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Variations and correlations of milk production, fertility, longevity, and type traits over time in Australian Holstein cattle

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ABSTRACT

When using historical data, it is often assumed that the genetic correlation of the same trait recorded at different time points is reasonably close to 1. However, selection and possible changes in trait definitions means that this may not necessarily be the case. Regularly monitoring genetic parameters over time is important, as changes could reduce the accuracy of genetic evaluations. About 20 yr (1993 to 2012) of data on milk yield as well as functional and type traits from Australian Holstein dairy cattle were analyzed to assess changes in genetic correlations within and among traits over time by considering 2 traits at a time using linear random regression (RR) and multitrait (MT) models. Both residual and genetic variances for milk yield traits and calving interval (CI) increased over time, with the highest increase observed for protein yield. For most type traits some fluctuations over time were noted in both the residual and additive genetic variances. Genetic correlations among survival (i.e., from first to second lactation), milk yield traits, CI, and some type traits varied over time. The genetic correlation of the same trait (e.g., protein yield, fat yield, and some type traits) measured in different years was also less than 1.0 (0.1–0.9), which is likely to be due to selection or changes in trait definitions. Estimates of parameters from the RR model were generally similar to those from MT models that considered the same trait recorded in different year groups as different traits. However, in the case of survival and CI (i.e., lowly heritable traits), the genetic correlations over time obtained from the MT model were lower (0.21 to 0.75) than those from the RR models (0.9–1.0). Genetic correlations of survival with milk, fat, and protein yields declined from ~0.4 to 0.5 at the beginning of the study period (1993/94) to zero or negative at the end (2009/10), whereas the correlation between CI and milk yield became more

unfavorable and increased from 0.3 to 0.5 over the same time period. The same pattern was observed for the genetic correlation between survival and CI, which also became more unfavorable over time and increased from 0.67 to 0.87 in absolute value. The genetic correlations of survival with type traits, such as angularity and body depth, decreased from near zero to negative (–0.3 to –0.4). But genetic correlations between pin set and survival showed less variation (0.2–0.3) over time. Similarly the genetic correlation of CI with body depth and angularity became more antagonistic over time. Over time the importance of traits such as milk yield and overall type as criteria for culling decreased, whereas the importance of fertility and possible disease incidence increased, implying that there has been a switch from voluntary to involuntary reasons dominating culling decisions. Changes in genetic correlations of the same trait and among traits over time have important implications on the accuracy of prediction of traits, such as survival and CI, which often rely on other traits as predictors and ultimately on the accuracy of genetic evaluations (traditional and genomic), and also the prediction of response to selection.

Key words: genetic correlation, random regression, genetic evaluation, type traits, functional traits

INTRODUCTION

In animal breeding, data collected over many years is often used for both genetic evaluation (traditional and genomic) and genome-wide association studies (GWAS). The main reason for using older data in genetic evaluations is to increase the amount of data used and ultimately the accuracy of EBV, and most models account for selection bias in this process. When using older or historical data, the basic assumption is that the genetic correlation of the same trait recorded at different time points is reasonably close to 1 and also variance component estimates are assumed to be constant over time. However, several factors, including selection, linkage disequilibrium, change in trait definition, and so on, could contribute to changes in variance of traits and correlations between traits.

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The correlation between the same trait over time can change either dramatically or gradually. For example, changes in correlations of survival with itself over time could happen gradually because of changes in culling reasons over time (Tsuruta et al., 2004a). However, change in definition of subjectively scored traits in particular, such as type and workability traits, can be more dramatic and may result in low correlations between data collected over time. This means that when functional traits are predicted from type and workability traits, the prediction equations need to be updated more frequently (Tsuruta et al., 2004a). Traits that have precise measurements, such as milk yield traits are less likely to change over time, but selection pressure on these traits could be high and this may cause changes in genetic variance and correlation among milk yield traits or their correlation with other traits (Tsuruta et al., 2004a). For example, genetic correlations among milk yield traits appear to have changed over the last 20 yr, presumably because of the strong of selection for protein yield (Bowman et al., 1996). Estimates based on data of Australian Holstein-Friesian cows collected before 1992 showed a genetic correlation between fat and milk yield of 0.78 (Visscher and Goddard, 1995), whereas the estimates based on more recent data are close to 0.3 [Kon Konstantinov, Australian Dairy Herd Improvement Scheme (ADHIS) Melbourne, Australia, personal communication]. Similar decreases in genetic correlations between milk and fat yield over time were also observed in the US Holstein data (Tsuruta et al., 2004a).

Knowing the extent of changes over time in genetic variances and covariances among traits could be useful to improve the effectiveness of selection schemes and accuracy of genetic or genomic evaluations. For example, if correlations between a trait measured at different time points are low, then genetic evaluations that consider the same trait recorded in different time periods as 2 different correlated traits may be better than models that ignore this information (Jamrozik and Schaeffer, 1991; De Jong and Harbers, 2002). If the changes that are observed in these traits are gradual, fitting an additive genetic effect with random regression (**RR**) on year of birth or calving to account for variation over time may be better (e.g., Tsuruta et al., 2004b). In fact, knowing the change in genetic covariances over time is very important, as large data sets that include a lot of historical data have been assembled for genomic prediction and GWAS. Knowing how covariances change over time can improve the subdivision of animals into training and validation groups for genomic prediction and GWAS as well as for improving prediction equations for economically important lowly

heritable traits where either the predicted trait or its predictors change over time.

The current study examined estimates of variances and covariances among traits over time using data on milk yield, 2 functional traits (survival and fertility), and some type traits from Australian Holstein cows collected over the last 20 yr. The type traits considered were those correlated with milk yield or functional traits (Pryce et al., 2009; Haile-Mariam et al., 2014). These were 4 linear traits (body depth, angularity, udder depth, and pin set) and 2 composite traits (mammary system and overall type). The 2 composite traits were selected because 2 analyses (Battagin et al., 2012, 2013) that used data from about 20 Interbull-member countries showed that the cluster to which Australian data belonged changed more frequently over the study period (2001–2010), which could be indicative of change in definition of the traits. Furthermore, genomic analyses of Australian data (Haile-Mariam et al., 2015) showed that the reliability of direct genomic value (**DGV**) for validation bulls was particularly lower for mammary system and overall type compared with other traits with similar heritability (h^2). In addition, the definitions of some traits changed in 2007 as part of the breed development program of Holstein Australia. Assessing the extent of the changes in the definitions of the traits and their correlation with other traits can give better insight into changes over time. Therefore the approach that was taken in our study was to carry out a series of bivariate analyses so that changes in one trait can be compared with another trait.

MATERIALS AND METHODS

Data

Two main data sets of first-parity Holstein-Friesian cows were used to estimate genetic parameters, including the relationship among dairy traits over time. The traits analyzed were fertility [calving interval (**CI**)], milk yield (305-d milk, fat, and protein yield), survival from first to second lactation (coded as 1 or 0), and some type traits (overall type, mammary system, body depth, angularity, udder depth, and pin set).

All the data used for our study were extracted from the ADHIS database. A detailed description of the data used for our study is given elsewhere (Haile-Mariam et al., 2014). Briefly, relatively large herds, with at least 1,000 calving records between January 1993 and December 2010, were selected. Only bulls that were part of AI programs and that had at least 5 daughters were included in our study. Additionally, the study was restricted to first-parity cows that calved between 18

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