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Microsatellite based genetic diversity and population structure of nine indigenous Chinese domestic goats

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ABSTRACT

Determination of genetic diversity and population structure plays an important role in supporting genetic improvement programs and future conservation plans. In this study, 352 individuals representing nine Chinese indigenous goat populations distributed in China were genotyped at 15 microsatellite loci. The mean number of alleles (MNA) per breed ranged from 3.867 (Matou goat, MT) to 5.400 (Ujumqin white goat, UW), the expected heterozygosity (H_e) varied from 0.482 (Hainan black goat, HNB) to 0.659 (UW). Allelic diversity and heterozygosity measures in the studied populations were much lower than Chinese Cashmere and meat type goats. Global F statistics revealed 9.8% of total variance explained among breeds while 90.2% of variance was due to diversities within breeds. Three major population clusters were observed broadly conforming to geographical locations of different goat populations. Three-dimensional scatterplot derived from three largest principal components supported the observed phylogeny based on genetic distance estimations. Goats from Northern China and Island region were distinct while strong admixture was observed among goat populations from Central China. The study revealed market orientation and geographical distances among populations might have contributed to the genetic structure and population sub-division among Chinese indigenous goats. Our study provided a new insight into understanding the genetic diversity and structure of Chinese indigenous goat breeds, and will be helpful to determine the strategies for breeding and conservation programs.

1. Introduction

The goat (*Capra hircus*), one of the first animal species domesticated in South-west Asia around 9000–7000 BCE (Zeuner, 1963), migrated east into central Asia and the high altitude areas of southwest China where modern Chinese indigenous goat breeds supposedly originated from (Tu, 1989). Currently, over 50 breeds of Chinese indigenous goats are listed in the Domestic Animal Diversity Information System (DAD-IS, http://dad.fao.org/) of FAO, that constitute more than 20% of total goat breeds available in Asia. Moreover, there are 188.03 million goats in China accounting for ~18% of global goat population (FAOSTAT, 2014). The Chinese indigenous goat breeds possess specific characteristics resulting from long-term natural selection and artificial breeding. These breeds are known for their high fitness levels under harsh conditions, ability to survive with coarse fodder, rapid growth rate and adaptability to a range of habitats from northern cold and harsh high altitude areas to southern warm and humid low altitude basins (Jiang and Tao., 1988; Zheng et al., 1989). These native goat breeds are valuable resources for trade and exchange in modern animal husbandry offering a variety of agricultural products such as wool, milk, chevon and kid leather. However, intensification of goat husbandry with emphasis on production has become an increasing threat to the conservation and utilization of indigenous goat breeds. Some of the breeds with low growth rate such as Maguan Horn Down goat and Guishan goat in Yunnan province became almost extinct in recent years. The primary objective of conservation is to retain as much as within and between breed diversities in indigenous goats. However, information on phenotypic and genetic characteristics like pedigree records, production performance, basic diversity measures and genetic distance estimates for most Chinese goat breeds are very limited. Therefore, the evaluation and analysis of genetic diversity and population structure may provide an approach to prioritize breeds for conservation. Also, the phylogenetic relationship among breeds would throw light on origin and migration of these goats. In this study, 15 microsatellite marker loci for 9 Chinese indigenous goat breeds

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Table 1
Details of nine Chinese indigenous goat breeds under study.

Breed	Breed code	Sample size	Locality	Utility
Arbas white cashmere goat	AWC	43	Inner Mongolia	Cashmere
Chuandong white goat	CDW	39	Si Chuan	Meat
Hainan black goat	HNB	41	Hai Nan	Meat
Matou goat	MT	33	Hu Bei	Meat
Nanjiang yellow goat	NJY	29	Si Chuan	Meat
Rongjiang xiang goat	RJX	63	Gui Zhou	Meat
Ujumqin white goat	UW	15	Inner Mongolia	Meat
Youyang black goat	YYB	33	Si Chuan	Meat
Youyang wu goat	YYW	56	Si Chuan	Meat

were investigated to identify the degree of genetic diversity and population structure.

2. Materials and methods

2.1. Biological samples

In total, 352 animals representing nine indigenous goat breeds (Table 1) were sampled from three geographical locations: northern, southern and island regions (Fig. 1). The southern region was further divided into two sub-regional groups, mid-west and mid-east. The unrelated animals were sampled based on pedigree records or after detailed interview of farmers on the breeding history. Genomic DNA was extracted from peripheral blood using the genomic DNA extraction kit (Omega bio-tek, USA).

2.2. Microsatellite loci

The polymerase chain reaction (PCR) amplification was carried out at 15 microsatellite marker loci (Supplementary Table ST1). These microsatellites were selected from the list of markers recommended by the Joint ISAG/FAO standing committee, MoDAD (Measurement of Domestic Animal Diversity) for the analysis of genetic diversity in goats (FAO, 2011) and some of them were extensively used in previous studies (Saitbekova et al., 1999; Li et al., 2002; Maudetr et al., 2002; Li and Valentini, 2004; Canon et al., 2006; Fan et al., 2008). Fluorescently labelled PCR primers (forward primers labelled with one of the following dyes: 6FAM, VIC, NED and PET) were used. Allele sizes at each locus were estimated relative to internal lane control (LIZ 500 size standards of length 35 bp–500 bp) and the genotypes were extracted using GENEMAPPER software V. 3.7.

2.3. Statistical analysis

The total number of alleles, expected heterozygosity (*He*) and sample size corrected allelic richness was characterized for all loci in the breeds. Wright's F-statistics, F_{IS}, F_{ST}, and F_{IT} (Weir and Cockerham, 1984) were estimated after jack-knifing over populations and loci using FSTAT v2.93 (Goudet, 1995). The He corrected for sampling bias (Nei, 1987), the observed heterozygosity (H_o), the polymorphic information content (*PIC*) and the estimated null allele frequency were calculated for each locus in the whole population using CERVUS v3.03 (Kalinowski et al., 2007). GENEPOP v3.4 package (Raymond and Rousset, 1995) was used to perform exact test for Hardy-Weinberg equilibrium considering both options (heterozygote deficit and heterozygosity excess) as alternative hypotheses. The exact test was conducted by microsatellite loci (test multi-population) and by population (test multi-locus) using Markov chain method with 1000 iterations. The neutrality of genetic markers was tested by LOSITAN workbench (Beaumont and Nichols, 1996; Antao et al., 2008) based on F_{ST} outlier approach. Gene flow (N_m) was estimated by approximation of Wright $F_{ST} \approx 1/(1+4Nm)$

Fig. 1. Schematic map illustrates of sampling location of nine Chinese indigenous goat breeds used in this study. The sample sizes for each breed are in brackets, and the breed abbreviations are given in Table 1.

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