

Estimation of test-day model (co)variance components across breeds using New Zealand dairy cattle data

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ABSTRACT

In New Zealand, a large proportion of cows are currently crossbreds, mostly Holstein-Friesians (HF) × Jersey (JE). The genetic evaluation system for milk yields is considering the same additive genetic effects for all breeds. The objective was to model different additive effects according to parental breeds to obtain first estimates of correlations among breed-specific effects and to study the usefulness of this type of random regression test-day model. Estimates of (co)variance components for purebred HF and JE cattle in purebred herds were computed by using a single-breed model. This analysis showed differences between the 2 breeds, with a greater variability in the HF breed. (Co)variance components for purebred HF and JE and crossbred HF × JE cattle were then estimated by using a complete multibreed model in which computations of complete across-breed (co)variances were simplified by correlating only eigenvectors for HF and JE random regressions of the same order as obtained from the single-breed analysis. Parameter estimates differed more strongly than expected between the single-breed and multibreed analyses, especially for JE. This could be due to differences between animals and management in purebred and nonpurebred herds. In addition, the model used only partially accounted for heterosis. The multibreed analysis showed additive genetic differences between the HF and JE breeds, expressed as genetic correlations of additive effects in both breeds, especially in linear and quadratic Legendre polynomials (respectively, 0.807 and 0.604). The differences were small for overall milk production (0.926). Results showed that permanent environmental lactation curves were highly correlated across breeds; however, intraherd lactation curves were also affected by the breed-environment interaction. This result may indicate the existence of breed-specific competition effects that vary through the

different lactation stages. In conclusion, a multibreed model similar to the one presented could optimally use the environmental and genetic parameters and provide breed-dependent additive breeding values. This model could also be a useful tool to evaluate crossbred dairy cattle populations like those in New Zealand. However, a routine evaluation would still require the development of an improved methodology. It would also be computationally very challenging because of the simultaneous presence of a large number of breeds.

Key words: crossbreeding, Holstein-Friesian, Jersey, multibreed model

INTRODUCTION

Crossbreeding is a method used for improving animal production in pigs, beef cattle, and poultry (e.g., Wei and van der Werf, 1995). However, it has not been widely used in dairy cattle in most temperate countries until recently because of the high milk production of the Holstein-Friesian (HF) breed (Touchberry, 1992). Most current purebred HF populations in the world were created by upgrading existing European Friesian or similar populations. Harris and Kolver (2001) gave a more detailed history of the New Zealand HF (NZHF) population that showed the different phases. The original NZHF population was first developed from animals imported from the West Coast of the United States before 1925, and it then remained as a closed population. Most of the cattle before 1960 (approximately 75%) were Jersey (JE). Therefore, until the early 1980s upgrading was first from JE to NZHF by using locally available sires. The descendants of this process remained lighter than overseas HF (OSHF) from North America or Europe. Since the 1980s, OSHF sires have become more popular. However, the daughters of these animals are heavier and seem to be less fertile and have decreased survival rates (Harris and Kolver, 2001). Therefore, most New Zealand dairy farmers have not upgraded to OSHF, and as a result of this experience, there has been even more widespread popularity of crossbreeding. Even though dairy farmers in North America and

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Europe were very reluctant to crossbreed at that time, crossbreeding has been a feature of the history of the dairy industry of New Zealand. Currently, more than one-third of dairy replacements are crossbred, mostly HF×JE. This is because both breeds, the HF and JE, are economically comparable under typical New Zealand production systems (e.g., Lopez-Villalobos and Garrick, 2002), and complementarity characteristics from these breeds and heterosis effects favor crossbreds (e.g., Lopez-Villalobos and Garrick, 2002). Crossbreeding provides a good opportunity to maximize the net income per hectare under New Zealand pastoral conditions by improving fertility and survival, and also by improving (or altering) the composition of milk, which is very important because the dairy company payment structures reward farmers for the amount of milk solids (fat and protein) produced. Therefore, crossbreds benefit from the high volumes achieved in the HF breed as well as from the beneficial fat and protein composition of the JE breed (Montgomerie, 2002). Several studies have demonstrated the economic superiority of crossbred HF×JE cows in New Zealand (e.g., Lopez-Villalobos and Garrick, 1996, 1997; Lopez-Villalobos et al., 2002) and potentially elsewhere (e.g., VanRaden and Sanders, 2001).

Additionally, crossbred bulls are currently being progeny tested by the major New Zealand breeding companies in response to farmer requests. Farmers are willing to accept a reduction in heterosis to have a type of cow that they recognize as being the most profitable for their system, even when heterosis effects are ignored.

From 1996 to the beginning of 2007, New Zealand dairy cattle were genetically evaluated across breeds for yield traits by using a 2-step test-day model, in which test-day production records were combined to predict 270-d yields, and an animal model was used for the genetic evaluation of these predicted yields (Harris, 1994, 1995). A new test-day model has been developed to use the milk production herd-test data to calculate breeding values, and this new system has been implemented since February 2007 (Harris et al., 2006). The evaluated production traits are then included in an economic index called breeding worth, which describes animal profitability per unit of feed (this is a feature of the across-breed evaluation; Johnson, 1996; Garrick et al., 1997). Heterosis is modeled as a fixed effect in the model, correcting for mean differences. Thus, genetic contributions from purebreds to crossbreds are only partly taken into account; therefore, it does not allow an optimal use of crossbred data. Moreover, a study by Wei and van der Werf (1995) showed that an optimal use of crossbred information jointly with purebred information in selection could bring more genetic progress

in crossbreds. To do this, genetic correlation of additive effects in different breeds has to be known. Such results are rare, if not nonexistent, in dairy cattle, whereas in swine or in beef cattle, such results are less unusual (e.g., Lutaaya et al., 2001; Newman et al., 2002; Roso et al., 2005; Zumbach et al., 2007).

The objective of this study was to model different additive effects according to breed composition to estimate correlations among breed-specific effects. The second objective was also to study the usefulness of this type of a more complicated random regression test-day model.

MATERIALS AND METHODS

Data

Data were provided by the Livestock Improvement Corporation, Hamilton, New Zealand, and comprised records on cows from dedicated progeny-testing herds. The original data comprised 223,141 animals in production and a total of 500,134 animals in the pedigree.

Only animals of HF and JE inheritance were kept to estimate (co)variance components; therefore, animals whose summed proportion of HF and JE genes was less than 100% were eliminated. No distinction was made among HF animals with different compositions of OSHF and NZHF genes; they were considered to belong to the same breed. This was also done to limit the study to a 2-breed situation. Data were limited to first-lactation test-day milk yields, which were recorded for 208,164 cows in 3,481 herds with test days, equally spaced across the lactation at 2-mo intervals. After these edits, the breed composition of animals with records in first lactation was approximately 54% HF, 21% JE, and 25% HF×JE, and the distribution of herds per breed composition showed that 65% of herds had HF×JE, HF, and JE or were entirely composed of HF×JE animals; 25% of herds were purebred HF and only 10% were purebred JE. In the context of this article, purebred means at least 95% of HF or JE genes. Crossbreds consequently were animals with a major breed composition of between 50% (included) and 95% (excluded) HF or JE genes.

Data sets were constructed based on a stratification of herds as a function of their average breed proportions. Herds with average breed compositions of 95% and more HF or JE genes were considered purebred herds. Similarly, herds with an average breed composition of between 50% (included) and 95% (excluded) HF or JE genes were considered crossbred herds. Within the purebred herds, only animals whose proportions of HF or JE genes were 95% or more were selected. Because the data set was still too large for analysis, ad-

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