

## Accurate genomic evaluation of small dairy cattle populations

Nearly all traits of economic interest, such as milk production of dairy cows, are "quantitative." These traits are determined by a large number of genes and are also affected by environmental factors. Until 2010, breeding of dairy cattle was based on the "progeny test scheme." Although bulls do not produce milk, most genetic improvement was based on sire selection; because female fertility is very limited, while male fertility via artificial insemination is nearly unlimited. Elite dairy bulls can have thousands of daughters. The genetic value of bulls was determined by producing 50 to 100 daughters for each candidate bull. Most bulls were culled after their first crop of daughters, while 90% of all cows were mated to elite bulls. The main defect in this scheme is that while bulls reach sexual maturity at one year, results from the progeny test only become available when the bulls is five years old.

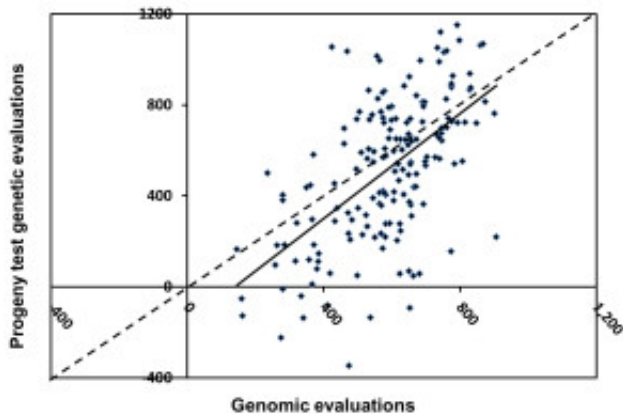


Fig. 1. Regression of progeny test genetic evaluations on genomic evaluations of 174 validation bulls for the Israeli selection index, PD11. Solid line is the regression, dotted line is the line of unbiased estimation of the progeny test genetic evaluations on the genomic evaluations.

Single nucleotide polymorphisms (SNP) are among the most common types of variability found in the genomes of higher organisms. In a typical SNP, A is replaced with T, or C with G at a specific position on a chromosome. With high density "SNP chips" an individual's genotype for tens of thousands of SNPs that cover the entire length of DNA can be determined for less than \$100. Although the vast majority of SNPs do not affect any specific trait, large chromosomal segments pass from parents to progeny. Therefore a specific SNP in close proximity to a gene affecting a trait of interest will generally be inherited together. By genotyping many animals for SNP chips the genetic value of an individual can be determined, merely from a sample of his DNA, which could be taken at any age.

Determination of a bulls' genetic value from their SNPs' genotype is hardly an exact science. The overwhelming majority of SNPs only add "noise" in the evaluations. To overcome this problem, it is necessary to genotype thousands of bulls in order to obtain accurate estimates of the effects of each individual SNP. These numbers of bulls are available only in the largest dairy cattle populations, such as the US Holstein populations. In smaller populations, the accuracy of genomic evaluations based on the genotypes of local bulls is no higher than a genetic evaluation computed as the mean of the bull's parents genetic evaluations.

We tested the hypothesis that higher accuracy genomic evaluations could be obtained for a relatively small population, the Israeli Holsteins, by combination of the data with a much larger population, the Dutch Holsteins. The joint population of bulls was divided into a "training" population, including 4,010 Dutch bulls and 713 older Israeli bulls; and a "validation" population of 185 younger Israeli bulls with daughter records for milk production traits. Effects of 40,947 valid SNPs were determined on the training populations, and these effects were then used to determine the genomic evaluations of the validation bulls.

Correlations of the evaluations of the validation bulls based on progeny tests with genomic evaluations were higher than the correlations of progeny tests evaluations with parent averages for 9 economic traits. Milk production evaluations were biased upwards for both genomic evaluations and parent averages, but bias was greater for parent averages. Regression of progeny test genetic evaluations on the genomic evaluations for the validation bulls for the Israeli selection index, PD11, is shown in Figure 1. If half of all inseminations are by young bulls with genomic evaluations, then the rate of annual genetic gain would be increased by 7%.

## **Publication**

[Genomic evaluation of a relatively small dairy cattle population by combination with a larger population.](#)

Weller JI, Stoop WM, Eding H, Schrooten C, Ezra E.

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