PCR-SSCP Genotype Effects of Growth Hormone, Prolactin and Insulin-Like Growth Factor-1 Genes on Milk Yield in Korean Cattle (Hanwoo)

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With recent advances in molecular genetic techniques, there has been international interest in the mapping of genes affecting quantitative traits. Genes involved in the biology of the trait of interest are candidate genes and are targets for genetic marker studies. Growth hormone (GH), prolactin (PRL) and insulin-like growth factor-1 (IGF-1) especially play an important regulatory function in growth, lactation, body composition and mammary gland development in cattle. Therefore, GH, PRL and IGF-1 are excellent candidate genes for linkage analysis with QTL because of their biological significance on the quantitative traits. Allelic variation in the structural or regulatory sequences of the GH, PRL and IGF-1 genes would be of interest because of possible direct or indirect effects on milk production and growth performance. If the DNA polymorphisms of these candidate genes are associated with economically important traits, they could serve as genetic markers for genetic improvement in future marker-assisted selection programs. It is well known that the milk production of beef cows has a large effect on calf growth. Recently, the importance of cow's milking ability to effect a greater weaning weight of calves has been recognised in Korean Cattle. The objective of this study was to analyse the single-strand conformation polymorphisms (SSCP) markers of GH, PRL and IGF-1 genes by using the PCR-SSCP method and to estimate the genotypic effects of these candidate loci on milk yield in Korean Hanwoo Cattle.

Hanwoo cows were selected for high and low breeding values for their milk yields and weaning weights of calves. Data on 200 cows with high (n=110) and low (n=90) milk were used in the analysis. For SSCP analysis of the GH, PRL and IGF-1 candidate genes, genomic DNA was extracted from the blood of the selected cows and amplified by PCR as previously described (Hart et al., 1993; Yao et al., 1996; Ge et al., 1997). The electrophoresis was carried out using 10-15% polyacrylamide TBE gels at 350 volts for 7hr at room temperature. The fragments in the gel were stained with silver nitrate. Preliminary data analysis was performed using the GLM procedure of the statistical package SAS (1990).

For GH and PRL, three alleles were identified at each gene, designated as A, B and C. Two alleles A and B were observed for the IGF-1 gene. The frequencies of AA, AB, AC, BB, BC and CC genotypes of GH were .13, .23, .19, .25, .15 and .06 for the high milk group and .10, .20, .12, .35, .20 and .02 for the low milk group, respectively. The frequencies of AA, AB, AC, BB, BC and CC genotypes of PRL were .75, .42, .94, .17, .19 and .06 for the high milk group and .12, .35, .16, .10, .25 and .02 for the low milk group, respectively. The frequencies of AA, AB and BB genotypes for IGF-1 were .51, .24 and .25 for high milk group and .32, .31 and .37 for low milk group, respectively. There were no significant differences in genotypic frequencies between high and low groups selected for milk yield for GH and PRL genes. However, significant differences (P<0.05) in genotype frequencies for the IGF-1 gene were observed between the two groups of cows. In the frequency of AA and BB genotypes for IGF-1, the differences between the two groups selected for high and low milk yield were 19% and 12%, respectively. Our results indicate that IGF-1 SSCP genotype may be a useful genetic marker for the genetic improvement of milk yield in Korean Cattle.


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