



Genomic evaluation of a relatively small dairy cattle population by combination with a larger population

J. I. Weller,^{*1} W. M. Stoop,[†] H. Eding,[†] C. Schrooten,[†] and E. Ezra[‡]

^{*}Institute of Animal Sciences, Agricultural Research Organization, The Volcani Center, Bet Dagan 50250, Israel

[†]CRV BV, 6800 AL Arnhem, the Netherlands

[‡]Israel Cattle Breeders Association, Caesaria Industrial Park 38900, Israel

ABSTRACT

The objectives were to investigate the accuracy of genomic evaluations obtained for a small dairy cattle population (Israeli Holsteins) via joint evaluation with a larger population (Dutch Holsteins), and to evaluate the use of pedigree data from foreign bulls computed by Interbull without daughter records in Israel. The training population included 4,010 Dutch bulls and 713 Israeli bulls. The validation population included 185 Israeli bulls with daughter records for milk production traits and slightly fewer bulls for the nonproduction traits. Milk, fat, and protein yields, somatic cell score, longevity, female fertility, direct and maternal calving ease, direct and maternal stillbirth, and the Israeli breeding index were analyzed. The genomic prediction model was based on the Bayesian multi-QTL model of Meuwissen and Goddard, where the effects of dense single nucleotide polymorphisms across the whole genome are fitted directly, without the use of haplotypes or identical-by-descent probabilities. Correlations of May 2014 estimated breeding values (EBV₁₄) with genomic EBV (GEBV) were higher than the correlations of EBV₁₄ with parent averages (PA) computed from the June 2009 evaluation for all traits. For the Israel selection index, the difference between EBV₁₄ and GEBV correlation on the one hand and EBV₁₄ and PA computed using Interbull data on the other hand was 15 percentage points. For protein, the difference between the corresponding correlations was 14 percentage points. Generally, correlations of EBV₁₄ with PA based on Israeli EBV only were similar to correlations of EBV₁₄ with PA including Interbull evaluations. Relative to EBV₁₄, milk production traits were biased upwards for both GEBV and PA, but the bias was greater for PA. The Y-intercepts of regressions of EBV₁₄ were significantly different from zero for regression on GEBV for all 3 milk production traits and the Israeli selection

index. This was not the case for regression of EBV₁₄ on PA. The regression line intersected with the line of unbiased estimation near the EBV of the bulls with highest values. Because only bulls with high evaluations are of interest for selection, GEBV for these bulls were less biased compared with that of bulls with lower evaluations. The difference in mean EBV₁₄ between bulls born during 2007–2008 selected by GEBV and PA was 65 units. If half of all inseminations are by young bulls, then the annual genetic gain obtained by implementation of genomic evaluation will be 8 units per year (65/8). Because annual gain is currently 107 units, this is a gain of 7%.

Key words: dairy cattle, genomic evaluation, Israeli Holsteins

INTRODUCTION

In the Netherlands, genomic selection based on a reference population of ~1,500 progeny-tested bulls genotyped with a custom 60K bead chip was first applied in 2007 (de Roos et al., 2009). Genomic selection of US Holsteins was introduced in 2008 with evaluation of 5,285 proven bulls (VanRaden, 2008). Generally, accuracy of genomic estimated breeding values (**GEBV**) is determined by dividing the population of genotyped individuals into a training population of older animals, and a validation population of younger animals (e.g., VanRaden et al., 2009). The individuals of both the training and validation populations are usually bulls with daughter yield deviations or EBV based on daughter records. Effects of the individual markers are determined in the training population based on the bulls' EBV or daughter yield deviations, and these effects are then used to derive GEBV for the validation population using only genomic and pedigree information. The GEBV for the validation population are then compared with EBV of these bulls based on daughter records.

The accuracy of GEBV is strongly dependent on the number of genotyped animals (VanRaden et al., 2009; Calus, 2010). With ~10,000 bulls in the training population, accuracies of the GEBV of young bulls without daughter records approach those of EBV obtained with

Received November 9, 2014.

Accepted March 8, 2015.

¹Corresponding author: joel.weller@mail.huji.ac.il

progeny tests with ~50 daughters per sire, (Lund et al., 2011; Wiggans et al., 2011), whereas accuracies of GEBV for young bulls derived from reference populations of ~1,000 genotyped bulls are generally no higher than traditional BLUP based only on pedigree information (Thomasen et al., 2012; Van Grevenhof et al., 2012). Jiménez-Montero et al. (2012) suggested that more accurate GEBV could be obtained with training populations consisting chiefly of genotyped cows with EBV computed based on their own records. The potential number of genotyped cows with records is much larger than the number of bulls with progeny tests. However, cow EBV based on their own records have much lower accuracy than bull EBV based on the production records of 50 to 100 daughters.

Various methods have been used to derive GEBV for the Israeli Holstein population, including “single stage” methodologies, in which marker effects are derived from the actual cow records rather than EBV (Lourenco et al., 2014), and derivation of GEBV based on all valid markers and selected subsets of markers (Weller et al., 2014), but none of these methods were able to derive GEBV for validation bulls with accuracies significantly greater than those obtained based only on pedigree data.

Because increasing the size of the training population significantly increases accuracy of GEBV for young bulls at least up to ~10,000 bulls, even organizations with relatively large dairy cattle populations have formed consortiums to pool data from different countries. Canada and the United States have shared genotypes for all dairy cattle breeds since 2007 (Wiggans et al., 2009) and have recently shared Holstein genotypes with the United Kingdom and Italy (VanRaden et al., 2012). EuroGenomics was founded in 2009 with 4 Holstein populations of at least 4,000 bulls each from ALLICE (France), VikingGenetics (Denmark, Sweden, Finland), DHV-VIT (Germany), and CRV (the Netherlands, Flanders) (Lund et al., 2011). Since 2011, CONAFE (the Spanish Confederation of Holstein Associations) and Genomika Polska, which represents the Polish Federation of Cattle Breeders, have joined EuroGenomics (<https://global.crv4all.com/aboutus/news/latestnews/288797/>).

Very little has been published with respect to the question of how differing climatic and management conditions among populations may affect the accuracy of GEBV computed with data pooled across populations. This problem is likely to be more severe if the populations differ greatly in size and climatic conditions or if relationships among populations are limited. The effects derived for specific markers will most likely reflect the conditions of the larger population and may not be effective for the much smaller population. For

example, although the polymorphism for *ABCG2* is present in many different populations, allelic frequencies across populations differ dramatically (Ron et al., 2006). Similarly, Glick et al. (2012) and Weller et al. (2014) demonstrated that the markers with the greatest effects on traits of interest change over time, due to changes in allelic frequencies.

Although both Israel and the Netherlands have advanced commercial dairy industries based chiefly on Holsteins, the populations differ significantly in their size, environmental conditions, and selection objectives. In Israel, average rainfall, excluding the Negev Desert, is ~550 mm, and there is virtually no rainfall in the summer. Winters are mild, summers are hot, and a large fraction of cattle feed is imported concentrates. Mean temperatures in the Netherlands are ~10°C, mean rainfall is ~720 mm, and is spread over the entire year. The typical Dutch dairy cattle ration includes a higher fraction of roughage than is common in Israel. Cheese and butter consumption per capita are higher in the Netherlands compared with Israel, where a larger fraction of milk produced is directed to liquid consumption. Most Israeli cows are in large, communal herds (average size of 300 cows) and are milked 3 times dairy, whereas most Dutch cows are in smaller family farms. Mean annual production is higher in Israel, but fat and protein concentrations are higher in the Netherlands. According to the most recent Interbull analysis (Interbull, 2014), the genetic correlation between Israel and the Netherlands for protein production of Holsteins is 0.77, which is among the lowest correlation for the Netherlands with other countries included in the analysis. With respect to Israel, this correlation is also lower than the correlation of Israel with most other countries. Both countries have imported significant quantities of semen from other countries, chiefly the United States.

In 2013, the 2 countries signed an agreement to compute joint GEBV in the Netherlands on the Israeli scale. Because the Israeli population is much smaller than the Dutch population, it is of major interest to determine the accuracy of GEBV for validation bulls of the Israeli population compared with EBV for these bulls computed from pedigree data. In addition to the accuracy of the evaluations, bias was also evaluated. The second objective was to evaluate the use of pedigree data and EBV from foreign bulls without daughter records in Israel, computed by Interbull.

MATERIALS AND METHODS

Animals Genotyped

A total of 1,488 Israeli Holstein bulls were genotyped: 912 bulls for the 54,001 SNP BeadChip (Illumina Inc.,

Download English Version:

<https://daneshyari.com/en/article/10975333>

Download Persian Version:

<https://daneshyari.com/article/10975333>

[Daneshyari.com](https://daneshyari.com)