Journal of Animal and Veterinary Advances 8 (6): 1070-1074, 2009
ISSN: 1680-5593

Influence of Environmental Factors on the Genetic Diversity of Sheep

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Abstract: Multivariate analysis was used to investigate the influence of environmental factors from animal habitat on the genetic diversity of sheep populations. Populations were classified based on their morphological features and environmental indices into 2 groups, the 1st group includes Mongolia sheep and Tan sheep, they were distributed in the pastoral and agro-pastoral area, respectively. The area was characterized by high elevation, low rainfall and low annual mean temperature. The 2nd group includes Han large-tailed sheep, Han small-tailed sheep, Tong sheep and Hu sheep, they were in agricultural area and the area was characterized by low elevation, high rainfall and high annual mean temperature. The result showed that the elevation and annual rainfall were play important role in the distribution of sheep populations.

Key words: Sheep, environmental factors, genetic diversity, influence, pastoral, agro-pastoral

INTRODUCTION

The realization that 32% of recorded animal genetic resources are at risk of being lost has stimulated national livestock conservation efforts (Scherf, 2000). The need for conservation is based on economic, cultural and ecological values; unique biological characteristics; shifts in market demand and research needs (Oldenbroek, 1999). It is generally accepted that environmental heterogeneity acts as a diversifying force by providing many selection pressures to which a species must adapt (Nevo, 2001). As such, one might expect that areas with the highest heterogeneity would tend to harbour the highest levels of genetic diversity within a species. There is little evidence of climate-forcing on mammalian evolution (Alroy *et al*., 2000). Jernvall and Fortelius (2002) was link between the drying climate of Europe during the Neogene and evolution of hypsodonty in mammals.

Qualitative and quantitative analyses of the links between morphological variations and both ecological factors and constraints have become increasingly widespread in the last decades (Klingenberg and Ekau, 1996; Schluter, 1996; Zani, 2000). Comparisons between a large number of species and assessments of morphological variability have been widely used in ecomorphology or community ecology (Klingenberg and Ekau, 1996; Zani, 2000), but few studies have depicted multi character morphological variation in an integrated way as it can be done with geometric morphometric tools (Rber and Adams, 2001; Claude *et al*., 2003). Multivariate analysis is the only meaningful technique that examines the relationships among several variables, which helps to determine affinities between individuals and considers the variation in such variables as a whole, allows exploration of variation in a multidimensional scale (Isabel *et al*., 2003). Multivariate analysis has been used extensively in ecological studies (Saila and Martin, 1987; Rodriguez and Magnan, 1995). In the present study, we used multivariate analysis to investigate the influence of environmental factors from animal habitat on the genetic diversity of sheep populations.

MATERIALS AND METHODS

Data collection: Data was collected from 6 Chinese sheep population in their habitat, these populations includes Hu sheep (HU) from Huzhou city of Zhejiang province and Tong sheep (TONG) from Baishui county of Shannxi Province, Han large-tailed sheep (DWH) and Han small-tailed (XWH) sheep from agricultural area, Mongolian sheep (MEG) from pastoral area and Tan sheep from agro-pastoral area (Zheng, 1980). The phenotypic data collected from sheep population includes body measurements (Height at withers, body length, heart girth, tail length and tail width) (Table 1), morphology characters (have horn, don't have horn, self fleece color,

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Corresponding Author: W. Sun, College of Animal Science and Technology, Yangzhou University, Yangzhou 25009, China head and legs with colored extremities, spotted fleece color and dark brown fleece color) (Table 2) and environmental indices (Elevation, average of annual temperature, average of the lowest temperature, average of the highest temperature, range of annual temperature and rainfall) (Table 3).

Statistical analysis: Q hierarchical clustering based on 17 quantitative indices was used to analyze the genetic diversity of sheep populations. Principal component with cumulative

$$\Lambda = \frac{\sum_{i=1}^{k} X}{\sum_{i=1}^{n} X} \geq 85\%$$

were selected for each population. Euclid distances among the populations were computed according to the principal components of each population and then R-type hierarchical cluster was used. All data were analyzed by SAS and SPSS statistical package.

Table 1: Body measurements of sheep populations

Population	(X_1)	(X_2)	(X_3)	(X_4)	(X_5)
			(cm)		
MEG	64.3	69.8	83.4	14.50	12.50
TAN	61.8	71.6	62.6	29.70	8.10
DWH	64.1	68.5	87.3	27.30	18.60
XWH	69.1	69.4	79.4	17.00	12.20
TONG	62.0	67.5	82.4	18.70	23.30
HU	67.2	78.5	87.3	10.98	9.41

X_1: Height at withers, X_2: Body length, X_3: Heart girth, X_4: Tail length and X_5: Tail width

Table 2: Phenotype frequencies of morphology characters on sheep population

	Horn			Fleece colors			
Population	(X_6)	(X_7)	(X_8)	(X_9)	(X_{10})	(X_{11})	Tail type
MEG	0	1	32.11	56.94	8.08	18.7	Short fat-tail
TAN	0	1	21.00	72.00	7.00	0.0	Long fat-tail
DWH	0	1	70.45	25.97	3.58	0.0	Long fat-tail
XWH	1	0	71.99	25.07	3.13	0.0	Short fat-tail
TONG	0	1	100.00	00.00	0.00	0.0	Long and short fat-tail
HU	0	1	94.00	5.00	1.00	0.0	Short fat-tail

X_6: Have horn, X_7: Don't have horn, X_8: Self fleece color; X_9: Head and legs with colored extremities; X_{10}: Spotted fleece color and X_{11}: Dark brown fleece color

Table 3: Distribution of the ecological characters of sheep habitat

	X_{12}	X_{13}	X_{14}	X_{15}	X_{16}	X_{17}	
Population	(m)			(°C)		(mm)	Natural characters
MEG	990	1.8	-39.5	36.9	75.9	269.3	Drought, high plain
TAN	1185	9.0	-23	35.9	58.9	228.0	Drought,d esert plain
DWH	36.7	12.8	-21.3	41.4	62.7	560.2	Wetness, plain, complement food
XWH	49.7	13.6	-20.4	42.0	62.4	691.7	Wetness, plain, complement food
TONG	368	13.3	-16.2	42.8	59.0	538.0	Wetness, plain, complement food
HU	7.2	16.2	-9.6	38.5	48.1	1246	Wetness, plain, complement food

X_{12}: Elevation, X_{13}: Average of annual temperature, X_{14}: Average of the lowest temperature, X_{15}: Average of the highest temperature, X_{16}: Range of annual temperature and X_{17}: Rainfall

RESULTS

Influence of environmental factors on sheep distribution: Using the multivariate cluster analysis based on environmental indices, sheep populations were classified into 2 groups (Fig. 1), the 1st includes Mongolia sheep and Tan sheep, are respectively distributed in the pastoral and agro-pastoral area, the area characterized by high elevation, low rainfall and low annual mean temperature. The 2nd includes Han large-tailed sheep, Han small-tailed sheep, Tong sheep and Hu sheep, they were in agricultural area. The area characterized by low elevation, high rainfall and high annual mean temperature. The cumulative rate of the 1st-4th Eigen value was 48.51, 66.35, 83.14 and 96.95%, respectively. The 1st principal component comprises the information of self-color, elevation, annual mean temperature, annual rainfall, etc. The 2nd principal component comprises the height at withers, body length, tail width, etc. The 3rd principal component comprised the annual mean temperature, range, horned or polled, etc. The 4th principal component comprised horned or polled, heart girth, etc.

Euclid distances among the populations were estimated based on 4 principal components of each population (Table 4). Thereafter, the populations were cluster by R-type hierarchical using nearest distance method (Fig. 2). The populations were clustered into 2 groups; one includes Mongolia sheep in pastoral area and Tan sheep in agro-pastoral area. The other Han large-tailed sheep, Hu sheep, Han small-tailed sheep and Tong sheep were in agricultural area. Similarly, the morphological and environmental indices of sheep populations were clustered into 3 groups (Fig. 3). The elevation and annual rainfall were shown to play important role in the distribution of sheep populations.

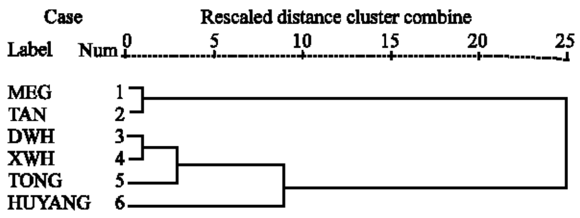

Fig. 1: Q-type cluster analysis based on environmental indices of sheep populations

Table 4: Principal components of sheep populations

	Principal component			
Population	1	2	3	4
MEG	-3.88616	-0.06169	1.17418	2.06998
TAN	-3.11025	-1.02084	-1.87838	-1.79286
DWH	0.56069	1.46898	-0.16888	-0.19695
XWH	1.40725	-0.78848	2.74091	-1.54089
TONG	1.64187	2.57369	-0.73592	0.11464
HU	3.38660	-2.17166	-1.13192	1.34608

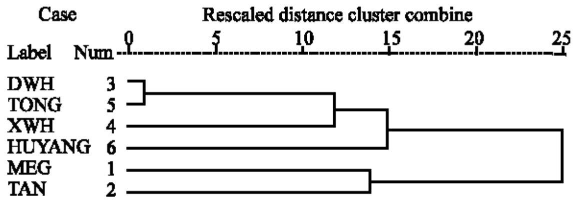

Fig. 2: R-type hierarchical cluster based on principal component values of sheep populations

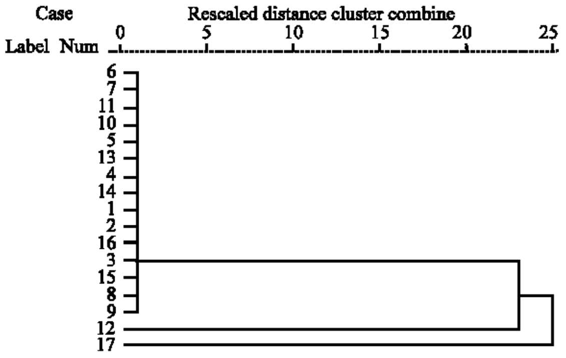

Fig. 3: Cluster analysis based on environmental indices and morphological features of sheep populations

DISCUSSION

Studies of geographically restricted species are of interest to evolutionary biologists because rapid evolutionary change often takes place in isolated populations (Zaghloul *et al.*, 2006). Information on the ecology and the genetics of these taxa is also important to those responsible for the management of rare species, a problem that is gaining increasing attention (Ledig, 1986; Zaghloul *et al.*, 2006). Phylogenetic analyses of variance were used to test the hypothesis that populations in different macrohabitat types differ morphologically (Losos and Chu, 1998). In this study, multivariate analyses find strong differences between sheep populations in different macrohabitat types. Sheep in pastoral and agro-pastoral area were cluster in one group; the area was characterized by high elevation, low rainfall and low annual mean temperature. However, the sheep in agricultural area were cluster in the 2nd group; the area was characterized by low elevation, high rainfall and high annual mean temperature. Most researchers consider an organism's phenotype as a multivariate set of variables and the covariation of traits an important analytical consideration (Collyer and Adams, 2007). Populations are dynamic units very precisely adapted physiologically and genetically to their environments and sensitive to and within limits responsive to, any change in their environmental conditions (Merrell, 1981). Variation in habitat use and morphology may be strongly correlated among populations independent of their phylogenetic relatedness (Harvey and Pagel, 1991; Wainwright and Reilly, 1994), which suggests an important role for natural selection. Directional selection may produce independent evolution of similar morphological features in lineages that enter similar habitats, whereas stabilizing selection may produce long-term morphological stability in lineages that maintain a particular habitat type (Schluter, 2000; Levinton, 2001). The results also showed that the elevation and annual rainfall were play important role in the distribution of sheep populations. Similarly, Scheiner (1993) indicated that the environment was plays an important role in the evolutionary process. In addition, Glor *et al.* (2003) reported that the distantly related populations from similar habitats are morphologically similar and closely related populations in different habitats are morphologically divergent. Molecular markers provide important measures of population genetic structure and geographic differentiation and have been employed to assess evolutionary questions (Avise, 1994). The extent of geographic variation results from a balance of forces tending to produce local genetic differentiation and forces standing to produce genetic homogeneity (Slatkin, 1987). However, the effects of environment on population genetic structure vary among different species (Huang *et al.*, 2005).

CONCLUSION

Both Q-type hierarchical clustering and the principal component analysis were used to study the influence of environmental factors on the genetic diversity of Chinese sheep population. The populations studied were divided into those reared in pastoral and agro-pastoral area and those reared in agricultural area. Finally, we conclude that although, it is difficult to judge the phylogenetic degree of populations based on environmental indices and morphological features of populations, their weight in genetic diversity should be consider beside the molecular markers.

ACKNOWLEDGEMENTS

This research was supported by the International Cooperation Item of the National Natural Science Foundation of China (30410103150), China Postdoctoral Science Foundation (No. 20080430470), State Scientific Basic Research platform Program (No. 2005DKA21101), National High Technology Research and Development Program of China (863 Program) (No. 2006AA10Z198), Support Foundation of China during the 11th 5 years Plan Period (No. 2006BAD13B08), Natural Science Foundation of Jiangsu Province of China (BK2007556), Basic Natural Science Foundation for Colleges and Universities Jiangsu Province (NK051039), Jiangsu Government Scholarship for Overseas Studies Project and Qing Lan Project for Colleges and Universities of Jiangsu Province in China.

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