

## ASSESSMENT OF GENETIC VARIABILITY BASED ON DNA POLYMORPHISM IN NEI MONGOL CASHMERE GOATS

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### INTRODUCTION

Cashmere goat is gaining in popularity all over the world, where cashmere, meat and leather production are economically important. Nei Mongol (NM) Cashmere Goat is one of the country's most famous breed and whose cashmere is a most important exchange earner in China. There are 13 million cashmere goats totally in Nei Mongolia, China, which amount to 21.67% of numbers of down-bearing goats in all China. NM is situated in northern China, a narrow belt, stretching more than 5000 kilometers from east to west. Typical continental plateau climate, which is very much different in the year around and seasons, dry and hot summer, cold winter and windy spring and autumn, precipitation and humidity decrease from east to west (600-50 mm). Vegetation change drastically in different seasons and regions. Forest grassland, meadow grassland and typical (good) grassland are distributed in mid and eastern NM, arid and semi-arid grassland, even only Gobi are mostly in western NM. Grass grows relatively well in summer and autumn, and wilts in winter and spring, and also decreases in the species and numbers from east to west. The composition of vegetation in the area around are primarily *Caragana stenophylla* poiark, *Caragana tibetica kom*, *Caragana rorsninskii kom*, *Caragana intermedia kaung*, *Agriopyron cristutum gaertn*, *Agriopyron cristutum schut*, *Alium polyrhizum turcz*, *Artemisia frigidi willd*, *Artemisia ordosica praschen*, *Atipa breviflora griseb*, *Haloxylon ammodendron bunge*, *Ammopiptanthus mongolicus cheng.f.*, which are usual forage for goats, and some of them are grazed only by goats. So NM has many different types cashmere goats from east to west. Cashmere quality and yield are currently in different performance in much of NM region. Is the difference among NM cashmere goats were lead from environment? What is about the genetic variability? To improve the growth, size and fiber quality of the best-adapted NM cashmere goats and to reduce the number, genetic variability among them should be study as quickly as possible.

In the present work, we report the variability of mitochondrial DNAs and genomic DNAs in different regions NM cashmere goat. This study also provides some primary data for further investigation of the breeding in NM cashmere goats.

### MATERIAL AND METHODS

**Source and description of animal.** The entire 32 animals are collected from different regions in Inner Mongolia Black Mountain Breeding Farm, which is located in mid of NM.

**Mitochondrial DNA and Genomic DNA.** Mt DNA was extracted from liver or kidney mitochondria and further purified as described (Zhang, 1997). Genomic DNA was extracted from NM cashmere goats blood cell and purified as described (Zhao, 1998).

**DNA RFLP and RAPD analyses.** Restriction enzyme fragments of mtDNA were digested using based on 15 different restriction enzymes listed in Table 1.

**Table 1. The restriction morphs of mt DNA of goats**

Restriction Endonucleases	Number Of site	Length of fragments (kb)							Molecular Size (kb)
<i>Apa I</i>	2	12.5	3.5						16.0
	2	11.7	4.3						16.0
<i>BamH I</i>	1	16.2							16.2
	2	9.6	6.8						16.4
	4	7.6	3.6	3.4	1.9				16.5
	4	6.8	4.2	3.8	1.2				16.0
	4	6.8	5.0	4.2					17.0
<i>Bgl I</i>	1	16.0							16.0
	4	6.7	6.7	1.8	1.3				16.5
<i>Bgl II</i>	4	6.5	6.1	2.0	1.4				16.0
	3	7.5	6.5	2.0					16.0
<i>Dra I</i>	7	3.9	3.5	2.3	1.9	1.6	1.5	1.3	16.0
	6	3.9	3.5	2.8	2.3	1.9	1.6		16.0
<i>EcoR I</i>	4	5.1	4.3	3.8	3.2				16.4
	4	4.9	4.6	3.7	3.1				16.3
	4	8.5	3.3	2.7	1.5				16.0
	5	4.5	4.0	3.3	2.7	1.5			16.0
	5	4.7	4.2	3.4	2.6	1.4			16.3
<i>EcoR V</i>	1	16.4							16.4
<i>Hae II</i>	4	8.0	3.6	3.0	1.4				16.0
<i>Hind III</i>	4	8.0	4.0	2.5	1.5				16.0
	4	9.3	3.0	2.5	1.8				16.6
<i>Kpn I</i>	1	16.0							16.0
<i>Pst I</i>	2	12.2	4.8						17.0
	2	11.5	5.0						16.5
<i>Pvu II</i>	3	6.5	5.2	4.3					16.0
<i>Sac I</i>	1	16.0							16.0
<i>Sal I</i>	1	16.0							16.0
	2	8.1	7.9						16.0
<i>Xho I</i>	2	15.1	0.9						16.0

Random primer PCR reaction were performed through the method as described (Zhang, 1997).

The length data were handled and analyzed using the program developed by our group (Zhang, 1997).

## RESULTS AND DISCUSSION

**Mt DNA RFLP.** Mt DNA is usually maternally inherited in the egg cytoplasm with one haplotype occurring in individuals. The restriction morphs of mt DNA of NM cashmere goat is shown in Table 1. There were 97 sites in total among the 32 cashmere goats from different region. In the experiment 92 restriction sites and 30 restriction morphs were detected. Interspecific differences are ascertained in all regions of the cashmere goats. NM cashmere goats are highly variable in mt DNA. The mt DNA molecular size is 16.2kb in average, which is close to Upholt and David (1977). This work provides a basic data for restriction map of NM cashmere goat in the future and the sequence should be done soon for correct assessment and selection of goat.

**Genomic RAPD.** To display the genetic deviations from cashmere goats, random primers PCR were carried out, the result was Table 2.

**Table 2 Primers used for RAPD analyses and the number of amplified fragments**

Sequences of primers	No. Of Markers	No. Of poly-morphic	Sequences of primers	No. Of markers	No. Of poly-morphic
AAGGCACGAG	16	16	CCTCACGTCC	10	7
AAGGCGGCAG	15	12	CCTCTAGACC	6	2
AAGGCTCACC	7	7	CCTGATCACC	6	3
AATGCCCCAG	3	1	GACCGCTTGT	3	2
ACAACGCCTC	6	4	GACGTGGTGA	14	14
ACAACGCGAG	6	4	GAGCGTCGAA	7	4
ACACACGCTG	4	4	GGGAACGTGT	6	4
ACCCCCAAG	6	3	GGGAATTCGG	3	2
ACGCTGCGAC	10	8	GGGCCAATGT	3	2
ACGTAGCGTC	3	3	GGGCCAATGT	3	3
AGAGCCGTC	6	4	GGGTCTCGGT	5	5
AGCCAGCGAA	7	4	GGTCGATCGT	11	3
AGGCAGAGCA	1	1	GGTCGATCTG	4	3
AGGGTCGTTT	3	1	GGTGCACGTT	3	2
CAAACGTCGG	4	3	GTGGAGTCAG	9	7
CAAACGTGGG	14	13	GTGTCGCGAG	3	2
CAAAGCGCTC	10	10	TCAGAGCGCC	3	3
CAATCGCCGT	6	4	TCAGTCCGGG	5	2
CATCGCCGA	5	5	TCGCGGAACC	11	9
CCAGATGCGA	7	5	TGAGGGTCCC	7	7
CCAGCTTAGG	6	3	TGCCCCGTCGT	3	1
CCCAGTCACT	4	4	TGGTGCACCTC	11	8
CCCTACCGAC	6	2	TTCCGAACCC	4	3
CCGCGTCTTG	11	10	Average	6.5	4.9

As shown in Table 2, the amplified bands were 306 in all, and 229 bands with polymorphism among them; The polymorphism in RAPD fragments reveals a highly variable type among NM

cashmere goats.

Our results of DNA polymorphism within and between regions allow some conclusions and raise a number of questions regarding the correct breeding scheme of NM cashmere goat.

#### **CONCLUSION**

Inner Mongolia cashmere goats have a good production performances and adaptability to the local natural environment. There is large variability in NM cashmere goats based on DNA polymorphism so that there are still margins potential for selections. At the present some primary information have been achieved on genetic variability for NM cashmere goats. The genetic variability estimated in the current study appears reliable so it provides an authentic basis for the cashmere goat breeding scheme. Maternal genetic effects cannot be ignored also. According to the results obtained here it is suggested that the schemes of selections, assortment and genetic improvement of cashmere goats be made as soon as only based on right cluster by DNA polymorphism

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