

## Study on Origin and Phylogeny Status of Hu Sheep

R. Q. Geng, H. Chang\*, Z. P. Yang, W. Sun, L. P. Wang, S. X. Lu, K. Tsunoda<sup>1</sup> and Z. J. Ren<sup>2</sup>

Animal Science & Veterinary Medical College, Yangzhou University Yangzhou, Jiangsu Province, 225009, China

**ABSTRACT** : Applying simple random sampling in typical colony methods in the central area of habitat, 14 structural loci and 31 alleles in blood enzyme and other protein variations of Hu sheep population are examined. After collecting the same data of 11 loci about the 22 sheep colonies in China and other countries, it clusters the 23 sheep populations by fuzzy cluster analysis. The study proves that the phylogenetic relationship between Hu sheep population and Mongolia populations is relatively closed. This result obtained is shown to conform to the historical data. (*Asian-Aust. J. Anim. Sci.* 2003, Vol 16, No. 5 : 743-747)

**Key Words** : Hu Sheep, Origin, Phylogeny Status, Phylogenetic Relationship

### INTRODUCTION

Hu sheep, as a special local sheep breed of China, it also is one of the several white breeds of the world. Now, there are about 1 million Hu sheep in partial regions of Zhejiang province, Jiangsu province and Shanghai city. Under the given environment of Taihu Lake valley, it has premature, perennial oestrus and other excellent traits with high reproduction character. For a long time, there are several different views about the origin of Hu sheep. Someone thinks it originated from Mongol sheep of Yuan Dynasty. Someone thinks it originated from Mongol sheep or Han sheep in Shandong of Nansong dynasty. Someone thinks it originated from north sheep of "Five Dynasties" times (A. D. 907-A. D. 960). The aim of this paper is to provide new bases for discussing the origin and phylogenetic status among other sheep populations in Asian and European.

### MATERIALS AND METHODS

#### Sampling methods

Applying simple random sampling in typical colony methods in the central area of habitat (Huzhou City Zhejiang Province), 63 Hu sheep were selected. Blood samples are collected and treated according to references (Zhang et al., 1997; Li, 1982).

#### Multiloci electrophoresis

Starch gel electrophoresis is used to determine the variations of the 14 loci in encoded hemoglobin- $\beta$  (Hb- $\beta$ ), Albumin (Al), Post-albumin (P<sub>2</sub>), Transferrin (Tf),

Alkalinephosphatase (Alp), Leucine aminopeptidase (Lap), Arylesterase (Ary-Es), X-protein (X-P), Carbonic anhydrase (CA), Malate dehydrogenase (MDH), Catalase (Cat), Glucosephosphate isomerase (GPI), Lysine (Ly) and potassium (Ke). 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 references (Tsunoda et al., 1988, 1990, 1992).

#### Statistical analysis

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

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

In the above formula, P and V (P) stand for gene frequency and variance, respectively;  $\lambda$  is the standardized deviation of the estimate and is suitable for the first formula when its standardized deviation is  $\lambda = 0.5 \div [V(P)^{\frac{1}{2}}]$ .

Phylogenetic relationship cluster According to the frequency of the genetic loci 11 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.

$$\mu R_{ij}(x, y) = \frac{1}{2} \ln( J_x, y^i \sqrt{J_x \cdot J_y} ) + 1$$

In the above formula, J<sub>x</sub>, J<sub>y</sub> and J<sub>x,y</sub> stand respectively

\* Reprint request to: H. Chang, Tel: +86-514-979350, Fax: +86-514-7350440, E-mail: rqgeng@sohu.com

<sup>1</sup> Showa University School of Medicine, 1-5-8 Hatanodai, Tokyo, Japan.

<sup>2</sup> Northwest Agriculture University, Yangling, Shanxi Province, 712100, P.R. China.

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**Table 1.** Abbreviation, sampling source and data source of 23 sheep populations in China and other countries

Population abbreviation	Sampling population and location	Data source
Kha-KH	Khalkhas Kharkhorin, Mongolia	Tsunoda et al., 1999
Kha-UB	Khalkhas Ulaanhaatar, Mongolia	Tsunoda et al., 1999
Vie-NS	Ninh Son, Vietnam	Tsunoda et al., 1998
Yun-LF	Lufeng, Yunnan Province, China	Tsunoda et al., 1995
Yun-LN	Lunan, Yunnan Province, China	Tsunoda et al., 1995
Bar-SO	Baruwal Solu, Nepal	Tsunoda et al., 1992
Bar-KO	Baruwal Kodari, Nepal	Tsunoda et al., 1992
Bar-KG	Baruwal Kali Gandaki, Nepal	Tsunoda et al., 1992
Kag-KT	Kagi, Kathmandu, Nepal	Tsunoda et al., 1992
Kag-CH	Kagi, Chitlang, Nepal	Tsunoda et al., 1992
Ban-JK	Jessore Khulna, Bangladesh	Tsunoda et al., 1989
Ban-MY	Mymensingh, Bangladesh	Tsunoda et al., 1989
Ban-NO	Noakhali, Bangladesh	Tsunoda et al., 1989
Bhy-KO	Bhyanglung Kodari, Nepal	Tsunoda et al., 1992
Bhy-KG	Bhyanglung Kali Gandaki, Nepal	Tsunoda et al., 1992
Lam-NS	Lampuchhre Narayangath Somnath, Nepal	Tsunoda et al., 1992
Lam-L	Large Lampuchhre, Lumbini, Nepal	Tsunoda et al., 1992
Suf	Suffolk Sheep, raised in Japan	Tsunoda et al., 1988, 1990
Che	Cheviot Sheep, raised in Japan	Tsunoda et al., 1988, 1990
Cor	Corriedale Sheep, raised in Japan	Tsunoda et al., 1988, 1990
Bor	Border Leicester Sheep, raised in Japan	Tsunoda et al., 1988, 1990
Fin	Finnish Landrace Sheep, raised in Japan	Tsunoda et al., 1988, 1990
HY	Hu Sheep, Huzhou city, Zhejiang Province, China	This study, 2001

for population X, population Y and the probability average among loci of the same alleles acquired at random from the first two populations.  $\mu_{\mathbb{R}}(X, Y)$  stands for the membership function under the fuzzy consistency relation  $\mathbb{R}$  between X and Y populations.

#### Quotation of source materials

In the above phylogenetic relationship clusters, the data information of 23 colonies are shown in table 1. These data are reported by other researchers with the same techniques (Tsunoda et al., 1988, 1990, 1992, 1995, 1998, 1999).

Table 1. Abbreviation, sampling source and data source of 23 sheep populations in China and other countries

## RESULTS

**Table 2.** The estimators of gene frequencies in structural loci of Hu sheep population

Locus	Allele	P	V (P)	$\eta$	$\beta$
Al	C	1.0000	0	0	1.0000
Po	F	0.0167	$1.3916 \times 10^{-4}$	1.4128	0.5222
	S	0.9833	$1.3916 \times 10^{-4}$	0.0240	1.0000
Tf	A	0.0416	$3.3788 \times 10^{-4}$	0.8837	0.7416
	B	0.1500	$1.0805 \times 10^{-3}$	0.4383	0.9774
	C	0.3000	$1.7797 \times 10^{-3}$	0.2812	0.9997
	D	0.3417	$1.9063 \times 10^{-3}$	0.2556	0.9999
	E	0.1500	$1.0805 \times 10^{-3}$	0.4383	0.9774
	F	0.0167	$1.3916 \times 10^{-4}$	1.4128	0.5222
Alp	B+	0.3945	$2.0243 \times 10^{-3}$	0.2281	1.0000
	B-	0.6055	$2.0243 \times 10^{-3}$	0.1486	1.0000
Ary-Es	Es+	0.3292	$1.8714 \times 10^{-3}$	0.2628	0.9999
	Es-	0.6708	$1.8714 \times 10^{-3}$	0.1290	1.0000
Lap	A	0.4373	$2.0853 \times 10^{-3}$	0.2089	1.0000
	B	0.5627	$2.0853 \times 10^{-3}$	0.1623	1.0000
Hb- $\beta$	F	0.0238	$1.8737 \times 10^{-4}$	1.1503	0.6156
	S	0.9762	$1.8737 \times 10^{-4}$	0.0280	1.0000
X-p	X	0.2546	$1.5305 \times 10^{-3}$	0.3073	0.9990
	x	0.7454	$1.5305 \times 10^{-3}$	0.1050	1.0000
CA	F	0.0794	$5.8948 \times 10^{-4}$	0.6116	0.8990
	S	0.9206	$5.8948 \times 10^{-4}$	0.0527	1.0000
MDH	F	0.5000	$2.0161 \times 10^{-3}$	0.1796	1.0000
	S	0.5000	$2.0161 \times 10^{-3}$	0.1796	1.0000
Cat	B	0.4444	$1.9912 \times 10^{-3}$	0.2008	1.0000
	C	0.5556	$1.9912 \times 10^{-3}$	0.1606	1.0000
GPI	1	0.7857	$1.3579 \times 10^{-3}$	0.0938	1.0000
	2	0.2143	$1.3579 \times 10^{-3}$	0.3439	0.9964
Ly	A	0.7183	$1.6318 \times 10^{-3}$	0.1125	0.9994
	a	0.2817	$1.6318 \times 10^{-3}$	0.2868	1.0000
Ke	L	0.0828	$6.1245 \times 10^{-4}$	0.5978	0.9050
	h	0.9172	$6.1245 \times 10^{-4}$	0.0540	1.0000

Frequency distribution of blood enzyme and other protein loci accuracy and reliability of the estimate of gene frequencies of Hu sheep are shown in Table 2.

Table 2 The estimators of gene frequencies in structural loci of Hu sheep population of the 14 loci tested, 13 have polymorphism. It is seen from table 2 that the reliability of estimate of 25 alleles apart from  $P_0^F$ ,  $Tf^A$ ,  $Tf^F$ ,  $Hb-\beta^F$ ,  $CA^F$ ,  $Ke^L$  and their reliability is 0.5222, 0.7416, 0.5222, 0.6156, 0.8990 and 0.9050 respectively. So these data may serve as statistical analysis of phylogenetic relationship (Chang et al., 1995).

#### Phylogenetic clusters

The interal and external data are quoted, phylogenetic clusters are performed as standard genetic distance based on gene frequency of 11 blood enzymes and other protein loci

**Table 3.** Fuzzy resemblance relation R (upper right) and fuzzy similarity relation R<sub>23</sub> (lower left)

HY	Kha-KH	Kha-UB	Vie-NS	Yun-LF	Yun-LN	Bai-SO	Bai-KO	Bar-KG	Kag-KT	Kag-CH	Bai-KJ	Ban-MY	Ban-NO	Bhy-KO	Bhy-KG	Lam-NS	Lam-L	Suf	Che	Cor	Ber	Fin
1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23
1.	.9783	.9605	.9342	.9302	.9600	.9366	.9362	.9065	.9234	.9493	.9573	.9317	.9137	.9142	.9257	.9315	.9280	.9674	.9558	.9317	.9575	.9260
.9783	1	.9923	.9596	.9509	.9786	.9397	.9512	.9370	.9334	.9562	.9624	.9217	.9041	.9605	.9659	.9455	.9242	.9618	.9572	.9432	.9669	.9516
.9783	.9923	1	.9491	.9506	.9614	.9224	.9244	.9069	.9028	.9273	.9508	.9137	.8961	.9429	.9416	.9231	.9156	.9351	.9309	.9135	.9413	.9196
.9764	.9764	.9764	1	.9349	.9617	.9177	.9474	.9516	.9522	.9659	.9756	.9255	.8874	.9745	.9545	.9848	.9557	.9659	.9580	.9655	.9713	.9507
.9509	.9509	.9509	.9509	1	.9442	.9441	.9492	.9451	.9481	.9498	.9475	.9417	.9028	.9299	.9020	.9358	.9291	.9255	.9327	.9180	.9156	.9029
.9783	.9786	.9786	.9764	.9509	1	.9421	.9761	.9508	.9443	.9737	.9678	.9088	.9098	.9518	.9597	.9590	.9468	.9747	.9596	.9490	.9764	.9261
.9764	.9764	.9764	.9766	.9509	.9764	1	.9766	.9649	.9659	.9730	.9760	.9723	.9690	.8965	.8927	.9503	.9004	.9275	.9134	.9392	.9328	.9166
.9764	.9764	.9764	.9843	.9509	.9764	.9766	1	.9787	.9791	.9917	.9718	.9375	.9359	.9426	.9406	.9673	.9402	.9578	.9410	.9509	.9640	.9335
.9764	.9764	.9764	.9843	.9509	.9764	.9766	.9857	1	.9857	.9829	.9624	.9376	.9092	.9599	.9459	.9759	.9023	.9352	.9391	.9690	.9471	.9581
.9764	.9764	.9764	.9843	.9509	.9764	.9766	.9858	.9857	1	.9858	.9673	.9659	.9210	.9440	.9204	.9798	.9434	.9444	.9321	.9661	.9480	.9545
.9764	.9764	.9764	.9843	.9509	.9764	.9766	.9917	.9857	.9858	1	.9823	.9477	.9310	.9469	.9599	.9843	.9411	.9756	.9630	.9742	.9796	.9513
.9764	.9764	.9764	.9848	.9509	.9764	.9766	.9843	.9843	.9843	.9843	1	.9702	.9640	.9567	.9280	.9861	.9503	.9689	.9499	.9667	.9664	.9363
.9723	.9723	.9723	.9723	.9509	.9723	.9723	.9723	.9723	.9723	.9723	.9723	1	.9604	.8834	.8898	.9496	.9337	.9089	.8885	.9298	.9050	.9042
.9690	.9690	.9690	.9690	.9509	.9690	.9690	.9690	.9690	.9690	.9690	.9690	.9690	1	.8399	.8405	.9196	.8945	.8965	.8619	.8899	.8869	.8518
.9745	.9745	.9745	.9745	.9509	.9745	.9745	.9745	.9745	.9745	.9745	.9745	.9723	.9690	1	.9881	.9560	.9166	.9331	.9416	.9439	.9505	.9678
.9745	.9745	.9745	.9745	.9509	.9745	.9745	.9745	.9745	.9745	.9745	.9745	.9723	.9690	.9881	1	.9403	.8878	.9360	.9403	.9306	.9493	.9628
.9764	.9764	.9764	.9848	.9509	.9764	.9766	.9843	.9843	.9843	.9843	.9861	.9723	.9690	.9745	.9745	1	.9486	.9684	.9594	.9837	.9682	.9589
.9557	.9557	.9557	.9557	.9509	.9557	.9557	.9557	.9557	.9557	.9557	.9557	.9557	.9557	.9557	.9557	.9557	1	.9406	.9047	.9082	.9278	.8745
.9764	.9764	.9764	.9796	.9509	.9764	.9766	.9796	.9796	.9796	.9796	.9796	.9723	.9690	.9745	.9745	.9796	.9557	1	.9826	.9707	.9865	.9417
.9764	.9764	.9764	.9796	.9509	.9764	.9766	.9796	.9796	.9796	.9796	.9796	.9723	.9690	.9745	.9745	.9796	.9557	.9826	1	.9784	.9798	.9574
.9764	.9764	.9764	.9837	.9509	.9764	.9766	.9837	.9837	.9837	.9837	.9837	.9723	.9690	.9745	.9745	.9837	.9557	.9796	.9796	1	.9780	.9735
.9764	.9764	.9764	.9796	.9509	.9764	.9766	.9796	.9796	.9796	.9796	.9796	.9723	.9690	.9745	.9745	.9796	.9557	.9865	.9826	.9796	1	.9556
.9735	.9735	.9735	.9735	.9509	.9735	.9735	.9735	.9735	.9735	.9735	.9735	.9723	.9690	.9735	.9735	.9735	.9557	.9735	.9735	.9735	.9735	1

\* The zero before the decimal point of the data is omitted in this table.

in 23 sheep populations. The fuzzy resemblance relation  $\underline{R}$  (upper right) and fuzzy similarity relation  $\underline{R}_{23}$  (lower left) are shown in table 3.

Figure 1 shows the phylogenetic relationship among 23 populations, the base of which is the fuzzy similarity matrix.

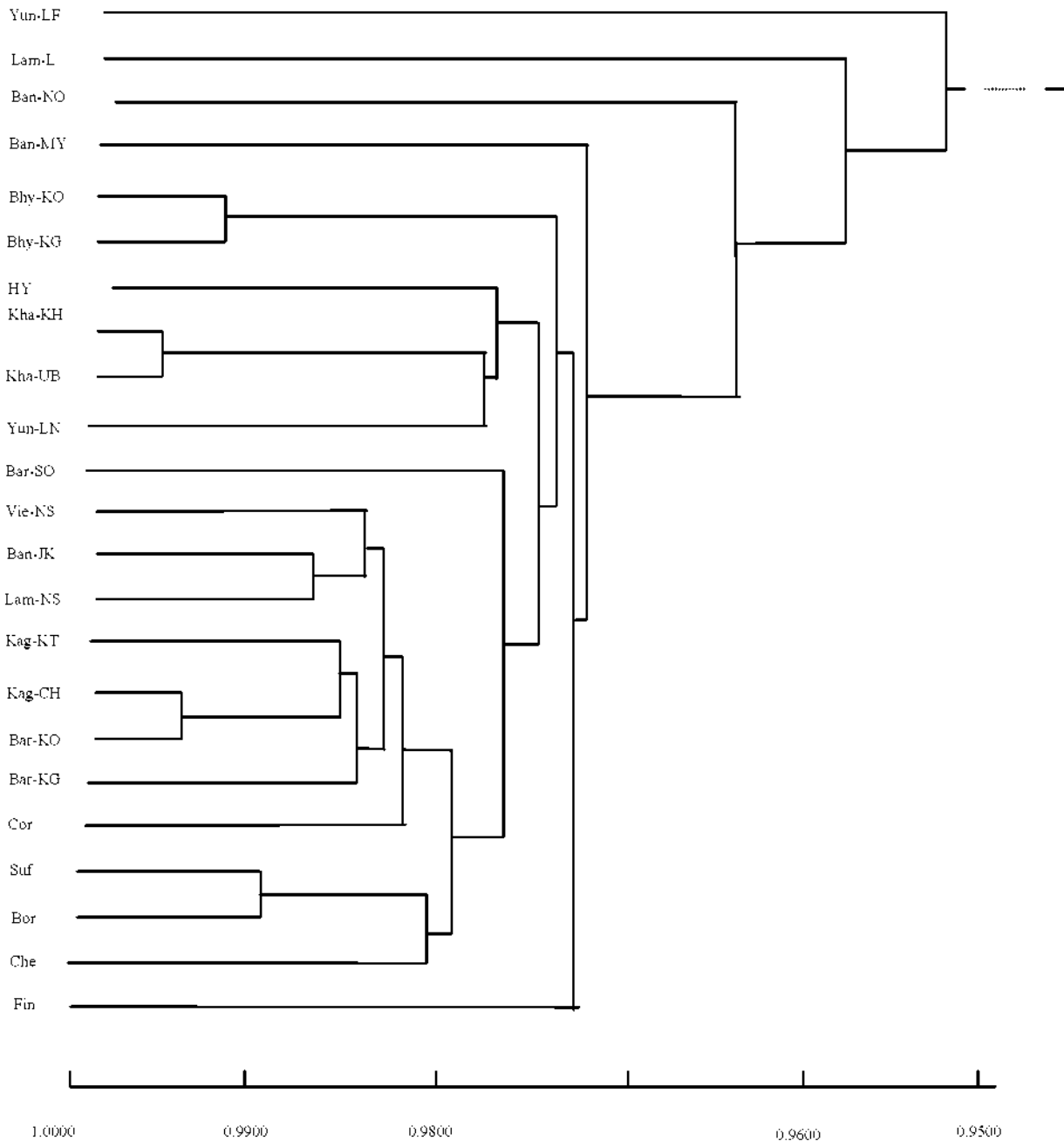
From figure 1, we can see that on the value level of 0.9783, Hu sheep population, Kha-KH, Kha-UB populations of Mongolia and Yun-LN populations of Yunnan are clustered; Corriedale sheep and 7 Asian populations are clustered on the value level of 0.9837. Finnish Landrace sheep dissociate from some Asian and European populations.

### DISCUSSION AND CONCLUSIONS

Phylogenetic clusters is a basic methods to analyze

origin of livestock and poultry, probing relative osculation degree among breeds within species or populations quantitatively. It represents a new idea, makes up the shortcoming of classical clusters which ignores the continuity of difference among breeds. It may reflect a dynamic bloodline.

Hu sheep is generally recognized as belonging to the Mongolian family. This study proves that the phylogenetic relationship is relatively closed between Hu sheep and Mongolian populations. It shows that they may share the same origin in fairly recent times. This result obtained conforms to the historical data. According to recorded historical data, the sheep of the Mongolian family lives on the Mongolian grassland early. Along the evolve of history, large quantities of numbers of the Mongolian sheep moves to Taihu Valley which is recorded in "shu guo chun qiu"(Wu, Qing Dynasty). Under the effects of natural, economic and



**Figure 1.** Phylogenetic relationship among populations

social factors, it forms a unique sheep breed---Hu sheep gradually.

Finnish Landrace sheep dissociates among some Asian and European populations. This fact reminds us of the background of evolution. Until the 16th century, there has no record about Finnish, which belongs to ural phylum. Some linguists think that ural and Altai belongs to the same phylum. Under this society background, it is possible to keep part neutral stactual loci which restricts blood protein for Finnish Lardrace sheep.

In addition, the phylogenetic relationship between

Corriedale sheep and some Asian sheep populations is relatively closer, the cause of which awaits further investigation (Note: Mr. Geng Rongqing now is in the Teacher College of Yancheng).

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