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Annals of Biological Research, 2012, 3 (9):4442-4443
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Bovine LTF gene polymorphism, is associated with somatic cell score in Isfahan Holstein cows

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ABSTRACT

The purpose of this study was to estimate the association between bovine lactoferrin (LTF) gene polymorphism and somatic cell score (SCS) of milk. According to general linear model, the relationship of bovine LTF gene with SCS of milk was studied. Association of LTF genotypes with SCS in milk was relatively high ($p < 0.05$). The results showed that DNA marker could be used in selection to improve susceptibility and mastitis resistance in Holstein dairy cows.

Key words: Holstein dairy cows, SCS, mastitis, LTF gene, milk.

INTRODUCTION

Bovine LTF, a member of the transferrin gene family, is an iron-binding 80 kilodalton (kDa) glycoprotein that found in milk and exocrine secretions like tears, bile, mucous secretion and sperm [1]. This glycoprotein synthesized by granulocytes and mammary epithelial cells in response to the infection [2]. LTF gene is located on the BTA22 chromosome and consists of 17 exons, 1122 bp of promoter region and spans about 34.5 kb of the genomic DNA [3]. Bovine LTF gene considered as a candidate marker for mastitis susceptibility/resistance due to relation to the innate immunity and it would be a potential candidate gene for imparting resistance mastitis in dairy cows [1, 4]. The purpose of this study was to estimate the association between bovine LTF gene polymorphism and SCS of milk.

MATERIALS AND METHODS

Genomic DNA samples were obtained in summer 2009 from 404 Holstein dairy cows belonging to five different herds. Animals were between 3 to 6 years of age and kept in identical environmental conditions. Genomic data related with SCS was used in statistical analysis. DNA samples were extracted from whole blood. PCR conditions described by Asadallahpor Nanaei *et al.* [5]. Polymorphic variants of the LTF gene on recorded traits were analysed using SAS package (Statistical Analysis System) [6]. The following model was employed:

$$Y_{ijk} = \mu + G_i + HYS_j + b_1(z_{ijk} + \bar{Z}) + b_2(N_{ijk} + \bar{N}) + e_{ijk}$$

Where, Y_{ijk} = somatic cell score, μ = overall mean, G_i = fixed effect of the i th genotype, HYS_j = herd-year-season effect, z_{ijk} = milk yield, b_1 = the linear regression coefficient of milk yield, N_{ijk} = open days, b_2 = the linear regression coefficient of open days, and e_{ijk} = random error.

RESULTS AND DISCUSSION

As previously reported (Asadallahpor Nanaei *et al.*) the genotypic frequencies were 0.606 for AA and 0.394 for AB as followed by 0.803 for A allele and 0.197 for B allele which were in linkage disequilibrium [5]. Molecular basis of this polymorphism was the silent mutation (C→T) located within intron 6 of the LTF gene. The genotypes were considered to be in the association analysis between LTF/*EcoRI* polymorphism genotypes and SCS of milk (Table 1). Results showed that there was an association between genotypes and SCS. Genotype AA had lower amount of SCS in milk than AB groups ($p < 0.05$). Besides, association between SCS with open days and corrected milk production for 305 days were not significantly different among the two groups ($p > 0.05$). However there was a high statistically significant effect ($p < 0.01$) of HYS on SCS.

Table1. Association between SCS and the analysed factors

Source of variability (analysed factors)	Degrees of freedom	Statistic F	Probability P	Significance of associations
LTF genotype	1	4.34	0.038	*
Herd-year-season (HYS)	35	2.35	0.001	***
305-day milk yield (kg)	1	0.00	0.949	n.s.
open days	1	0.21	0.647	n.s.

* $P \leq 0.05$; *** $P \leq 0.001$; n.s. = non significant

Bovine LTF gene is highly polymorphic. Investigation of the polymorphism for this gene first reported by Seyfert and Kuhn, that found two alleles A and B with frequencies of 0.755 and 0.245 respectively [7]. According to some authors, there is an association between bovine LTF gene polymorphism in the intron 6 region and somatic cell count of milk [4, 8]. Wojdak- Maksymiec *et. al.* reported that animals with AA genotypes are associated with lower SCC than AB groups [4]. However, Sender *et. al.* provided contrary results as the genotype BB animals showed the lowest SCC than other animals [8]. Another investigation for polymorphism of this gene in the same region has been reported by Sharifzadeh and Doosti, who reported that the frequency of A allele was 67.74% and B allele 32.26%, which controlled three possible genotypes AA, AB and BB with frequencies 32.50%, 57.50% and 10% respectively [9].

CONCLUSION

In summary, according to the results of current study homozygosity for AA genotype of LTF gene is associated with lower somatic cell score of milk in Holstein dairy cattle. It is suggested that this could be due to selection of the somatic cell concentration in milk and as a marker for susceptibility and mastitis resistance in Holstein dairy cows.

Acknowledgments

To Isfahan University of Technology for supporting Hojjat Asadallahpor Nanaei's M.Sc. thesis Financially.

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