Electronic Journal of Biotechnology ISSN: 0717-3458
http://www.ejbiotechnology.info
DOI: 10.2225/vol16-issue4-fulltext-13 *RESEARCH ARTICLE*

Polymorphism of four microsatellites and their polymerisation effect on litter size in Boer goats

Jian Gang Wang[1] · Jin-Xing Hou[1] · Guang Li[1] · Guang Qin Zhu[1] · Bin Yun Cao[1] ✉

1 Northwest A&F University, College of Animal Science and Technology, Yangling, Shaanxi, P.R. China

✉ Corresponding author: caobinyun@126.com
Received November 14, 2012 / Accepted June 5, 2013
Published online: July 15, 2013

Abstract

Background: Finding molecular markers linked to quantitative trait loci is the first step in marker-assisted selection (MAS). Microsatellites are excellent molecular markers because of their large numbers, even distribution in the genome, and high polymorphism. In this study, the polymerisation effect of four microsatellites (OarAE101, BM1329, BM143, and LSCV043) on litter size was analysed using microsatellite markers and pedigrees.
Results: The results indicate that the polymerisation effect of four microsatellite loci significantly affected the litter size. $E_5E_{10}F_2F_6G_1G_5H_6H_{11}$ and $E_3E_8F_5F_7G_1G_5H_3H_9$ had the highest and lowest litter sizes in the F2 generation, respectively. The polymerisation effect value (v) of the E_5E_{10} genotype was 3.18% higher than that of the E_2E_7 genotype. The v of genotype F_2F_6 was 14.47% higher than that of the F_5F_7 genotype. The v of genotype G_1G_5 was 58.99% higher than that of the G_2G_7 genotype. The v of the H_6H_{11} genotype was 5.60% to 49.74% higher than those of the H_4H_{10} and H_1H_7 genotypes. The v of the H_3H_9 genotype was 17.22% higher than that of the H_1H_7 genotype.
Conclusions: The results of the present study are vital to improving the reproductive performance in goat breeds MAS.

Keywords: microsatellite marker, pedigrees, polymerisation effect, polymorphism.

INTRODUCTION

Selective breeding in goats is relatively effective because of the low heritability of the litter sizes. Marker-assisted selection (MAS) can improve the efficiency of selective breeding for traits with low heritability by controlling the selection time, selection strength, and accuracy. The search for molecular markers linked to quantitative trait loci is the first step in MAS (Dekkers, 2004; Williams, 2005). Microsatellites are excellent molecular markers because of their large numbers, even distribution in the genome, and high polymorphism (Scali et al. 2012).

Polymerisation is a breeding method for developing new breeds or lines. In this technique, favourable genes from several different breeds or lines are integrated into a breed or line through genetic engineering and hybridisation, backcrossing, and multiple cross (Yadav et al. 1990; Servin et al. 2003). Polymerisation affects the contribution rates of different genotypes to the performance in genotype combinations (Li et al. 2011). Marker-assisted gene pyramiding provides a way for animal and plant breeders to integrate the favourable genes identified in different breeds (lines) and to build an ideal genotype or genotype combination through optimal mating of individuals based on their genotypes at the target loci. Gene pyramiding has been successfully applied in several crop breeding programs to improve the disease and insect pest resistance of crops, consequently producing a number of varieties

and lines (Huang et al. 1997; Hittalmani et al. 2000; Barloy et al. 2007). However, gene pyramiding in animals has not been practiced to date because of low fertility, long generation intervals, inability to perform self-fertilisation, and inbreeding depression in animals.

One copy of the FecB gene increases the ovulation rate by 1.3 to 1.6, while two copies increase the rate by 2.7 to 3.0. The litter size is increased by 0.9 to 1.2 in ewes that carry a single copy and by 1.1 to 1.7 in ewes with two copies of the FecB gene (Davis et al. 1982; Piper et al. 1985). Four microsatellite loci (OarAE101, LSCV043, BM1329, and BM143) are linked to the FecB gene on ovine chromosome 6 (Montgomery et al. 1993; Lord et al. 1996; Zhang et al. 2009). Montgomery et al. (1993) found that microsatellite marker OarAE101 is linked to the FecB gene, with a maximum likelihood-of-the-odds (lod) score of 17.33 at a distance of 13 centimorgans (cM). Lord et al. (1998) mapped the FecB gene to a 10 cM region between microsatellites BM1329 and OarAE101. Mulsant et al. (1998) reported that the closest flanking markers of the FecB gene are caprine microsatellite LSCV043, which are situated approximately 2 cM on either side of the gene.

Based on the above considerations, we detected the polymorphisms of caprine OarAE101, LSCV043, BM1329, and BM143 in the present study and investigated the relationship between these genetic markers and litter size. This study would provide a number of useful information on goat genetic resources and breeding.

MATERIALS AND METHODS

DNA samples

All animals were maintained according to the No. 5 proclamation of the Ministry of Agriculture (P.R. China). Sample collection was approved by the Institutional Animal Care and Use Ethics Committee of Northwest A&F University and was performed in accordance with the ‘‘Guidelines for Experimental Animals’’ of the Ministry of Science and Technology (Beijing, China). Blood samples were obtained from 279 Boer goats, which were reared in Liuyou County of Shaanxi Province (P.R. China). The litter size and pedigree records of each female goat were collected for statistical analysis. DNA samples were extracted from leucocytes (Mullenbach et al. 1989).

PCR conditions and microsatellite marker

According to sheep and bovine microsatellites: OarAE101, BM1329, LSCV043, and BM143 (GenBank accession nos. L13692, G18422, and G18387 and NCBI accession no. 279530, respectively), four primer pairs (P1 to P4) were designed to amplify goat microsatellites OarAE101, BM1329, LSCV043, and BM143 (Table 1), respectively. The 12 µL volume contained 6.0 µL dH_2O, 2.0 µL 10 x buffer, 1.0 µL genomic DNA template, 0.5 µL of each primer (10 pmol/µL), 1.0 µL dNTPs (dATP, dTTP, dCTP, and dGTP), 1.0 µL Taq DNA polymerase (MBI), and 1.5 mM $MgCl_2$. The cycling protocol was 4 min at 95ºC, 35 cycles of denaturation at 94ºC for 30 sec, annealing at XºC (Table 1) for 30 sec, extension at 72ºC for 40 sec, and a final extension at 72ºC for 10 min. Aliquots (5 µL) of the PCR products were mixed with 2 µL bromophenol blue, and the mixed PCR products were subjected to PAGE (80 mm x 73 mm x 0.75 mm) in a 1 x TBE buffer at constant voltage (200 V) for 3.5 hrs. The gel (29:1 acrylamide:bis) was stained with 0.1% silver nitrate (Ji et al. 2007).

Statistical analysis

Genotypic frequencies were directly calculated. Statistical analysis was performed using the general linear model in the analysis menu of the SPSS 16 statistical software. Multiple comparisons of the means were performed using the least-significant difference method. The model applied was as follows:

$$Y_{ilm} = \mu + G_i + S_l + E_{ilm}$$

[Model 1]

where Y_{ilm} is the trait measured on each of the ilm^{th} animal, μ is the overall population mean, G_i is the fixed effect associated with the i^{th} genotype, S_l is the random effect associated with the l^{th} sire, and E_{ilm} is the random error. The combination effects of the four microsatellites on litter size were analysed using the following model:

$$Y_{ilm} = \mu + C_i + S_l + E_{ilm}$$

[Model 2]

where Y_{ilm}, μ, and S_l are the same as those in Model 1 and C_i is the fixed effect associated with the i^{th} combined genotype. Effects associated with farm, birth year, and season of birth were not matched in the linear model because preliminary statistical analyses indicated that these factors do not have a significant effect on the variability of traits in the analysed populations.

The polymerisation effect values (v) of the genotypic combinations of four microsatellites were calculated using Equation 1.

$$v = \frac{c-d}{d}$$

[Equation 1]

where c and d are the least-square means of different genotypic combinations at average parity, respectively.

RESULTS

Polymorphism of microsatellite loci

Eleven alleles were found at the microsatellite OarAE101 locus (135, 132, 129, 126, 124, 120 bp, 116, 114, 111, 109, and 106 bp) and were subsequently labelled as E_1, E_2, E_3, E_4, E_5, E_6, E_7, E_8, E_9, E_{10}, and E_{11}, respectively (Figure 1, Table 2). Seven alleles were detected at the microsatellite BM1329 locus (220, 217, 215, 210, 207, 190, and 187 bp) and were labelled as F_1, F_2, F_3, F_4, F_5, F_6, and F_7, respectively (Figure 2, Table 2). Meanwhile, nine alleles were found at the microsatellite LSCV043 locus (167, 162, 155, 150, 145, 140, 135, 130, and 120 bp) and were subsequently labelled as G_1, G_2, G_3, G_4, G_5, G_6, G_7, G_8, and G_9, respectively (Figure 3, Table 2). Eleven alleles were found at the microsatellite BM143 locus (137, 135, 132, 129, 127, 124, 120, 119, 115, 114, and 110 bp) and were labelled as H_1, H_2, H_3, H_4, H_5, H_6, H_7, H_8, H_9, H_{10}, and H_{11} respectively (Figure 4, Table 2). The different genotypes of the four microsatellite loci are shown in Table 3.

Association of the four microsatellite polymorphisms with litter size

The different genotypes of the four microsatellite loci exhibited significant effects on the litter size. The results indicate that individuals with E_5E_{10} and E_2E_7 genotypes had the largest and smallest litter sizes, respectively, compared with those of other genotypes in the OarAE101 locus ($P < 0.05$). In the BM1329 locus, individuals with the F_2F_6 genotype had larger litter sizes than those with the F_4F_7 and F_5F_7 genotypes ($P < 0.05$). In the LSCV043 locus, individuals with the G_1G_5 genotype had the largest litter size compared with those of other genotypes ($P < 0.05$). In the BM143 locus, individuals with the H_6H_{11} genotype had larger litter sizes than those with the H_2H_8 genotype ($P < 0.05$).

Individuals with $E_5E_{10}F_2F_6G_1G_5H_6H_{11}$ had larger litter sizes than those with $E_5E_{10}F_2F_6G_1G_5H_4H_{10}$, $E_5E_{10}F_5F_7G_2G_6H_6H_{11}$, and $E_5E_{10}F_2F_6G_2G_6H_6H_{11}$ at average parity ($P < 0.05$) (Table 4). Compared with $E_5E_{10}F_2F_6G_1G_5H_4H_{10}$, the polymerisation effect value (v) of the H_6H_{11} genotype of $E_5E_{10}F_2F_6G_1G_5H_6H_{11}$ was 16.80% higher than that of the H_4H_{10} genotype. A comparison of $E_5E_{10}F_2F_6G_2G_6H_6H_{11}$ and $E_5E_{10}F_5F_7G_2G_6H_6H_{11}$ showed that the v of the F_2F_6 genotype was 14.47% higher than that of the F_5F_7

genotype. Meanwhile, a comparison of $E_5E_{10}F_2F_6G_1G_5H_6H_{11}$ and $E_5E_{10}F_2F_6G_2G_6H_6H_{11}$ indicated that the *v* of the G_1G_5 genotype was 8.55% higher than that of the G_2G_6 genotype (Table 4).

Individuals with $E_5E_{10}F_2F_6G_1G_5H_1H_7$ had larger litter sizes than those with $E_5E_{10}F_2F_6G_2G_6H_4H_{10}$, $E_2E_7F_2F_6G_2G_7H_6H_{11}$, and $E_2E_7F_5F_7G_1G_5H_6H_{11}$ at average parity ($P < 0.05$) (Table 5). A comparison of $E_5E_{10}F_2F_6G_1G_5H_6H_{11}$ of the F_1 generation and $E_5E_{10}F_2F_6G_2G_6H_4H_{10}$ of the F_0 generation showed that the *v* of the H_6H_{11} genotype was 49.74% higher than that of the H_4H_{10} genotype. A comparison of $E_2E_7F_2F_6G_1G_5H_6H_{11}$ of the F_1 generation and $E_2E_7F_2F_6G_2G_7H_6H_{11}$ of the F_0 generation indicated that the *v* of the G_1G_5 genotype was 58.99% higher than that of the G_2G_7 genotype. A comparison of $E_2E_7F_2F_6G_1G_5H_6H_{11}$ of the F_1 generation and $E_5E_{10}F_2F_6G_1G_5H_1H_7$ of the F_0 generation showed that the *v* of the H_6H_{11} genotype was 13.20% higher than that of the H_1H_7 genotype (Table 5).

Individuals with $E_5E_{10}F_2F_6G_1G_5H_6H_{11}$ had larger litter sizes than those with $E_2E_7F_2F_6G_1G_5H_1H_7$ and $E_3E_8F_5F_7G_1G_5H_3H_9$ at average parity ($P < 0.05$) (Table 6). In the F_2 generation, the *v* of H_3H_9 of the $E_5E_{10}F_5F_7G_1G_5H_3H_9$ genotype was 21.53% higher than that of the H_1H_7 genotype compared with $E_5E_{10}F_5F_7G_1G_5H_1H_7$. A comparison of $E_5E_{10}F_2F_6G_1G_5H_6H_{11}$ and $E_5E_{10}F_2F_6G_2G_6H_6H_{11}$ showed that the *v* of the G_1G_5 genotype was 19.18% higher than that of the G_2G_6 genotype. A comparison of $E_2E_7F_2F_6G_1G_5H_6H_{11}$ of the F_1 generation and $E_2E_7F_2F_6G_1G_5H_1H_7$ of F_2 generation indicated that the *v* value of the H_6H_{11} genotype was 70.48% higher than that of the H_1H_7 genotype. A comparison of $E_5E_{10}F_5F_7G_2G_6H_6H_{11}$ of the F_1 generation and $E_5E_{10}F_5F_7G_3G_8H_6H_{11}$ of the F_2 generation showed that the *v* of the G_2G_6 genotype was 6.82% higher than that of the G_3G_8 genotype.

DISCUSSION

The 107 bp/113 bp genotype of OarAE101 and 146 bp/158 bp genotype of BM1329 exhibited significant positive correlations with the litter size in Small Tail Han sheep (Chu et al. 2001). Ouyang et al. (2006) reported that individuals with the 107 bp/111 bp genotype had the largest litter size compared with those of other genotypes in microsatellite OarAE101. In addition, individuals with the 100 bp/106 bp and 106 bp/112 bp genotypes had larger litter sizes than those of other genotypes in microsatellite BM143. In the present study, the results indicate that individuals with the E_5E_{10} and E_2E_7 genotypes had the highest and lowest litter sizes, respectively, in the OarAE101 locus ($P < 0.05$). Individuals with the F_2F_6 genotype had larger litter sizes than those with the F_4F_7 and F_5F_7 genotypes in the BM1329 locus ($P < 0.05$). Individuals with the G_1G_5 genotype had the largest litter size in the LSCV043 locus ($P < 0.05$). Individuals with the H_6H_{11} genotype had larger litter sizes than those with the H_2H_8 genotype in the BM143 locus ($P < 0.05$).

Reproductive traits are complex quantitative traits that involve multiple genes, loci, and interactions. Therefore, investigations on the combined effects of multiple genes or loci on reproductive traits are important (An et al. 2013). In the present study, the association between multiple loci and litter size from the first to the fourth parity was analysed. The results show that the polymerisation effects of $E_5E_{10}F_2F_6G_1G_5H_6H_{11}$ and $E_5E_{10}F_2F_6G_1G_5H_1H_7$ on litter size were greater than those of other combination genotypes. Compared with $E_5E_{10}F_2F_6G_1G_5H_4H_{10}$, the polymerisation effect value (*v*) of the H_6H_{11} genotype of $E_5E_{10}F_2F_6G_1G_5H_6H_{11}$ was 16.80% higher than that of the H_4H_{10} genotype. A comparison of $E_5E_{10}F_2F_6G_2G_6H_6H_{11}$ and $E_5E_{10}F_5F_7G_2G_6H_6H_{11}$ showed that the *v* of the F_2F_6 genotype was 14.47% higher than that of the F_5F_7 genotype. A comparison of $E_5E_{10}F_2F_6G_1G_5H_6H_{11}$ of the F_1 generation and $E_5E_{10}F_2F_6G_2G_6H_4H_{10}$ of the F_0 generation indicated that the *v* of the H_6H_{11} genotype was 49.74% higher than that of the H_4H_{10} genotype. A comparison of $E_2E_7F_2F_6G_1G_5H_6H_{11}$ of the F_1 generation and $E_2E_7F_2F_6G_2G_7H_6H_{11}$ of the F_0 generation showed that the *v* of the G_1G_5 genotype was 58.99% higher than that of the G_2G_7 genotype. Compared with $E_5E_{10}F_5F_7G_1G_5H_1H_7$, the *v* of H_3H_9 of the $E_5E_{10}F_5F_7G_1G_5H_3H_9$ genotype was 21.53% higher than that of the H_1H_7 genotype. A comparison of $E_2E_7F_2F_6G_1G_5H_6H_{11}$ of the F_1 generation and $E_2E_7F_2F_6G_1G_5H_1H_7$ of the F_2 generation showed that the *v* value of the H_6H_{11} genotype was 70.48% higher than that of the H_1H_7 genotype. The results of the previous studies, together with the results obtained in the present study, indicate that the four microsatellite polymorphisms associated with litter size have potential applications in MAS programs for goat breeding.

Financial support: This study was supported by the National Support Program of China (2011BAD28B05-3) and Technology Innovation Project of Shaanxi Province (2011KTCL02-09).

REFERENCES

AN, X.P.; HOU, J.X.; ZHAO, H.B.; LI, G.; BAI, L.; PENG, J.Y.; YAN, Q.M.; SONG, Y.X.; WANG, J.G. and CAO, B.Y. (2013). Polymorphism identification in goat *GNRH1* and *GDF9* genes and their association analysis with litter size. *Animal Genetics*, vol. 44, no. 2, p. 234-238. **[CrossRef]**

BARLOY, D.; LEMOINE, J.; ABELARD, P.; TANGUY, A.M.; RIVOAL, R. and JAHIER, J. (2007). Marker-assisted pyramiding of two cereal cyst nematode resistance genes from *Aegilops variabilis* in wheat. *Molecular Breeding*, vol. 20, no. 1, p. 31-40. **[CrossRef]**

CHU, M.X.; CHENG, J.H. and GUO, W. (2001). Preliminary studies of microsatellite markers OarAE101 and BM1329 in five sheep breeds. *Acta Genetica Sinica*, vol. 28, no. 6, p. 510-517.

DAVIS, G.H.; MONTGOMERY, G.W.; ALLISON, A.J.; KELLY, R.W. and BRAY, A.R. (1982). Segregation of a major gene influencing fecundity in progeny of Booroola sheep. *New Zealand Journal of Agricultural Research*, vol. 25, no. 4, p. 525-529. **[CrossRef]**

DEKKERS, J.C.M. (2004). Commercial application of marker and gene-assisted selection in livestock: Strategies and lessons. *Journal of Animal Science*, vol. 82, no. 13, p. 313-328.

HITTALMANI, S.; PARCO, A.; MEW, T.V.; ZEIGLER, R.S. and HUANG, N. (2000). Fine mapping and DNA marker-assisted pyramiding of the three major genes for blast resistance in rice. *Theoretical and Applied Genetics*, vol. 100, no. 7, p. 1121-1128. **[CrossRef]**

HUANG, N.; ANGELES, E.R.; DOMINGO, J.; MAGPANTAY, G.; SINGH, S.; ZHANG, G.; KUMARAVADIVEL, N.; BENNETT, J. and KHUSH, G.S. (1997). Pyramiding of bacterial blight resistance genes in rice: Marker-assisted selection using RFLP and PCR. *Theoretical and Applied Genetics*, vol. 95, no. 3, p. 313-320. **[CrossRef]**

JI, Y.T.; QU, C.Q. and CAO, B.Y. (2007). An optimal method of DNA silver staining in polyacrylamide gels. *Electrophoresis*, vol. 28, no. 8, p. 1173-1175. **[CrossRef]**

LI, G.; AN, X.P.; FU, M.Z.; HOU, J.X.; SUN, R.P.; ZHU, G.Q.; WANG, J.G. and CAO, B.Y. (2011). Polymorphism of *PRLR* and *LHβ* genes by sscp marker and their association with litter size in Boer goats. *Livestock Science,* vol. 136, no. 2-3, p. 281-286. **[CrossRef]**

LORD, E.A.; LUMSDEN, J.M.; DODDS, K.G.; HENRY, H.M.; CRAWFORD, A.M.; ANSARI, H.A.; PEARCE, P.D.; MAHER, D.W.; STONE, R.T.; KAPPES, S.M.; BEATTIE, C.W. and MONTGOMERY, G.W. (1996). The linkage map of sheep chromosome 6 compared with orthologous regions in other species. *Mammalian Genome*, vol. 7, no. 5, p. 373-376. **[CrossRef]**

LORD, E.A.; DAVIS, G.H.; DODDS, K.G.; HENRY, H.M.; LUMSDEN, J.M. and MONTGOMERY, G.W. (1998). Identification of Booroola carriers using microsatellite markers. *Wool Technology and Sheep Breeding*, vol. 46, no. 3, p. 245-249.

MONTGOMERY, G.W.; CRAWFORD, A.M.; PANTY, J.M.; DODDS, K.G.; EDE, A.J.; HENRY, H.M.; PIERSON, C.A.; LORD, E.A.; GALLOWAY, S.M.; SCHMACK, A.E.; SISE, J.A.; SWARBRICK, P.A.; HANRAHAN, V.; BUCHANAN, F.C. and HILL, D.F. (1993). The ovine Booroola fecundity gene (*FecB*) is linked to markers from a region of human chromosome 4q. *Nature Genetics*, vol. 4, no. 4, p. 410-414. **[CrossRef]**

MULLENBACH, R.; LAGODA, P.J. and WELTER, C. (1989). An efficient salt-chloroform extraction of DNA from blood and tissue. *Trends in Genetics*, vol. 5, no. 12, p. 391.

MULSANT, P.; SCHIBLER, L.; LECERF, F.; RIQUET, J.; CHITOUR, N.; EGGEN, A.; CRIBIU, E.; LANNELUC, I. and ELSEN, J.M. (1998). Regional mapping of the FecB (Booroola) region of sheep chromosome 6. *Animal Genetics*, vol. 29, supp. S1, p. 36-37.

OUYANG, X.X.; SHI, Q.S.; DENG, Z.F.; HUANG, S.Q.; LIU, H.X.; YIN, X.P.; TAN, S.P. and HU, S.G. (2006). Studies of microsatellite markers OarAE101 and BM143 in 4 goat breeds. *Acta Veterinaria et Zootechnica Sinica,* vol. 37, no. 7, p. 640-645.

PIPER, L.R.; BINDON, B.M. and DAVIS, G.H. (1985). The single gene inheritance of the high litter size of the Booroola Merino. In: LAND, R.B. and ROBINSON, D.W. eds. *Genetics of Reproduction in Sheep*. Butterworths, London. p. 115-125.

SCALI, M.; VIGNANI, R.; BIGLIAZZI, J.; PAOLUCCI, E.; BERNINI, A.; SPIGA, O.; NICCOLAI, N. and CRESTI, M. (2012). Genetic differentiation between Cinta Senese and commercial pig breeds using microsatellite. *Electronic Journal of Biotechnology*, vol. 15, no. 2. **[CrossRef]**

SERVIN, B.; MARTIN, O.C.; MEZARD, M. and HOSPITAL, F. (2003). Towards a theory of marker-assisted gene pyramiding. *Genetics,* vol. 168, no. 1, p. 513-523. **[CrossRef]**

WILLIAMS, J.L. (2005). The use of marker-assisted selection in animal breeding and biotechnology. *Revue Scientifique et Technique-Office International Des Epizootics*, vol. 24, no. 1, p. 379-391.

YADAV, R.D.S.; SINGH, S.B.; RAI, M.; SINGH, S.N.; SINGH, B.N.; MAURYA, M.L. and SINGH, A. (1990). Gene pyramiding and horizontal resistance to diara stress in mustards. *National Academy Science Letters*, vol. 13, no. 9, p. 325-327.

ZHANG, L.; LI, C.M.; CHU, M.X.; CHEN, H.Q.; LI, X.W.; LI, F.; DI, R.; MA, Y.H. and LI, K. (2009). Linkage analysis between microsatellite locus LSCV043 and FecB gene in small tail han sheep. *Journal of Agricultural Biotechnology,* vol. 17, no. 4, p. 621-628.

How to reference this article:

WANG, J.G.; HOU, J.X.; LI, G.; ZHU, G.Q. and CAO, B.Y. (2013). Polymorphism of four microsatellites and their polymerisation effect on litter size in Boer goats. *Electronic Journal of Biotechnology*, vol. 16, no. 4. http://dx.doi.org/10.2225/vol16-issue4-fulltext-13

Tables

Table 1. Primer information of four microsatellite loci.

Locus	Primer sequence	Tm (°C)	Allele size (bp)
OarAE101	F: 5-TTCTTATAGATGCACTCAAGCTAGG-3 R: 5-TAAGAAATATATTTGAAAAAACTGTATCTCCC-3	63.0	109-135
BM1329	F: 5-TTGTTTAGGCAAGTCCAAAGTC-3 R: 5-AACACCGCAGCTTCATCC-3	62.0	105-140
LSCV043	F: 5-CCAGAATATAGAGTTTTGTCAAG-3 R: 5-GCCTGATTTGTATTTGTATGAG-3	54.7	130-167
BM143	F: 5-ACCTGGGAAGCCTCCATATC-3 R: 5-CTGCAGGCAGATTCTTTATCG-3	63·0	182-234

Table 2. Distribution of alleles at each microsatellite locus in Boer goats.

Locus	Number of allele	Distribution of allelic frequency
OarAE101	11	135bp 132bp 129bp 126bp 124bp 120bp 116bp 114bp 111bp 109bp 106bp 0.067 0.031 0.164 0.122 0.055 0.128 0.031 0.183 0.122 0.055 0.061
BM1329	7	220bp 217bp 215bp 210bp 207bp 190bp 187bp 0.049 0.013 0.020 0.110 0.085 0.049 0.116
LCV043	9	167bp 162bp 155bp 150bp 145bp 140bp 135bp 130bp 120bp 0.061 0.329 0.049 0.043 0.061 0.031 0.146 0.262 0.018
BM143	11	137bp 135bp 132bp 129bp 127bp 124bp 120bp 119bp 115bp 114bp 110bp 0.049 0.043 0.140 0.079 0.134 0.055 0.049 0.043 0.140 0.079 0.189

DOI: 10.2225/vol16-issue4-fulltext-13

Table 3. Association of four microsatellite locus genotypes with litter size (mean ± S.E.) in Boer goats.

Locus	Genotype	Name	Frequency	Litter size
OarAE101	135/120 (11)	E_1E_6	0.14	1.75 ± 0.40^{a}
	132/116 (5)	E_2E_7	0.06	1.45 ± 0.16^{b}
	129/114 (24)	E_3E_8	0.30	1.77 ± 0.38^{a}
	126/111 (20)	E_4E_9	0.25	1.69 ± 0.33^{a}
	124/109 (9)	E_5E_{10}	0.11	2.06 ± 0.26^{c}
	120/106 (10)	E_6E_{11}	0.13	1.78 ± 0.21^{a}
BM1329	220/207 (8)	F_1F_5	0.10	1.78 ± 0.31^{ab}
	217/190 (49)	F_2F_6	0.23	1.97 ± 0.38^{b}
	215/190 (23)	F_3F_6	0.28	1.77 ± 0.33^{ab}
	210/187 (18)	F_4F_7	0.22	1.69 ± 0.30^{a}
	207/187 (14)	F_5F_7	0.17	1.59 ± 0.28^{a}
LSCV043	167/145 (10)	G_1G_5	0.12	2.08 ± 0.46^{d}
	162/140 (5)	G_2G_6	0.06	1.66 ± 0.26^{ab}
	162/135 (21)	G_2G_7	0.26	1.87 ± 0.32^{c}
	162/130 (28)	G_2G_8	0.34	1.76 ± 0.29^{bc}
	155/130 (8)	G_3G_8	0.10	1.59 ± 0.2^{a}
	150/130 (7)	G_4G_8	0.09	1.50 ± 0.19^{a}
	135/120 (3)	G_7G_9	0.04	1.40 ± 0.40^{a}
BM143	137/120 (8)	H_1H_7	0.10	1.73 ± 0.27^{ab}
	135/119 (7)	H_2H_8	0.09	1.63 ± 0.36^{a}
	132/115 (23)	H_3H_9	0.28	1.75 ± 0.34^{ab}
	129/114 (13)	H_4H_{10}	0.16	1.77 ± 0.27^{ab}
	127/110 (22)	H_5H_{11}	0.27	1.72 ± 0.33^{ab}
	124/110 (9)	H_6H_{11}	0.11	2.08 ± 0.43^{b}

Note: Values with different superscripts within the same column differ significantly at $P < 0.05$. Numbers in brackets indicate the number of samples.

Table 4. Association of F_1 generation combination genotypes with litter size (mean ± S.E.) in Boer goats.

Combination genotype	Frequency	Litter size				
		1st parity	2nd parity	3rd parity	4th parity	Average parity
$E_2E_7F_2F_6G_1G_5H_6H_{11}$ (5)	0.1364	2.33 ± 0.22^{c}	3.00 ± 0.25^{a}	3.00 ± 0.21^{a}	3.00 ± 0.14^{A}	2.83 ± 0.12^{a}
$E_5E_{10}F_2F_6G_1G_5H_4H_{10}$ (9)	0.3182	1.75 ± 0.19^{B}	2.50 ± 0.21^{b}	2.75 ± 0.18^{b}	3.00 ± 0.12^{A}	2.50 ± 0.10^{b}
$E_5E_{10}F_2F_6G_1G_5H_6H_{11}$ (5)	0.1364	2.66 ± 0.22^{A}	3.00 ± 0.24^{a}	3.00 ± 0.21^{a}	3.00 ± 0.14^{A}	2.92 ± 0.12^{a}
$E_5E_{10}F_5F_7G_2G_6H_6H_{11}$ (7)	0.2272	2.00 ± 0.17^{d}	2.80 ± 0.19^{c}	2.40 ± 0.16^{c}	2.20 ± 0.11^{B}	2.35 ± 0.09^{c}
$E_5E_{10}F_2F_6G_2G_6H_6H_{11}$ (6)	0.1818	2.00 ± 0.19^{d}	2.75 ± 0.21^{c}	3.00 ± 0.18^{a}	3.00 ± 0.12^{A}	2.69 ± 0.10^{b}

Note: Values with different superscripts within the same column differ significantly at $P < 0.05$ or $P < 0.01$. Numbers in brackets indicate the number of samples.

Table 5. Association of parental generation (F_0) combination genotypes with litter size (mean ± S.E.) in Boer goats.

Combination genotype	Frequency	Litter size				
		1st parity	2nd parity	3rd parity	4th parity	Average parity
$E_5E_{10}F_2F_6G_2G_6H_4H_{10}$ (11)	0.3704	1.70 ± 0.15^{c}	1.90 ± 0.19^{c}	2.00 ± 0.20^{c}	2.20 ± 0.16^{B}	1.95 ± 0.13^{c}
$E_2E_7F_2F_6G_2G_7H_6H_{11}$ (8)	0.2593	1.43 ± 0.18^{B}	1.86 ± 0.22^{c}	1.86 ± 0.24^{B}	2.00 ± 0.18^{B}	1.78 ± 0.15^{b}
$E_5E_{10}F_2F_6G_1G_5H_1H_7$ (5)	0.1481	2.00 ± 0.24^{A}	2.25 ± 0.30^{A}	2.75 ± 0.32^{A}	3.00 ± 0.25^{A}	2.50 ± 0.20^{a}
$E_2E_7F_5F_7G_1G_5H_6H_{11}$ (7)	0.2222	1.33 ± 0.19^{B}	1.50 ± 0.24^{B}	2.00 ± 0.26^{c}	2.00 ± 0.20^{B}	1.71 ± 0.16^{b}

Note: Values with different superscripts within the same column differ significantly at $P < 0.05$ or $P < 0.01$. Numbers in brackets indicate the number of samples.

Table 6. Association of F_2 generation combination genotypes with litter size (mean ± S.E.) in Boer goats.

Combination genotype	Frequency	Litter size			
		1st parity	2nd parity	3rd parity	Average parity
$E_5E_{10}F_5F_7G_3G_8H_6H_{11}$ (16)	0.1136	1.80 ± 0.14^{d}	2.30 ± 0.14^{Ac}	2.50 ± 0.17^{Aa}	2.20 ± 0.09^{Ab}
$E_2E_7F_2F_6G_1G_5H_1H_7$ (15)	0.1023	1.44 ± 0.14^{Bb}	1.66 ± 0.15^{Bb}	1.89 ± 0.18^{e}	1.66 ± 0.09^{B}
$E_5E_{10}F_5F_7G_1G_5H_1H_7$ (17)	0.1250	1.91 ± 0.13^{d}	2.09 ± 0.14^{Ac}	2.27 ± 0.16^{Ac}	2.09 ± 0.08^{Ab}
$E_5E_{10}F_2F_6G_1G_5H_6H_{11}$ (16)	0.1136	2.70 ± 0.14^{A}	2.95 ± 0.14^{Ac}	3.06 ± 0.16^{Ab}	2.92 ± 0.08^{Aa}
$E_5E_{10}F_2F_6G_2G_6H_6H_{11}$ (17)	0.1250	2.09 ± 0.13^{Ae}	2.73 ± 0.13^{Ac}	2.54 ± 0.16^{Aa}	2.45 ± 0.08^{A}
$E_3E_8F_5F_7G_1G_5H_3H_9$ (14)	0.0910	1.25 ± 0.15^{Bc}	1.87 ± 0.16^{b}	1.50 ± 0.19^{B}	1.54 ± 0.10^{B}
$E_5E_{10}F_2F_6G_2G_6H_2H_8$ (17)	0.1250	1.54 ± 0.13^{Bb}	2.54 ± 0.13^{Ac}	2.45 ± 0.16^{Aa}	2.18 ± 0.08^{Ab}
$E_5E_{10}F_5F_7G_1G_5H_6H_{11}$ (16)	0.1136	2.30 ± 0.14^{Ae}	2.70 ± 0.14^{Ac}	2.94 ± 0.17^{Aa}	2.64 ± 0.09^{Aa}
$E_5E_{10}F_5F_7G_1G_5H_3H_9$ (14)	0.0910	2.00 ± 0.15^{Ae}	2.62 ± 0.16^{Ac}	3.00 ± 0.19^{Ab}	2.54 ± 0.10^{Aa}

Note: Values with different superscripts within the same column differ significantly at $P < 0.05$ or $P < 0.01$. Numbers in brackets indicate the number of samples.

Figures

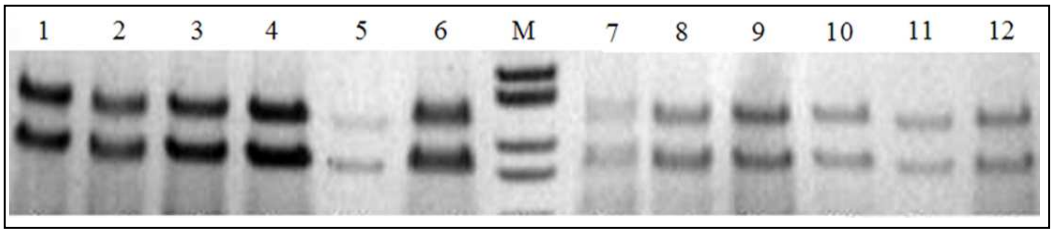

Fig. 1 PAGE results of PCR products at the microsatellite *OarAE101* locus in Boer goats 1 to 12. Different goats; M. pBR322DNA/Msp I Markers, fragment sizes are 147, 133, 110, and 90 bp, top to bottom.

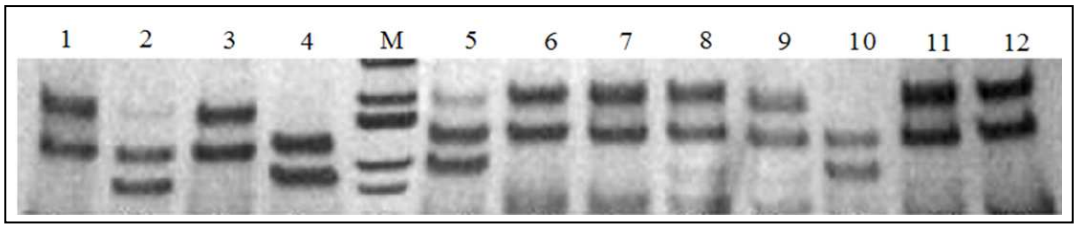

Fig. 2 PAGE results of PCR products at the microsatellite *BM1329* locus in Boer goats 1 to 12. Different goats; M. pBR322DNA/Msp I Markers, fragment sizes are 225, 201, 190, 180, and 170 bp, from top to bottom.

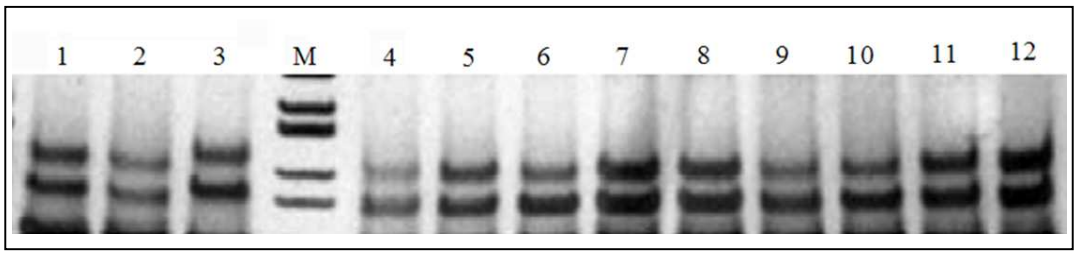

Fig. 3 PAGE results of PCR products at the microsatellite *LSCV043* locus in Boer goats 1 to 12. Different goats; M. pBR322DNA/Msp I Markers, fragment sizes are 175, 160, 147, 132, and 124 bp, from top to bottom.

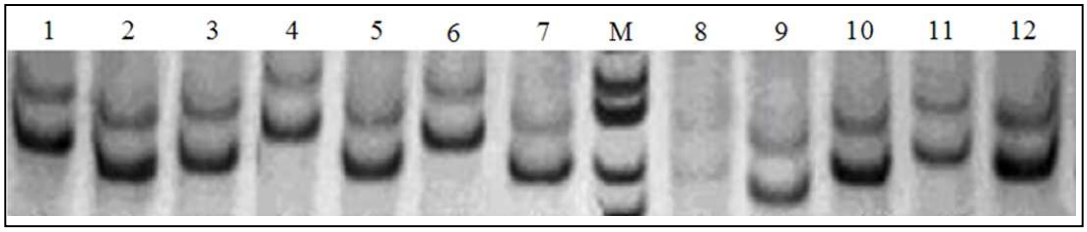

Fig. 4 PAGE results of PCR products at the microsatellite *BM143* locus in Boer goats 1 to 12. Different goats; M. pBR322DNA/Msp I Markers, fragment sizes are 147, 123, 110, and 90 bp, from top to bottom.