

MILK PROTEIN GENOTYPE EFFECTS ON MILK PRODUCTION IN BEEF HEIFERS AND CALF PERFORMANCE: PRELIMINARY RESULTS

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Story in Brief

Genotypes at the β -lactoglobulin and κ -casein loci were determined on 72 first calf heifers to study the effects of cow genotype on milk production and preweaning calf performance. Genotypes were resolved using polymerase chain reaction and restriction fragment length polymorphism analyses on genomic DNA. Estimates of 12-hour milk production, obtained by the weigh-suckle-weigh method, and calf weights were obtained at 28 day intervals through the first third of lactation. Effects on age-adjusted weaning weight were also analyzed. The dam's genotype at the β -lactoglobulin locus was observed to have no effect on milk production, nor on any measure of calf performance. The AA genotype at the κ -casein locus was associated with increased calf ADG and increased milk production among Angus-sired dams. Weaning weights were also heavier among calves out of AA heifers by Angus sires, when compared to heifers with the AB genotype (507.1 vs. 454.7 lb). Among heifers by Polled Hereford sires, the AA genotype increased calf ADG, but the difference was not as large as in Angus-sired heifers. The AB genotype in this breed group tended to increase milk production during early lactation, but differences in weaning weight of their calves were not attributable to the dam's genotype at this locus. These results are preliminary, but indicate possible effects of the κ -casein gene and further investigation is certainly warranted.

(Key Words: Beef Cattle, Kappa-casein, Beta-lactoglobulin, Preweaning, Markers.)

Introduction

In livestock, most traits of economic importance are influenced by many different genes. One assumption made in the development of genetic theory is

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that since there are many genes affecting quantitative traits, the effect of each of the genes on a given trait is very small. Through many years of research, there is little evidence to suggest that this is a poor assumption. However, the discovery of the "F" gene, a single gene resulting in a marked increase in ovulation and lambing rate in Booroola Merino sheep, indicated that there are possible exceptions to the rule. Although genes with large effects (major genes) date back to the earliest genetics studies, this was probably the first major gene known to affect a truly quantitative trait (reproductive rate).

Recent advancements in molecular genetic techniques have given researchers a new tool that may help identify other major genes. The effects of these potential major genes, however, will probably not be as obvious as that of the "F" gene. These new techniques have allowed for a large number of polymorphic genetic markers to be identified in several different species, including cattle. Polymorphic genetic markers are relatively short segments of chromosomal DNA, for which more than one variation of the segment's base sequence is found among individuals in a population. These markers may be part of a gene, or they may be found between genes on a chromosome. When base sequence variations are found within a gene, they can result in variations in the gene products, which may also cause differences in a trait or traits that are economically important.

Two such markers identified in dairy cattle are located within the genes that code for two milk proteins, β -lactoglobulin and κ -casein. The two variants of each of these two genes (and the proteins for which they code) are known to affect the cheese-making properties of milk. The purpose of this study was to determine the effects of genotypes for these markers on milk production in beef cows, as well as preweaning performance of their calves. These markers were chosen as candidate genes due to the known variants of the two proteins, and because they were known to be polymorphic in the Hereford breed (suggesting polymorphism in other beef breeds). Results presented in this report are from analyses of data from the first year of the study (first calf heifers) for the effects of cow genotype on milk production and calf performance through the first third of lactation, and on calf weaning weight.

Materials and Methods

Blood samples were collected from cows ($n=72$) in the maternal EPD study described by Buchanan et al. (1992, 1993). DNA was extracted from white blood cells by salt extraction. Known regions of the β -lactoglobulin and κ -casein loci were amplified for each cow by polymerase chain reaction (PCR). PCR is a procedure that allows us to make over a billion copies of a specific segment of chromosomal DNA, or a gene marker, so that it can be isolated from all of the other genes. Restriction fragment length polymorphism (RFLP) analyses were performed on PCR products, and genotypes (AA, AB or BB)

were determined by the resulting banding patterns separated with agarose gel electrophoresis. RFLP analyses and gel electrophoresis are lab procedures that allow us to visualize certain DNA sequence differences between animals. The reaction systems for determining genotypes at these two loci were first described by Medrano and Aguilar-Cordova (1990a, 1990b).

To obtain milk production and calf performance data, seven trial dates were arranged at 28 d intervals during each lactation period. On the evening prior to each trial, calves were sorted and held off their dams overnight. At 6:00 am the following morning, calves were allowed to suckle their dams until the cows appeared to be nursed out. Calves were again removed for two consecutive 6-hour periods, and milk production was estimated by the weigh-suckle-weigh method at the end of each calf removal period. The first trial each season was conducted when the oldest calves reached approximately 45 d of age, and cows with calves less than 15 d of age were not subjected to trial.

Results obtained from first calf heifers in the first year of the study are reported. Performance information includes 12-hour milk production, calf weight and calf ADG (to date) on the first three of seven trial dates. Calf weaning weights were also analyzed, and were adjusted to 205 and 240 d for spring- and fall-born calves, respectively.

All traits were analyzed with a model that included the effects of the cow's sire breed, maternal EPD group within the sire's breed, cow's sire within breed and maternal EPD group, sex of calf, calving season and cow genotype within her sire's breed. Preliminary analyses indicated that the sire of the calf was not an important source of variation, so this effect was not included in the final analyses. For milk production and early calf performance traits, a covariate was included to adjust for age (d) of the calf on the test date. Two- and three-way interactions in which all subclasses were represented were included in the model, but due to the small number of observations within subclasses, only adjusted means for cow genotypes within sire breed are reported.

Results and Discussion

The heifers utilized in this study were by sires that represented the extremes for maternal EPD within their respective breeds. It might be anticipated that there would be an association of heifer genotype with sire maternal EPD group, if genotype had an effect on milk production or preweaning calf performance. This, however, was not the case, as genotypes for both loci were distributed approximately equally among low and high maternal EPD groups. A possible explanation may be that the anticipated effects of either gene on the traits measured are potentially small. Therefore, a much larger sample of sires might be needed to detect differences in heifer genotype frequencies among maternal EPD groups.

β -lactoglobulin

Although all three genotypes for β -lactoglobulin were present in both sire breed groups, only five of the 72 cows were found to have the AA genotype. For this reason, only records from cows with AB or BB genotypes were analyzed. Genotypic frequencies were .083, .361 and .556 in cows by Angus sires, and .056, .250 and .694 in cows by Polled Hereford sires, for AA, AB and BB, respectively.

Cow genotype at the β -lactoglobulin locus did not affect any of the calf traits measured. Differences ($P < .05$) due to cow genotype were observed in 12-hour milk production levels among Angus-sired cows at the first and second test dates. These differences were inconsistent, however, as the ranking of the two genotypes was reversed between the two test dates. Upon further analysis, this inconsistency was completely explained by the records of two AB cows in the Angus, high maternal EPD sire group, and the differences were therefore considered to be artificial.

κ -casein

Only the AA and AB genotypes for κ -casein were present among the cows in the study. Genotypic frequencies were .694 and .306 in cows by Angus sires, and .583 and .417 in cows by Polled Hereford sires, for AA and AB, respectively.

Cow genotype at the κ -casein locus affected 12-hour milk production only at the first of the three trial dates. Figure 1 shows tendencies for the AA

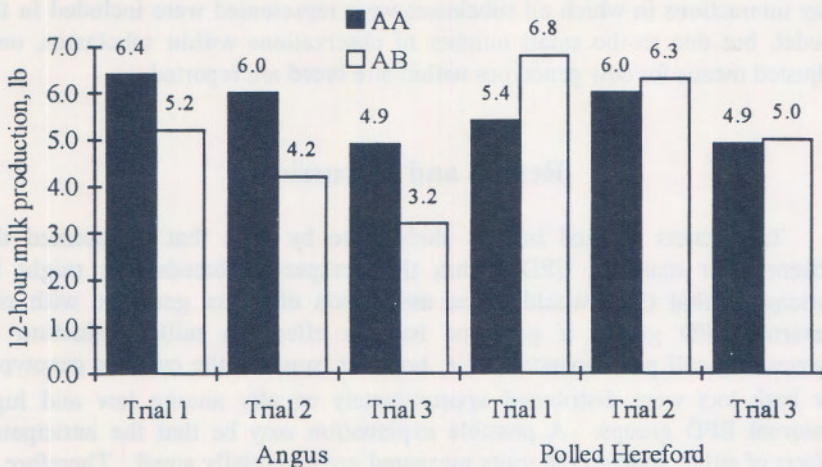


Figure 1. Adjusted means of the effects of heifer κ -casein genotype on milk production during early lactation.

genotype to be superior in Angus-sired cows across trials, but the AB genotype tended to be superior in cows by Polled Hereford sires, at least for the first trial period ($P < .1$).

Figures 2 and 3 show the effects of the cow's genotype on calf growth rate. Among cows by Angus sires, those with the AA genotype had calves that grew faster and were heavier at all three trial dates ($P < .05$). Among cows by Polled Hereford sires, the trend was in similar, but the genotypes differed only at the first trial date for calf ADG ($P < .05$), and calf weights were similar across trial dates ($P > .3$).

Figure 4 illustrates the effect of cow genotype on calf weaning weight. Among Angus-sired cows, those with the AA genotype weaned calves that were 52 lb heavier than those with the AB genotype ($P < .05$). Both genotypes weaned calves of similar weight among cows by Polled Hereford sires ($P > .5$).

It should be stressed that these results are preliminary, but this study indicates that the κ -casein locus may have an effect on the maternal component of preweaning calf growth. The underlying basis appears to be increased milk production, but milk quality may also be involved. Much more information is needed before any definitive conclusions should be drawn. As this study continues, data will become available to help determine the validity of these results, as well as the effects of these and other genetic markers on both immature and mature females.

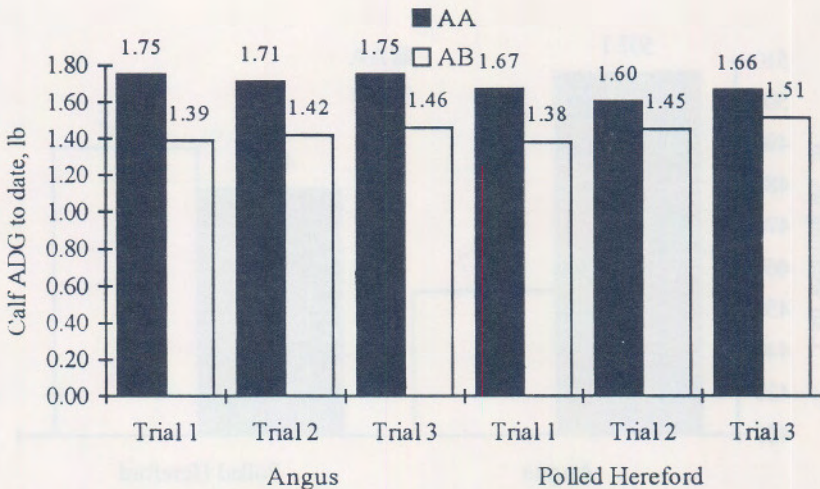


Figure 2. Adjusted means of the effects of heifer κ -casein genotype on calf ADG during early lactation.

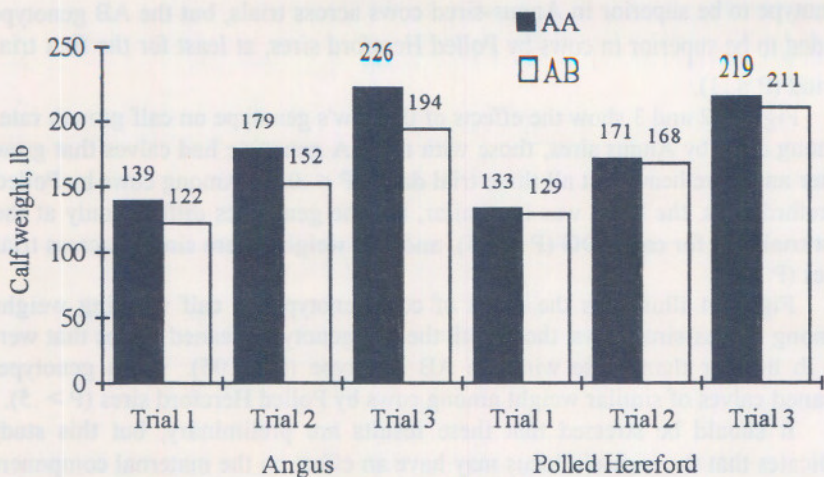


Figure 3. Adjusted means of the effects of heifer κ -casein genotype on calf weight during early lactation.

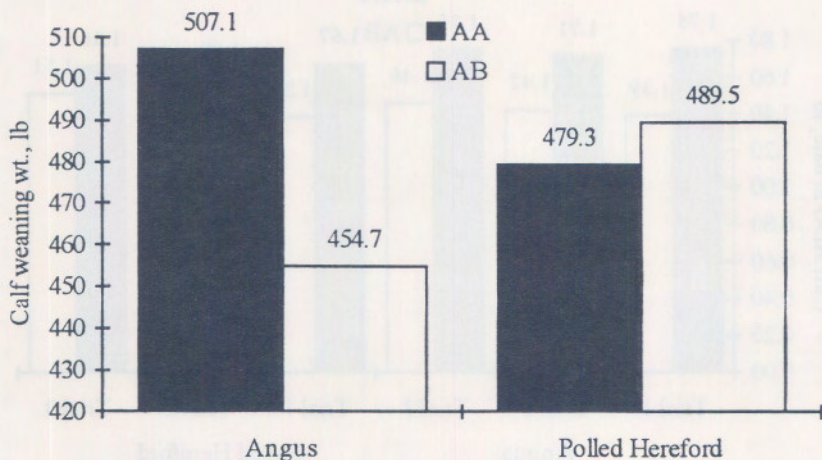


Figure 4. Adjusted means of the effects of heifer κ -casein genotype on calf age-adjusted weaning weight.

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