# ASSOCIATIONS OF FIVE GENES WITH GROWTH AND MATERNAL TRAITS IN LINE 1 HEREFORD CATTLE

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## Story in Brief

A total of 414 cattle representing the Line 1 Hereford population was genotyped for DNA polymorphisms in the Kappa Casein, Beta Lactoglobulin, Growth Hormone, Insulin-like Growth Factor I and Pit-1 genes. Two alleles for each gene were segregating in the population. Regression analysis was used to estimate the average effect of replacing an A allele with a B allele of each gene on expected progeny differences (EPD) for birth weight, weaning weight, yearling weight and maternal ability. Kappa-Casein allele substitution had significant effects on birth weight EPD and maternal EPD, accounting for 11% and 14% of the variation in EPD, respectively. These effects would be large enough to warrant further study for inclusion of Kappa-Casein genotype in a marker assisted selection program. Several other significant effects accounting for smaller percentages of variation in EPD were found.

(Key Words: Genotype, EPD, DNA, Beef Cattle, Growth, Milk.)

## Introduction

Traditionally, genetic improvement of livestock has been accomplished by selecting animals that express superior phenotypes or have quantitative genetic evaluations predictive of superior additive genetic merit for particular traits of interest. Techniques in molecular genetics now enable the actual genotype of an animal to be determined for specific genes. This information may accelerate future genetic improvement of livestock through marker assisted selection, if significant associations can be found between specific genotypes and traits of economic importance, such as growth and milk production.

The Line 1 population of Hereford cattle was established at the Fort Keogh Livestock and Range Research Laboratory (Miles City, MT) in 1931 as part of a project to develop a line of cattle superior in genetic merit for growth (MacNeil et al., 1992). The population was closed to outside introduction of germplasm in 1935 and has since been selected for increased post weaning growth. Line 1 cattle are recognized for genetic superiority of growth traits and have been used extensively throughout the Hereford breed. Therefore, Line 1

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Herefords are a unique population in which to study the effects of DNA polymorphisms on growth traits.

Growth hormone (GH), through the effects of Insulin like Growth Factor 1 (IGF-I), is known to have a major effect on the hormonal regulation of growth (Isaksson et al., 1985). Pit-1 has been identified as a protein produced in the pituitary which is necessary for the expression of growth hormone (Ingraham et al., 1988). Therefore, genes for GH, IGF-I and Pit-1 are all logical candidates for molecular markers of growth traits. Kappa casein (K-Cas) and Beta lactoglobulin (B-Lac) are both proteins expressed in milk. K-Cas (Medrano and Aguilar-Cordova, 1990a) and B-Lac (Medrano and Aguilar-Cordova, 1990b) genes may be informative in evaluating genetic potential for milk production, as expressed by maternal ability in cattle. The objective of this study was to characterize genetic variability at these five candidate genes and to evaluate allelic effects on growth and maternal traits in USDA Line 1 Hereford cattle.

## Materials and Methods

***Source Population and Data Collection:*** The Line 1 Hereford population was used in this study. Data for the present study comprised calf crops born in 1991 to 1993. Husbandry and management practices of Line 1 are described in MacNeil et al. (1992). All calves were weighed within 24 hours after birth. Those surviving were weighed at weaning and at 1 year of age. For the present study, yearling weights on 1993-born calves were not yet available.

***Genotyping:*** DNA was extracted from blood or semen. Polymerase Chain Reaction (PCR) was used to genotype 414 animals at polymorphisms within the K-Cas, B-Lac, GH, IGF-I and Pit-1 genes. K-Cas, B-Lac and GH genotypes were determined using PCR amplification and restriction enzyme digestion as described by Medrano and Aguilar-Cordova (1990a), Medrano and Aguilar-Cordova (1990b), and Zhang et al. (1992), respectively. IGF-I genotypes were determined by a method similar to that described by Kirkpatrick (1992). A polymorphism not previously described was identified in the bovine Pit-1 gene. PCR was used to amplify a portion of the Pit-1 gene, and restriction endonuclease digestion of the resulting PCR products revealed two different Pit-1 alleles.

***Statistical Analyses:*** Birth weight (BW), weaning weight (WW), yearling weight (YW), and maternal (MILK) expected progeny differences (EPD) were obtained as part of the American Hereford Association National Cattle Evaluation. Regression analyses were performed in which the EPD were the dependent variables and genotype was the independent variable. As described by Falconer (1989), the regression coefficient estimates the average effect of gene substitution, or the predicted change in EPD caused by replacing an A

allele with a B allele. $R^2$ values from these analyses represent the percent of variability in EPD explained by genotype.

## Results and Discussion

Observed gene and genotype frequencies are shown in Figure 1. Frequency of the A allele in Line 1 for K-Cas was .64, compared to earlier reports of .85 for Holstein (Medrano, 1990) and .1 for Jersey (Medrano and Aguilar-Cordova, 1990a). Medrano (1990) also reported a B-Lac A allele frequency of .4 in Holstein, which is much lower than the frequency of .72 observed in Line 1.

Zhang et al. (1993) reported GH A allele frequencies of .91, .73, .74 and .65 for Holstein, Simmental, Angus and Herefords, respectively. GH A allele frequency observed in Line 1 was .35 which is considerably lower than the previous estimate for Herefords. This may well be a result of sampling variance at the initiation of Line 1, or alternatively may be a direct result of selection. However, the magnitude of this difference is surprising considering the wide distribution of Line 1 cattle within the Hereford breed. Kirkpatrick (1992) reported an A allele frequency of .26 for IGF-I in a mixed-breed population, compared to .62 observed in Line 1. These results indicate significant between-breed variation in allele frequencies at many loci.

Results from the regression analyses of BW, MILK, WW and YW EPD on genotype are presented in Tables 1 and 2. Substituting a B allele for an A allele had significant effects ($P<.01$) on BW EPD for K-Cas, B-Lac, IGF-I, and Pit-1, but the effect was not significant for GH. Substituting a B allele for an A allele had significant effects ($P<.01$) on MILK EPD for K-Cas, B-Lac, GH and IGF-I, and was also significant for Pit-1 ($P<.05$). $R^2$ values for these analyses ranged from 0.5 to 14.3%.

The average effect of allele substitution had a significant effect on both WW and YW EPD for K-Cas ($P<.01$) and for IGF-I ($P<.05$). The average effect of allele substitution on YW EPD was also significant ($P<.05$) for GH and Pit-1. $R^2$ values for these analyses were small, ranging from .4 to 2.2%.

These results indicate the average effect of allele substitution was significant for all genes studied at one or more traits analyzed, even though the magnitude of the effect was small in most cases. However, variation in K-Cas genotype accounted for 11.0% of variability in BW EPD and 14.3% of variability in MILK EPD. These effects would be large enough to warrant further study for inclusion of K-Cas genotype in a marker assisted selection program. Unfortunately, K-Cas B allele substitution produced a desirable effect of decreasing BW EPD along with a potentially undesirable effect of decreasing MILK EPD. This latter effect agrees with some reports but is in contrast with others on the effects of K-Cas genotype on milk production in dairy cattle (see Bovenhuis et al., 1992). Ziehe et al. (1993) reported results similar to the present study for the effects of K-Cas genotype on milk production in Angus and Polled Hereford sired beef cows.

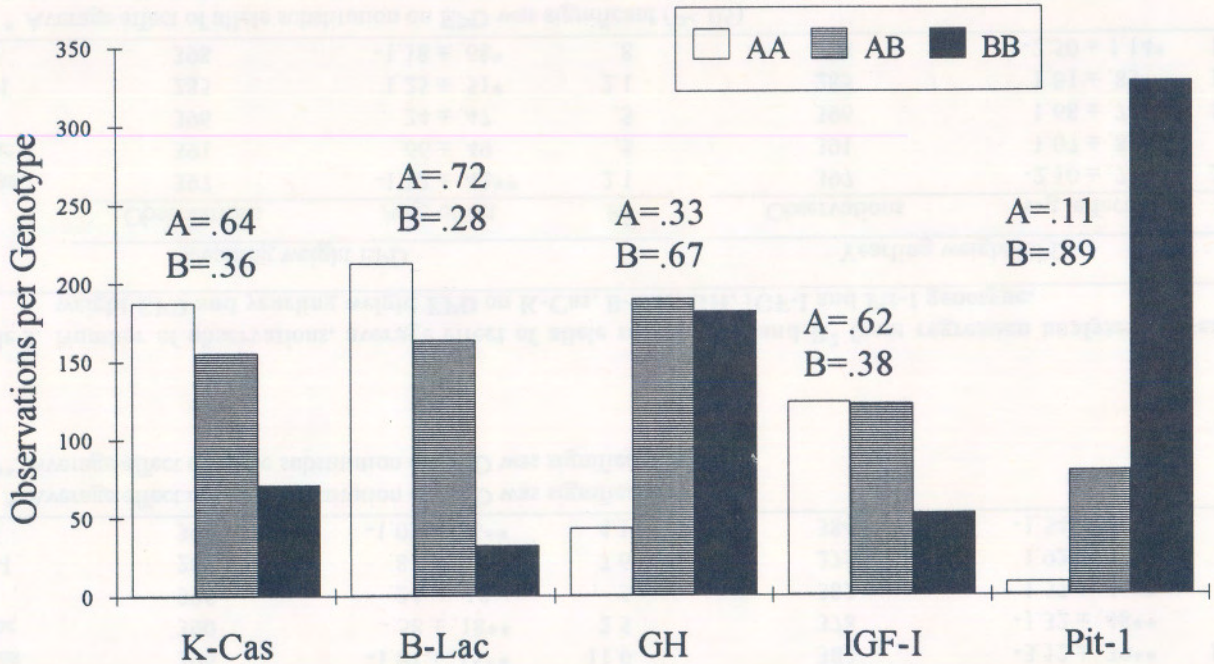


**Figure 1. Gene and genotype frequencies of K-Cas, B-Lac, GH, IGF-I and Pit-1 genes in Line 1 Herefords.**

**Table 1. Number of observations, average effect of allele substitution and $R^2$ from regression analyses of birth weight EPD and maternal EPD on K-Cas, B-Lac, GH, IGF-I and Pit-1 genotype.**

| | Birth weight EPD | | | Maternal EPD | | |
|---|---|---|---|---|---|---|
| | Observations | Avg. effect | $R^2$ | Observations | Avg. effect | $R^2$ |
| K-Cas | 396 | -1.07 ± .15** | 11.0 | 383 | -3.12 ± .39** | 14.3 |
| B-Lac | 390 | -.58 ± .18** | 2.5 | 378 | -1.32 ± .48** | 2.0 |
| GH | 395 | .24 ± .18 | .5 | 382 | 1.57 ± .46** | 3.0 |
| IGF-I | 284 | .87 ± .18** | 7.6 | 275 | 1.92 ± .53** | 4.7 |
| Pit-1 | 397 | -1.05 ± .26** | 4.1 | 384 | -1.54 ± .68* | 1.3 |

* Average effect of allele substitution on EPD was significant (P<.05).
** Average effect of allele substitution on EPD was significant (P<.01).

**Table 2. Number of observations, average effect of allele substitution and $R^2$ from regression analyses of weaning weight EPD and yearling weight EPD on K-Cas, B-Lac, GH, IGF-I and Pit-1 genotype.**

| | Weaning weight EPD | | | Yearling weight EPD | | |
|---|---|---|---|---|---|---|
| | Observations | Avg. effect | $R^2$ | Observations | Avg. effect | $R^2$ |
| K-Cas | 397 | -1.22 ± .42** | 2.1 | 397 | -2.10 ± .70** | 2.2 |
| B-Lac | 391 | .66 ± .49 | .5 | 391 | 1.07 ± .82 | .4 |
| GH | 396 | .24 ± .47 | .5 | 396 | 1.68 ± .79* | 1.1 |
| IGF-I | 285 | 1.25 ± .51* | 2.1 | 285 | 1.81 ± .83* | 1.6 |
| Pit-1 | 398 | -1.18 ± .68* | .8 | 398 | -2.50 ± 1.14* | 1.2 |

* Average effect of allele substitution on EPD was significant (P<.05).
** Average effect of allele substitution on EPD was significant (P<.01).

The effects of the IGF-I and Pit-1 markers should be interpreted with caution because they are both polymorphisms which likely do not alter or effect the proteins translated from different alleles. Therefore, IGF-I and Pit-1 may be markers for other genes influencing BW. In contrast, A and B alleles of K-Cas do produce different forms of K-Cas, and the large effects of K-Cas genotype on BW EPD and MILK EPD may be a direct result of the differences in K-Cas proteins. Analysis of IGF-I and Pit-1 markers in well defined, segregating resource families is required to accurately quantify their influence on phenotypic traits of interest.

The small magnitude of effects found in this study (indicated by low $R^2$ values) was not unexpected when considering the effects of single genes on quantitative phenotypic traits such as growth and milk production. Traditionally, quantitative traits are assumed to be controlled by several genes, each contributing small effects. In order for selection utilizing molecular marker information to be effective in improving quantitative traits, small effects of many different genes will have to be identified and understood.

This study emphasizes the need for more research on the associations between molecular markers and their effects on phenotypic traits. Several small but significant associations were identified between molecular markers and EPD in Line 1 Herefords. More information, including consideration of combinations of small effects contributed by different genes, will be needed in order for marker assisted selection to become a practical selection tool.

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