

## Diversity of Chinese Indigenous Goat Breeds: A Conservation Perspective - A Review -

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**ABSTRACT** : In this manuscript, a review of the diversity of Chinese indigenous goat breeds according to data from body stature and appearance, chromosome group, blood proteins, DNA molecular markers (mitochondria DNA, random amplified polymorphic DNA, microsatellite DNA, major histocompatibility complex) has been introduced. All of these provide efficient tools for the diversity analysis of Chinese indigenous goat breeds and are very important for biodiversity conservation, restoration of declining goat breeds, the priority defining in Chinese indigenous goat breeds' protection and the selection of nature preservation zones. Many Chinese indigenous goat breeds with small population size in the isolated mountains or reservoir areas are verging the potential threat of extinction, effectively lost with the rapid destroying of ecological environment. On the other hand, as a result of the introduction of modern commercial goat breeds and shortage of effective conservation, some populations, such as *Small-xiang* goat and *Tibetan* goat decrease rapidly in number of sires. In the interests of the long-term future of the goat breeds in China, conservation of goat breeds' genetic resources should be considered urgently and some conservation measures should be adopted. In addition, the continuing development of molecular biology will further enhance conservation of diversity of Chinese indigenous goat breeds. (*Asian-Aust. J. Anim. Sci.* 2004, Vol 17, No. 5 : 726-732)

**Key Words** : Diversity, Conservation, Chinese Indigenous Goat

### INTRODUCTION

Goat (*Capra*) is one of the ancient livestock. Generally it was considered that domestic goat (*Capra hircus*) originated from two kinds of wild goat (*Capra aegagrus* and *Capra falconeri*) (Tu, 1989). Goat was first domesticated in west Asia at the period of 9000-7000 B.C. (Zeuner, 1963). Based on the abundant results of archaeological history and animal researches, it was extensively accepted that Chinese goat breeds originated from the territorial plateau of southwest China and the adjacent mid-Asia area (Tu, 1989). There are 48 Chinese indigenous goat breeds and all of them are valuable reservoir in the world goat breed resource of 300-400 goat breeds (Yue, 2000). The Chinese indigenous goat breeds are also the natural gene pool for goat breeding. Some breeds possess specific gene resources endowed by nature. For example, the genes controlling properties of fur coat in *Zhongwei* goat, the genes controlling the high reproductive capacity and the genes deciding the color of lambskin in *Jining* grey goat (Xiao, 1996).

Resulted from the long-term natural selection and artificial breeding, Chinese indigenous goat breeds formed some instinctive merits: extensively adaptability, strong

disease-resistant and cold-resistant ability, strong coarse fodder enduring ability, abundant breeds, manifold animal product, high reproductive capacity, and rapid growth rate (Jiang et al., 1988). However, with the rapid development of goat industry in China and the introduction of exotic goat breeds, most Chinese indigenous goat breeds were facing the challenge of modern commercial goat breeds. In addition, as a substitute in goat breeding, frozen exotic goat embryos exerted a powerful impact on Chinese indigenous goat breed resource. Some local goat breeds were replaced by exotic goat breeds in the scale of county or district (Yue, 2000). The introgression from other native goat populations might also result in the loss of original genetic variations (Guo, 2001). Hence, Chinese indigenous goat breeds are not only threatened by extinction due to breed replacement, but also by the genetic erosion of native populations.

It is commonly accepted that the breed diversity is the genetic ability of a breed or a population adapting to human demand variation. The diversity of Chinese goat breeds just leads to the extensive adaptability. Moreover, the diversity of Chinese goat breeds contributes to the heterosis of goat. Since the genetic resources required for the future are unknown, it has been suggested that one criterion that be used to identify breeds for conservation is 'taxonomic distinctness' (Hall and Bradley, 1995). Many conservation strategies for Chinese indigenous goat have been considered and carried out. This manuscript will briefly introduce the diversity of Chinese indigenous goat as follows, with the aim of hoping that the diversity conservation of Chinese goat breeds could be strengthened.

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## DIVERSITY OF CHINESE INDIGENOUS GOAT BREEDS

### Body stature and appearance

Goat industry in China has experienced a long history and it can be seen from the recorded history of the Xia Dynasty (21<sup>st</sup>-16<sup>th</sup> century B.C.) and can be proved by the plenty of historical relics unearthed in the archaeological studies (Li, 1993). Chinese indigenous goats have two horn types: sickle type and spire type. This phenomenon can be traced to its ancestors of *Capra aegagrus* with sickle type horn and *Capra falconeri* with spire type horn. There are distinctive appearances forming the exterior diversity of Chinese indigenous goat breeds. With the enriching of knowledge of genetics and breeding, the diversity of appearance was gradually expressed by the specific values, such as height at withers, body height, heart girth and cannon circumference (Tu, 1989). The multivariate statistics analysis of three sides (body measurement, morphology and ecological characteristics) was carried out by Chang et al. (1998). Their results indicated that the body measurement and morphology had intimate relationships with ecological characteristics and the ecological characteristics also played an important effect on goat breed evolution. The goats in high altitude area had a little larger body height and heart girth than those of goats in the low altitude area. On the other hand, the percentage of goats with horn in high altitude was also a little more than that of goats in the low altitude. The size and weight of goat breeds in northern areas were larger than those of goat breeds in southern areas. The relationship of animal's body size and climate condition was consistent with that reported by Campbell et al. (1975). In some Chinese indigenous goat breeds, owing to different ecological environments, such as altitude and climate, they could be divided into several ecotypes. For instance, *Tibetan* goat was divided into three ecotypes (Plateau type, Mountain-valley type and Ou-la type) according to their ecological characteristics, body stature and exterior appearance (Qin et al., 1997).

The coat color is another important economical characteristics for Cashmere goat and fur coat goat. It is also a genetic sign for breed classification and reflects the diversity of Chinese indigenous goat breeds. Coat color in goat has eight calligraphic models: Bezour, silver Bezour, grey, pure white, light bluish white, Bezour with Toggenburg whitespot and white with Dutch belt (Chang, 1998). Major coat color variation in goat is Mendel traits controlled by a few gene loci. The gene loci are agouti locus, locus of color dilution factor, locus of the interaction white, and white spot locus (Nozawa, 1988). All the four genes are in the euchromosome and have no linkage relationships (Lush, 1926; Asdell, 1928; Searle, 1968). However, because coat color inheritance of goat is a

complicated genetic issue, some problems involved in coat color inheritance in the process of Chinese indigenous goat improvement still wait for us to work out a solution. For example, what degree of genetic limitation exists in the different shades of purple Cashmere down in the savannah-type goat (Chang, 1998)?

Generally, goat breeds are named by their places of origin and classified by their uses of product. As the effect of different ecological conditions and long-term artificial selection, goat breeds with different genetic characteristics and product orientation are formed, such as ordinary goat, wool goat, Cashmere goat, pelt goat, lambskin goat, mutton goat and milk goat (Yue, 2000). The majority of goats in China are ordinary goat breed and there are no indigenous wool and milk goat breeds in China (Yue, 2000). The goat breeds with different product uses have different appearances and spread in different ecological zones. For example, the majority of Cashmere goat breeds with good Cashmere down exist in temperate zones (Shi, 2000). It was considered that the domestic goat breeds in the world were from a single origin and their separations in different ecological areas followed (Nozawa, 1988). Additionally, Cashmere down of Chinese indigenous goat has three colors of white, grey and purple. The white Cashmere down is the most valuable down. The fineness, mean length and mean intensity of Cashmere down are not the same in different Cashmere goat breeds (Jia et al., 1999b). The phenotypes of Chinese indigenous goat breeds are important factors for breed differentiation. However, besides the genetic factors, the environment also exerts a tremendous influence on the exterior appearance of goat. Therefore the accuracy and reliability of exterior appearance is not so good as chromosome, biochemical markers and molecular DNA in breed differentiation (Fang et al., 2001).

### Chromosome group

At the beginning of this century, Sokolov (1930) set about the study of the chromosome number and banding pattern of goat. With the technique improvement of chromosome detection such as *in vitro* culturing and peripheral blood lymphocytes culturing, people are gradually acquainted with chromosome pattern of different goat breeds. Normal goat has twenty-nine pairs of cavillose euchromosome and one pair of sex chromosome. The sex chromosome of male goat is XY and that of female goat is XX. The X chromosome is also cavillose and is the biggest. The Y chromosome is the smallest with mediocentromere and twenty-nine pairs of euchromosome are acrocentric chromosome (Li, 1998). The abnormal chromosome including Robertsonian translocation could be found in the chromosome of goat. Especially, XX/XY mosaicism goat was often reported and it had relative relationship with the

horn of their parents (Feng et al., 1988). The intersex chromosome and interzonal fusion revealed that Ag-NORs had strong genetic characteristics and were the genetic feature of chromosome. It was also found that the frequencies of Ag-NORs in different breeds were markedly different and they were highly polymorphic (Sun, 1998). The study on the polymorphism of Ag-NORs could be used as important genetic markers for goat breeds' classification (Zhong et al., 1985; Zhao, 1993; Xie, 1999). The size of C-band and intensity of staining also had obvious polymorphisms. As a kind of genetic marker, C-band provided important cell genetic data for goat breed identification. Many studies of cytogenetics indicated that goat and sheep had high homology on the pattern of G-banding. The chromosome study of mountain-valley type *Tibetan* goat and *Tibetan* sheep also revealed that they originated from common ancestors (Zhong, 1985).

Since the late 1970s, molecular methods have provided new markers for the study of genetic variation. Genetic markers, based on unique sequence DNA mutations located within protein-coding regions, have long been used in genetic population studies and the diversity analysis of animal breeds, with most of the markers being biochemical polymorphism identified on the basis of electrophoresis differences (Arranz et al., 1996; Mo et al., 2003).

### Blood proteins

The polymorphisms of blood proteins of goats played an important role in studying the breed structure of goat and finding out the affinity within and between goat populations. The gene frequency difference of blood proteins between Chinese indigenous goat populations was the reflection of different origins, extremely slow and long-term natural selection, geographic isolation, and genetic drift (Pan, 1998). Therefore, the polymorphic blood proteins of Chinese indigenous goat breeds provided a method to trace breed relationship before artificial selection. The study on blood proteins of goat was the earliest and now it lagged far behind that of other domestic animals. Moreover, this study at home was less than that of abroad. The studies over the past 20 years on blood protein polymorphisms of goat indicated that the AKP, LDH, X-P, Np, Hb, Tf and Alb were polymorphic. However, the Am, Es, Cp and PHI had no polymorphism (Zhang, 1993; Pan, 1998). It was also suggested by Zhang et al. (1990) that the goat in the world could be divided into three populations according to the Hb gene frequency. 1196 samples of forty-two southeast-Asia goat populations were genotyped for 33 blood protein and enzyme loci. Fifteen loci were polymorphic. The percent of polymorphic loci was 6.1-24.2% and the average heterozygosity was 0.4-5.1%. Compared with corresponding value of other livestock, the values were very low. It indicated that the differentiation degree was low and

the domestic goat (*Capra hircus*) might be single-origin (Li, 1998). The phylogenetic relationship study of sixteen native goat populations with eighteen blood enzyme and other protein variations proved that the middle Yellow River valley was one of the taming and disseminating centers of domestic goats to the east and south of central Asia. The native goat colonies to the east and south of central Asia could be classified into two phylogenetic systems-the east Asian group and the south Asian group (Chang, 1998). Intro and inter population genetic variation were also measured with biochemical markers on *Tibetan* goat. The results showed that *Yadong* colony (Mountain-valley type) and the plateau type of *Tibetan* goats belonged to the south Asian and the east Asian group respectively (Chang, 1998). The low variation and low heterozygosity of blood protein loci in *Tibetan* goats showed that there was little artificial selection in it and it was a primitive indigenous goat breed. *Tibetan* goat breed also provided the basic material for Chinese indigenous goat conservation (Guo, 2001).

### DNA molecular markers

In recent years, molecular genetics has experienced considerable advances, and polymerase chain reaction (PCR) amplified DNA now offers a convenient way for characterization of population structure. Owing to the revealing genetic essence of goat population directly and not being affected by evolution and environment, DNA molecular markers are extensively applied to the goat breed classification instead of blood protein and isoenzyme nowadays.

mtDNA (mitochondria DNA) is an important maternal genetic marker in studying the genetic relationships of livestock species and breeds (Awise, 1991). The mtDNA has proven to be especially valuable in the study of genetic variation and evolution because it shows maternal inheritance and evolves much more rapidly than single-copy nuclear DNA in mammals (Brown et al., 1982). Compared with analyses of allozymic variations, analyses of mtDNA polymorphism at the nucleotide level have shown to be very useful for detection of genetic variation. The mtDNA has the following distinctive characteristics: (1) Molecular weight is small; (2) Molecular architecture is simple and stable; (3) The genetic pattern is unisexual matrilinear inheritance; (4) In the process of metagenesis, it has no recombination and can keep the same mtDNA type as its wild ancestors. In 1997, Upholt found that the length of mtDNA in goat was 15.8 kb with electron microscope. The study on mtDNA polymorphism analysis of Chinese indigenous goat was later than that of other species and lacked the systematicness. On the other hand, the depth in study was far inferior to that of swine and ox. Fourteen restriction endonuclease (ApaI, BamHI, BglI, BglII, DraI, EcoRI, EcoRV, KpnI, PvuII, PstI, SacI, SalI, SmaI, XhoI)

were used to investigate the mtDNA polymorphism of eleven Chinese indigenous goat breeds from twelve provinces and autonomous regions (Li et al., 1997; Li et al., 2000). Among more than 300 individuals, nineteen restriction patterns were detected, which could be classified into eight haplotypes. The results pointed out that the Chinese indigenous goat breeds might originate from two different maternal sides and mtDNA differentiation degree of Chinese indigenous goat breeds was low. The report on mtDNA polymorphism of *Inner Mongolia* Cashmere goat and *Guizhou* goat breeds also fully proved the above results (Jia et al., 1999a; Zhang et al., 2000).

Random amplified polymorphic DNA (RAPD) is a new PCR based DNA marker technique (Welsh and McClelland, 1990; Williams et al., 1990). This technique has been showed to be very useful for detection of genetic variation. RAPD marker has the following distinctive merits: (1) No prior knowledge of genomic sequences is necessary; (2) One set of primers can be used by different genomic DNA; (3) Only minimal amount of genomic DNA is needed for routine RAPD amplification; (4) Harmful radioisotopes is not needed. The study of "RAPD Variation and Genetic Distances among *Tibetan*, *Inner Mongolia* and *Liaoning* Cashmere Goats" showed that the Nei's (1972) standard genetic distances and the genetic heterozygosity of these Chinese indigenous goat populations were consistent with their geographic location and their development history respectively (Cheng et al., 2001). The technique of RAPD could also be applied to the goat breed identification and paternity tests (Li et al., 2001; Li et al., 2002). The study on RAPD marker of *Tibetan* goat indicated that the arbitrary primer (5'-TGGTGCCTC-3') could be confirmed as a marked primer to discern Mountain-valley type and Plateau type *Tibetan* goats (Qin et al., 1998). A vast amount of scientific data revealed that some RAPD markers had relative relationships with the economic traits and the body figure of goat (Li et al., 1999). Though the technique of RAPD is short of stability, it is a simple and convenient method in studying the genetic diversity of Chinese indigenous goat breeds.

Among these molecular markers, microsatellite DNA has been found to be common in all eukaryotic genomes so far examined, with frequency as high as one every 6kb (Beckmann et al., 1992). As it provides much more information, microsatellite markers have been proven to be useful in assessing genetic relationships among different animal populations (Li et al., 2000). Microsatellite DNA is short tandem repeat of 100-360 bp made up of 1-6 bp repeated oligonucleotide. It exists extensively in the genome of eukaryotic organism and is polymorphic resulted from the different repeat unit and repeat number. The microsatellite study of goat is relatively later than that of ovine, bovine and swine (Vaimain et al., 1996). Because of

the highly conservative of ruminant animal genome, some scholars suggested applying the cloned microsatellite of bovine and ovine to the study of goat (Barker, 1994). The 233 microsatellite markers in the first genetic map of goat published by Vaimain et al. in 1996, in which there were 165 from bovine, 47 from ovine and 11 from goat itself, were suitable for the breed diversity analysis of goat. With eight ovine microsatellite and five bovine microsatellite, the genetic relationships between five Chinese indigenous goat breeds, which included four Cashmere goat breeds (*Tibetan* goat, *Neimongol* goat, *Liaoning* goat, *Taihang* goat) and one *Hubei* local goat breed (*Matou* goat) used for mutton production were analyzed. The results pointed out that the genetic relationships of five Chinese goat breeds were in accordance with the known history, geographic origin and the production type of corresponding goat breeds (Yang, 1999). Eleven Chinese indigenous goat populations (High plateau type *Tibetan* goat, Mountain-valley type *Tibetan* goat, *Neimongol* goat, *Liaoning* goat, *Taihang* goat, *Small-xiang* goat, *Matou* goat, *Wu* goat, *Chuandong-white* goat, *Nanjiang-brown* goat, *Black* goat) were also investigated with the panel of microsatellite recommended by EU Sheep and Goat Biodiversity Project (<http://139.222.64.94>). The results proved that the ecological factor, genetic origin, geographic location and artificial selection contributed to breed diversity of Chinese indigenous goat (Li et al., 2002). Besides, nine microsatellite were applied to the genetic variation analysis between Korean goat and Chinese goat, the mean expected heterozygosity showed the highest genetic heterozygosity existed in Chinese native goat breeds, whereas the lowest heterozygosity was within Korean goat breeds (Kim et al., 2002).

Different from the microsatellite DNA, major histocompatibility complex (MHC) is distinct haplotype resulted from disequilibria distribution of alleles. The MHC genes play an important role in the immune system of all vertebrates, as restriction elements presenting antigens to T lymphocytes. These genes encode some of the most polymorphic molecules known (Juul-Madsen et al., 2000). Three kinds of molecules (I, II, III) are encoded by MHC. These molecules are codominant inheritance and have an important effect on the antigen recognition, immune response, immunological regulation and destroying the exotic antigen target cell. MHC is highly homogenous in ruminant animals. MHC of goat was discovered by Van Dam et al. (1979) and was located in the 23rd chromosome by Vaimain et al. (1996). The studies later showed that there were a high level of polymorphisms in the MHC I, II loci. However, it was not often reported that MHC marker was applied to the genetic resource classification of goat breeds. The study of "PCR-RFLP Analysis of MHC-DRB3 Gene in *Wuzhumuqin* Goat and *Kazakh* Goat" pointed out that the MHC-DRB3 was highly polymorphic and there were

significant differences of genotypic frequencies and allelic frequencies between two populations (Sun, 2001). The results indicated that MHC was an effective marker for goat breed classification in China. Recently, genomic regions encoding the MHC appeared promising for further analysis in genetic relationship study in our lab.

### DIVERSITY CONSERVATION OF CHINESE INDIGENOUS GOAT BREEDS

In the past ninety years, goat industry in China had made considerable headway due to exotic excellent goat breeds. However, the tides of exotic goat breeds exerted a great impact on Chinese indigenous goat breeds. The threat to the Chinese indigenous goat is that almost one-third goat breeds are verging on the extinct. It includes the following causes (Xiao, 1996; Chang, 1998; Guo, 2001): (1) Sixty percent of goat breeds in the developing districts are short of funds to found and defend the basic installation for goat breeds diversity protection; (2) Protection the goat breeds which people have no interests in is not paid enough attention; (3) Generally, the systematic monitoring strategy has not been formed and it is deficient of the basic trait information of most Chinese indigenous goat breeds; (4) The regulation of rural economic structure and the west exploiting policy will pound the native goat breeds once again; (5) Fourteen native goat breeds which are rarely utilized are being substituted by the introduced goat breeds with high production capability; (6) Of the goat breeds in the imminent danger, two thirds of goat breeds which are short of any protection and management are threatened by the extinct.

It is not easy to predict the genetic requirements that farmers will need to meet future agricultural demands. Therefore, breeding strategies that preserve original native genes in Chinese goat breeds should be considered by the animal geneticists and commercial breeders in order to prevent the long-term loss of genetic variation within the breeds. Some measures should be adopted to conserve the diversity of Chinese indigenous goat breeds (Chang, 1998; Yue, 2000; Guo, 2001). The protection of genetic diversity of Chinese indigenous goat breeds include the following series of activities: (1) The identification, charactering and monitoring of goat breeds existed; (2) The sustained utilization of goat breeds - a effective method of preserving unusual gene; (3) Enough genetic material sample should be stored in order to guarantee that the descends can get unique threatened Chinese indigenous goat breeds; (4) The national policy and international cooperation which can guarantee the practical strategy should be fulfilled; (5) The research and training should be related to goat breed genetic resource; (6) The traditional knowledge beneficial to the protection of goat breed diversity should not be

overviewed; (7) The goat breeds which have large quantity and distribute widely can be protected and assortatively bred in reserve areas; on the other hand, the goat breeds with small quantity can be reserved in the protection farm; (8) Biological technology such as super-low-temperature-freezing method and genetic engineering should be applied in the genetic resource protection of Chinese indigenous goat breeds.

### CONCLUSION

The Chinese indigenous goat breeds are the precious genetic resource in the world. These goat breeds play an important role, not only on the goat industry in China, but also on the genetic improvement of goat industry in the world. In order to provide theoretical foundation for the conservation and utilization of Chinese indigenous goat breed resources, the origin, genetic characteristic, distribution and relationship of goat breeds should be studied further. With the development of molecular biology, the studies on genetic diversity are advancing from morphological markers to cytohistological markers and from biochemical markers to DNA molecular markers. We believe that the studies on the diversity of Chinese indigenous goat breeds will reflect their genetic variation from essence more precisely with the development of molecular genetic markers and molecular ecology. What's more, because of enormous loss of Chinese indigenous goat breed resources nowadays, the studies on diversity of Chinese indigenous goat breeds are becoming imminent. Conservation of genetic diversity should be considered by breeders and geneticists urgently.

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