middle and lower valley in the Yellow River has something to do with the geographical location in their native areas.

If the 18 colonies in the whole country are taken into consideration, the Nielamu Goat and the Plateau Goat in Tibet cluster with the colonies to the east of Ziwuling Mountain Chain in the middle Yellow River valley on the level value of 0.9991; the Yadong Goat in Tibet enters this community on 0.9987. The white Goat at the Yangtze Delta and the Guishan Goat in the Lunan District of Yunnan Province cluster on the level value of 0.9989; however, when they cluster with Yunling Goat, another colony in Yunnan Province, on 0.9978, they have already clustered with Liaoning Cashmere Goat which originates from the northeast of China. Shaannan White Goat along the Yangtze River valley does not enter the community until the colonies along the Yangtze and to the south of the Yangtze cluster with those in the middle Yellow River valley and Tibet (0.9977).

The 38 goat colonies to the east and south of Central Asia are clearly classified, on the level value of $\mu_{R37}(x,y) \geq 0.9971$, into the group dominated by South Asian colonies and the group dominated by the Chinese and Japanese goat colonies. The colonies in the Southeast Asia enter either into the first group or into the second, showing scattered relation. On this

Table 2. The gene frequencies in 22 populations quoted by this study

Population	Hb- α II			Hb- β			Tf			Cited from	
	1	2	3	1	2	3	A	A'	B		C
Japan JS	1	0	0	0.9547	0.0453	0	0.9163	0	0.0837	0	Nozawa, K. et al., 1994
Shiba	1	0	0	0.9878	0	0.0122	0.9939	0	0.0061	0	Nozawa, K. et al., 1994
Okinawa	1	0	0	0.9643	0.0262	0.0095	0.9638	0	0.0339	0.0023	Nozawa, K. et al., 1994
Tokara	1	0	0	1	0	0	0.8594	0	0.1406	0	Nozawa, K. et al., 1994
Ogasawara	1	0	0	1	0	0	1	0	0	0	Nozawa, K. et al., 1994
Yunling	1	0	0	1	0	0	0.9923	0	0.0077	0	Nozawa, K. et al., 1995
Guishan	1	0	0	1	0	0	1	0	0	0	Nozawa, K. et al., 1995
Bangladesh JP	0.8333	0.1667	0	1	0	0	0.4722	0	0.5278	0	Nozawa, K. et al., 1998
KJ	1	0	0	1	0	0	0.2059	0	0.7941	0	Nozawa, K. et al., 1998
MY	0.9878	0	0.0122	1	0	0	0.3780	0	0.6220	0	Nozawa, K. et al., 1998
Indonesia P ₃ T	1	0	0	1	0	0	0.3000	0	0.7000	0	Katsumata, M. et al., 1983
CA	1	0	0	1	0	0	0.6470	0	0.3530	0	Katsumata, M. et al., 1983
CR	1	0	0	1	0	0	0.3077	0	0.6923	0	Katsumata, M. et al., 1983
CG	1	0	0	1	0	0	0.5250	0	0.4750	0	Katsumata, M. et al., 1983
KA	1	0	0	1	0	0	0.7692	0	0.2308	0	Katsumata, M. et al., 1983
CS	1	0	0	1	0	0	0.8529	0	0.1471	0	Katsumata, M. et al., 1983
PP	1	0	0	1	0	0	0.8333	0	0.1667	0	Katsumata, M. et al., 1983
Sri Lanka UPE	1	0	0	1	0	0	0.1667	0	0.8333	0	Shotake, T. et al., 1986
GAL	1	0	0	0.9000	0	0.1000	0.2167	0.0833	0.6500	0.0500	Shotake, T. et al., 1986
NEG	1	0	0	1	0	0	0	0	1.000	0	Shotake, T. et al., 1986
HBT	1	0	0	0.9667	0	0.0333	0.0167	0.0333	0.9000	0.0500	Shotake, T. et al., 1986
SIG	1	0	0	1	0	0	0.0833	0	0.9167	0	Shotake, T. et al., 1986

JS: Japanese Saanen, JP: Jamnapari, KJ: Khulna Jessere, My: Mymensingh, P₃T: Pusat penelitian dan pengembangan, CA: Cianjur, CR: Cirebon, CG: Cigombong, KA: Kiaralawang, CS: Ciangsa, PP: Pasar Padarg, UPE: University of Peradeniya, Gal: Galle, NEG: Negombo, HBT: Hambatota, SIG: Sigiriya.

Table 2. The gene frequencies in 22 populations quoted by this study (continued)

Population	ES		Alp		PA-3		Amy			Cited from
	A	B	O	F	1	2	1	2	3	
Japan JS	0.9980	0.0020	0.8207	0.1793	0.5714	0.4286	0.9979	0.0021	0	Nozawa, K. et al., 1994
Shiba	1	0	0.9815	0.0185	0.8567	0.1433	1	0	0	Nozawa, K. et al., 1994
Okinawa	0.9942	0.0058	0.8979	0.1021	0.7275	0.2725	0.9707	0.0293	0	Nozawa, K. et al., 1994
Tokara	1	0	0.8660	0.1340	0.9531	0.0469	1	0	0	Nozawa, K. et al., 1994
Ogasawara	1	0	0.6786	0.3214	0.1296	0.8704	0.9643	0.0357	0	Nozawa, K. et al., 1994
Yunling	1	0	0.7545	0.2455	0.6846	0.3154	1	0	0	Nozawa, K. et al., 1995
Guishan	1	0	0.6901	0.3099	0.5467	0.4524	1	0	0	Nozawa, K. et al., 1995
Bangladesh JP	1	0	0.9718	0.0282	0.6944	0.3056	1	0	0	Nozawa, K. et al., 1998
KJ	1	0	0.8402	0.1598	0.2647	0.7353	0.9412	0	0.0588	Nozawa, K. et al., 1998
MY	1	0	0.9627	0.0373	0.5244	0.4756	1	0	0	Nozawa, K. et al., 1998
Indonesia P ₃ T	1	0	1	0	0.3500	0.6500	1	0	1	Katsumata, M. et al., 1983
CA	1	0	1	0	0.5588	0.4412	1	0	0	Katsumata, M. et al., 1983
CR	1	0	0.8770	0.1230	0.6923	0.3077	1	0	0	Katsumata, M. et al., 1983
CG	1	0	0.9486	0.0514	0.4000	0.6000	1	0	0	Katsumata, M. et al., 1983
KA	1	0	0.7337	0.2663	0.4231	0.5769	1	0	0	Katsumata, M. et al., 1983
CS	1	0	0.8043	0.1957	0.7059	0.2941	1	0	0	Katsumata, M. et al., 1983
PP	1	0	0.6324	0.3676	0.3667	0.6333	1	0	0	Katsumata, M. et al., 1983
Sri Lanka UPE	1	0	1	0	0.2667	0.7333	1	0	0	Shotake, T. et al., 1986
GAL	1	0	0.9129	0.0871	0.3500	0.6500	1	0	0	Shotake, T. et al., 1986
NEG	1	0	0.9487	0.0513	0.2000	0.8000	0.8000	0	0.2000	Shotake, T. et al., 1986
HBT	1	0	0.9832	0.0168	0.2833	0.7167	1	0	0	Shotake, T. et al., 1986
SIG	1	0	0.9280	0.0720	0.1389	0.8611	1	0	0	Shotake, T. et al., 1986

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Table 2. The gene frequencies in 22 populations quoted by this study (continued)

Population	Es-D		MDH		LDH-A		CEs-1		Cited from
	1	2	1	2	1	2	1	2	
Japan JS	0.9775	0.0225	1	0	1	0	0.9959	0.0041	Nozawa, K. et al., 1994
Shiba	0.9939	0.0061	1	0	1	0	1	0	Nozawa, K. et al., 1994
Okinawa	0.9603	0.0397	1	0	1	0	1	0	Nozawa, K. et al., 1994
Tokara	0.9545	0.0455	1	0	1	0	1	0	Nozawa, K. et al., 1994
Ogasawara	0.9286	0.0714	0.9815	0.0185	1	0	1	0	Nozawa, K. et al., 1994
Yunling	0.6692	0.3308	1	0	1	0	1	0	Nozawa, K. et al., 1995
Guishan	0.9211	0.0789	1	0	1	0	1	0	Nozawa, K. et al., 1995
Bangladesh JP	1	0	0.9444	0.0556	0.9722	0.0278	1	0	Nozawa, K. et al., 1998
KJ	1	0	1	0	1	0	1	0	Nozawa, K. et al., 1998
MY	1	0	1	0	0.9756	0.0244	1	0	Nozawa, K. et al., 1998
Indonesia P ₃ T	1	0	1	0	1	0	1	0	Katsumata, M. et al., 1983
CA	1	0	1	0	1	0	1	0	Katsumata, M. et al., 1983
CR	1	0	1	0	1	0	1	0	Katsumata, M. et al., 1983
CG	0.9250	0.0750	1	0	1	0	1	0	Katsumata, M. et al., 1983
KA	0.8446	0.1154	1	0	1	0	1	0	Katsumata, M. et al., 1983
CS	1	0	1	0	1	0	1	0	Katsumata, M. et al., 1983
PP	1	0	1	0	1	0	1	0	Katsumata, M. et al., 1983
Sri Lanka UPE	1	0	1	0	1	0	1	0	Shotake, T. et al., 1986
GAL	0.8667	0.1333	1	0	1	0	1	0	Shotake, T. et al., 1986
NEG	0.9500	0.0500	1	0	1	0	1	0	Shotake, T. et al., 1986
HBT	0.9667	0.0333	1	0	1	0	1	0	Shotake, T. et al., 1986
SIG	0.9444	0.0556	0.9861	0.0139	1	0	1	0	Shotake, T. et al., 1986

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Table 2. The gene frequencies in 22 populations quoted by this study (continued)

Population	PHI			AK		Pep-B			IDH		Cited from
	1	2	0	1	2	A	B	C	1	2	
Japan JS	0.8837	0.0055	0.1108	0.9980	0.0020	0.9713	0.0103	0.0184	1	0	Nozawa, K. et al., 1994
Shiba	1	0	0	1	0	0.9780	0.0189	0.0031	1	0	Nozawa, K. et al., 1994
Okinawa	1	0	0	1	0	0.9891	0.0109	0	1	0	Nozawa, K. et al., 1994
Tokara	1	0	0	1	0	1	0	0	1	0	Nozawa, K. et al., 1994
Ogasawara	1	0	0	1	0	1	0	0	0.9815	0.0185	Nozawa, K. et al., 1994
Yunling	1	0	0	1	0	0.7373	0.2627	0	1	0	Nozawa, K. et al., 1995
Guishan	1	0	0	1	0	0.9333	0.0667	0	1	0	Nozawa, K. et al., 1995
Bangladesh JP	1	0	0	1	0	1	0	0	1	0	Nozawa, K. et al., 1998
KJ	1	0	0	1	0	1	0	0	1	0	Nozawa, K. et al., 1998
MY	1	0	0	1	0	1	0	0	1	0	Nozawa, K. et al., 1998
Indonesia P ₃ T	1	0	0	1	0	1	0	0	1	0	Katsumata, M. et al., 1983
CA	1	0	0	1	0	1	0	0	1	0	Katsumata, M. et al., 1983
CR	1	0	0	1	0	1	0	0	1	0	Katsumata, M. et al., 1983
CG	1	0	0	1	0	1	0	0	1	0	Katsumata, M. et al., 1983
KA	1	0	0	1	0	1	0	0	1	0	Katsumata, M. et al., 1983
CS	1	0	0	1	0	1	0	0	1	0	Katsumata, M. et al., 1983
PP	1	0	0	1	0	1	0	0	1	0	Katsumata, M. et al., 1983
Sri Lanka UPE	1	0	0	1	0	1	0	0	1	0	Shotake, T. et al., 1986
GAL	1	0	0	1	0	1	0	0	1	0	Shotake, T. et al., 1986
NEG	1	0	0	1	0	1	0	0	1	0	Shotake, T. et al., 1986
HBT	1	0	0	1	0	1	0	0	1	0	Shotake, T. et al., 1986
SIG	1	0	0	1	0	1	0	0	1	0	Shotake, T. et al., 1986

JS: Japanese Saanen, JP: Jamnapari, KJ: Khulna Jessere, My: Mymensingh, P₃T: Pusat penelitian dan pengembangan, CA: Cianjur, CR: Cirebon, CG: Cigombong, KA: Kiaralawang, CS: Ciangsa, PP: Pasar Padarg, UPE: University of Peradeniya, Gal: Galle, NEG: Negombo, HBT: Hambatota, SIG: Sigiriya.

Table 3. Sampling estimators of gene frequencies and their reliability and precision

Population	Parameter	Tf				LAP		AIP		PA-3	
		A	A'	B	C	A	B	O	F	1	2
AMR	P	0.8875	0	0.1125	0	1	0	0.8625	0.1375	0.7750	0.2250
	β	1.0000		0.9756		1	0	1.0000	0.9876	1.0000	0.9996
	η	0.0563		0.4444				0.0571	0.4000	0.0816	0.2811
ZHW	P	0.9260	0	0.0740	0	0.8809	0.1191	0.9110	0.0890	0.6910	0.3090
	β	1.0000		0.9070		1.0000	0.9720	1.0000	1.0000	1.0000	0.9999
	η	0.0475		0.5946		0.0613	0.4534	0.0134	0.1369	0.1120	0.2500
ZWX	P	0.8190		0.1810	0	0.8500	0.1510	0.6625	0.3375	0.6313	0.3687
	β	1.0000		1.0000		1.0000	0.8660	0.9970	0.8660	1.0000	1.0000
	η	0.0153		0.0689		0.2350	1.3330	0.3395	0.6670	0.0990	0.0500
ZWD	P	0.8720	0	0.1280	0	1	0	0.8138	0.1862	0.5660	0.4340
	β	1.0000		0.9580				1.0000	1.0000	1.0000	1.0000
	η	0.0722		0.4918				0.0297	0.1305	0.1793	0.2338
LLH	P	0.8737	0	0.1263	0	1	0	0.6250	0.3750	0.6387	0.3613
	β	1.0000		0.9850				1.0000	0.9880	1.0000	0.9950
	η	0.0597		0.4128				0.2370	0.3950	0.2000	0.3536
TAH	P	0.9236	0	0.0764	0	0.8333	0.1667	0.6806	0.3194	0.4923	0.5077
	β	1.0000	0	0.9230	0	1.0000	0.9999	1.0000	1.0000	1.0000	1.0000
	η	0.0585	0	0.5656	0	0.1103	0.2036	0.1190	0.0745	0.1619	0.1186
FUN	P	0.9375	0	0.0625	0	0.7422	0.2578	0.5938	0.4062	0.4375	0.5625
	β	1.0000		0.8487		1.0000	0.9989	1.0000	1.0000	1.0000	1.0000
	η	0.0465		0.6969		0.1067	0.3071	0.1496	0.2187	0.1965	0.1528
JNQ	P	0.9667	0	0.0333	0	0.9734	0.0266	0.2267	0.7733	0.4000	0.6000
	β	1.0000		0.5435		1.0000	0.9840	0.7383	0.9997	1.0000	0.9379
	η	0.0462		1.3430		0.0113	0.4149	0.8910	0.2791	0.0274	0.5359
WDB	P	0.9652	0	0.0348	0	1	0	0.2778	0.7222	0.5319	0.4681
	β	1.0000		0.7815				0.9998	1.0000	1.0000	1.0000
	η	0.0293		0.8129				0.2694	0.1036	0.1594	0.1924
CSB	P	0.9767	0	0.0233	0	0.8733	0.1267	0.7534	0.2466	0.4736	0.5264
	β	1.0000		0.7512		1.0000	0.9995	1.0000	1.0000	1.0000	1.0000
	η	0.0207		0.8671		0.0895	0.2804	0.0954	0.2910	0.1561	0.1735
CDM	P	0.7976	0	0.2024	0	0.7738	0.2262	0.5476	0.4524	0.7500	0.2500
	β	1.0000		0.9774		1.0000	0.9856	1.0000	1.0000	1.0000	0.9911
	η	0.1113		0.4384		0.1194	0.4085	0.2007	0.2430	0.1275	0.3825
SNB	P	0.9582	0	0.0418	0	1	0	0.4830	0.5170	0.6515	0.3485
	β	1.0000		0.4453				1.0000	1.0000	1.0000	1.0000
	η	0.0739		1.6928				0.3419	0.3195	0.1104	0.2064
LNR	P	0.9250	0	0.0750	0	1	0	0.8120	0.1880	0.6906	0.3094
	β	1.0000		1.0000				1.0000	1.0000	1.0000	1.0000
	η	0.0206		0.2544				0.0348	0.1500	0.1086	0.2425
YAD	P	0.8890	0	0.1110	0	0.9440	0.0556	0.5330	0.4670	0.5670	0.4830
	β	1.0000		0.9025		1.0000	0.7449	1.0000	1.0000	1.0000	1.0000
	η	0.0753		0.6034		0.0519	0.8786	0.1996	0.2278	0.1863	0.2206
NLM	P	0.8570	0	0.1430	0	0.9290	0.0710	0.7500	0.2500	0.5890	0.4110
	β	1.0000		0.8666		1.0000	0.6903	1.0000	0.9661	1.0000	0.9978
	η	0.1112		0.6663		0.0752	0.9845	0.1571	0.4714	0.2274	0.3258
ZGY	P	0.8110	0	0.1890	0	0.9000	0.1000	0.7780	0.2220	0.4330	0.5670
	β	1.0000		0.9764		1.0000	0.8821	1.0000	0.9878	1.0000	1.0000
	η	0.1029		0.4416		0.0711	0.6396	0.1139	0.3991	0.2339	0.1863

Table 3. Sampling estimators of gene frequencies and their reliability and precision (continued)

Population	Parameter	Amy			Es-D		Cat		Pep-B			GO-1	
		1	2	3	1	2	A	B	A	B	C	1	2
AMR	P	0.9937	0.0063	0	0.3438	0.6562	0.9625	0.0375	1	0	0	1	0
	β	1.0000	0.8764		0.9747	1.0000	1.0000	0.9576					
	η	0.0041	0.6498		0.2647	0.1386	0.0192	0.4964					
ZHW	P	0.9920	0.0080	0	0.2380	0.7620	0.9920	0.0080	0.9630	0.0370	0	0.9750	0.0250
	β	1.0000	0.4060		0.9991	1.0000	1.0000	0.4060	1.0000	0.7623		1.0000	0.7030
	η	0.0149	1.8750		0.3000	0.0937	0.0149	1.8750	0.0330	0.8650		0.0250	0.9600
ZWX	P	0.9500	0.0500	0	0.5250	0.4750	1	0	1	0	0	1	0
	β	1.0000	0.3830		1.0000	1.0000							
	η	0.1050	2.0000		0.0950	0.1050							
ZWD	P	1	0	0	0.4609	0.5391	1	0	1	0	0	1	0
	β				1.0000	1.0000							
	η				0.1466	0.1253							
LLH	P	0.9939	0.0061	0	0.5584	0.4416	0.5785	0.2415	0.9756	0.0244	0	0.9429	0.0571
	β	1.0000	0.4320		1.0000	0.9880	1.0000	0.9748	1.0000	0.9500		1.0000	0.3940
	η	0.0114	1.9410		0.3120	0.3939	0.9100	1.1770	0.3900	1.5330		0.1170	1.9360
TAH	P	1	0	0	0.6319	0.3681	1	0	0.9931	0.0069	0	1	0
	β				1.000	0.9999			1.0000	0.4413			
	η				0.0120	0.2407			0.0539	1.2321			
FUN	P	0.8750	0.1250	0	0.6641	0.3359	1	0	0.9808	0.0716	0.0017	1	0
	β	1.0000	0.9662		1.0000	1.0000			1.0000	0.3109	0.0322		
	η	0.0673	0.4712		0.1269	0.2509			0.0379	1.9545	3.9412		
JNQ	P	0.9667	0.0333	0	0.4931	0.5069	1	0	0.9666	0.0267	0.0067	1	0
	β	1.0000	0.6636		0.9732	0.9772			1.0000	1.0000	0.7105		
	η	0.0358	1.0403		0.4517	0.4394			0.0146	0.2369	0.9444	1	0
WDB	P	0.9722	0.0278	0	0.3472	0.6528	1	0	0.9931	0.0069	0	1	0
	β	1.0000	0.6743		1.0000	1.0000			1.0000	0.1226			
	η	0.0291	0.0174		0.1594	0.1924			0.0450	6.4814			
CSB	P	0.9057	0.0943	0	0.8676	0.1324	0.9884	0.0116	0.9605	0.0395	0	1	0
	β	1.0000	0.9772		1.0000	0.9628	1.0000	0.5802	1.0000	0.7141			
	η	0.0457	0.4392		0.0738	0.4798	0.0145	1.2394	0.0385	0.9371			
CDM	P	0.9762	0.0238	0	0.8810	0.1190	1	0	1	0	0	1	0
	β	1.0000	0.5204		1.0000	0.9039							
	η	0.0345	1.4145		0.0812	0.6009							
SNB	P	1	0	0	0.7603	0.2397	1	0	1	0	0	1	0
	β				1.0000	0.9808							
	η				0.1346	0.4270							
LNR	P	1	0	0	0.7415	0.2585	1	0	0.9811	0.0126	0.0063	1	0
	β				1.0000	1.0000			1.0000	0.6575	0.2867		
	η				0.0119	0.0342			0.0212	1.0534	2.7216		
YAD	P	1	0	0	0.4890	0.5110	1	0	0.9780	0.0220	0	1	0
	β				1.0000	1.0000			1.0000	0.0583			
	η				0.2179	0.2086			0.0320	1.4215			
NLM	P	1	0	0	0.4110	0.5890	1	0	0.9670	0.0330	0	1	0
	β				0.9978	1.0000			1.0000	0.9901			
	η				0.3258	0.2274			0.0503	0.3878			
ZGY	P	1	0	0	0.4560	0.5440	1	0	0.9560	0.0440	0	1	0
	β				1.0000	1.0000			1.0000	0.6856			
	η				0.2329	0.1952			0.0457	0.9938			

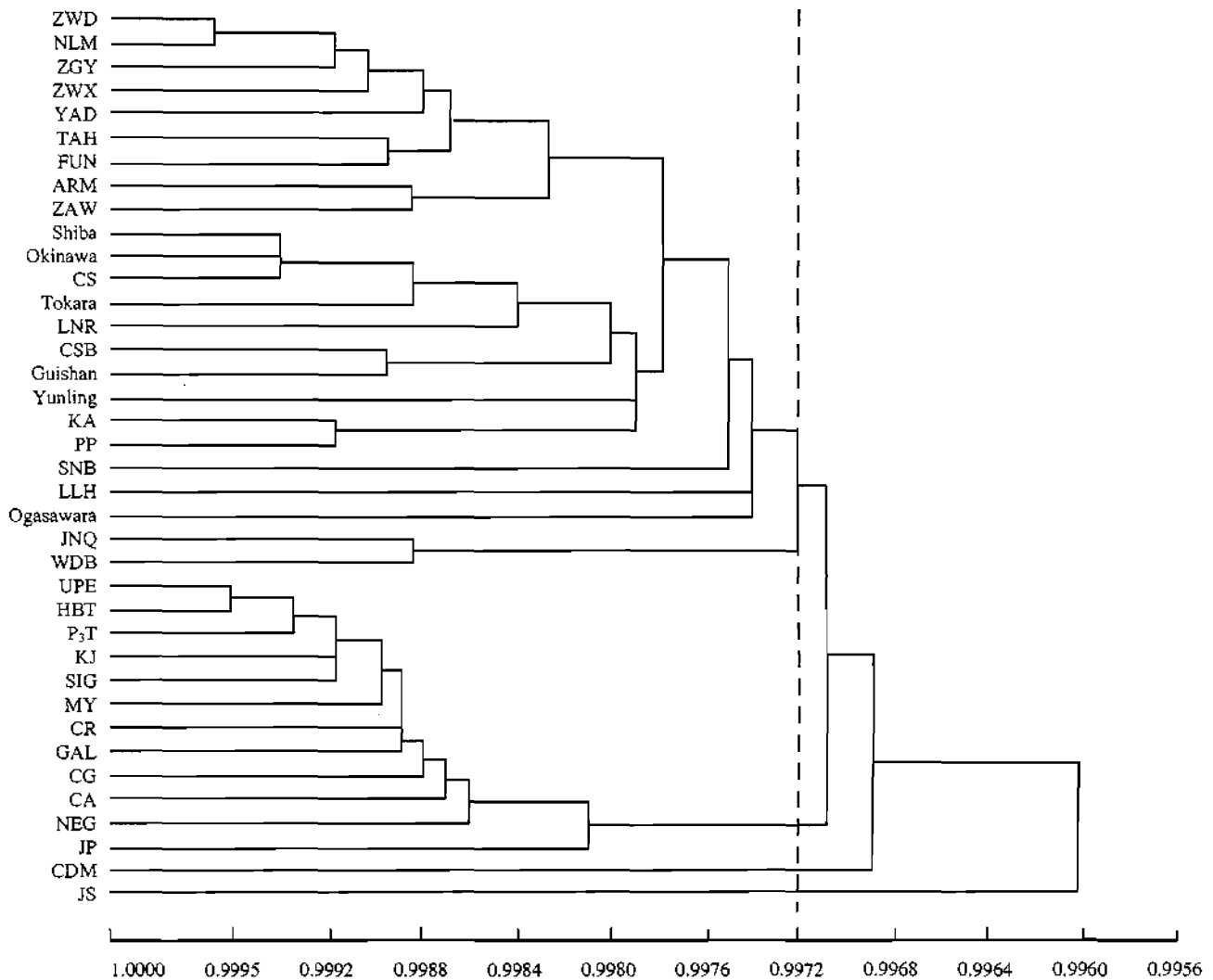


Figure 3. The fuzzy cluster figure of 38 internal and external goat populations

level value, Chengdu Grey Goat and the Japanese Saanen Goat dissociate from all other groups.

DISCUSSION

1. The goats on the two sides of Ziwoiling Mountain Chain and the Alashan Cashmere Goats in Inner Mongolia are generally recognized as belonging to the Mongolian family. The close relationship between the 6 colonies in the middle valley of the Yellow River and the 3 colonies in Tibet indicates that the native goat colonies on the eastern Mongolian Plateau, the Qinghai-Tibetan Plateau and along the middle valley of the Yellow River are of the same origin in their evolution, compared with other goat colonies in China, other countries of East Asia, South Asia and Southeast Asia. Those colonies in the middle valley of the Yellow River are relatively remote in their relation with the colonies in its lower valley near

the sea.

2. This study does not show any cluster trend between colonies along and to the south of the Yangtze valley. They are, basically, approaching the group centered on the colonies along the middle Yellow River valley.

3. The colonies in East Asia and South Asia have each formed their own systems. The colonies in Southeast Asia which are scattered, cluster either with a East Asian group or a South Asian group. They do not cluster among themselves.

4. The afore-mentioned facts prove that the middle valley of the Yellow River is the dissemination center of domestic goats in China and East Asia. The blood lineage of the ancestor colonies in this area comes from the west Mongolian Plateau and the Qinghai-Tibetan Plateau. The goats in this area after long periods of domestication spread eastwards and southwards. Southeastwardly, they finally entered the islands in Southeast Asia and met the gene current

from the sub-continent of India and Pakistan. The result is identical with the conclusion of Nozawa (1991) on the history of the domestication of goats. The "gap" problem in this respect merits further investigation from different angles.

5. On the level value of $\mu_{R37}(x,y) \geq 0.9971$, the Saanen Goat of Japan dissociates from any Asian goat groups, which tallies with the known history of breeding; so does Chengdu Grey Goat, the cause of which awaits further investigation.

CONCLUSIONS

The middle Yellow River valley is one of the taming and disseminating centers of domestic goats in the East and South of Central Asia. Compared with other goat colonies in the East and South of Central Asia, the native goat colonies on western Mongolia Plateau, the Qinghai-Tibetan Plateau and along the middle Yellow River valley share the same origin. The phylogenetic relationship between the colonies along the lower and middle valley of the Yellow River is relatively distant. The native goat colonies in the East and South of Central Asia may be classified into two phylogenetic systems—the East Asian and the South Asian groups. The colonies in Southeast Asia belong either to the former or the latter.

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