African Journal of Biotechnology Vol. 10(73), pp. 16691-16696, 21 November, 2011
Available online at http://www.academicjournals.org/AJB
DOI: 10.5897/AJB11.1414
ISSN 1684–5315 © 2011 Academic Journals

Full Length Research Paper

Weaver gene 3'UTR novel mutations: Associations with production traits and milk composition in dairy goat

Zhuanjian Li, Wenjiao Guo, Xianyong Lan, Jing Wang, Mingxun Li, Yongzhen Huang, Bao Zhang, Chuzhao Lei and Hong Chen*

College of Animal Science and Technology, Northwest A&F University, Shaanxi Key Laboratory of Molecular Biology for Agriculture, Yangling, Shaanxi 712100, China.

Accepted 19 September, 2011

Our recent report on a parallel increase in the milk yield of *weaver* gene mutation suggests that *weaver* gene is a candidate marker for quantitative traits in farm animals with respect to milk production traits. To further understand the effects of *weaver* gene variant on fat, protein, solids-not-fat, lactose and total solids percentage, two novel single nucleotide polymorphisms (SNPs) located on the flanking 3'UTR region were investigated by *Taq*I polymerase chain reaction-restriction fragment length polymorphism (PCR-RFLP) and *Hha*I forced PCR-RFLP in a sample of 1,019 individuals from four Chinese indigenous goat breeds. In the *Taq*I and *Hha*I analyses, the frequencies of allele T_2 and H_2 in Xinong Sannen dairy (XNSN dairy) and Guanzhong dairy (GZ dairy) populations were significantly greater than those of Shanbei White Cashmere (SBWC) and Xinjiang White Cashmere (XJWC) goats, respectively. Relationships analyses between the two SNPs and milk performance traits and growth traits were performed. T_2T_2 animals had significantly greater milk yield, protein and solids-not-fat percentage than those with the T_1T_1 genotype. Thus, *weaver*/*Taq*I polymorphism appears to be a promising marker to improve milk production traits in goat.

Key words: Dairy goat, weaver gene, milk performance traits, single nucleotide polymorphism.

INTRODUCTION

Many important genes have been discovered to be involved in controlling milk traits in livestock. And it is important to realize that milk traits are controlled by polygenes with pleiotropic effect (Moioli et al., 2007; Dagnachew et al., 2011; Glantz et al., 2011). However, the major gene model suggests that a few genes may account for relatively large proportion of the genetic variation. The *weaver* gene (also named as *KCNJ6*) encodes for the GIRK2 protein subunits of a human ATP-sensitive K^+-channel that is widely and distinctively expressed in the central nervous system (Ikeda et al., 2003). Two silent mutations (rs702859 and rs2070995) with similar frequencies in normal and non-insulin-dependent diabetic patients were identified (Sakura et al., 1995). One nonsense mutation (rs59497335) has been listed in the NCBI dbSNP database. The mice phenotype *weaver* mutation (Gly-Ser) in the H5 region caused ataxia, tremor, male infertility, tonic-clonic seizures and the degeneration of cerebellum granule neurons (Goldowitz, 1989; Patil et al., 1995). Moreover the *GIRK1/GIRK2* gene may be involved in the inhibitory regulation of the release of oxytocin and vasopressin from the supraoptic nucleus in rat (Li et al., 2001). Therefore, weaver gene participates in a wide range of physiologic responses (Alexander et al., 2008; Benarroch, 2009).

The weaver gene with 5 exons located on cattle chromosome 1 (NC_007299) encodes for the GIRK2 protein. In 1973, cattle weaver syndrome was a cattle progressive degenerative myeloencephalopathy and recessive genetic disease which was found in 36 purebred Brown Swiss cattle (Stuart and Leipold, 1985; Tenhumberg et al., 1994). Interestingly, weaver carriers produce more milk than noncarriers (Hoeschele and Meinert, 1990).

*Corresponding author. E-mail: lizhuanjian@yahoo.com.cn or chenhong1212@263.net. Tel: +86-029-8709 2004. Fax: +86-029-8709 2164.

Cattle weaver syndrome is related to cattle milk production (Georges et al., 1993). Seven single nucleotide polymorphisms (SNPs) (rs41706488, rs41706492 and rs41615623) have been reported in the bovine *weaver* gene in GenBank (http://www.ncbi.nlm.nih.gov). Moreover, genetic characteristics of seven microsatellite loci linked with *weaver* gene on BTA1 revealed that BM6438, BMS711, BMS2321 and TGLA116 were potential DNA markers of milk production (Shan et al., 2002). Thus, *weaver* gene is an important potential candidate gene for the production performance in livestock.

Therefore, the aim of this study was to scan SNPs within the caprine *weaver* gene by using DNA sequencing and PCR-RFLP methods and to determine the associations of the polymorphisms between milk production traits and milk composition.

MATERIALS AND METHODS

Animal data

DNA was extracted from blood (white blood cell) collected from 1,019 healthy and unrelated individuals belonging to ourf indigenous Chinese goat breeds, namely, Xinong Sannen dairy (XNSN, dairy breed, n = 268), Guanzhong dairy (GZ, dairy breed, n = 440), Xinjiang White Cashmere (XJWC, wool breed, n = 119), and Shanbei White Cashmere (SBWC, wool breed, n = 192), which were from Shaanxi, Shaanxi, Xinjiang Uygur Autonomous Region and Shaanxi province, respectively. Body height, length and chest circumference were measured on 268 XNSN and 440 GZ animals. Records of total milk yield as well as fat, protein, solids-not-fat, lactose and total solids percentage during a whole lactation, which were collected from 268 XNSN dairy goats two to three years, were used for statistical analysis. Milk compositions were measured by MilkoScan FT120 following the instruction. There were no milk yield records of GZ dairy goats, because the farm of GZ dairy goats was a new farm.

PCR conditions

Based on the bovine sequence (GenBank accession No. NC_007299), four pair of primers for the amplification of different fragments of the caprine *weaver* gene (P1-P4) were designed (Table 1). The 25 µl volume contained: 50 ng genomic DNA, 0.5 µM of each primer, 1 × buffer (including 1.5 mM $MgCl_2$), 200 µM dNTPs and 0.625 units of *Taq* DNA polymerase (MBI, Vilnius, Lithuania). The cycling protocol was 5 min at 95°C, 35 cycles of 94°C for 30 s, annealing for 30 s, 72°C for 40 s, with a final extension at 72°C for 10 min. The expected sizes of the amplifications, which are shown in Table 1, were confirmed by 1.0% agarose gels electrophoresis stained with ethidium bromide.

Detecting novel polymorphisms within goat *weaver* gene by PCR-SSCP and DNA sequencing

PCR products were analyzed for single-strand conformation polymorphisms (SSCP) in four loci. Aliquots of 5 µl PCR products from 80 randomly selected individuals for each breed were mixed with 5 µl denaturing solution (95% formamide, 25 mM EDTA, 0.025% Xylene-Cyanole and 0.025% bromophenol blue), heated for 10 min at 98°C and chilled on the ice. Denatured DNA was subjected to PAGE (80 × 73 × 0.75 mm) in 1 × TBE buffer and constant voltage (200 V) for 2.5 to 3.0 h at 4°C. The gels were stained with 0.1% silver nitrate (Lan et al., 2007). Based on the findings of SSCP, the putative polymorphic DNA samples were sequenced with the forward and reverse directions in ABI PRISM 3730 DNA analyzer and sequences were analyzed with BioXM software (Version 2.6).

Genotyping of TaqI and HhaI weaver allele by PCR-RFLP

The 20 µl 173 bp PCR products of P4 locus were digested with 10 U *Taq*I (MBI, Vilnius, Lithuania) for 5 h at 65°C and *Hha*I (MBI, Vilnius, Lithuania) for 5 h at 37°C following the supplier's protocol, respectively. The digested products were analyzed by electrophoresis for 2 h in 3.0% agarose gels stained with ethidium bromide.

Statistical analysis

Estimate of linkage disequilibrium was performed by SHEsis software (Li et al., 2009). Genotypic and allelic frequencies and Hardy-Weinberg equilibrium were directly calculated according to the *Taq*I, *Hha*I PCR-RFLP analysis of the goat *weaver* P4 locus. Homozygosity was calculated by Yeh's method using PopGene software (Version 1.3.1) (Yeh et al., 1999). Differences for these frequencies among/between different populations were analyzed using the chi-square test, which was performed by SPSS software (Version 16.0).

A full animal model and then a reduced animal model were used in a joint analysis of the growth traits and genotypes according to the description from Lan et al. (2007). Mixed model analyses for milk traits were performed using the SAS mixed procedure (SAS, 1999). The model for XNSN included marker genotype, sire, lambing season, age and lactation number as fixed effects, the linear and quadratic effects of lactation length as covariates and doe as a random effect. The factor number of kids was not included in the statistical model, because XNSN does predominantly had one kid, but does that lambed twins were also part of the dataset. Data were presented as least squares means with associated standard error according to the following model:

$$Y_{ijklmn} = \mu + A_i + G_j + LN_k + LS_l + S_m + E_{ijkln}$$

where Y_{ijklmn} = the trait measured on each of the *ijklmn*th animal; μ = the overall population mean; A_i = fixed effect due to the *i*th age; Gj = fixed effect associated with *j*th genotype; LN_k = fixed effect due to the *k*th lactation number; LS_l = fixed effect associated with *l*th lambing season; S_m = fixed effect due to the *m*th sire; E_{ijklmn} = the random error.

RESULTS AND DISCUSSION

Based on the PCR-SSCP, flanking 3'UTR region showed polymorphism (Figure 1a). DNA from eight randomly chosen goats with different SSCP patterns were sequenced in both directions and some of their sequences were deposited in the GenBank database (Accession No. FJ973156-FJ973159). High homology identity was identical with the bovine *weaver* gene (GenBank accession No. NC_007299) after the

Table 1. Primers information of goat *weaver* gene.

Loci	Primer (5'-3')	Fragment (bp)	Tm (℃)	Note
P1	1F: CAGTGTTATGACTGGCAGTCTG 1R: TGGGCACGAATGCAAATAC	319	58.5	Exon 1 and part of intron 1 (18-336)*
P2	2F: CTACTCAGGCTGCCCTAACA 2R: CCATCAGGACAAGGCTCAC	515	62.0	Part of intron 2, exon 3 and part of intron 3 (4812-5326)
P3	3F: GCATCCAAGAGTTTCCCTG 3R: TCAGAACAGAAATGCCTACT	376	55.0	Part of 3' flanking (98970-99345)
P4	4F: GCATCCAAGAGTTTCCCTG 4R:CTTCACCTCACCTGGGTCCTGTAAGC	173	56.0	Part of 3' flanking (98970-99142)

The reverse primer of P4 was designed to genotype the two mutations which were detected by SSCP in P3. The underlined base shows the incorporated mismatch creating a restriction site. * Ref. NC_007299.

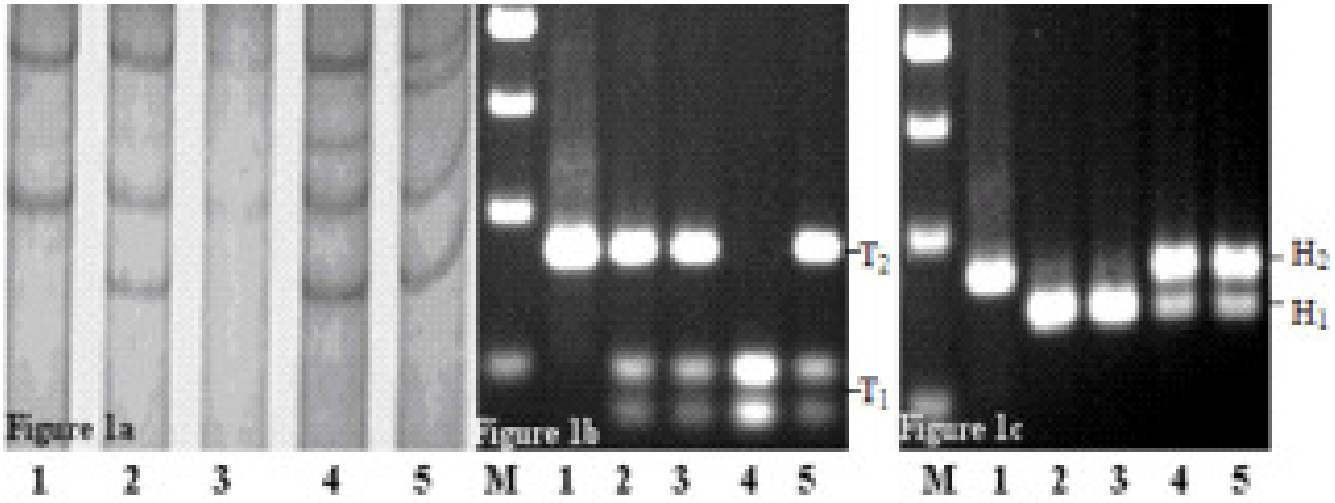

Figure 1. Electrophoretic patterns of PCR-SSCP and PCR-RFLP of goat *weaver* gene. 1a, PCR-SSCP of goat *weaver* gene; Lane 1, 3, C-C/C-C); lane 2, C-C/C-T; lane 4, (C-T/C-C) and lane 5, (T-T/C-T); 1b, the *Taq*I PCR-RFLP of goat *weaver* gene; lane 1, T_2T_2 genotype; lane 2, 3 and 5, T_1T_2 genotype; lane 4, T_1T_1 genotype; 1c the *Hha*I forced PCR-RFLP of goat *weaver* gene; lane 1, H_2H_2 genotype; lane 2 to3, H_1H_1 genotype; lane 4 to 5; H_1H_2 genotype; M, (400, 300, 200, and 100 bp).

comparison among the goat sequences following the SSCP two novel SNPs: NC_007299:g.99045C > T; NC_007299:g.99116C > T in the flanking 3'UTR region of *weaver* gene. Interestingly, the NC_007299:g.99045C > T mutation abolished a *Taq*I endonuclease restriction site (TCGA). In order to exactly detect the NC_007299:g.99116C > T mutation, the forced PCR-RFLP method was used to detect this mutation (Cox, 2006). The reverse primer (Table 1-P4R) was redesigned. Therefore, the 173 bp amplification contains two endonuclease restriction recognition sites for the detection of the mutations in *weaver* gene. At the *Taq*I locus, digestion of the 173 bp PCR fragment with *Taq*I resulted in fragment lengths of 98 and 75 bp bands for genotype T_1T_1 individual (homozygous); T_1T_2 (heterozygous) showed 173, 98 and 75 bp bands; T_2T_2 (homozygous) showed 173 bp (Figure 1b). At the *Hha*I locus, digestion of the 173 bp PCR fragment with *Hha*I resulted in fragment lengths of 148 and 25 bp bands for genotype H_1H_1 individual (homozygous); H_1H_2 (heterozygous) showed 173, 148, and 25 bp bands; H_2H_2 (homozygous) showed 173 bp (Figure 1c). It was noted that the 25 bp fragment was too short to be visible in Figure 1c.

The two novel SNPs of *weaver* gene were investigated by PCR-RFLP and forced PCR-RFLP methods. Allelic and genotypic frequencies are shown by breed in Table 2, as well as homozygosity.

Table 2. Genotypic and allelic frequencies of *weaver* gene at two polymorphic loci in the four Chinese indigenous goat breeds.

Breed	Type	N	Genotypic and allelic frequency					Ho
			T_1T_1	T_1T_2	T_2T_2	T_1	T_2	
XNSN	Dairy	268	0.369	0.481	0.150	0.610	0.390	0.524
GZ**	Dairy	440	0.275	0.557	0.168	0.553	0.447	0.506
SBWC	Wool	192	0.943	0.057	\	0.971	0.029	0.944
XJWC	Wool	119	0.950	0.050	\	0.975	0.025	0.951
			H_1H_1	H_1H_2	H_2H_2	H_1	H_2	
XNSN	Dairy	268	0.664	0.313	0.023	0.821	0.179	0.706
GZ**	Dairy	440	0.625	0.366	0.009	0.808	0.192	0.690
SBWC	Wool	192	0.953	0.047	\	0.977	0.023	0.954
XJWC	Wool	119	0.941	0.059	\	0.971	0.029	0.943

** $P < 0.01$(Hardy-Weinberg equilibrium); "\" corresponds to "0.000".

Table 3. The χ^2 (df) from genotypic and allelic frequencies among the four breeds at goat *weaver-Taq*I and *Hha*I loci.

Loci	Breed	XNSN	GZ	SBWC	XJWC
*Taq*I locus $\chi 2$ (df)[1]	XNSN		6.943* (2)	155.150*** (2)	112.266*** (2)
	GZ	4.377* (1)		239.350*** (2)	175.332*** (2)
	SBWC	160.491*** (1)	214.743*** (1)		0.067 (1)
	XJWC	109.280*** (1)	144.927*** (1)	0.065 (1)	
*Hha*I locus $\chi 2$ (df) [1]	XNSN		3.810 (2)	55.512*** (2)	33.821*** (2)
	GZ	0.367 (1)		72.185*** (2)	43.998*** (2)
	SBWC	53.620*** (1)	62.816*** (1)		0.215 (1)
	XJWC	32.013*** (1)	37.356*** (1)	0.209 (1)	

[1] χ^2 (df) represent differences of genotypic frequencies between four breeds in the up-triangle; χ^2 (df) represent differences of allelic frequencies between the four breeds in the down-triangle. *$P < 0.05$; ***$P < 0.001$.

In the *Taq*I and *Hha*I analyses, genotypes of goat *weaver* gene were in Hardy-Weinberg equilibrium except in GZ population. The r^2 parameters of LD were 0.103, 0.139, 0.187 and 0.192 for XNSN, GZ, SBWC and XJWC respectively, which indicated that the two SNPs were not linked strongly in the populations. Genotypic and allelic frequencies in the PCR-RFLP analysis with *Taq*I and *Hha*I were found to be different among XNSN dairy, GZ dairy, SBWC wool and XJWC wool based on chi-square tests ($\chi^2 = 354.862$, df = 6, ***$P < 0.001$ and $\chi^2 = 328.463$, df = 3, ***$P < 0.001$ for *Taq*I; $\chi^2 = 110.861$, df = 6, ***$P < 0.001$ and $\chi^2 = 95.249$, df = 3, ***$P < 0.001$ for *Hha*I, respectively) (Table 3). Moreover, frequencies of genotype T_2T_2 and H_2H_2, allele T_2 and H_2 were higher in dairy utility (XNSN and GZ) than those of wool utility (SBWC and XJWC), which implies that allele T_2 and H_2 may be associated with the milk performance. Hence, caprine *weaver* gene was considered having positive effects on dairy traits. The frequencies of T_2 and H_2 allele were low in the dairy utility breeds, compared with the alternate allele, consisting the XNSN and GZ genetic background of the breeds. Both breeds were identified as dairy goat breeds about 20 years ago which were needed for further selection during breeding. This assumes that the markers could be useful in breeding strategy in goat by marker-assisted selection. Taken together, the observations suggest that the distributions of genotypic and allelic frequencies of goat *weaver* gene were significantly associated with different goat utility and different selection diverges affected the frequency of *weaver* gene that played multiple roles in dairy and wool producing traits.

We previously reported that one SNP located on exon 4 was associated with milk yield ($P = 0.045$) (Li et al., 2010). However, no difference was found in milk composition ($P > 0.05$). In this study, we revealed the association of the *Taq*I polymorphisms within the 3'UTR of *weaver* gene with milk yield, protein and solids-not-fat percentage in the XNSN (Table 4). Statistical results were found in milk yield between different genotypes in *Taq*I polymorphism locus ($P = 0.015 < 0.05$, Table 4). Protein and solids-not-fat content were higher in milk

Table 4. Associations of different genotypes within the *weaver* gene with milk yield and milk composition in Xinong Sannen dairy goat.

Trait	SNP genotype (mean ± S.E.)			*P*-value
	T_2T_2	T_1T_2	T_1T_1	
MY (kg)	628.17 ± 13.66[a]	624.39 ± 8.14[a]	590.47 ± 9.66[b]	0.015
Fat (%)	2.87 ± 0.20	2.68 ± 0.15	2.65 ± 0.16	0.696
Protein (%)	3.52 ± 0.10[a]	3.21 ± 0.07[b]	3.11 ± 0.07[b]	0.027
Lactose (%)	4.13 ± 0.06	4.10 ± 0.04	4.08 ± 0.04	0.729
SNF (%)	8.76 ± 0.09[a]	8.60 ± 0.07[a]	8.33 ± 0.08[b]	0.032
TS (%)	11.63 ± 0.30	11.40 ± 0.16	11.44 ± 0.20	0.264

MY = milk yield; SNF = solids-not-fat; TS = total solids; S.E. = standard error of the mean. Values with different superscripts within the same line differ significantly; $P < 0.05$ (a, b).

from T_2T_2 compared with T_1T_1 genotypes (3.52 vs. 3.11% and 8.76 vs. 8.33%, $P < 0.05$, respectively). Moreover, no relationships were observed between the polymorphisms and growth traits (body height, body length and chest circumference) ($P > 0.05$, data not shown). In dairy cattle, the influence of *weaver* gene on milk production traits has already been described (Georges et al., 1993; Shan et al., 2002). *Taq*I polymorphism (g.99045C > T) locus in the 3'UTR of *weaver* showed the stronger association with milk traits in the XNSN breed. However, no influence of *weaver* gene variant on milk traits was detected in the *Hha*I polymorphism locus ($P > 0.05$, data not shown). We also estimated the effect of the combination of the two SNPs. However, no differences were found in milk traits ($P > 0.05$). It was considered that these associations can be explained by the following possible reasons. Although the mutation of 3'UTR did not change amino acid sequence, it may regulate the expression of *weaver* gene. It has been observed that the sequences in the 3'UTR can affect mRNA deadenylation and degradation (Xu et al., 1998) and significantly is associated with mRNA stability (Kamiyama et al., 2007). T (*Taq*I-T_2) in the 3′UTR may be the functional nucleotide that increased *weaver* expression. Alternatively, linkage disequilibrium with the causal mutation possibly affected variation in milk traits. If *Taq*I-T_2 was in linkage disequilibrium with a gene affecting variation in milk traits, segregation based on marker alleles would result in phenotypic differences (Ester et al., 2009). If $r^2 > 0.33$, then the linkage disequilibrium was considered strong (Li et al., 2009). The linkage disequilibrium between the two SNPs was estimated, which indicated that the two SNPs were not linked strongly in the analyzed populations ($r^2 = 0.103$). Hence, the *Taq*I-T_2 allele may be beneficial for improving milk yield but not the *Hha*I-H_2 allele. Therefore, NC_007299:g.99045C > T mutation may directly or indirectly influence the stability of the mRNA of *weaver*, and consequently, the amount of protein produced, which needs further study.

Conclusions

To summarize, we firstly reported the *Taq*I and *Hha*I polymorphisms in goat *weaver* gene and their associations with the production traits and milk composition in XNSN dairy goat breed. Some of those with better performance of T_2T_2 genotype could be used for the breeding of new breeds of dairy goat in China. Moreover, this study contributed to its evaluation as genetic marker in goat breeding and extension of the spectrum of genetic variation of caprine *weaver* gene.

ACKNOWLEDGEMENTS

This work was supported by Research Fund for the Doctor Program of Higher Education of China (No.20080712001), the Young Topnotch Researcher Support Project of Northwest A&F University (No.QNGG-2009-007), Natural Science Foundation of Shaanxi Province of China (No. 2011JQ3009), and Special Fund for animal breeding of Northwest A&F University (X.Y. Lan). We thank Professor Jun Luo for collecting the dairy goat blood samples.

REFERENCES

Alexander SP, Mathie A, Peters JA (2008). Guide to Receptors and Channels (GRAC), 3rd edition. Br. J. Pharmacol. 153(2): 1-209.

Benarroch EE (2009). Potassium channels: brief overview and implications in epilepsy. Neurology, 72: 664-669.

Cox MP (2006). Minimal hierarchical analysis of global human Y-chromosome SNP diversity by PCR-RFLP. Anthropol. Sci. 114: 69-74.

Dagnachew BS, Thaller G, Lien S, Adnoy T (2011). Casein SNP in Norwegian goats: additive and dominance effects on milk composition and quality. Gene. Sel Evol. 43(1): p. 31.

Ester WA, Van-Meurs JB, Arends NJ, Uitterlinden AG, De-Ridder MA, Hokken-Koelega AC (2009). Birth Size, Postnatal Growth and Growth during Growth Hormone Treatment in Small-for-Gestational-Age Children: Associations with IGF1 Gene Polymorphisms and Haplotypes. Horm. Res. 72: 15-24.

Georges M, Dietz AB, Mishra A, Nielsen D, Sargeant LS, Sorensen A, Steele MR, Zhao X, Leipold H, Womack JE (1993). Microsatellite mapping of the gene causing weaver disease in cattle will allow the study of an associated quantitative trait locus. Proc. Natl. Acad. Sci. 90: 1058-1062.

Glantz M, Lindmark Månsson H, Stålhammar H, Paulsson M (2011). Effect of polymorphisms in the leptin, leptin receptor, and acyl-coenzyme A:diacylglycerol acyltransferase 1 genes and genetic polymorphism of milk proteins on cheese characteristics. J. Dairy Sci. 94(7): 3295-3304.

Goldowitz D (1989). The weaver granuloprival phenotype is due to intrinsic action of the mutant locus in granule cells: evidence from homozygous weaver chimeras. Neuron. 2: 1565-1575.

Hoeschele I, Meinert TR (1990). Association of genetic defects with yield and type traits: the weaver locus effect on yield. J. Dairy Sci. 73: 2503-2515.

Ikeda K, Yoshii M, Sora I, Kobayashi T (2003). Opioid receptor coupling to GIRK channels. In vitro studies using a Xenopus oocyte expression system and in vivo studies on weaver mutant mice. Methods Mol. Med. 84: 53-64.

Kamiyama M, Kobayashi M, Araki S, Iida A, Tsunoda T, Kawai K, Imanishi M, Nomura M, Babazono T, Iwamoto Y, Kashiwagi A, Kaku K, Kawamori R, Ng DP, Hansen T, Gaede P, Pedersen O, Nakamura Y, Maeda S (2007). Polymorphisms in the 3' UTR in the neurocalcin delta gene affect mRNA stability, and confer susceptibility to diabetic nephropathy. Hum. Genet. 122: 397-407.

Lan XY, Pan CY, Chen H, Zhang CL, Li JY, Zhao M, Lei CZ, Zhang AL, Zhang L (2007). An AluI PCR-RFLP detecting a silent allele at the goat POU1F1 locus and its association with production traits. Small Rumin. Res. 73: 8-12.

Li JH, You ZD, Song CY, Lu CL, He C (2001). The expression of G-protein-gated inwardly rectifying K+ channels GIRK1 and GIRK2 mRNAs in the supraoptic nucleus of the rat and possible role involved. Neuroreport. 12: 1007-1010.

Li ZJ, Chen ZQ, Lan XY, Ma L, Qu YJ, Liu YL, Li MJ, Wang P, Li F, Chen H (2010). Two novel cSNPs of weaver gene in Chinese indigenous goat and their associations with milk yield. Mol. Biol. Rep. 37: 563-569.

Li Z, Zhang Z, He Z, Tang W, Li T, Zeng Z, He L, Shi Y (2009). A partition ligation combination subdivision EM algorithm for haplotype inference with multiallelic markers: update of the SHEsis (http://analysis.bio-x.cn). Cell Res. 19: 519-523.

Moioli B, Contarini G, Avalli A, Catillo G, Orru L, De Matteis G, Masoero G, Napolitano F (2007). Effect of stearoyl-coenzyme A desaturase polymorphism on fatty acid composition of milk. J. Dairy Sci. 90: 3553–3558.

Patil N, Cox DR, Bhat D, Faham M, Myers RM, Peterson AS (1995). A potassium channel mutation in weaver mice implicates membrane excitability in granule cell differentiation. Nat. Genet. 11: 126-129.

Sakura H, Bond C, Warren-Perry M, Horsley S, Kearney L, Tucker S, Adelman J, Turner R, Ashcroft FM (1995). Characterization and variation of a human inwardly rectifying K+ channel gene: a putative ATP-sensitive K+ channel subunit. FEBS. Lett. 367: 193-197.

SAS (1999). Statistical Analysis Systems user's guide SAS Institute Inc., Cary, North Carolina, USA. 6: p. 4.

Shan XS, Zhang Y, Li N (2002). Effects of several microsatellite DNA loci on milk production in dairy cattle. Acta Genet. Sin. 29: 430-433.

Stuart LD, Leipold HW (1985). Lesions in bovine progressive degenerative myeloencephalopathy ("Weaver") of Brown Swiss cattle. Vet. Pathol. 22: 13-23.

Tenhumberg H, Trela T, Matzke P, Averdunk G, Dirksen G (1994). Bovine progressive degenerative myeloencephalopathy in brown Swiss x Braunvieh cattle: reproductive occurrences, results of embryo transfer. Berl. Munch. Tierarztl. Wochenschr. 107: 400-404.

Xu N, Loflin P, Chen CY, Shyu AB (1998). A broader role for AU-rich element-mediated mRNA turnover revealed by a new transcriptional pulse strategy. Nucleic Acids Res. 26: 558-565.

Yeh FC, Yang RC, Boyle T (1999). POPGENE. Microsoft Windows-based freeware for population genetic analysis. University of Alberta, Edmonton. 1: p. 31.