J. Dairy Sci. 99:2413–2427
http://dx.doi.org/10.3168/jds.2015-9970

Using genomics to enhance selection of novel traits in North American dairy cattle[1,2]

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ABSTRACT

The objectives of this paper were to briefly review progress in the genetic evaluation of novel traits in Canada and the United States, assess methods to predict selection accuracy based on cow reference populations, and illustrate how the use of indicator traits could increase genomic selection accuracy. Traits reviewed are grouped into the following categories: udder health, hoof health, other health traits, feed efficiency and methane emissions, and other novel traits. The status of activities expected to lead to national genetic evaluations is indicated for each group of traits. For traits that are more difficult to measure or expensive to collect, such as individual feed intake or immune response, the development of a cow reference population is the most effective approach. Several deterministic methods can be used to predict the reliability of genomic evaluations based on cow reference population size, trait heritability, and other population parameters. To provide an empirical validation of those methods, predicted accuracies were compared with observed accuracies for several cow reference populations and traits. Reference populations of 2,000 to 20,000 cows were created through random sampling of genotyped Holstein cows in Canada and the United States. The effects of single nucleotide polymorphisms (SNP) were estimated from those cow records, after excluding the dams of validation bulls. Bulls that were first progeny tested in 2013 and 2014 were then used to carry out a validation and estimate the observed accuracy of genomic selection based on those SNP effects. Over the various cow population sizes and traits considered in the study, even the best prediction methods were found, on average, to either under-evaluate observed accuracy by 0.20 or over-evaluate it by 0.22, depending on the approach used to estimate the number of independently segregating chromosome segments. In some instances, differences between observed and predicted accuracies were as large as 0.47. Indicator traits can be very useful for the selection of novel traits. To illustrate this, protein yield, body weight, and mid-infrared data were used as indicator traits for feed efficiency. Using those traits in conjunction with 5,000 cow records for dry matter intake increased the reliability of genomic predictions for young animals from 0.20 to 0.50.

Key words: genetic evaluation, novel trait, prediction accuracy, genomics, selection

INTRODUCTION

For many years, dairy cattle selection has focused primarily on milk production and cow conformation; however, many functional traits have negative correlations with production, which has led to reductions in health and fitness. Several traits were introduced in North American selection objectives over the last 10 to 20 yr to address this issue, notably SCS, herd life or productive life (longevity), and daughter fertility traits. In addition, several traits affect product quality, cost efficiency, and the environmental impact of dairying. These traits are gaining in importance in the industry, and genomics provides new opportunities for their selection. The objectives of this paper were to carry out a brief review of the status of research and genetic evaluation for those novel traits, to assess their expected selection accuracy in industry selection schemes, and to illustrate how the use of indicator traits could increase that accuracy.

Received June 15, 2015.
Accepted November 20, 2015.

[1] The use of trade, firm, or corporation names in this publication is for the information and convenience of the reader. Such use does not constitute an official endorsement or approval by USDA or the Agricultural Research Service of any product or service to the exclusion of others that may be suitable.

[2] Presented as part of the Joint Interbull/JAM Symposium: Use of Genomics to Improve Limited and Novel Phenotypes in Animal Breeding at the ADSA-ASAS Joint Annual Meeting, Orlando, Florida, July 2015.

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BRIEF REVIEW OF NOVEL TRAITS IN NORTH AMERICA

A comprehensive review of novel traits in dairy cattle can be found in Egger-Danner et al. (2015a). That review provides useful information on worldwide research for those traits and on phenotyping strategies that can be used for their selection. An existing trait in one country may be a novel trait in another. Scandinavian countries, in particular, have accumulated data and produced genetic evaluations for many health traits that are novel in other countries. In the current study, the purpose was to provide a brief description of the status of selection for novel traits in North America, including activities expected to lead to national genetic evaluations for those traits within the next 5 yr. Table 1 summarizes current status separately for Canada and the United States, including for each trait of (a) no or very little research, (b) actively researched, (c) preliminary evaluations produced, or (d) national evaluations officially implemented. Traits were categorized as udder health, hoof health, other health traits, feed efficiency and methane emissions, or other novel traits. For actively researched traits, only research projects undertaken with the goal of providing national evaluations over the next 5 yr were described.

Udder Health

Several studies have shown that incorporating mastitis incidence data into breeding value estimation can improve genetic progress for mastitis resistance compared with the use of SCS alone (Heringstad et al., 2007). In Canada, the development of a national health-recording program began in 2007 as collaboration between the Canadian Dairy Network (**CDN**; Guelph, ON, Canada) and Canadian DHI organizations and has led to the collection of large amounts of data on mastitis incidence. Those incidence data, which are recorded by producers or veterinarians, are analyzed in a multitrait model with data on SCS and other indicator traits (namely, mean SCS in early lactation, standard deviation of SCS, excessive test-day SCC, fore udder attachment, udder depth, and BCS) to produce traditional as well as genomic evaluations for mastitis resistance (Koeck et al., 2012a,c; Jamrozik et al., 2013; Miglior et al., 2014). Genomic breeding values for mastitis resistance have been published officially in Canada since August 2014 and have become part of national selection indices (Pro$, a new profit-based index expressed in dollar terms, and LPI, the current lifetime performance index; Beavers and Van Doormaal, 2015) since August 2015.

Table 1. Novel traits with ongoing research or official evaluations in the United States and Canada (AR = actively researched; PE = preliminary evaluations produced; OE = official evaluations nationally implemented)

Trait	United States	Canada
Udder health		
Mastitis incidence (recorded by producer or veterinarian)	AR	OE
Alternative definitions of SCS	—	OE
New predictors of mastitis incidence [conductivity, mid-infrared (MIR)]	—	AR
Hoof health (hoof trimming, locomotion, lameness)	AR	PE
Other health traits		
Reproductive disorders [incidence of retained placenta, metritis, cystic ovaries, predictors (e.g., activity monitor data, hormones)]	AR	AR
Metabolic diseases [incidence of ketosis, displaced abomasum, predictors (e.g., BHB, fat:protein ratio)]	AR	PE
Resistance to Johne's disease (*Mycobacterium avium* ssp. *paratuberculosis*)	AR	AR
Immune response (antibody, cell-mediated)	—	E[1]
Feed efficiency and methane emissions		
Individual feed intake [e.g., DMI, residual feed intake, energy balance, predictors (production, direct or indirect cow weight, MIR)]	AR	AR
Emission of methane (calorimeter, other methods) and predictors (e.g., MIR)	AR	AR
Other novel traits		
Workability		
Milking speed (measured or subjective)	—	OE
Milking temperament (subjective)	—	OE
Profitability		
Number of embryos produced (for embryo transfer)	—	AR
Profit per cow to 6 yr of age	—	OE[2]
Milk composition (fatty acids, lactoferrin) and predictors (e.g., MIR)	—	AR

[1] Evaluations within one AI organization.

[2] Used for derivation of a national selection index.