The availability of thousands of molecular markers allows us to characterize the genetic structure of groups of individuals or populations. In particular, microsatellites (MS) are broadly used to describe the evolutionary relationships of closely related populations because of their highly polymorphic nature. The patterns and extent of genetic variation observed within and between populations could provide useful information concerning the genetic affinities and phylogenetic inference of domesticated animals. It is well known that evolutionary forces such as mutations, recombination, selection, genetic drift and gene flow influence and shape the genetic variation observed within and between populations.

A phylogeographic study based on mtDNA reported that the genetic differences among goat breeds sampled from Europe, Africa and Asia were small compared to the differences observed between cattle breeds (Luikart et al., 2001). Several studies on genetic structure and variation between different goat populations based on MS markers have been published, finding small to moderate genetic differentiation among goat populations (Barker et al., 2001; de Araújo et al., 2006). The relatively low level of genetic differentiation between goat populations could be related to extensive transportation of these animals in the past. The aims of this study were to estimate population genetic parameters such as allele frequency, heterozygosities, and polymorphic information content (PIC), deviations from Hardy-Weinberg Equilibrium (HWE), genetic distances and FST statistic for five goat populations from Mongolia and Australia and to infer genetic variation within and between goat populations using these genetic parameters.

**MATERIALS AND METHODS**

**Resource populations**

This study included genotype information from Australian Angora and Cashmere goats and three Mongolian Cashmere goat populations (Bayandelger, Zavkhan Buural, and Gobi Gurvan Saikhan). Australian
* Different annealing temperatures were used for different primer pairs.

** I duration and number of cycles was used for different annealing temperatures were used for different primer pairs.

Table 1. Cycling parameters for PCR amplification

| Step | Purpose | Temperature (°C) | I** | Cycle No. | Duration | Cycle No. | II** |
|------|---------|-----------------|-----|-----------|----------|-----------|------|
| 1    | Activation of enzyme | 94   | 2.55 minutes | 1 | 1 | 2 minutes | 1 |
| 2    | Denaturation | 95   | 05 seconds | 35 | 45 seconds | 30 |
|      | Annealing   | 55-63*| 30 seconds | 35 | 45 seconds | 30 |
|      | Elongation  | 72   | 30 seconds | 35 | 60 seconds | 30 |
| 3    | Final extension | 72   | 2.30 minutes | 1 | 7 minutes | 1 |
|      | Total period | 1.27 h|          | 1 | 1.57 h |           |    |

Angora and Cashmere goats were drawn from separate commercial herds of each breed. The Angora herd initially comprised 250-300 does of mixed Australian, Texan and South African blood which was upgraded to a minimum of 87% South African blood. Australian Cashmere goats were drawn from a single Cashmere goat herd. The herd was established in 1985 and bucks and does were sourced from a wide variety of sources over the years including Kinross, the WA group breeding scheme, Noel Waters, Bess Vickers, Fred Brown and Northumbria. Animals from three other Cashmere goat populations (Bayandelger/BD, Zavkhan buural/ZB, and Gobi Gurvan Saikhan/GGS) were included in this study for phylogenetic comparison. These animals were randomly sampled from different herds in the experimental stations of the Institute of Animal Husbandry (IAH) in Ulaanbaatar and its branch in southern region of Mongolia. Around 350 goats of each BD and ZB goat strains were originally shifted from the Eastern and North-Western regions of Mongolia to the experimental station of the IAH in 1996 and 1998, respectively.

Microsatellite genotype analysis

DNA of animals of these populations was extracted from blood and ear punch samples according to the phenol/chloroform extraction protocol described by Sambrook et al. (1989). In total, fourteen microsatellite markers (Tables 2 and 3) were used in genotyping analysis from the “goat map” website: http://dga.jouy.inra.fr/cgi-bin/lgeb/carte.pl?BASE=goat&NOM=schibler_1998.

PCRs were conducted in 4 μl reagent volumes containing ~10 ng genomic DNA. Optimization of PCR conditions was carried out by changing the concentrations of MgCl₂ (1.5-4.5 mM) and 4dNTP’s (62.5 μM, 80.0 μM and 100.0 μM). 4dNTP’s in PCR reagent volumes were prepared with a 1 (dATP):10 (dGTP, dCTP and dTTP) ratio because a lower concentration of dATP helps for more efficient incorporation of 33P-dATP. For running PCR, two different durations and numbers of thermal cycles were used for the different primers based on PCR optimization (Table 1).

Visualization of PCR products was done using gel electrophoresis and autoradiography. 5 μl of 500 fmol plasmid dsDNA template (pGEM™-3ZfR+) control DNA) was used to prepare the sequencing ladders for sizing PCR products (Promega, 2001). PCR products and the four sequencing ladders (adenine (A), cytosine (C), guanine (G), and thymine (T)) were loaded on a 6% polyacrylamide gel electrophoresis. After completion of electrophoresis, the gel was exposed to BioMax™ or X-Omat K autoradiography (Kodak) film for 18-72 h depending on the activity of the 33P-dATP used. The absolute length of the PCR product (sizes of two alleles per each animal or a sample) was determined by visual comparisons with the sequencing bands or ladders, which were observed as four lanes of sequenced nucleotide in the middle of the film.

In total, 1,118 goats representing five goat populations were screened for their genotypes at fourteen MS loci. The total number of genotypes studied was 15,652. From these, 15,614 genotypes were identified. The sample size of each population varied from 47 to 548 across populations (Tables 2 and 3).

Population genetic parameter analysis

In order to describe the genetic variation within and amongst studied goat populations, the allele frequency, observed and expected heterozygosities of each locus, and the amount of polymorphism (PIC) at a single locus were calculated using ARLEQUIN program (Schneider et al., 2000). Departures from the Hardy-Weinberg equilibrium were detected using the GENEPOP program (Raymond and Rousset, 1995), which implemented the modified version of the Markov-chain random walk algorithm described by Guo and Thompson (1992) and used a method analogous to Fisher’s exact test. The calculation was carried out on genotypic data of all individuals of each population with Markov chain of 100 batches of 1,000 iterations. The calculation of HWE was based on allele frequencies. If a population deviated from HWE, a score test (U-test) (Rousset and Raymond, 1995) was then performed to examine whether the observation was caused by excess or
deficit of heterozygote individuals. F coefficients ($F_{IS}$ and $F_{ST}$) were used to estimate the amount of genetic variation within and between the five goat populations, respectively. Estimates of $F$ coefficients, their standard deviation and confidence intervals were calculated using the GENEPOP.

Genetic distances (Nei, 1978) between populations and their confidence intervals were calculated using the GENEPOP.

Table 3. Number of observed microsatellite alleles, observed and expected heterozygosity and deviation from Hardy-Weinberg equilibrium on each locus for three Mongolian goat populations

| Locus | GGS (47*) | ZB (47*) | BD (48*) |
|-------|-----------|-----------|-----------|
|       | Alleles   | H_e | PIC | H_e | PIC | H_e | PIC | Alleles | H_e | PIC | H_e | PIC | Alleles | H_e | PIC | H_e | PIC |
| OarFCB20 | 9.072 0.730 0.467 0.362 82-112 | 0.060 0.759 0.717 0.057 96-124 | 6.732 0.740 0.686 0.634 96-124 |
| ILSTS29 | 9.017 0.678 0.644 0.200 154-186 | 0.553 0.608 0.579 0.099 154-182 | 7.053 0.487 0.451 0.977 154-182 |
| SRCRSP07 | 5.956 0.492 0.453 0.526 119-129 | 0.511 0.499 0.454 0.402 123-133 | 5.563 0.539 0.494 0.278 119-129 |
| BM906 | 12.745 0.501 0.478 0.504 100-122 | 0.702 0.784 0.751 0.533 100-124 | 0.805 0.800 0.764 0.797 98-126 |
| LSCV44 | 11.957 0.847 0.815 0.894 112-134 | 0.936 0.892 0.872 0.505 112-134 | 0.938 0.821 0.790 0.609 112-130 |
| ILSTS3 | 9.002 0.741 0.701 0.538 266-282 | 0.609 0.757 0.709 0.087 266-282 | 0.750 0.741 0.687 0.986 266-282 |
| TLG43 | 11.723 0.700 0.666 0.687 117-141 | 0.617 0.713 0.673 0.274 117-131 | 0.813 0.797 0.763 0.749 117-139 |
| INRABERN185 | 5.739 0.714 0.652 0.827 164-172 | 0.766 0.712 0.655 0.111 164-172 | 0.702 0.672 0.628 0.738 164-172 |
| BM1258 | 5.340 0.333 0.332 0.630 256-282 | 0.426 0.412 0.383 0.102 266-282 | 0.479 0.419 0.399 0.626 256-282 |
| INRABERN172 | 11.894 0.855 0.830 0.865 160-182 | 0.702 0.736 0.708 0.481 158-180 | 0.658 0.754 0.715 0.881 158-180 |
| OarCP73 | 21.872 0.904 0.886 0.101 154-210 | 0.851 0.921 0.905 0.048* 154-216 | 0.854 0.902 0.885 0.121 154-242 |
| BM1358 | 9.151 0.636 0.794 0.555 102-130 | 0.936 0.869 0.845 0.170 102-136 | 0.813 0.866 0.841 0.711 102-128 |
| MGH108 | 11.891 0.863 0.838 0.103* 250-270 | 0.850 0.805 0.777 0.344 252-268 | 0.750 0.790 0.756 0.263 250-270 |
| INRABERN172 | 7.723 0.760 0.713 0.345 236-250 | 0.660 0.704 0.650 0.612 236-246 | 0.813 0.782 0.743 0.687 236-246 |
| MNA | 9.574 0.744 0.734 0.699 | 9.607 0.717 0.727 0.691 | 8.753 0.737 0.723 0.686 |

*Number of individuals.

**Significant deviations from HWE (p<0.05); MNA = Mean number of alleles; H_e = Expected heterozygosity; PIC = Polymorphic information content.
frequencies within populations never exceeded 19% (Table 4). Such private alleles were found at eleven loci. The number of private alleles was higher in all four Cashmere populations (2-3 alleles) than in the Angora_Aus population (1 allele). Interestingly, the Angora population contains a private allele (120 at locus BM1258) with a high frequency (18.6%). Also, allele 115 at locus TGLA53 with 11.9% frequency was specific to the Cashmere_Aus population (Table 4). The remaining private alleles across the populations had low frequencies.

Deviations from HWE at the studied loci were tested for all five populations (Tables 2 and 3). Out of a total seventy tests, only four cases showed statistically significant deviations from HWE (p<0.05). One of these four significant deviations was found in locus BM1818 in the GGS population and two were observed in locus OarCP73 in the Cashmere_Aus and ZB populations. The remaining one was found in locus SRCRSP07.

All five studied goat populations displayed a quite similar and high mean observed heterozygosity (Ho), ranging from 0.711 for the ZB population to 0.744 for GGS (Tables 2 and 3). Compared with Ho, the mean estimated gene diversity (He) the studied loci was slightly lower and it ranged from 0.710 for the Cashmere_Aus population to 0.734 for the GGS population. Regarding either heterozygote deficiency or heterozygote excess (Rousset and Raymond, 1995) the f-statistic was used to test for statistically significant differences between the observed and the expected frequencies of heterozygotes. As shown in Table 5, five negative f values (locus SRCRSP07 in GGS, RM096 in both Australian populations, LSCV44 in BD and BM1258 in Angora_Aus populations) indicated significant excess of heterozygotes (p<0.01) or higher level of heterozygosity than that expected from HWE. A significant deficit of heterozygotes (p<0.01) was observed at loci OarFCB20 in Cashmere_Aus, SRCRSP07 in Angora_Aus, and OarCP73 and BM1818 in BD populations (significant positive f values as shown in Table 5).

The overall pattern of PIC values concords with values of heterozygosity (Tables 2 and 3). PIC values were high for all studied loci except for the loci that showed low values of either He or Ho. The range of the mean PIC across all loci was between 0.686 for the BD population and 0.710 for the Cashmere_Aus population.

### Genetic variation between populations

Genetic differentiation of the studied populations (Table 6) was investigated by comparing mean values of the FST statistic using Weir and Cockerham's methodology (Weir and Cockerham, 1984). The results of FST statistic analysis are presented in Table 6.
show greater differentiation of the Angora goat from the four Cashmere goat populations than between any of the Cashmere populations. This indicates genetic distinction of the Angora goat population. The lowest $F_{ST}$ values were found between Mongolian Cashmere goat populations. Australian Cashmere goats displayed a greater genetic differentiation from Angora goats (0.087) than Mongolian Cashmere goats (0.061-0.081). Another way to assess genetic differentiation using $F_{ST}$ statistics is grouping the studied populations according to their known origins (Table 7). The average $F_{ST}$ for grouping of all five populations across all loci was 0.075, indicating a moderate level of genetic differentiation between the five populations. This means that 7.5% of total genetic variation can be explained by the difference between the five populations. In other words, only 7.5% of the total number of shared alleles has been lost since the populations separated. The grouping of three Mongolian Cashmere goat populations displayed the lowest mean $F_{ST}$ values (0.011), reflecting a high degree of genetic similarity among them. After adding the Cashmere_Aus population to the Mongolian Cashmere group, the differences between all four Cashmere goat populations accounted for 4.4% of the total genetic variation.

The standard genetic distance measure (Nei, 1978) revealed reliable genetic relationships between the five populations (Table 8). The greatest distances were observed between the Angora and four Cashmere populations (0.201-0.276); the shortest distances were between the Mongolian Cashmere goat populations (0.026-0.031). Compared with other Cashmere goat populations, the GGS (crossbred) population had the smallest pairwise genetic distance with Angora population (0.192). The comparisons between Australian Cashmere and Mongolian Cashmere goat populations indicated that ZB population displayed the highest pairwise distance with Australian Cashmere goats (0.150). As expected, the pairwise genetic distance between two Mongolian goat breed, ZB and BD, was the shortest.

### Table 6. Population differentiation coefficients ($F_{ST}$) for all pairwise combinations of Australian and Mongolian goat populations

| Markers | Total number of alleles | $F_{ST}$ in all Mongolian Cashmere goat populations | $F_{ST}$ in all Cashmere goat populations studied | $F_{ST}$ in all Cashmere and Angora goat populations |
|---------|------------------------|---------------------------------------------------|---------------------------------------------------|--------------------------------------------------|
| OarFCB020 | 10 | 0.003 | 0.036 | 0.075 |
| ILSTS029 | 14 | 0.013 | 0.049 | 0.054 |
| SRCRSP07 | 15 | 0.000 | 0.044 | 0.093 |
| RM096 | 12 | 0.015 | 0.074 | 0.114 |
| LSCV44 | 11 | 0.017 | 0.051 | 0.035 |
| ILSTS11 | 14 | 0.005 | 0.023 | 0.060 |
| TGLA53 | 5 | 0.015 | 0.012 | 0.011 |
| INRA0463 | 9 | 0.001 | 0.043 | 0.060 |
| INRABERN185 | 13 | 0.023 | 0.067 | 0.070 |
| OarCP73 | 27 | 0.010 | 0.046 | 0.099 |
| BM1258 | 15 | 0.009 | 0.041 | 0.052 |
| BM1818 | 11 | 0.020 | 0.055 | 0.158 |
| INRABERN172 | 10 | 0.007 | 0.050 | 0.083 |
| All loci | 174 | 0.011 | 0.045 | 0.075 |
| Standard deviation | 0.002 | 0.004 | 0.011 |
| Confidence interval | 0.0073-0.0148 | 0.0371-0.0532 | 0.0552-0.0950 |

### Table 7. Coefficient of gene differentiation ($F_{ST}$) for the fourteen microsatellite loci applied in the studied goat populations

| Markers | Total number of alleles | $F_{ST}$ in all Mongolian Cashmere goat populations | $F_{ST}$ in all Cashmere goat populations studied | $F_{ST}$ in all Cashmere and Angora goat populations |
|---------|------------------------|---------------------------------------------------|---------------------------------------------------|--------------------------------------------------|
| OarFCB020 | 10 | 0.003 | 0.036 | 0.075 |
| ILSTS029 | 14 | 0.013 | 0.049 | 0.054 |
| SRCRSP07 | 8 | 0.003 | 0.028 | 0.052 |
| RM096 | 15 | 0.000 | 0.044 | 0.093 |
| LSCV44 | 12 | 0.015 | 0.074 | 0.114 |
| ILSTS11 | 11 | 0.017 | 0.051 | 0.035 |
| TGLA53 | 14 | 0.005 | 0.023 | 0.060 |
| INRA0463 | 5 | 0.015 | 0.012 | 0.011 |
| INRABERN185 | 9 | 0.001 | 0.043 | 0.060 |
| SRCRSP05 | 13 | 0.023 | 0.067 | 0.070 |
| OarCP73 | 27 | 0.010 | 0.046 | 0.099 |
| BM1258 | 15 | 0.009 | 0.041 | 0.052 |
| BM1818 | 11 | 0.020 | 0.055 | 0.158 |
| INRABERN172 | 10 | 0.007 | 0.050 | 0.083 |
| All loci | 174 | 0.011 | 0.045 | 0.075 |
| Standard deviation | 0.002 | 0.004 | 0.011 |
| Confidence interval | 0.0073-0.0148 | 0.0371-0.0532 | 0.0552-0.0950 |

### Table 8. Pairwise genetic distance (Nei, 1978) among the studied goat populations

| Markers | Total number of alleles | $F_{ST}$ in all Mongolian Cashmere goat populations | $F_{ST}$ in all Cashmere goat populations studied | $F_{ST}$ in all Cashmere and Angora goat populations |
|---------|------------------------|---------------------------------------------------|---------------------------------------------------|--------------------------------------------------|
| OarFCB020 | 10 | 0.003 | 0.036 | 0.075 |
| ILSTS029 | 14 | 0.013 | 0.049 | 0.054 |
| SRCRSP07 | 8 | 0.003 | 0.028 | 0.052 |
| RM096 | 15 | 0.000 | 0.044 | 0.093 |
| LSCV44 | 12 | 0.015 | 0.074 | 0.114 |
| ILSTS11 | 11 | 0.017 | 0.051 | 0.035 |
| TGLA53 | 14 | 0.005 | 0.023 | 0.060 |
| INRA0463 | 5 | 0.015 | 0.012 | 0.011 |
| INRABERN185 | 9 | 0.001 | 0.043 | 0.060 |
| SRCRSP05 | 13 | 0.023 | 0.067 | 0.070 |
| OarCP73 | 27 | 0.010 | 0.046 | 0.099 |
| BM1258 | 15 | 0.009 | 0.041 | 0.052 |
| BM1818 | 11 | 0.020 | 0.055 | 0.158 |
| INRABERN172 | 10 | 0.007 | 0.050 | 0.083 |
| All loci | 174 | 0.011 | 0.045 | 0.075 |
| Standard deviation | 0.002 | 0.004 | 0.011 |
| Confidence interval | 0.0073-0.0148 | 0.0371-0.0532 | 0.0552-0.0950 |
-0.026 (Table 8). The standard errors of genetic distances between the studied populations were rather small.

Figure 1 shows a neighbour-joining tree illustrating that two native Mongolian populations are clustered in the same branch, which is closely related to the crossbred population (GGS), and then to the Australian Cashmere population. The Angora forms a branch alone, which was distinct from the four Cashmere populations. Separation between Angora and Cashmere populations as well as between Australian Cashmere and Mongolian Cashmere populations is strongly supported by bootstrap probability (100%, not shown on the tree). However, the divergence between Mongolian Cashmere goat populations was not strong (~48%), thus indicating a degree of admixture among these three populations. These results corroborate well with our data ($F_{ST}$ values) showing that the Australian Angora and Cashmere populations belong to different and less related populations, with the Australian Cashmere more closely related to the three Mongolian Cashmere populations. The three Mongolian populations were the most similar or closely related populations among the five studied goat populations. This is in agreement with information about the origin and history of the populations.

A three-factorial correspondence analysis using GENETIX program (Belkhir et al., 1996) was performed to study the degree of differentiation between all individuals of the five goat populations. Figure 2 is a graphical representation of this analysis based on allele frequencies of 14 MS markers in a three-dimensional space. The first two factors (axes 1 and 2) accounted for 58% and 30% of total variation respectively and clearly distinguished the Angora_Aus, Cashmere_Aus and the Mongolian Cashmere goats, seen as three separate blocks (Figure 2). On the other hand, the three different Mongolian Cashmere populations can hardly be distinguished from each other. They are mixed and present as groupings belonging to one population rather than being three separate populations. The Mongolian goats appear closer to the Cashmere_Aus population.

**DISCUSSION**

The number and range of described alleles in the fourteen loci differed considerably for each population. From the mean number of alleles per locus, it can be said that the four studied Cashmere populations (8.57-9.57 alleles/locus) are more diverse than the Angora_Aus population (7.50 alleles). Compared with the five populations in this study, twelve Chinese goat populations had lower mean number of alleles, ranging from 5.24 to 7.77 (Li et al., 2002). However, the mean number of alleles could be different depending on nature of MS markers studied and populations concerned.

The presence of private or population-specific alleles could underline the divergence between populations depending on their allele frequency. Generally a high frequency of private alleles reflects a low level of gene flow between populations. The frequency of private alleles in subpopulations decreases with increase of rate of migration. Angora_Aus and Cashmere_Aus populations presented at least one private allele (allele 120 on BM1258 and 115 on TGLA53, respectively) with a reasonably high frequency, indicating a low level of gene flow between these two populations. The existence of such population-specific alleles with high frequency can be explained in two ways. Firstly, the new alleles (private alleles) could appear after a goat lineage split into Angora and Cashmere and further split. Secondly, some populations may have lost these alleles during their evolution.

In four cases, statistically significant deviations from
HWE were observed for these five populations. From the results of the $f$-statistic, the reason for significant deviations from HWE on loci BM1818 in GGS and SRCRSP07 in Angora_Aus was due to deficiency of heterozygotes at these two loci. Based on likelihood parentage analysis, the heterozygote deficiency at SRCRSP07 in Angora_Aus was probably associated with the presence of a null allele. Surprisingly, the extremely variable locus OarCP73 demonstrated p-values (deviations from HWE test) close to significance across all populations. This might be caused by the presence of many alleles with low frequencies. Low frequencies of alleles can lead to spurious rejection of the null hypothesis (Zapata et al., 2001). To avoid this we also examined the deviations from HWE in the data set, which included only alleles with frequencies >3%. With such data p-values for deviations from HWE in this locus generally increased for each population. However, a significant deviation ($p = 0.0476$) at OarCP73 still remained in the Cash_Aus population even after excluding 6 alleles with frequency <3%. Therefore, beside low-frequency alleles, other factors might also cause the deviations from HWE in this locus. On the other hand, the observed significant deviations from HWE could be simply due to chance if we set a strict threshold for Multiple test (e.g. $p<0.05$ with the sequential Bonferroni correction).

The level and pattern of observed and expected heterozygosity and polymorphic information content at the fourteen loci studied across the populations were high, indicating a high power of these markers for this population genetic study. A similar amount of heterozygosity and PIC was observed by other researchers working with Chinese indigenous (Li et al., 2002) and Mongolian Cashmere goat and Angora (Turkey) goat populations (Luikart et al., 1999). A slightly lower variability was observed in Swiss goat breeds as well as in two feral (Creole and Bezoar) goat species (Saitbekova et al., 1999).

The level of the $F_{ST}$ values reflects the level of divergence among the populations. The mean $F_{ST}$ value (0.075) for all the five populations demonstrates that only 7.5% of total genetic variation is attributable to differences between the populations. Such limited differentiation between the Australian and Mongolian goat breeds is not very surprising if we consider previous findings in literature. For example, Luikart et al. (2001) using mtDNA diversity analysis found that around 10.7% of the total genetic variation was explained by a difference between goat breeds from different continents (Europe, Africa, Asia and Middle and Near East) and also they noted that mitochondrial DNA types found in Mongolian goat samples were represented in all three domestic goat lineages. Furthermore, Mannen et al. (2004) found in their mitochondrial analysis that 20% of Mongolian cattle carried B. indicus mitochondrial haplotypes whereas Japanese and Korean

Figure 2. Correspondence analysis of allele frequencies from fourteen MS loci based on the genotypes of all individuals representing the five goat populations.
cattle carried only B. taurus haplotype. They postulated that this may have been due to the import of zebu and other cattle during the Mongol Empire era with subsequent crossing with native taurine cattle. Compared with cattle, goats are small portable animals and have been transported widely for food supply and trading purposes from one place to another by land or sea. Therefore widespread transportation and dispersal may be a factor contributing to lower than expected genetic diversity between some goat populations.

The results of pairwise $F_{ST}$ values as well as genetic distances between the studied populations indicated that the Angora goats are genetically distinct from the Cashmere goat populations. However the magnitude of the difference between Angora and Cashmere goat populations was small for animals of different breeds. This may be true for all Australian Cashmere goat populations as crossbreeding with Angoras was commonly used in the early establishment of cashmere-bearing goats. The Australian Cashmere goat population showed slightly higher pairwise $F_{ST}$ values and larger genetic distance from the Angora population, than did the Mongolian Cashmere goat populations, suggesting that the Mongolian Cashmere goats had a genetic link with Angora goats in the past. Russian Pri-Don and Gorno-Altai goats, which produce mohair, were brought in Mongolia in 1954 and 1970s, respectively, and were used in crossbreeding programs to improve the productivity of the Mongolian native goats in southern and south-western regions of Mongolia. Therefore, admixture or gene flow at some degrees may have occurred between crossbred goat populations and Mongolian native goat populations. Within the studied Mongolian Cashmere goat populations, a high level of polymorphism existed between individuals within populations (about 99%), but not between populations, which indicates a high rate of gene flow between these populations. As additional proof, according to the correspondence analysis, the three Mongolian goat populations appeared as a single population (Figure 2). Similar observations (negligible genetic difference) were made by Naymsamba (2003) in studies of genetic relationships among eight native Mongolian goat populations based on 33 biochemical genetic markers.

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