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Detection of phylogenetic extraction of sheep populations in East and South Asia based on fuzzy discriminants analysis

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Based on the previous research, according to the Hierarchy clustering, the sheep populations in East and South Asia were divided into 3 groups: Mongolia group, South-Asia group and European group. In this study, the extraction of sheep was demonstrated by two discriminants based on fuzzy discriminants analysis. The discriminants were verified with sheep populations presented 34 alleles in 10 loci. The result showed the second discriminant might be the best known discriminant, which is derived from the theory of genetic approach degree formula: $(I, X) = 1 - \xi(I, X) = 1 - \frac{2}{K} \sum_{j=1}^K |\mu_I(P_j) - \mu_X(P_j)|$

Where $\mu_I(P_j)$ is the membership function of allele No, j is the group No I, $\mu_X(P_j)$ is the allele No, j is to distinguished population X, viz., the gene frequencies of allele j in group I, in population X, respectively; K is the number of allele; $\xi(I, X)$ is the linear genetic fuzzy degree. The extraction of an unknown population was checked using the second discriminant, the result proved that the genetic approach degree was reliable for discriminant of extraction in East and South Asia, which also might reflect the course of extraction breeding of Tong Sheep, Hu Sheep and Yunnan Sheep in China, and of course, it might be extended to other genetic markers.

Key words: Sheep, genetic approach degree, extraction, fuzzy discriminant.

INTRODUCTION

Hierarchy clustering analysis played a great role in indicating the phylogenetic relationship of livestock and poultry and is still the useful method. But the phylogenetic relationships of most animal and poultry in an abroad field have been known and some data have been obtained, we only want to judge the extraction belonging to single

breed or few breeds. Fuzzy discriminants analysis is more accurate and convenient method; it uses discriminants to judge the belonging of population through the comparison of different approach degree.

Since there are different degree phylogenetic relationship among populations of the same species, the fuzzy discriminants analysis is practical than that of classical mathematics. From 1980s, there were many hierarchy clustering data about the sheep populations in East and South Asia (Tsunoda et al., 1988; 1990; 1992; 1995; 1998; 1999; 2004; 2006); the previous research found

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that the sheep populations in the East and South of Central Asia could be classified in the three genetic groups: Mongolia sheep, South-Asia sheep and European sheep (Sun et al., 2002).

The origin of many sheep populations is still unknown in this area; to determine the genetic origin of sheep populations, we used the fuzzy discriminant of sheep extraction in the present study.

Theory discussion

The known groups and unknown population were regarded as the fuzzy subset of limited discussion area of the sheep populations in East and South of Central Asia, all the targeted alleles were regarded as element and the gene frequencies in the groups or population were regarded as the membership function of the fuzzy subset. So: first, the first discriminant can be made according to the thought of approach degree (Lou, 1987) and the genetic approach degree which was described by inner product and exterior product of fuzzy subset:

$$(\underline{I}, \underline{X}) = \frac{1}{2} \left[\underline{I} \cdot \underline{X} + 1 - (\underline{I} \odot \underline{X}) \right]$$

in which

$$\underline{I} \cdot \underline{X} = \bigvee_{P_j \in P} [\mu_{\underline{I}}(P_j) \wedge \mu_{\underline{X}}(P_j)]$$

$$\underline{I} \odot \underline{X} = \bigwedge_{P_j \in P} [\mu_{\underline{I}}(P_j) \vee \mu_{\underline{X}}(P_j)]$$

where \wedge stands for the selection of the minimum value between its two sides, and \vee the maximum value.

Second, since the gene frequency is the maker of gene pool, the fuzzy degree between the known group and unknown population may be logically defined as "the linear genetic fuzzy degree", the genetic approach degree is given a definition as remainder which is 1 minus the liner genetic fuzzy degree, mathematically and genetically is indicated in the following formula:

$$(\underline{I}, \underline{X}) = 1 - \xi(\underline{I}, \underline{X}) = 1 - \frac{2}{K} \sum_{j=1}^K |\mu_{\underline{I}}(P_j) - \mu_{\underline{X}}(P_j)|$$

Where $\mu_{\underline{I}}(P_j)$ is the membership function of j^{th} to the known group Ith, $\mu_{\underline{X}}(P_j)$ is the j^{th} allele to distinguished

population X, that is , the gene frequencies of allele j in group I and population X, respectively; K is the number of alleles; $\xi(\underline{I}, \underline{X})$ is the linear genetic fuzzy degree.

Practical demonstration

Demonstrative way

The two discriminants were used hypothetically to judge some populations whose belonging extractions were known. The better discriminant was selected on the basis of hypothetically judged result, and then used the best discriminant to judge the extraction belonging of an unknown population.

MATERIALS

Known materials

The known materials include the average 34 gene frequencies from 10 loci in 3 groups, the gene frequencies of 10 judged populations from the same loci, all data were the raw materials of our research in East and South Asia (Sun et al., 2002). The materials are showed in Table 1.

Materials need to be judged

Sampling

Tong sheep whose extraction unknown was sampled in the Baishui country of Shannxi province of China by "Random sampling in typical colonies of central area" and any two (or more) individual with traceable phylogenetic relationship were avoided.

Multiloci electrophoresis

Starch gel electrophoresis was used to determine the variations of the 11 loci: albumin (Al), post-albumin (Po), transferrin (Tf), alkaline phosphatase (Alp), leucine aminopeptidase (Lap), arylesterase (Ary-Es), hemoglobin- β (Hb- β), X-protein(X-p), carbonic anhydrase (CA), catalase (Cat) and malate dehydrogenase (MDH), lysine (Ly) was tested with cellulose acetate film electrophoresis. The types of the variations were determined according to the standards universally accepted in the countries neighboring China (Tsunoda et al., 1998; 1992).

Statistical analysis

Gene frequencies for polymorphic traits were computed by the gene counting method for the Al, Gc, Tf, Hb- β , CA, Cat and MDH loci and by the square root method for the Alp, Lap, Ary-Es, X-p and Ly loci (Tsunoda et al., 1990).

The following two formulae were used to calculate the reliability that ensures the estimate not to deviate from the true value more than 0.5 times (β) and the relative deviation when the reliability reaches 0.9545(η) (Chang et al., 1995).

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

In the above formula, P and V(p) stand for gene frequency and gene variance, respectively; λ is the standardized deviation of the estimated and is suitable for the first formula when its standardized deviation is:

Table 1a. The means of gene frequencies in known 3 groups and the gene frequencies in 10 populations.

Population	Al				Tf												Alp
	A	B	C	X	A	B	C	D	E	F	G	H	I	J	K	M	B ⁺
Yunnan	0	0	1	0	0.714	0.2143	0	0.0286	0.6857	0	0	0	0	0	0	0	0.2829
Hu	0	0	1	0	0.0982	0.0357	0.2857	0.2054	0.1518	0.1875	0	0	0	0	0	0.0357	0.3945
Lam	0	0	1	0	0	0	0.2955	0.1136	0.5909	0	0	0	0	0	0	0	0
Bhy	0	0	1	0	0.0732	0.061	0.3658	0.1219	0.3537	0.0122	0.0122	0	0	0	0	0	0.5583
Ban	0.197	0	0.803	0	0.039	0.013	0.178	0	0.757	0.013	0	0	0	0	0	0	0.02
Kh	0	0	1	0	0.0859	0.1263	0.3131	0.1768	0.197	0.0404	0	0.005	0.0101	0.0101	0.0353	0	0.215
Viet	0	0	1	0	0	0	0.5441	0	0.3824	0.0735	0	0	0	0	0	0	0
Suf	0	0	1	0	0.122	0	0.265	0.187	0.135	0.291	0	0	0	0	0	0	0.334
Che	0	0	1	0	0	0.052	0.276	0.586	0.069	0.017	0	0	0	0	0	0	0.475
Cor	0	0	1	0	0.175	0.042	0.15	0.425	0.142	0.066	0	0	0	0	0	0	0.051
Mongolia	0	0	1	0	0.2413	0.1368	0.2435	0.1703	0.3252	0.0207	0.0026	0.0013	0.0025	0.0025	0.0088	0	0.2732
South-Asia	0.0394	0	0.9606	0	0.0101	0.0073	0.2352	0.0252	0.6976	0.0197	0.0197	0.0024	0	0	0	0	0.014
European	0	0	1	0	0.1114	0.0292	0.3265	0.3240	0.1363	0.0707	0.0020	0	0	0	0	0	0.2594
Tong	0	0	1	0	0.0781	0.0625	0.25	0.0469	0.4922	0.0313	0	0	0	0	0.0234	0.0156	0.1497

Yunnan (Yunnan sheep, Yunnan Province of China), Hu sheep (Huzhou city of China), Lam (Lampuchhre sheep, Nepalese), Bhy (Bhyanglung sheep, Bangladeshi), Kh (Kharkhorin sheep, Central Mmongolia), Viet (Vietnamese sheep, Vietamese), Suf (Suffolk sheep, breeds in Japan), Che (Cheviot sheep, breeds in Japan), Cor (Corriedale sheep, breeds in Japan).

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

RESULTS

The contrast between judged and practical extraction in 10 known populations

The judged extraction conformed with the practical extraction by discriminant 2 (Table 2). While using discriminant 1, the judged extraction either did not conform with the practical extraction or was not certain. The reason derived from the judging

method, which valued alleles frequencies 0 or 1, resulting in high inner product (near 1) and low exterior product (near 0) among 10 known populations and a higher approach degree value.

The estimates of gene frequencies and their reliability and precision

The accuracy and reliability of estimate of gene frequencies of Tong sheep are shown in Table 3. From the 12 loci tested, 11 loci have polymorphism. The reliability of the estimate of 29 alleles reached 0.95 except TfA, TfB, Tf^D, Tf^K, Tf^M and

CA^F. So "Random sampling in typical colonies of central area" was a useful method, these data might be used in statistical analysis of phylogenetic relationship.

The judgement of extraction for Tong sheep by the second discriminant

The extraction of Tong sheep belonged to the "Mongolia group" by discriminant 2 (Table 4), which conformed with the known history (Lei, 1999): Tong sheep was bred between Xiwei Dynasty and Tang Dynasty about 1200 to 1500

Table 1b. The means of gene frequencies in known 3 groups and the gene Frequencies in 10 populations (continued).

Population	Alp	Es		Lap		Hb- β			x-p		CA		Cat			Ly	
	B ⁻	Es ⁺	Es ⁻	A	B	A	B	C	X	x	F	S	A	B	C	A	a
Yunnan	0.7171	0.1894	0.8106	0.4145	0.5855	0.1571	0.5857	0.2572	0.0438	0.9562	0	1	0	0.7571	0.2429	0.7072	0.2928
Hu	0.6055	0.3292	0.6708	0.4373	0.5627	0.0574	0.5492	0.3934	0.22546	0.7454	0.0794	0.9206	0	0.2128	0.7872	0.7183	0.2817
Lam	1	0.0707	0.9293	0.7868	0.2132	0.4546	0.5227	0.0227	0.4359	0.5641	0.0454	0.9546	0	0.4444	0.5556	0.5821	0.4179
Bhy	0.4417	0.5583	0.4417	0.4156	0.5844	0.7805	0.0122	0.2073	0	1	0	1	0	0.9756	0.0244	0.7791	0.2209
Ban	0.98	0.089	0.911	0.719	0.281	0.1908	0.8092	0	0.372	0.628	0.007	0.993	0	0.414	0.586	0.771	0.229
Kh	0.785	0.414	0.586	0.414	0.586	0.1515	0.5152	0.3333	0.518	0.9482	0	1	0	0.5455	0.4545	0.7706	0.2294
Viet	1	0	1	0.4577	0.5423	0.6029	0.3971	0	0.2724	0.7276	0	1	0	0.8971	0.1029	0.5528	0.4472
Suf	0.666	0.095	0.904	0.502	0.498	0.074	0.926	0	0.29	0.71	0	1	0.013	0.94	0.047	1	0
Che	0.525	0.035	0.965	0.646	0.354	0.31	0.69	0	0.035	0.965	0	1	0	0.977	0.023	1	0
Cor	0.949	0.017	0.983	1	0	0.392	0.608	0	0.204	0.796	0	1	0	0.977	0.023	1	0
Mongolia	0.7268	0.3091	0.6909	0.3924	0.6076	0.1231	0.6005	0.2765	0.2229	0.9046	0.0199	0.9802	0	0.5283	0.4718	0.7229	0.2771
South-Asia	0.986	0.1425	0.8575	0.7522	0.2478	0.3117	0.5083	0.18	0.2591	0.7409	0.0105	0.9895	0	0.6926	0.3072	0.737	0.263
European	0.7406	0.2264	0.7736	0.6861	0.3139	0.3688	0.5967	0.0346	0.1078	0.8922	0	1	0.0022	0.9689	0.0289	0.967	0.037
Tong	0.8503	0.5196	0.4804	0.4886	0.5114	0.1746	0.4762	0.3492	0.1129	0.8871	0.0462	0.9538	0	0.2846	0.7154	0.7519	0.2481

Lam (Lampuchhre sheep, Nepalese), Bhy (Bhyanglung sheep, Bangladeshi), Kh (Kharkhorin sheep, Central Mmongolia), Viet (Vietnamese sheep, Vietramese), Suf (Suffolk sheep, breeds in Japan), Che (Cheviot sheep, breeds in Japan), Cor (Corriedale sheep, breeds in Japan).

Table 2. The contrast between judged and practical extraction in sheep.

Populatio n	Genetic approach degree						Extraction		
	Discriminant 1			Discriminant 2			Discriminant 1	Discriminant 2	Practical
	“Mongolia”	“South-Asia”	“European”	“Mongolia”	“South-Asia”	“European”	Judged	Judged	
Yunan	1	0.99475	1	0.8506	0.7758	0.7447	“Mongolia”, “European”	“Mongolia”	“Mongolia”
Hu	1	0.9803	1	0.8637	0.7216	0.7553	“Mongolia”, “European”	“Mongolia”	“Mongolia”
Lam	1	0.993	1	0.7383	0.8680	0.7164	“Mongolia”, “European”	“South-Asia”	“South-Asia”
Bhy	1	0.99475	1	0.7422	0.6631	0.7473	“Mongolia”, “European”	“European”	“European”
Ban	0.9015	0.99475	0.9965	0.7369	0.8687	0.7015	“European”	“South-Asia”	“South-Asia”
Kh	1	0.99475	1	0.9099	0.7641	0.7636	“Mongolia”, “European”	“Mongolia”	“Mongolia”
Viet	1	0.99475	1	0.7227	0.8103	0.7496	“Mongolia”, “European”	“South-Asia”	“South-Asia”
Suf	1	0.99475	1	0.7638	0.7191	0.8550	“Mongolia”, “European”	“European”	“European”
Che	1	0.99475	1	0.7089	0.7173	0.8859	“Mongolia”, “European”	“European”	“European”
Cor	1	0.9895	1	0.6866	0.7649	0.8680	“Mongolia”, “European”	“European”	“European”

Table 3. The estimates of gene frequencies and their reliability and precision.

Locus	Alleles	P	V _p	λ	β	η
Al	Al ^C	1	0	0	1	0
	Po ^S	1	0	0	1	0
Tf	Tf ^A	0.0781	5.625×10 ⁻⁴	1.647	0.9010	0.6074
	Tf ^B	0.0625	4.578×10 ⁻⁴	1.461	0.8558	0.6846
	Tf ^C	0.25	1.465×10 ⁻³	3.267	1	0.3062
	Tf ^D	0.0469	3.4922×10 ⁻⁴	1.2541	0.7888	0.7969
	Tf ^E	0.4922	1.953×10 ⁻³	1.017	1	0.1796
	Tf ^F	0.0313	2.369×10 ⁻⁴	0.876	0.6922	0.9834
	Tf ^K	0.0234	1.785×10 ⁻⁴	0.712	0.6212	1.1420
Alp	Tf ^M	0.0156	1.120×10 ⁻⁴		0.5222	1.4043
	B ⁺	0.1497	9.792×10 ⁻⁴	2.392	0.9832	0.4181
Es	B ⁻	0.8503	9.792×10 ⁻⁴	13.587	1	0.0736
	Es ⁺	0.5196	1.920×10 ⁻³	5.929	1	0.1687
Lap	Es ⁻	0.4804	1.920×10 ⁻³	5.482	1	0.1824
	Lap ^A	0.4886	1.922×10 ⁻³	5.572	1	0.1795
Hb-β	Lap ^B	0.5114	1.922×10 ⁻³	5.832	1	0.1715
	A	0.1746	1.144×10 ⁻³	2.5813	0.9901	0.3874
X-p	B	0.4762	1.980×10 ⁻³	5.3514	1	0.1869
	C	0.3492	1.804×10 ⁻³	4.1112	1	0.2432
CA	X	0.1129	8.209×10 ⁻³	1.9702	0.9512	0.5076
	X	0.8871	8.209×10 ⁻³	15.4807	1	0.0646
MDH	CA ^F	0.0462	3.390×10 ⁻⁴	1.255	0.7924	0.7970
	MDH ^F	0.3615	1.776×10 ⁻³	4.390	1	0.2331
Cat	MDH ^S	0.6385	1.776×10 ⁻³	7.576	1	0.1320
	Cat ^B	0.2846	1.566×10 ⁻³	3.5957	1	0.2781
Ly	Cat ^C	0.7154	1.566×10 ⁻³	9.0385	1	0.1106
	Ly ^A	0.7519	1.435×10 ⁻³	9.924	1	0.1008
	Ly ^a	0.2481	1.435×10 ⁻³	3.275	1	0.3054

years ago, and it is the descendant of Mongolia sheep.

DISCUSSION

The result of first discriminant can not wholly reflect the difference of gene frequencies between judged populations and known groups, and the extreme value of allele frequencies will make great effect on the result, so the first discriminant is not the best. The second discriminant may reflect the difference of all alleles frequencies between judged population and known groups, its fact is 1 minus average genetic distance between known group and judged population, and it is more strict in mathematics and genetics, adapting this discriminant not only may let the genetic approach degree conform with the fact that the extraction of each population is in the term of fuzzy change, but also may judge the extraction belonging of judged population according to the approach principle of fuzzy set.

The genetic approach degree between kh sheep, Hu sheep, Yunnan sheep, Tong sheep and Mongolia sheep is 0.9099, 0.8637, 0.8506 and 0.8359, respectively (Tables 2 and 4), which also conformed by the breeding course, indicating that the four populations have the same origin. The Mongolia sheep is the origin of Hu sheep, Yunnan sheep and Tong sheep. The findings can also be supported by the known history of breeding: Mongolia sheep immigrated into the Taihu valley when the Nan-Song Dynasty moved their former capital to Linan (that is, Hangzhou) (Editorial committee of the "breeds of domestic animal and poultry in China et al., 1989). The study can prove the origin of Hu sheep. Yunnan sheep distributed in the Tibet-Dian area, there were gene exchanging in this area according to the history, the genetic structure of Yunnan sheep may be affected by gene exchanging in certain degree (Animal Bureau of Yunnan Province et al., 1989). Therefore, the relationship between Yunnan sheep and Mongolia group is further than that of between Hu sheep and Mongolia

Table 4. The judgement of extraction for Tong sheep in China.

Population	Group	Genetic approach degree	Belonging of extraction
Tong sheep	"Mongolia"	0.8359	"Mongolia"
	"South-Asia"	0.7581	
	"European"	0.7779	

sheep, but the main gene resource of Yunnan sheep belong to Mongolia group, and the Yunnan sheep cluster with the Mongolia sheep, the genetic approach degree between Yunnan sheep and Mongolia Sheep, South-Asia sheep and European sheep is 0.8506, 0.7758 and 0.7447, respectively, which also reflect the known history.

The extraction of Tong sheep comprise some extraction of Han Large-tailed sheep, while the Han Large-tailed sheep originated from the fat-tailed sheep in ancient central Asia and west Asia, it extended to Xinjiang, Gansu and Shannxi in China along the Silk Road" (Li, 1993), and inevitably the Tong sheep may mix some extrinsic extraction. The genetic approach degree between Tong sheep and Mongolia group, South Asia group and European group is 0.8359, 0.7779 and 0.7581, respectively (Table 4). It is reasonable to believe that South Asia group and European group exerted more effect on the extraction of Tong sheep than that of Hu sheep and Yunnan sheep, which may reflect the known history.

Conclusion

The genetic approach degree defined by the second discriminant is reliable grounds for the discriminant of extraction in East and South Asia, and it may be extended to other genetic markers. The genetic approach degree defined by the second discriminant may reflect the breeding course of Tong sheep, Hu sheep and Yunnan sheep in China.

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