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Association of Polymorphism of Microsatellite Markers with Litter Size in Chinese Funiu White Goat

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Abstract: With the aim to detect micro-satellites loci affecting prolific in Funiu White Goat, Eight micro-satellites loci (OarAE101, BM1329, BM 143, LSCV043, GC101, TGLA68, OarHH55 and OarHH35) were selected to study the genetic polymorphisms in Funiu White goats and to analyze their association with litter size of the goat breeds. Within these seven loci, Polymorphism Information Content (PIC), Number of effective alleles (Ne) and Heterozygosity (H) were calculated. The results showed that the mean number of alleles per locus was 7.63±1.60 (range from 6-11) and the mean Ne was 5.34±0.41 (range, 4.74-5.61) and the mean PIC was 0.79±0.02 (range, 0.756-0.799), the mean heterozygosity was 0.88±0.03 (range, 0.84-0.92). It is indicated that the 8 microsatellite loci on the litter size of goat showed that 110 and 110/110 bp at OarAE101, 147/160 bp at 1329, 108/118 and 108 bp at BM143, 160 and 123/160 bp at OarHH35, 115 and 115/115 bp at TGLA68, 123/123 and 145/150 bp at OarHH55, 95/160 bp at LSCV043 had positive effects on the litter size in Funiu White goat. While 155 bp at BM1329, 100/123 bp at BM143 has negative effects on the second litter size and 119/135 bp at OarHH 55,115/160 bp at LSCV043 has negative effects on the total litter size in Funiu White goat. These results may be applied to marker-assisted selection and molecular breeding of Funiu White goat in future.

Key words: Microsatellite loci, goat, genetic polymorphism, litter size, Funiu White goat, range

INTRODUCTION

Microsatellite is also called Simple Sequence Repeat (SSR). This is a new kind of DNA mark developed from the late 1980s. It is generally accepted for its abundant quantity, wider distribution, richer polymorphism, dominant heredity and its quicker and convenient inspecting method. Microsatellite has rapidly become the favorite method for population genetic studies as it shows advantages over other methods and has been used extensively in designing the genetic chain map, orienting quantity character loci and evaluating the genetic diversity (Saitbekova *et al*., 1999; Farid *et al*., 2000; Gour *et al*., 2006; Mao *et al*., 2008; Ligdaa *et al*., 2009).

In resent years, a lot of work on microsatellite markers useful for determining genetic variability and correlation analysis of economic traits has been done in sheep (Chu *et al*., 2001; Wang and Wu, 2006; Sun *et al*., 2006; Guan *et al*., 2007) and goat (Jandurova *et al*., 2004; Marrube *et al*., 2007; Jin *et al*., 2006) production all over the world.

Henan is one of the pioneer provinces in China, about 20.38 million goats in 2008 which occupied 7.26% of the gross quantity in the China. The Funiu White goat is one of the local goat breed of Henan province. It is a prolific and major meat-skin producing animal. This breed kid twice a year or more commonly thrice in 2 years and the number of kids at one time varies from single to septuplet. This goat breed has an average adult body weight of 37.31 kg and produces 7.37% single births, 68.42% twins, 24.74% triplets or more with an average litter size of 2.11% in Neixiang county lying in south food of Funiu Mountain. This breed is also available in others Yuxi mountain region such as Xichuang, Xixia, Nanzhao and Zhenping County and the part north food of Funiu Mountain. Funiu White goat has better adaptability to extensive management in mountain areas; better immunity against diseases, higher reproduction rate and better meat-skin quality which are natural gene reservoir and the good original material of crossbreed predominance and high yield. Due to the higher reproductive performance, rearing this goat breed already brought local farmers

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considerable economic benefits. Because of no scientific selecting system and cultivating were conducted in recent year, some dominant genes of recessive were not protected perfectly which restrict the development of this goat breeding. Further researches on genetic basis theories have not been carried out. How to protect and use this indigenous goat breed resources is most hot research problems in local goat's genetics and breeding. eight microsatellite loci including OarAE101, BM1329, BM143, LSCV043, GC101, TGLA68, OarHH55 and OarHH35 reported affecting reproductive performance of goats such as Boar goat, Huanghuai goat and Xiang dong goat (Song *et al*., 2008; Guan *et al*., 2007; Ouyang *et al*., 2006a, b). How about in Funiu White goat, unknown. So it is essential to study on the polymorphisms of those microsatellite locous to analyze the correlation between litter size and locus from the molecular level, to provide useful information for effective strategies of selection system and conservation programs for local goat breeds.

MATERIALS AND METHODS

Animal and sample collection: Blood samples of 100 adult individuals were collected from the jugular vein using ACD (sodium citrate anticoagulant) as anticoagulant by a random sampling from 10 villages of Neixiang country. Analyzed animals can be as a representative sample of the breed of origin as they were collected from different Villages trying to avoid closely related individuals. For each doe, the number of kids born, the date of kidding, the flock number, the season of kidding and the prolific performance of the first three parities were recorded. Doe with incomplete performance records, doe lacking birth information and records with other obvious errors were removed.

DNA extraction and PCR amplification: A modified phenol/chloroform extraction method was used to isolate genomic DNA from blood (Jandurova *et al*., 2004). Blood (800 μL) was digested in 350 μL lyses buffer (10 mmol L^{-1} Tris-HCl, 1 mmol L^{-1} EDTA, 100 mmol L^{-1} NaCl, pH 8.0) with 10 μL proteinase K (10 mg mL^{-1}) for 12 h at 55°C. The extraction was repeated three times. After precipitation by adding two volumes of ice-cold ethanol, DNA was isolated by centrifugation and then stored at -20°C for future use. DNA pellets were resuspended in TE buffer and the total genomic DNA was quantified using agarose gelelectrophoresis.

The DNA concentration was calculated according to the standards. Eight microsatellite loci were selected according to published relatives; they are OarAE101, BM1329, BM143, LSCV043, GC101, TGLA68, OarHH55 and OarHH35. The PCR primers are shown in Table 1. All primers were synthesized by the Shanghai Sangon Biotech Co., Ltd.

Polymerase Chain Reaction (PCR) amplifications were performed with modifications to improve PCR amplification. A total reaction volume of 20 μL with 2 μL of 10×buffer, 1 μL of 25 mmol $MgCl_2$, 0.3 μL of 10 mmol dNTPs, 0.3 μL of 5U μL^{-1} Taq DNA polymerase, 0.7 μL of 10 pmol μL^{-1} each primers and approximately 50 ng of genomic DNA. The reaction was carried out by denaturing at 94°C for 30 sec, annealing at the temperature optimized for each primer pair for 1 min and extending at 72°C for 10 min for 35 cycles, followed by an extra extension step at 72°C for 10 min. The optimized annealing temperatures of different primer pairs are also listed in it.

Statistical analysis: Base on the microsatellite and the generated allele frequencies, Polymorphism Information Content (PIC), effective Number of alleles (Ne) and Heterozygosity (H) were calculated by the following formula:

Table 1: Information on the eight polymorphic microsatellite loci selected in this study

Loci	Primer (5'→3')	Anneal temp. (°C)	No. of gene bank	Source
OarAE101	F:TTCTTATAGATGCACTCAAGCTAGG R:TAAGAAATATATTTGAAAAAACTGTATCTCCC	63.0	L13692	*Ovis aries*
BM1329	F:TTGTTTAGGCAAGTCCAAAGTC R:AACACCGCAGCTTCATCC	63.0	G18422	*Bos taurus*
BM143	F:ACCTGGGAAGCCTCCATATC R:CTGCAGGCAGATTCTTTATCG	63.0	G18387	*Ovis aries*
LSCV043	F:CCAGAATATAGAGTTTTGTCAAG R:GCCTGATTTGATTTTGTATGAG	52.5	NW279530	*Bos taurus*
GC101	F:ATCCTCACCCTTCAAACAG R:CTGGGGAGTTTTCTCTGAC	59.5	AY690675	*Ovis aries*
TGLA68	F:ATCTTACTTACCTTCTCAGAGCT R:GGGACAAAATTTTACATATACACTT	58.0	AY036611	*Ovis aries*
OarHH55	F:GTTATTCCATATTCTTTCCTCCATCATAAGC R:CCACACAGACAACTAAAACCCAGC	62.5	L13693	*Ovis aries*
OarHH35	F:AATTGCATTCAGTATCTTTAACATCTGGC R:ATGAAAATATAAAGAGAATGAACCACACGG	63.0	L12554	*Ovis aries*

F: Forward Primer; R: Reverse primer

$$PIC=1-\left(\sum_{J=1}^{n}p_i^2\right)\left(\sum_{j=1}^{n-1}\sum_{j=j+1}^{n}2p_i^2p_j^2\right)$$

where, pi and pj were the frequency of ith and jth allele of a microsatellite DNA:

$$Ne=1/\sum_{i=1}^{n}p_i^2$$

where, pi was the frequency of ith allele of a microsatellite DNA:

$$H=1-\sum_{i=1}^{n}qi^2$$

where, qi was the frequency of ith allele of a microsatellite DNA. Associations of the animal genotypes with litter size were calculated using General Linear Model of SAS (SAS Inst. Inc., Cary, NC). The model showed as follows:

$$Y_{ijk}=\mu+\alpha_i+\beta_j+N_k+\varepsilon_{ijk}$$

Where:

Y_{ijk} = The phenotypic value of litter size
μ = The population mean
α_i = The fixed effect of genotype
β_j = The fixed effect of contemporary group
N_k = The fixed effect of year
ε_{ijk} = The random residual error

RESULTS AND DISCUSSION

Allele frequency of the microsatellite loci: All the microsatellite markers were successfully amplified in Fu Niu White goat and with high polymorphism as shown in Table 2. From a total of 864 sampling, about 61 alleles were detected in 8 microsatellite loci. The number of alleles per locus ranged from 6 (TGLA68) to 11 (GC101) with a mean of 7.625. About 11 allele were obtained in the GC101, the variance ranged from 220-280 bp. About 9 allele were found in BM1329 which ranged from 145-180 bp. About 7 allele were found in the OarAE101, BM143, LSCV043, OarHH 55, OarHH 35 which ranged from 106-147, 100-123, 95-160, 119-150 and 100-160 bp, respectively. The results showed that these 8 microsatellite loci had polymorphism in Funiu White goat and thus those can be used to evaluate the genetic polymorphism of goat.

Genetic information of 8 microsatellite loci: This study calculated mean PIC, mean Ne and mean H in goat breed according to allelic gene frequency at 8 microsatellite loci (Table 3). The higher variance of OarHH55 and the lower variance of BM143 were 0.803 and 0.756, respectively. Ne ranged form 5.319 (TGLA68) to 5.747 (OarHH55). All the H analyzed were higher than 0.843 and the highest was 0.92 in OarHH35.

Correlation analysis between litter size and microsatellite loci: Least square means and standard errors of the litter size obtained for the genotypes of the 8 microsatellite loci. There are total 103 genotypes were found in 8 microsatellite loci, of those, 9 genotypes in OarAE101, 14 in BM1329, 13 in BM143, 16 in OarHH35, 17 in GC101, 14 in TGLA68, 10 in OarHH55 and 10 in LSCV043, respectively.

For data analysis, microsatellite loci would not be considered if the appearance frequency of the genotype was <3 because too low an appearance frequency of the genotypes had little analytical value.

In this study, the first three parities of litter size and the total mean litter size of Funiu White goat were calculated by least square means and standard errors. Calculation results showed that some favorable genotype was found only for the mean litter size at first kidding, not for the mean litter size at the second and the total kidding. Most part of favorable genotypes were detected for both the mean litter size at second kidding and the total mean litter size, economic benefits to

Table 2: Distribution of alleles of 8 microsatellite loci in Funiu White goat

Loci	OarAE101	BM1329	BM143	LSCV043	GC101	TGLA68	OarHH 55	OarHH 35
Samples	86.000	82.000	82.000	66.000	90.000	74.000	84.000	84.000
alleles	7.000	9.000	7.000	7.000	11.000	6.000	7.000	7.000
Allele	106 bp (0.070)	145 bp (0.012)	100 bp (0.085)	95 bp (0.242)	220 bp (0.011)	105 bp (0.186)	119 bp (0.202)	100 bp (0.095)
(frequency)	110 bp (0.349)	147 bp (0.329)	106 bp (0.037)	123 bp (0.076)	225 bp (0.033)	110 bp (0.186)	123 bp (0.095)	120 bp (0.107)
	115 bp (0.140)	150 bp (0.110)	108 bp (0.195)	147 bp (0.106)	230 bp (0.056)	115 bp (0.267)	125 bp (0.167)	123 bp (0.262)
	130 bp (0.115)	155 bp (0.146)	110 bp (0.049)	115 bp (0.197)	235 bp (0.311)	118 bp (0.151)	135 bp (0.131)	135 bp (0.202)
	123 bp (0.186)	160 bp (0.159)	115 bp (0.073)	155 bp (0.212)	236 bp (0.022)	123 bp (0.140)	145 bp (0.083)	147 bp (0.048)
	145 bp (0.012)	165 bp (0.085)	118 bp (0.305)	110 bp (0.106)	238 bp (0.056)	125 bp (0.070)	147 bp (0.060)	155 bp (0.1910)
	147 bp (0.128)	170 bp (0.073)	123 bp (0.256)	160 bp (0.061)	239 bp (0.011)		150 bp (0.262)	160 bp (0.095)
		175 bp (0.049)			240 bp (0.056)			
		180 bp (0.037)			242 bp (0.233)			
					244 bp (0.089)			
					280 (0.122)			

Table 3: Genetic information of 8 microsatellite loci in Funiu White goats

Microsatellite loci	OarAE101	BM1329	BM143	LSCV043	GC101	TGLA68	OarHH55	OarHH35
PIC	0.762	0.796	0.756	0.802	0.793	0.785	0.803	0.799
Ne	4.739	5.435	4.695	5.731	5.405	5.319	5.747	5.618
H	0.88	0.909	0.878	0.843	0.850	0.905	0.883	0.920

be considered, the second and total mean litter size of different genotypes on each microsatellite locus in Funiu White goats was shown in Table 4.

The genotype 110/110 bp at OarAE101 was the favorable genotype for the mean litter size at second kidding and its value of significant difference ($p<0.05$) is higher than the genotype 123/147 bp. About 110/110 bp at OarAE101 also was the favorable genotype for the total mean litter size with a higher value of significant difference ($p<0.05$) than the genotype 110/130 and 130/130 bp.

The genotype 147/160 bp at BM1329 was the favorable genotype for the mean litter size at second kidding with a higher value of significant difference ($p<0.05$) than most of other genotypes. But the significant difference of the total mean litter size in different genotype was not found.

About 108/118 bp at BM143 was the favorable genotypes for the mean litter size at second kidding and was second higher value for the total mean litter size while 100/123 bp at BM143 was not the favorable genotypes for both the mean litter size at second kidding and the total mean litter size with lower values of significant difference ($p<0.05$) than most of other genotypes.

About 123/160 bp at OarHH 35 was the favorable genotype for the mean litter size at second kidding and its value was the highest value, 2.5 kids per does, 135/160 bp was the favorable genotype for the total mean litter size. Compared with other alleles, 160 bp at OarHH 35 has positive effects on the litter size of Fu Niu White goat.

About 235/244 bp at GC101 was the favorable genotype for the both the mean litter size at second kidding and the total mean litter size with the highest values. Compared with other alleles, no allele was believed to has positive or negative effects on the litter size of Fu Niu White goat.

About 115/115 bp at TGLA68 was the favorable genotype for both the mean litter size at second kidding and the total mean litter size with the highest value. The significant difference of the total mean litter size in different genotype was not found. The allele 115 bp at TGLA68 has positive effects on the litter size in Fu Niu White goat. About 123/123 bp and 145/150 bp at OarHH 55 was the favorable genotype for both the mean litter size at second kidding, 119/147 bp was the second favorable genotype.

About 95/160 bp at LSCV043 was the favorable genotype for the mean litter size at second kidding with a higher value of difference ($p>0.05$) than the most part of genotypes and was also for the total mean litter size with higher values of significant difference ($p>0.05$) than the genotype 95/95 and 115/160 bp.

Genetic polymorphism of microsatellite loci in Funiu White goat: Polymorphism Information Content (PIC) is a index to indicate the polymorphism of segments (Botstein *et al*., 1980) pointed out that PIC was used to study the degree of gene variance, a microsatellite locus has high polymorphism if PIC ≥ 0.5 and medium polymorphism if $0.5<PIC<0.25$. In this study, the PIC of eight locus ranged from 0.756-0.803 and thus has high polymorphism. To date, almost all published genetic linkage map for goats marked by microsatellite loci is notable that the PIC value for ideal microsatellite DNA should be >0.70 (Farid *et al*., 2000), so that when the locus of parents is heterozygous, distinct separation of alleles can be detected amongst their offspring. In this study, the average PIC value of 8 microsatellite loci was >0.70. The abundant polymorphism content could provide the theoretical bases for determination of QTL control to reproductive traits, as also the references for MAS study which is to accelerate the breeding of Funiu White goat.

Heterozygosis of neutral markers, such as microsatellite DNA marker is generally used to evaluate genetic diversity within populations. The results of this study indicated that microsatellite loci OarHH35 showed the greatest variability (0.920), the second was BM1329 with the 0.909 and LSCV043 showed the lowest one (0.843).

Previously study on the OarHH35 of Boar goat was 0.861 (Ouyang *et al*., 2006a, b) the result showed that the H of OarHH35 in Fu Niu White was higher than that of Boar goat. High heterozygosity indicted low genetic uniformity thus rich genetic diversity which may be suggest that the population size and the structure of the breeding group and reproduction (the number of sires in the studied population are properly.

Effective Number of alleles (Ne) represents the number of equally frequent variants that would give a PIC value. The comparison of this parameter with the number

Table 4: Least square means and standard errors of the litter size obtained for the genotypes of the 8 microsatellite loci in Fu Niu White goat

Loci (No.of genotypes)	Genotype (N)	The second mean litter size	Total mean litter size
OarAE101 (9)	106/106 bp (4)	2.00±0.68^{ab}	2.00±0.26^{ab}
	110/110 bp (14)	2.29±0.21^{a}	2.57±0.15^{a}
	110/130 bp (8)	1.88±0.27^{ab}	1.75±0.19^{b}
	110/123 bp (8)	1.88±0.54^{ab}	2.00±0.37^{ab}
	115/115 bp (4)	1.75±0.27^{ab}	1.88±0.19^{ab}
	115/147 bp (4)	2.00±0.38^{ab}	1.88±0.23^{ab}
	130/130 bp (8)	2.00±0.38^{ab}	1.75±0.24^{b}
	123/147 bp (12)	1.50±0.22^{b}	2.08±0.15^{ab}
BM1329 (14)	147/147 bp (6)	1.67±0.30^{b}	2.17±0.36^{a}
	150/180 bp (6)	1.67±0.30^{b}	1.50±0.12^{a}
	147/160 bp (14)	2.71±0.19^{a}	2.17±0.13^{a}
	150/170 bp (6)	1.67±0.30^{b}	1.64±0.14^{a}
	155/165 bp (6)	1.18±0.51^{b}	2.00±0.26^{a}
	147/155 bp (6)	1.33±0.297^{b}	2.33±0.26^{a}
	147/170 bp (4)	2.00±0.36^{ab}	1.75±0.24^{a}
BM143 (13)	100/118 bp (6)	1.50±0.34^{ab}	2.50±0.22^{ab}
	118/123 bp (14)	1.86±0.22^{ab}	1.79±0.14^{b}
	100/123 bp (4)	1.20±0.26^{B}	1.75±0.31^{b}
	108/118 bp (12)	2.33±0.24^{A}	2.83±0.22^{ab}
	115/123 bp (4)	2.00±0.41^{ab}	2.00±0.28^{ab}
	108/123 bp (10)	1.50±0.41^{ab}	3.00±0.36^{a}
	110/118 bp (4)	1.50±0.41^{ab}	2.00±0.26^{ab}
OarHH35 (16)	BF 110/155 bp (4)	1.50±0.24^{ab}	1.75±0.18^{ab}
	DF135/155 bp (10)	1.70±0.24^{ab}	1.80±0.37^{ab}
	DD135/135 bp (4)	1.50±0.17^{ab}	2.00±0.25^{ab}
	BC110/123 bp (8)	175.00±0.24^{ab}	1.75±0.13^{ab}
	CE123/147 bp (6)	1.67±0.15^{ab}	1.67±0.16^{ab}
	AD100/135 bp (8)	2.25±0.21^{ab}	1.75±0.24^{ab}
	CF123/135 bp (10)	1.60±0.19^{ab}	1.90±0.23^{ab}
	CH123/160 bp (6)	2.50±0.21^{a}	2.17±0.26^{ab}
	CC123/123 bp (6)	1.33±0.14^{b}	1.46±0.24^{a}
	AF100/155 bp (8)	1.75±0.36^{ab}	2.25±0.26^{ab}
	DH135/160 bp (4)	1.50±0.14^{ab}	2.50±0.18^{b}
GC101 (17)	235/242 bp (19)	1.05±0.18^{b}	2.11±0.19^{ab}
	235/235 bp (6)	1.33±0.33^{ab}	1.33±0.23^{a}
	240/280 bp (6)	1.83±0.307^{a}	2.00±0.20^{ab}
	235/244 bp (4)	2.00±0.00^{a}	2.75±0.215^{b}
	236/244 bp (3)	1.67±0.33^{ab}	2.00±0.22^{ab}
	238/244 bp (6)	1.17±0.601^{b}	1.50±0.33^{a}
	235/280 bp (4)	1.50±0.29^{ab}	2.25±0.35^{ab}
TGLA68 (14)	115/115 bp (10)	2.30±0.25^{a}	2.50±0.16^{a}
	105/118 bp (6)	1.00±0.29^{b}	2.00±0.17^{a}
	105/115 bp (6)	1.00±0.289^{b}	2.00±0.17^{a}
	110/123 bp (12)	2.00±0.20^{ab}	2.06±0.14^{a}
	105/110 bp (8)	2.13±0.250^{a}	1.89±0.17^{a}
	115/125 bp (6)	2.00±0.29^{ab}	2.17±0.18^{a}
	115/123 bp (4)	1.50±0.35^{ab}	1.75±0.20^{a}
	118/125 bp (4)	1.50±0.22^{ab}	2.00±0.22^{a}
	110/115 bp (4)	1.80±0.35^{ab}	1.75±0.22^{a}
OarHH55 (10)	CE125/145 bp (4)	1.75±0.46^{ab}	2.00±0.26^{a}
	BB123/123 bp (6)	2.00±0.38^{a}	2.25±0.23^{a}
	AD119/135 bp (10)	1.00±0.29^{b}	1.80±0.17^{a}
	AG119/150 bp (6)	1.33±0.38^{ab}	2.33±0.21^{a}
	CG125/150 bp (14)	2.00±0.25^{a}	2.21±0.15^{a}
	EG145/150 bp (8)	1.63±0.33^{ab}	2.25±0.20^{a}
	AF119/147 bp (8)	1.75±0.33^{ab}	1.89±0.18^{a}
	DG135/150 bp (6)	1.50±0.38^{ab}	2.33±0.21^{a}
LSCV043 (10)	95/95 bp (6)	1.18±0.41^{a}	1.67±0.25^{a}
	95/155 bp (12)	1.17±0.29^{a}	2.17±0.17^{ab}
	95/160 bp (4)	2.25±0.50^{b}	2.75±0.29^{b}
	123/147 bp (6)	1.33±0.41^{ab}	2.33±0.25^{ab}
	115/147 bp (18)	2.16±0.24^{b}	2.22±0.14^{ab}
	115/160 bp (6)	1.33±0.41^{ab}	1.50±0.27^{a}

of observed alleles at each locus gives information about the predominance of certain alleles in breed. Results of this study indicate that the average of Ne obtained from 8 loci ranged from 5.319 (TGLA68) to 5.747 (OarHH55). It is reported the Ne value of BM1329, BM143, TGLA68, OarHH55 and LSCV043 in Boar goat was 6.721, 5.493, 8.296, 4.809, 6.901, respectively (Xu *et al*., 2007) while in the study those values in Funiu White goat were 5.435,

4.695, 5.319, 5.747, 5.731, respectively of those only the Ne of OarHH55 in Funiu White goat was slightly higher than that of Boer goat.

The results indicate that a high level of genetic variation has been maintained in Funiu White goat breeds. A great deal of research on the genetic principle to improve the goat production should be done in the future.

Microsatellite loci and litter size of Funiu White goat: The Booroola (FecB) is a dominant gene located on sixth autosomal chromosome and is responsible for increasing the ovulation rate and litter size in sheep (Davis, 2005; Gootwine, 2005). Recently, study of polymorphism of microsatellite loci that linked to the fecundity gene FecB in the sheep chromosomes for goats are well documented (Martinez *et al*., 2006; Zhao *et al*., 2007; Glowatzki-Mullis *et al*., 2008). Reports on effect of microsatellite loci on economic traits of some goats were also available (Jin *et al*., 2006; Cano *et al*., 2007), also some studies described the polymorphism only, not the association analyses (Traore *et al*., 2009). The information on the effect of FecB allele on litter size in Funiu White goat is limited.

Some alleles that have effects on litter size of goats were documented. For example, it is reported that the allele 126 bp at OarAE101, the allele 120 bp and 124 bp at OarHH55, the allele 185 bp at BM1329 have positive effects on the litter size in Boer goat. The allele 108 bp, 114/126 bp at OarAE101, the allele 120 bp at OarHH55, the allele 185 bp at BM1329 have positive effects on the litter size in Xinong Shaanen goat (Song *et al*., 2008).

Microstaellite loci Lscv043 and GC101 on Huang huai goat were reported (Feng *et al*., 2006). The results showed that litter sizes at both the 1st kidding and the 2nd kidding of the population with 200/238 bp were significantly higher than those of other two genotypes population ($p<0.05$) but the litter size at third kidding among three population was not significant. The total mean litter size of population with 200/238 bp was the most significantly greater than those of other two genotypes population ($p<0.01$) but no significant difference between the later two population. They found that the Lscv043 may not be a factor of affection on the litter size of Huang huai goat. In this study, litter sizes at both the 2nd kidding and the total mean litter size of the population with 95/160 bp at Lscv043 was greater than other genotypes but 115/160 bp was lower, the number of individuals was considered, the affection on Funiu goats was not definite.

According to previously study (Ouyang *et al*., 2006b), three alleles of BM143 have positive effects on the litter size of Xiangdong black goat. Some alleles were also found to be significantly correlated with litter size of Boer goat (Xu *et al*., 2007). For example, 108 bp of BM143 were positively correlated to first parity litter size of Boer goat and we found the same results in Funiu goat. They reported that 216 bp of BM1329, 110 bp of BM143 had negative correlation with first parity litter size and we did found this. About 115 bp of TGLA68 was positively correlated to second parity litter size and this was consisting with this study in Funiu White goat.

Part of results of previously study summarized above are supported by this study but the size and numbers of alleles, the number of genotype were different in some microsatellite loci of those studies, the reason may be contributed to the breeds, the samples, the methods of analyzed and so on. Because there are no way to find out some definite genotype or loci associating with the number of kidding in low prolific goat breed and too small number of samples to represent the species characters especially reproductive performance and the number and size of genotype depends on the analyzing methods and correcting and so on.

In goat production, the total number of litter size during doe's lifetime is very important factor because it affects economic benefits of goat producers. Income from this should be considered as the only saleable product in most part of farm counties' producers. So the alleles and the genotypes that have positive effects on the total mean litter size are as favorable alleles and the genotypes. Secondly, the mean litter size at second kidding is often a paramount index to imply that a goat is withered a prolific one, so also is considered in this study. The mean litter size at third kidding is also important although, it is not shown in this study. Thus, in the study, some alleles and genotypes were found to be significantly correlate with litter size of Funiu White goat they were 110 and 110/110 bp at OarAE101, 147/160 at 1329, 108 and 108/118bp at BM143, 160 and 123/160 bp at OarHH 35, 115 and 115/115 bp at TGLA68, 123/123 and 145/150 bp at OarHH 55. While 155 bp at BM1329,100/123 bp at BM143, 115 bp160 bp at LSCV043, 119/135 bp at OarHH 55 has negative effects on the litter size in Funiu White goat. Those results would provide useful information for the MAS program.

CONCLUSION

The research is the first to study the correlation between microsatellite loci and litter size of Funiu White goat. Several favorable genotypes that affected litter size were analyzed for the first time. Whether if those alleles can be further used in genetic improvement programme based on marker assisted selection for goat prolific, further researches with more samples and more related goat species are needed.

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