Front. Agric. China 2007, 1(3): 324–328
DOI 10.1007/s11703-007-0054-3

RESEARCH ARTICLE

WANG Zhiguo, YANG Zhangping, MA Yuehui, WANG Qinghua, MAO Yongjiang, CHANG Hong, ZHOU Qunlan, XU Ming

Analysis of genetic diversity among seven goat populations in the middle and lower valley of Yangtse River and southeast coastal regions in China

Abstract The genomes of seven native goat populations were screened by using microsatellites as molecular markers; the populations were Yichang white, Matou, Xiangdong black, Fuqing, Daiyun, Huanghuai and Yangtse River Delta white goats. A total of 23 microsatellite markers were used and genetic diversities and genetic distances were also determined. The results showed that only 21 loci showed polymorphism in all populations. BM0203 was a homozygotic locus in every population, but more than one allele was found among all populations. Alleles of BM6444 were homozygotic in Xiangdong Black and Yichang White goats, but more than one allele was detected in other populations. Average heterozygosity of all populations was 0.819 0, and the mean polymorphism information content (*PIC*) of all seven populations was 0.630 5–0.691 9. An unweighted pair group method with arithmetic mean (UPGMA) dendrogram was constructed on Nei's standard genetic distance. Matou and Xiangdong black were grouped at first, then Fuqing, Daiyun, Yangtse River Delta white and Huanghuai goats joined them respectively. Finally, Yichang white goats clustered with all of the above.

Keywords goat, microsatellite, heterozygosity, genetic distance

1 Introduction

Microsatellites as reliable molecular markers have been used to study the genetic relationship of different populations. As being codominant, highly polymorphic, highly abundant, inheritant, locus specific, and easily analyzed, they are widely used in the analysis of population phylogenesis constitution. Wide-ranging, but still meager efforts, especially in developing countries, are in progress to characterize livestock at the phenotypic as well as molecular genetic level, and to document their genetic relationships, population status and production environments (Sodhi et al., 2006). Indigenous livestock breeds are considered, for diverse reasons, as treasured genetic resources that tend to disappear as a result of new market demands, crossbreeding or breed replacement, and mechanized agricultural operations. There is a terrible risk that most breeds may perish before they have been exclusively recognized and exploited (FAO, 2000).

There are about 40 indigenous goat breeds in China. Owing to long-term natural and artificial selection, transmutation of physical environment and hybridization, many illustrious local varieties have been formed from original breeds. More recently, with the generalization of modern livestock, numerous goat populations have become extinct (Editorial Group of Sheep and Goat Breeds in China, 1989). Faced with this serious situation, we have to provide valuable evidences to prioritize the breeds in terms of phylogenetic distinctness. Six microsatellite primers were applied to screen the genomes of 6 goat populations (Yang et al., 1999). The results from the application of structure locus and microsatellite markers in the analysis of genetic differentiation in sheep and goat populations were compared (Yang et al., 2004). Allele frequency, polymorphism information content, number of effective alleles, heterozygosity, and genetic distances were studied in Boer goat, Taihang goat and Hebei dairy goat using four microsatellite markers (Zhang et al., 2003). Five microsatellite loci were used to screen the polymorphism of six goat populations (Zhao et al., 2003). This study attempted to analyze the diversity of seven goat populations in the Middle and Lower Yangtse River Valley and Southeast Mainland near the sea by using 23 microsatellites as molecular markers, so as to help breeders to implement rational decisions for conservation and improvement of valuable germplasm.

Translated from *Acta Veterinaria et Zootechnica Sinica*, 2006, 37(1): 1–6 [译自: 畜牧兽医学报]

WANG Zhiguo, YANG Zhangping (✉), WANG Qinghua, MAO Yongjiang, CHANG Hong, ZHOU Qunlan, XU Ming
College of Animal Science and Technology, Yangzhou University, Yangzhou 225009, China
E-mail: zhangpy65@sohu.com

MA Yuehui
Institute of Animal Science, Chinese Academy of Agricultural Science, Beijing 100094, China

2 Materials and methods

2.1 Sampling methods and experiment materials

The tissue samples of seven goat populations were collected using the method of "randomly sampling in typical colonies of central area" (Chang, 1998). Forty Yichang white goats (YB) were from Yichang city of Hubei Province, 60 Matou goats (MT) and 55 Xiangdong black goats (XH) were from Shimen countryside of Hunan province, 50 Fuqing goats (FQ) and 50 Daiyun goats (DY) came from Fuqing and Dehua countrysides of Fujian Province, respectively, 50 Huanghuai goats (HH) and 40 Yangtse River Delta white goats (CB) came from Xiangshui and Haimen of Jiangsu Province. The genomic DNA was extracted from the tissues according to the procedure outlined by Wang et al. (2001).

2.2 Microsatellite primers

The information of 23 microsatellite primers was obtained from the following web sites: http:/locus.Jouy.inra.fr; http:/bos.cvm.tamu.edu; http:/www.marc.usda.gov and http:/www.roslin.ac.uk (The 23 primers were selected from 28 primers recommended by FAO, and the denotations of primers were seen in the table of statistical analysis). All of the primers were synthesized by Shanghai Sangon Biological Engineering Technology & Services CO., Ltd.

2.3 Reagent

10 × buffer, Taq, Mg^{+} and dNTPs were provided by Shanghai Sangon Biological Engineering Technology & Services CO., Ltd.

2.4 Polymerase chain reaction (PCR) protocol and electrophoresis

Polymerase chain reaction amplification was performed on a HBPX220 (Hybaid company). Each 20 μL PCR reaction contained 100 ng template DNA, 1–2 μL 8 pmol/μL each primer (GT and CA), 0.4 μL 10 mmol/μL dNTP, 1.0–1.8 μL 25 mmol $MgCl_2$, 0.2–0.4 μL 5 U Taq DNA polymerase, 2 μL 10 × buffer. An initial denaturizing at 94°C for 5 min was followed by 30 cycles of 60 s at 94°C denaturizing, 60 s of 53°C –63.5°C annealing, 60 s of 72°C extension. The final cycle was followed by an extension at 72°C for 10 min; then it was stored at 4°C.

The amplified fragments were electrophoresed on 8% polyacrylamide gels in 1 × TBE with 20 mA of running voltage. Then the gels were detected by ethidium bromide staining. The fragment sizes were calculated by using the Kodak Digital Science ID Image Analysis Software.

2.5 Statistical analysis

Twenty three microsatellite allele frequencies (*P*) were determined by direct counting. Genetic variability measures such as average heterozygosity (*H*) (Nei, 1978), information content of polymorphism (*PIC*) (Bostein et al., 1982), and number of effective allele (Ne) (Kimura and Crow, 1974) were calculated for each population. The standard genetic distances of Nei (*Ds*) (Nei, 1972) were calculated from the allele frequencies. All data were analyzed using FSTAT and POPGENE Software.

3 Results

3.1 Results of amplification and polymorphism of 23 microsatellite loci

The results showed that only 21 loci showed polymorphism in all populations in 23 loci. The locus of BM0203 was homozygotic in each population, but being polymorphic among populations. BM6444 was homozygotic in Xiangdong Black goats and Yichang White goats, but more than one allele was detected in other populations. Fig. 1 shows the electrophoresis patterns of PAGE in locus BM067 and MAF70.

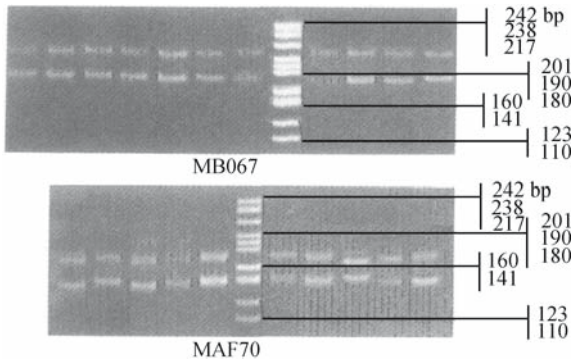

Fig. 1 The electrophoresis patterns of PAGE

3.2 Allele frequencies

According to the statistics, when comparing the allele frequencies of all the loci, the number of alleles (28) in BM1818 was the highest, in BMS1290 there were 24 alleles, and in MAF70 there were 21 alleles. BM0203, BM315 and MB023 had the least number of the alleles, in which there were 2, 3 and 6 alleles, respectively. Table 4 shows the number of effective alleles for each population. Except for homozygote loci, the number of effective alleles (*Ne*) in the seven populations (CB, HH, FQ, MT, XH, YB and DY) ranged from 1.867 8 to 8.325 2, 1.651 2 to 12.880 5, 2 to 9.639 9, 1.374 1 to 11.687 1, 2 to 10.240 0, 2 to 7.191 5 and 2 to 8.680 6, respectively. The average Nes were 4.323 9, 4.849 1, 5.111 2, 4.867 7, 5.211 0, 4.139 2 and 4.635 0, respectively. Among the seven populations, the XH goat had the most number of alleles, while the YB goat had the least.

3.3 Heterozygosity (*H*) and information content of polymorphism (*PIC*)

The heterozygosity (*H*) and information content of *PIC* of the seven populations are shown in Tables 1–3. Table 1 shows that the loci with the highest *H* value of the seven goat populations (CB, HH, FQ, MT, XH, YB and DY) were OarFCB193 (0.892), BMS1290 (0.940), BMS1678 (0.904), BM1818 (0.933), BMS1678 (0.911), OarFCB48 (0.870) and MAF70 (0.896), respectively. In all of the seven populations, the *H* value in BM0203 was 0, which showed that this locus was the highest homozygous. *H* values of BM6444 were 0.00 in Xiangdong black goat and Yichang white goat, and were also low in other populations (0.276–0.650); therefore, the diversity deduced from the loci was lower. The *H* values of MB023, BM315 and TGLA13 were 0.5 in all populations. In BMC1206, the *H* values were 0.5 in 6 populations except MT goat. The mean heterozygosity in seven populations was 0.705, 0.717, 0.737, 0.711, 0.709, 0.677 and 0.717, respectively. Table 2 shows that the highest *H* value was BM1818 (0.941) and the lowest was BM0203 (0.245) with an average value of 0.819. Table 3 shows that the locus of the highest *PIC* value of the seven goat populations (CB, HH, FQ, MT, XH, YB and DY) were OarFCB193, BMS1290, BMS1678, BM1818, BMS1678, OarFCB48, and MAF70, respectively; the values of *PIC* respectively were 0.868 4, 0.919 9, 0.887 2, 0.921 0, 0.893 5, 0.846 0, and 0.874 2. The average values of *PIC* in all loci in every population were 0.650 8, 0.670 4, 0.691 9, 0.684 8, 0.666 0, 0.630 5 and 0.663 7, respectively. From the *PIC* data, it was found that this result corresponded to analysis in *H*.

Table 1 Gene heterozygosity per locus and population

Locus	CB	HH	FQ	MT	XH	YB	DY
MB023	0.500	0.500	0.500	0.500	0.500	0.500	0.500
MAF70	0.817	0.873	0.877	0.874	0.906	0.856	0.896
BM1818	0.760	0.908	0.871	0.933	0.882	0.848	0.798
BMS1290	0.719	0.940	0.851	0.889	0.826	0.825	0.734
INRA063	0.653	0.850	0.830	0.706	0.822	0.835	0.780
BM0203	0.000	0.000	0.000	0.000	0.000	0.000	0.000
MAF65	0.884	0.815	0.730	0.744	0.716	0.699	0.757
BMS1678	0.870	0.802	0.904	0.790	0.911	0.770	0.814
BM6444	0.606	0.401	0.650	0.276	0.000	0.000	0.610
BMS1943	0.871	0.829	0.858	0.734	0.830	0.770	0.869
BM6404	0.771	0.811	0.827	0.795	0.862	0.860	0.858
BMS875	0.758	0.766	0.769	0.771	0.776	0.783	0.831
BMC3224	0.724	0.776	0.841	0.850	0.845	0.825	0.748
BMS1248	0.867	0.835	0.832	0.853	0.843	0.810	0.790
OarFCB193	0.892	0.887	0.860	0.647	0.862	0.798	0.810
MB067	0.776	0.750	0.867	0.875	0.879	0.773	0.766
BMS1724	0.768	0.795	0.837	0.822	0.854	0.754	0.880
OarFCB48	0.849	0.856	0.861	0.783	0.756	0.870	0.888
BM315	0.500	0.500	0.500	0.500	0.500	0.500	0.500
BMS812	0.843	0.845	0.842	0.860	0.854	0.772	0.846
BM1236	0.790	0.760	0.844	0.875	0.892	0.728	0.818
BMC1206	0.500	0.500	0.500	0.500	0.500	0.500	0.500
TGLA13	0.500	0.500	0.500	0.500	0.500	0.500	0.500
Average	0.705	0.717	0.737	0.711	0.709	0.677	0.717

3.4 Standard genetic distances

Table 5 shows Nei's standard genetic distances of the seven goat populations. The calculated observed genetic distances for the whole population were between 0.207 2 and 0.888 0. A UPGMA dendrogram was constructed based on Nei's standard genetic distance. Matou goat and Xiangdong black goat were grouped at first, then Fuqing goat, Daiyun goat, Yangtse River Delta white goat and Huanghuai goat joined them, respectively. Finally, Yichang white goats clustered with all the above (Fig. 2).

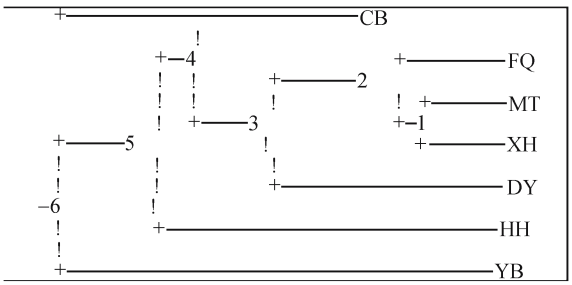

Fig. 2 Dendrogram of relationships among seven goat populations by using Nei's *Ds* and the UPGMA method of clustering

4 Discussion and conclusions

4.1 Genetic variation

Gene heterozygosity is gene variability. The average of heterozygosity could reflect the level of genetic variation.

Table 2 Gene heterozygosity at each locus

Locus	*Hs*	*Ht*	Locus	*Hs*	*Ht*	Locus	*Hs*	*Ht*
MB023	0.500	0.816	BM6444	0.364	0.430	BMS1724	0.816	0.879
MAF70	0.872	0.921	BMS1943	0.823	0.858	OarFCB48	0.838	0.901
BM1818	0.857	0.941	BM6404	0.826	0.898	BM315	0.500	0.561
BMS1290	0.827	0.924	BMS875	0.779	0.831	BMS812	0.838	0.930
INRA063	0.783	0.852	BMC3224	0.801	0.865	BM1236	0.815	0.901
BM0203	0.000	0.245	BMS1248	0.833	0.851	BMC1206	0.540	0.870
MAF65	0.763	0.815	OarFCB193	0.822	0.901	TGLA13	0.500	0.806
BMS1678	0.837	0.902	MB067	0.815	0.916	Average	0.711	0.819

Note: *Hs* represents heterozygosity for each group; *Ht* represents heterozygosity for the whole group.

Table 3 Polymorphism information content (*PIC*) per locus in seven populations

Locus	CB	HH	FQ	MT	XH	YB	DY
MB023	0.375 0	0.375 0	0.375 0	0.375 0	0.375 0	0.375 0	0.375 0
MAF70	0.783 1	0.849 6	0.856 0	0.852 3	0.888 5	0.828 4	0.874 2
BM1818	0.712 6	0.891 6	0.850 4	0.921 0	0.861 4	0.818 3	0.759 1
BMS1290	0.664 9	0.919 9	0.827 0	0.870 6	0.786 3	0.791 4	0.690 7
INRA063	0.589 1	0.823 8	0.798 7	0.648 2	0.788 4	0.798 5	0.736 0
BM0203	0.000 0	0.000 0	0.000 0	0.000 0	0.000 0	0.000 0	0.000 0
MAF65	0.858 2	0.780 1	0.675 6	0.702 1	0.662 7	0.640 2	0.707 1
BMS1678	0.842 2	0.765 1	0.887 2	0.753 8	0.893 5	0.721 9	0.7793
BM6444	0.531 9	0.364 2	0.590 4	0.243 2	0.000 0	0.000 0	0.535 0
BMS1943	0.842 4	0.794 8	0.832 8	0.690 6	0.800 9	0.726 4	0.837 0
BM6404	0.726 6	0.776 6	0.799 1	0.760 8	0.836 6	0.832 8	0.834 8
BMS875	0.711 9	0.721 9	0.725 7	0.729 9	0.734 1	0.738 8	0.800 9
BMC3224	0.668 3	0.731 5	0.813 6	0.824 5	0.816 9	0.789 7	0.700 9
BMS1248	0.838 4	0.807 5	0.803 3	0.827 6	0.815 4	0.771 8	0.752 9
OarFCB193	0.868 4	0.865 2	0.834 0	0.581 3	0.836 0	0.758 5	0.775 7
MB067	0.729 0	0.710 2	0.844 6	0.854 3	0.857 2	0.725 2	0.720 7
BMS1724	0.723 1	0.757 4	0.808 1	0.790 1	0.827 0	0.706 2	0.857 7
OarFCB48	0.816 7	0.830 6	0.838 0	0.745 9	0.713 9	0.846 0	0.868 3
BM315	0.375 0	0.375 0	0.375 0	0.375 0	0.375 0	0.375 0	0.375 0
BMS812	0.811 8	0.817 2	0.814 4	0.834 8	0.828 1	0.727 2	0.817 6
BM1236	0.750 0	0.713 1	0.816 7	0.868 9	0.872 2	0.782 2	0.718 8
BMC1206	0.375 0	0.375 0	0.752 3	0.375 0	0.375 0	0.375 0	0.375 0
TGLA13	0.375 0	0.375 0	0.375 0	0.375 0	0.375 0	0.375 0	0.375 0
Average	0.650 8	0.670 4	0.691 9	0.684 8	0.666 0	0.630 5	0.663 7

Table 4 Effective number of alleles (*Ne*) of 23 microsatellite loci in seven goat populations

Locus	CB	HH	FQ	MT	XH	YB	DY
MB023	2.000 0	2.000 0	2.000 0	2.000 0	2.000 0	2.000 0	2.000 0
MAF70	5.180 6	7.385 5	7.649 2	7.515 5	9.600 0	6.533 9	8.680 6
BM1818	4.029 4	7.722 6	6.022 3	11.687 1	6.564 1	6.195 5	4.449 1
BMS1290	1.867 8	12.880 5	6.430 4	7.662 7	5.260 3	5.443 3	3.693 6
INRA063	2.843 2	4.150 4	5.289 3	3.361 6	5.383 2	5.662 7	4.378 8
BM0203	1.000 0	1.000 0	1.000 0	1.000 0	1.000 0	1.000 0	1.000 0
MAF65	7.781 4	5.203 8	3.649 1	3.836 4	3.469 9	3.263 4	4.015 2
BMS1678	7.086 5	4.8972	9.639 9	4.643 1	10.240 0	4.216 1	5.205 0
BM6444	2.500 6	1.651 2	2.784 8	1.374 1	1.000 0	1.000 0	2.497 1
BMS1943	7.040 3	5.494 8	6.651 9	3.698 0	5.628 0	4.202 4	6.823 0
BM6404	4.205 3	5.111 5	5.563 8	4.760 0	6.847 9	6.685 2	6.750 0
BMS875	4.000 0	4.169 1	4.234 9	4.275 6	4.359 5	4.453 9	5.681 9
BMC3224	3.531 0	4.344 1	6.049 2	6.402 1	6.160 4	5.441 9	3.890 6
BMS1248	6.918 9	5.846 5	5.741 0	6.526 4	6.087 2	5.053 2	4.642 5
OarFCB193	8.325 2	8.165 3	6.743 1	2.814 0	6.836 8	4.760 6	5.097 7
MB067	4.293 5	3.913 0	7.134 6	7.591 0	7.757 6	4.278 5	4.165 4
BMS1724	4.160 2	4.710 3	5.891 1	5.426 0	6.517 7	3.966 1	7.736 4
OarFCB48	6.160 3	6.627 5	6.854 2	4.501 5	4.007 0	7.191 5	8.372 6
BM315	2.000 0	2.000 0	2.000 0	2.000 0	2.000 0	2.000 0	2.000 0
BMS812	5.953 5	6.168 7	6.083 2	6.805 4	6.536 2	4.254 5	6.205 3
BM1236	4.571 4	4.087 7	6.145 5	9.591 0	8.597 0	3.600 0	5.320 1
BMC1206	2.000 0	2.000 0	2.000 0	4.484 8	2.000 0	2.000 0	2.000 0
TGLA13	2.000 0	2.000 0	2.000 0	2.000 0	2.000 0	2.000 0	2.000 0
Mean	4.323 9	4.849 1	5.111 2	4.867 7	5.211 0	4.139 2	4.635 0
St.Dev	2.148 9	2.670 5	2.233 7	2.583 0	2.670 6	1.808 4	2.147 8

Information content of polymorphism (*PIC*) is a diversity index. The higher the *PIC* value is, the greater the rate of heterozygote, the more genetic information the locus provides (Nyamsamba and Nozawa, 2003). Generally, when $PIC > 0.50$, it is highly polymorphic; when $0.25 < PIC < 0.50$, it is medium polymorphic; when $PIC < 0.25$, it is lowly polymorphic. In this study, the calculated observed mean *Ht* for 23 microsatellite loci in the seven populations was 0.819 9 (0.245–0.941), the average value of *Hs* for the whole population was 0.711, the highest mean *PIC* value was 0.691 9 and the lowest mean *PIC* value was 0.630 5, which showed the high genetic polymorphism in the seven populations. The BM0203 and BM6444 had the lowest *PIC* value ($PIC < 0.25$), in all populations the *PIC* value of BM0203 was 0.00. The *PIC* value of locus BM6444 was 0.50 in Xiangdong black goat (XH) and Yichang white goat (YB), but 0.243 2 in Matou goat (MT). The medium *PIC* values (0.25–0.50) were BM023 and BM315, with an average of 0.375, so were BMC1206 and TGLA13 except in Matou goat (MT). Except for the above information, *PIC* values in all loci were more than 0.50. The higher variability of microsatellite DNA, the higher was the *PIC* value in each population. From this study, all loci were polymorphic, which could provide a foundation for QTL research (Wang et al., 2004), except BM0203 and BM6444. However, even though BM0203 was homozygotic in each population, it was variable among the seven populations. BM6444 displayed homozygosis in 2 populations, but was heterozygotic in the other five populations, which is seldom seen in microsatellite DNA research. Therefore, although it had lower polymorphism in the two loci, it is still very important for the researches on genetic relationship.

The number of effective alleles (*Ne*) was also an important index to reflect the level of genetic variation. If the allele was well-distributed in the population, the *Ne* would approach the observed. In this study, the number of effective alleles (*Ne*) in 5 loci (MB023, BM0203, BM315, BMC1206 and TGLA13) was equal to the observed. In BM6444, the number of effective alleles (*Ne*) was equal to the observed in XH and YB, and were close to the observed in other populations. In BMS875 and BMS812, the number of effective alleles (*Ne*) was very close to the observed, and the difference was less than two alleles. Except for those mentioned above, the number of effective alleles (*Ne*) on other loci was different from the observed. Thus, we could conclude that these alleles were not well-distributed in the goat population. This unbalance could result from region isolation, artificial selection and natural selection.

Table 5 Nei's original measures of genetic identity and genetic distance

	CB	HH	FQ	MT	XH	YB	DY
CB	****	0.458 7	0.536 1	0.587 4	0.503 1	0.470 8	0.548 1
HH	0.779 4	****	0.546 9	0.560 8	0.576 8	0.304 8	0.448 0
FQ	0.623 4	0.603 5	****	0.715 3	0.773 4	0.443 3	0.582 3
MT	0.532 0	0.578 5	0.335 1	****	0.812 9	0.463 5	0.612 5
XH	0.686 9	0.550 2	0.257 0	0.207 2	****	0.847 7	0.643 5
YB	0.753 2	0.888 0	0.813 6	0.768 8	0.768 1	****	0.543 8
DY	0.601 3	0.803 0	0.540 7	0.490 2	0.440 8	0.609 3	****

Note: Nei's genetic identity (above diagonal) and genetic distance (below diagonal).

4.2 Genetic dendrogram

Generally, different populations, which distribute in a similar area, may have a coincided genetic foundation, because ecological environments and artificial selection orientation of populations are similar, resulting in similar gene migrating efficiency. Our study encountered this result. Matou goat (MT) and Xiangdong black goat (XH) were grouped at first ($D = 0.207\ 2$), then Fuqing goat (FQ), Daiyun goat (DY), Yangtse River Delta white goat (CB), Huanghuai goat (HH) joined them, respectively. Finally, Yichang White goat (YB) clustered with all the above. Because YB came from a mountain area (Yichang City of Hubei Province), which was isolated from outsiders, the genetic relationships with the other six populations were far.

Acknowledgements This work was supported by the National Natural Science Foundation of China (Grant No. 30371026), the Special-purpose Foundation of Technology Department (No. 2001DEA10006) and the Natural Science Foundation of Jiangsu Province (No. BK2003040).

References

Bostein D, White R L, Skolnek M (1982). Construction of a genetic linkage map in man using restriction fragment length polymorphisms. Am J Human Genetics, 32: 314–331

Chang H (1998). Studies on Animal Genetic Resources in China. Xi'an: Shanxi People's Education Press, 45–51 (in Chinese)

Editorial Group of Sheep and Goat Breeds in China (1989). Sheep and Goat Breeds in China. Shanghai: Scientific and Technical Publishers, 1–16 (in Chinese)

FAO (2000). World watch list for domestic animal diversity, 3rd ed. Rome: Food and Agriculture Organization

Kimura M, Crow J F (1974). The number of alleles that can be maintained in a finite population. Genetics, 49: 725–738

Nei M (1972). Genetic distance between populations. American Naturalist, 106: 283–292

Nei M (1978). Estimation of average heterozygosity and genetic distance from a small number of individuals. Genetics, 89(3): 583–590

Nyamsamba D, Nozawa K N (2003). Genetic relationship among Mongolian native goat populations estimated by blood protein polymorphism. Small Ruminant Research, 47: 171–181

Sodhi M, Muhesh M, Prakash B, Ahlawat S P S, Sobti R C (2006). Microsatellite DNA typing for assessment of genetic variability in Tharparkar breed of Indian zebu (*Bos indicus*) cattle, a major breed of Rajasthan. Journal of Genetics, 85(3): 165–170

Wang H Y, Chang H, Xu W, Chang G B (2004). Genetic analysis of microsatellite DNA markers in domestic quail and wild Japanese quail populations. Acta Veterinaria et Zootechnica Sinica, 35(4): 367–371 (in Chinese)

Wang Y Q, Wang X G, Xu L X, Zhang Z B (2001). A new rapid method for extraction of high quality of genomic DNA from animal tissues. Chinese Journal of Zoology, 36(1):27–29 (in Chinese)

Yang L, Zhao S H, Li K, Peng Z Z, Montgomery G W (1999). Determination of genetic relationships among five indigenous Chinese goat breeds with six microsatellite markers. Anim Genet, 30(6): 452–455

Yang Z P, Chang H, Sun W, Gen R Q, Mao Y J, Tsunoda K (2004). A comparison of two kinds of markers applied in analysis of genetic diversity in sheep and goat populations. Asian Aust J Anim Sci, 17(7): 892–896

Zhang Y J, Zhao Y Z, Liu Y Q, Li Y, Sun S H, Sun H X (2003). Genetic polymorphism of 4 microsatellites markers in 3 goat populations. China Herbivore, 23 (4): 7–8 (in Chinese)

Zhao Y H, Ma Y H, Zhang L L (2003). Evaluation of Genetic Diversity of Some Goat Breeds by Microsatellite Marker. In: Proc 12th Ann Meet China Assoc Anim Breed. Beijing: Agricultural Publishing House, 263–265 (in Chinese)