

New Zealand Society of Animal Production online archive

This paper is from the New Zealand Society for Animal Production online archive. NZSAP holds a regular annual conference in June or July each year for the presentation of technical and applied topics in animal production. NZSAP plays an important role as a forum fostering research in all areas of animal production including production systems, nutrition, meat science, animal welfare, wool science, animal breeding and genetics.

An invitation is extended to all those involved in the field of animal production to apply for membership of the New Zealand Society of Animal Production at our website www.nzsap.org.nz

[View All Proceedings](#)

[Next Conference](#)

[Join NZSAP](#)

The New Zealand Society of Animal Production in publishing the conference proceedings is engaged in disseminating information, not rendering professional advice or services. The views expressed herein do not necessarily represent the views of the New Zealand Society of Animal Production and the New Zealand Society of Animal Production expressly disclaims any form of liability with respect to anything done or omitted to be done in reliance upon the contents of these proceedings.

This work is licensed under a [Creative Commons Attribution-NonCommercial-NoDerivatives 4.0 International License](http://creativecommons.org/licenses/by-nc-nd/4.0/).



You are free to:

Share— copy and redistribute the material in any medium or format

Under the following terms:

Attribution — You must give [appropriate credit](#), provide a link to the license, and [indicate if changes were made](#). You may do so in any reasonable manner, but not in any way that suggests the licensor endorses you or your use.

NonCommercial — You may not use the material for [commercial purposes](#).

NoDerivatives — If you [remix, transform, or build upon](#) the material, you may not distribute the modified material.

<http://creativecommons.org.nz/licences/licences-explained/>

blood metabolites (e.g., urea). The performance characteristics (e.g., heritabilities and genetic correlations with production traits) required to make greater genetic gains in the resulting proven sires and hence the NZ dairy cattle population have been defined.

CONCLUSION

A method for evaluating the benefits of new technologies to Livestock Improvement's breeding scheme

has been outlined. The method focuses on the NZDB/LIC mission statement. Several applications of the approach have been outlined.

REFERENCES

- Hill, W.G. 1974. Prediction and evaluation of response to selection with overlapping generations. *Animal Production* **18**: 117-139
- Van Vleck, L.D.; Pollak, E.J.; Oltenacu, E.A.B. 1987. Genetics for the Animal Sciences. W.H. Freeman and Company, New York

Associations between milk protein genetic variants and production traits in New Zealand dairy cattle

A.M. WINKELMAN AND B.W. WICKHAM

Livestock Improvement Corporation, Private Bag 3016, Hamilton, New Zealand.

ABSTRACT

Records on 7574 first lactation cows were used to investigate the associations between milk protein genetic variants and 305-day milk, fat, and protein yields. Friesians, Jerseys and Ayrshires and their crosses were represented in the data. Milk samples were typed for 3 casein (CN) proteins α_{s1} -CN (B,C), β -CN (A¹, A²), κ -CN (A,B) and 1 whey protein β -lactoglobulin (LG) (A,B). The model used to describe the data included the additive genetic effect of animal and the four protein phenotypes.

The interaction between breed and α_{s1} -CN phenotype and between breed and β -CN phenotype was significant ($P < 0.05$) for milk, fat and protein yields while the interaction between breed and κ -CN phenotype was significant ($P < 0.05$) only for protein yield. The interactions associated with the α_{s1} -CN and κ -CN phenotypes were scale effects while the interactions associated with β -CN resulted from reranking of protein phenotype across the breeds. Friesian and Jersey α_{s1} -CN BB cows had higher (2.8% and 0.8%, respectively) milk production and lower (0.3% and 1.2%, respectively) protein production than BC animals while the differences between the phenotypes for fat production were small. The β -CN A² allele was associated with increased production in the Friesians with A²A² cows producing approximately 2% more milk, fat and protein than A¹A¹ cows. The opposite effect was found in Jerseys where A²A² cows produced 3-4% less milk, fat, and protein than A¹A¹ cows. The B allele of κ -CN was associated with a 0.6 to 3.5% increase in production. The β -LG BB phenotypes produced approximately 1.3% less milk and protein and 1.2% more fat than the AA phenotypes. The dominance effect was not significant ($P < 0.05$) for any of the protein phenotypes.

Keywords: milk protein polymorphism; production traits.

INTRODUCTION

Genetic polymorphism exists in 3 casein (CN) proteins (α_{s1} -CN, β -CN and κ -CN) and 1 whey protein (β -lactoglobulin (LG)) of milk produced by the common breeds of Western cattle (for a review see Ng-Kwai-Hang and Grosclaude; 1992). The polymorphs, referred to as genetic variants, differ in their amino acid composition through either deletions or substitutions. Associations have been found between the genetic variant composition of the milk and its manufacturing properties. For example, Hill *et al.* (1995) found that β -LG BB milk had higher casein content, lower whey protein content, significantly higher curd firming rate and greater cheese yield than

β -LG AA milk. Other research found associations between genetic variants and yield traits. Bovenhuis *et al.* (1992) and Aleandri *et al.* (1990) found β -LG BB cows had lower milk and protein but higher fat production than β -LG AA cows. However, agreement between the two studies with respect to the associations of the casein proteins with production traits were less consistent with certain variants associated with increased production in one study but decreased production in the other study.

Given the potential manufacturing benefits of milk of a specific genetic variant composition as well as the associations between genetic variants with production traits, the value of genetic variants as selection criteria should be assessed. The economic value of milk of a specific genetic

variant composition is a function of its benefits from a manufacturing point of view and its associations with both production and nonproduction traits of economic importance. The purpose of this study was to investigate the associations between milk protein genetic variants and lactation yield traits in New Zealand dairy cattle.

MATERIALS AND METHODS

Electrophoretic methods developed by the New Zealand Dairy Research Institute (J. Hill, personal communication) were used to determine the genetic variants of α_{s1} -CN, β -CN and κ -CN and β -LG in milk sampled from 7574 first lactation cows. The genetic variant composition of an animal determined in this manner will be referred to as its protein phenotype for each protein of interest. The cows were distributed across 208 Sire Proving Scheme herds and were the progeny of 174 identified sires and 7476 identified dams. The production traits measured were 305-day milk, fat and protein yields. The breed composition and allelic frequencies of the data are shown in Table 1. The samples were also typed for A³ and B alleles of β -CN but their frequencies were low (< 0.10) and will not be referred to explicitly in this study. Given that there were two alleles for each protein studied, there were three protein phenotypes - two homozygotes and one heterozygote - for each protein. However, the frequency of the C allele of α_{s1} -CN was low resulting in a very low frequency (³ 2%) of CC cows. Because of the low number of animals, they were not included in the tests of hypotheses.

Univariate animal models were used for the analyses. All models included the fixed effects of herd, month of calving, phenotype for each of the four proteins (α_{s1} -CN, β -CN and κ -CN and β -LG), fraction of Ayrshire, Friesian and Jersey genes, breed heterozygosity based on breed composition of parents and days in milk. When tests of breed by protein phenotype were performed (see below) the model also included the appropriate breed by protein interaction terms. Prior to analyses of the associations between protein phenotype and production traits, heritabilities were estimated for the three traits using Restricted Maximum Likelihood. The heritabilities were 0.32, 0.18, and 0.22 for milk, fat and protein yield, respectively. Hypothesis testing involved tests of the breed by protein phenotype interaction for each of the 4 proteins and, where appropriate, tests of the main effect of the protein. For these tests, two contrasts were considered. One involved a comparison between the homozygous

phenotypes (eg. AA-BB for β -LG) and the other involved a test to determine whether the homozygote was midway between the two homozygotes (eg. AA+BB-2AB) i.e. a test of nonadditive gene action. Hypothesis testing was done using the PEST programme of Groeneveld *et al.* (1990). Tests of significance were done at the 5% level.

RESULTS

The interaction between breed and α_{s1} -CN phenotype and between breed and β -CN phenotype was significant for milk, fat and protein yields while the interaction between breed and κ -CN phenotype was significant only for protein yield. The significant interaction for κ -CN was mainly a scale effect where the BB phenotypes had higher production than the AA animals for both Friesians and Jerseys but with the magnitude of the difference being larger for Friesians than Jerseys. For β -CN, there was reranking of protein phenotypes across breed where the A² allele increased production of all three traits in the Friesians but decreased production in the Jerseys.

The difference between α_{s1} -CN BB and BC phenotypes was greatest for the Ayrshires with the BB cows having higher yields than the BC cows for all three traits. BB Friesians had 2.8% higher milk production and 0.3% lower protein production than BC Friesians. A similar trend was found for Jerseys where BB animals had 0.8% higher milk production and 1.2% lower protein production than BC animals. Differences between the phenotypes for fat production were small for both the Friesian and Jersey breeds.

Contrasts between each phenotype and a chosen "base" phenotype expressed as a percentage of the "base" phenotypic mean are shown in Figures 1 (β -CN), 2 (κ -CN) and 3 (β -LG). The base means were taken as the A¹A¹ phenotype for β -CN and the AA phenotypes for κ -CN and β -LG. Thus, Figure 1 indicates the effect of substitution of the A¹ allele by the A² allele while Figures 2 and 3 represent the effect of substituting the A allele by the B allele within each protein. For β -CN, the trends are shown within the Friesians and Jerseys while for κ -CN and β -LG the trends are across all breeds.

The β -CN A² allele was associated with increased production in the Friesians but decreased production in the Jerseys for all three traits. The relative increase of A²A² Friesians over A¹A¹ Friesians was approximately 2% while the relative decrease for the Jerseys was 3-4%. The greater

TABLE 1: Within breed allelic frequencies for each of the four milk proteins.

Milk Protein Breed ¹	n	α_{s1} -CN		β -CN		κ -CN		β -LG	
		B	C	A ¹	A ²	A	B	A	B
Ayrshire	37	0.932	0.068	0.432	0.527	0.797	0.203	0.297	0.703
Friesian	3761	0.972	0.026	0.465	0.510	0.826	0.174	0.487	0.513
Jersey	1328	0.703	0.297	0.123	0.591	0.519	0.481	0.316	0.684
Cross	825	0.830	0.170	0.297	0.549	0.643	0.357	0.397	0.603
Other	1623	0.885	0.115	0.340	0.556	0.725	0.275	0.431	0.569

¹ Ayrshires, Friesians, and Jerseys are (15/16 pure bred).
 Crosses are 7/16-9/16 Friesian and 7/16-9/16 Jersey (i.e. close to a 50/50 cross).
 Other includes all crossbred animals that were not 50/50 crosses.

FIGURE 1: Relationship between β -CN phenotype and milk, fat and protein yield within Friesian and Jersey cows. (The standard error of the difference between Friesian A¹A¹ and A²A² cows vs. Jersey A¹A¹ and A²A² cows, as a percentage of A¹A¹ production, was 2.25, 2.23, and 2.07 for milk, fat, and protein production, respectively.)

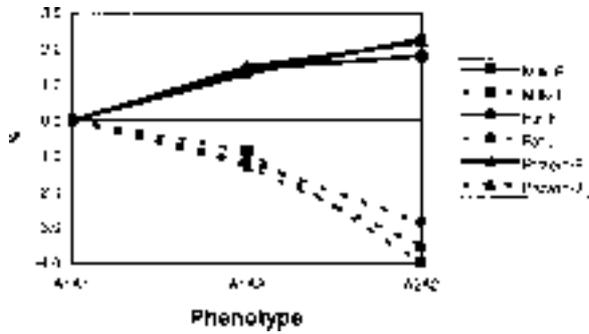


FIGURE 2: Relationship between κ -CN phenotype and milk, fat and protein yield. (The standard error of the difference between AA and BB production, as a percentage of AA production, was 0.73, 0.71, and 0.66 for milk, fat, and protein yield, respectively.)

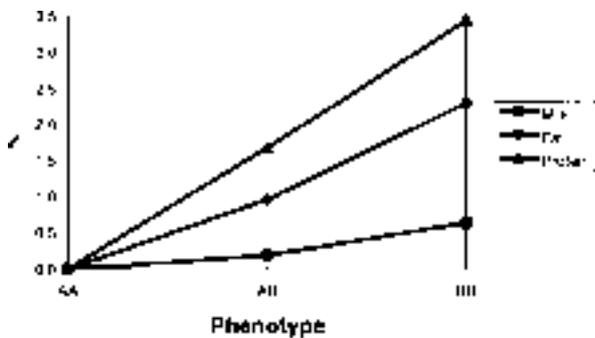
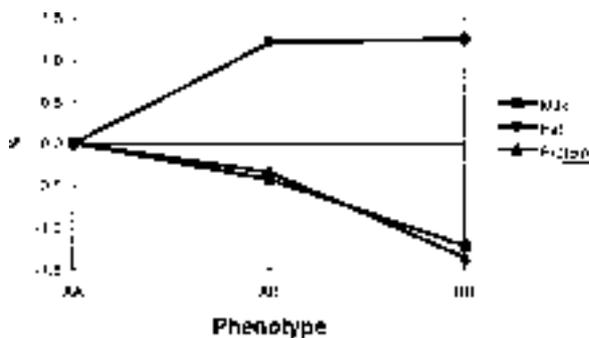


FIGURE 3: Relationship between β -LG phenotype and milk, fat and protein yield. (The standard error of the difference between AA and BB production, as a percentage of AA production, was 0.50, 0.49, and 0.45 for milk, fat, and protein yield, respectively.)



effect in the Jerseys reflects both the lower production levels of this breed as well as larger absolute differences between the production of the two phenotypes. Tests for the presence of dominance were not significant in either breed with production of A¹A² animals lying close to the midpoint of the A¹A¹ and A²A² animals.

For κ -CN, the B allele was associated with a significantly higher fat and protein production with BB animals producing 3.5% more protein and 2.3% more fat than AA animals. While not significant, a similar trend was evident for milk with BB animals producing 0.6%

more milk than AA animals. The dominance effect was not significant for any of the traits.

The β -LG BB phenotypes produced significantly less milk and protein and more fat than the AA phenotypes. The relative difference between the homozygous phenotypes was approximately 1.3% for all traits. While not significant at the 5% level, the results show evidence of a dominance effect for fat production with the production of AB animals being closer to that of BB animals than AA animals.

DISCUSSION

The presence of a breed by protein phenotype interaction warrants further discussion. Jakob (1995) considered the underlying mechanisms by which milk protein variants affect milk protein composition. He indicated that if the same trend is seen in any breed, then the effect is probably due to a direct gene effect. Such a condition was found with the β -LG phenotypes. However, if the effect is due to a linked gene, the effects observed in different breeds may be contradictory. He used the example of the κ -CN B allele having a positive effect on casein content in Friesian cattle, but not Simmental or Brown cattle. Another point that he considered was the mistyping of alleles that could occur from the commonly used analytical techniques. This would result in a number of different alleles being identified as the same allele. Such a situation could account for discrepancies across different studies where different populations are considered. H. Geldermann (1995) indicated that the haplotypes of the promoter regions of the genes could be different for different breeds or populations of the same breed and that the effect of the protein variants on milk composition could depend on the haplotypes in these promoter regions. The results from this study where the A² allele of β -CN increased production in the Friesians but decreased it in the Jerseys could be attributed to the above causes. Neither Bovenhuis (1992) or Aleandri (1990) found significant differences in production between A¹A¹ phenotypes and A²A² phenotypes.

Bovenhuis *et al.* (1992) found no significant effect of α_{s1} -CN phenotype on production traits. However, the relationships shown between the protein phenotype and the fat and protein production were similar to those found in the present study with differences between the phenotypes being small for fat production but with BC animals producing higher protein than BB animals. Differences occurred with milk production where Bovenhuis *et al.* (1992) found higher production in BC animals while in the present study, the BB animals had higher production than the BC animals.

The positive association between the B allele of κ -CN with production raises the question as to why the frequency is relatively low (³0.17) in the Friesians. It is possible that there is a deleterious effect associated with the allele. This avenue needs to be further explored.

The results for β -LG parallel those found by Bovenhuis *et al.* (1992) and Aleandri *et al.* (1990) in that the B allele increased fat production and decreased milk

and protein production. While the magnitude of the changes differed across the studies, a function of the different production levels of the cows in these studies, the change in protein production as a fraction of the change in milk production was in close agreement among the studies. The values (as a percentage) were 4.0 in the present study compared to 3.7 (Aleandri *et al.*, 1990) and 3.0 (Bovenhuis *et al.*, 1992). Analogous figures for fat production were 4.7, 2.9 and 2.3, respectively. While these changes were not as in close agreement as for protein production the results still indicate a similar effect of protein phenotype across the studies.

The benefits of including protein phenotype in the breeding objective depends on its value as from a processing perspective and its association with traits of economic importance. While β -LG BB milk was found to have beneficial aspects from a processing perspective, the results in this study indicate that total protein production from BB cows would be lower than that of AA cows, thus partially negating the value of this phenotype. Such issues must be taken into account when determining the net value of the different milk protein phenotypes.

The present work is a first study to examine the associations between milk protein phenotype and production traits in New Zealand dairy cattle. Future work will investigate the relationships between protein phenotype and nonproduction traits such as reproductive performance, somatic cell count and conformation. The measure of protein yield considered in this study did not differentiate between casein and whey proteins. In order to properly assess the value of milk of a specific milk protein genetic variant composition for a given manufactured

product it will be necessary to determine the association of protein phenotype with casein and whey production. Finally, in the case of the casein proteins, it will be necessary to establish whether the effect on production is due to the genetic variants themselves or to linked alleles. Given a situation of linkage, the success of a breeding programme aimed at changing the frequencies will be influenced by the closeness of the linkage.

REFERENCES

- Aleandri, R., Buttazzoni, L.G. and Schneider, J.C. 1990. The effects of milk protein polymorphisms on milk components and cheese-producing ability. *Journal of Dairy Science* **73**:241-255.
- Bovenhuis, H., van Arendonk, J.A.M. and Korver, S. 1992. Associations between milk protein polymorphisms and milk protein traits. *Journal of Dairy Science* **75**:2549-2559.
- Geldermann, H. 1995. Aspects of genetic variants in dairy cattle breeding. In Implications of Genetic Polymorphism of Milk Proteins on Production and Processing of Milk. *International Dairy Federation* **304**: 22-22.
- Groeneveld, E., Kovac, M., and Wang, T. 1990. PEST, a general purpose BLUP package for multivariate prediction and estimation. In *Proceedings of the 4th World Congress on Genetics Applied to Livestock Production*, **13**:488-491.
- Hill, J.P., Paterson, G.R., Lowe, R. and Johnston, K.A. 1995. Effect of (-lactoglobulin variants on curd firming rate, yield, maturation and sensory properties of Cheddar cheese. In Implications of Genetic Polymorphism of Milk Proteins on Production and Processing of Milk. *International Dairy Federation* **304**:18-19.
- Jakob, E. 1995. Effect of genetic polymorphism on milk protein composition. In Implications of Genetic Polymorphism of Milk Proteins on Production and Processing of Milk. *International Dairy Federation* **304**:7-8.
- Ng-Kwai-Hang, K.F. and Grosclaude, F. 1992. Genetic polymorphism of milk proteins. In *Advanced Dairy Chemistry - 1: Proteins* (Ed. Fox P F) Elsevier Science Publishers Ltd, London, pp 405-455.

Assessment of female traits for genetic improvement of fertility in dairy cattle

T. GROSSHANS, Z.Z. XU AND L.J. BURTON

ABSTRACT

The objective of the present study was to investigate the suitability of various fertility traits for describing the reproductive performance of dairy cows in New Zealand. Using a data set from herds participating in the Livestock Improvement Sire Proving Scheme over the 1986/87 to 1992/93 seasons, the following female fertility traits have been investigated. Based on the start of mating (STOM) in a particular herd, the intervals from STOM to first mating (SMFM) and to the successful mating (SMCO) were calculated and compared to the internationally used traits that are based on the calving date, such as, calving to first mating (CFM) and calving to successful mating (days open, DO). Further traits considered are age at calving (AC), number of matings per conception (NS), first to successful mating (FMCO), calving interval (CI) and two traits that indicate whether a cow became pregnant within 21 or 42 days of STOM (PR21, PR42). The traits defined for the unique conditions in New Zealand, SMFM, SMCO, PR21 and PR42 emphasize the economic importance of reproduction to dairy production. The comparison to overseas studies using DO, FMCO and CI showed that New Zealand dairy cows had a better fertility performance than overseas cows.

INTRODUCTION

With the seasonal nature of dairy production in New Zealand, reproductive performance, or fertility, is a

key determinant of production efficiency and genetic gain. However, up till now there has been no deliberate selection for female fertility traits in New Zealand. Overseas results have shown sufficient genetic variation in fertility