

Improving Selection Tools for Economically Important Traits in Dairy Cattle

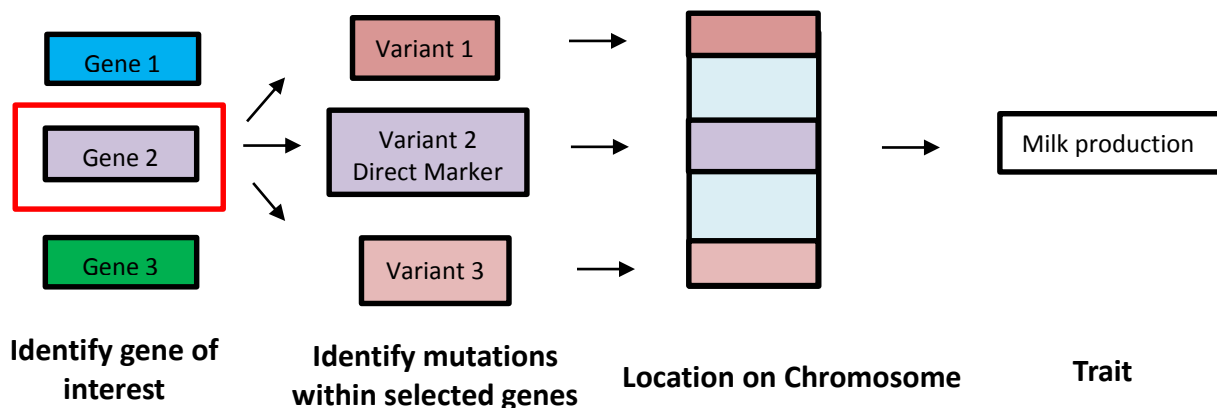
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Why is this important?

Milk production and fertility are two important traits that affect overall efficiency and profitability in the dairy cattle industry. Accurate genomic selection increases the likelihood of gaining a desirable improvement in these traits (i.e. increased milk production). Accuracy can be further increased by identifying markers in DNA that are associated with the trait.

Selection for production traits was first based on phenotype (physical characteristics) of the animal such as breeding cows with the highest milk yield. Today, selection is based on markers within DNA. With the application of DNA markers we identify genes (or DNA sequence) at a known location on the chromosome that is passed down to offspring and can contribute to the phenotype of the desired trait. These DNA markers are also called variants in a genome. The most common variations in the genome are SNPs, where only a single nucleotide is different. The other variations occur due to mutations resulting in larger sequence differences.

SNP: single nucleotide polymorphism



Genotyping is required to determine which genetic variants, or markers, are present in an individual. This can be done through a variety of methods.

Currently, most of the variants that are identified as markers are not directly associated with the desired traits. If we can identify variants that do directly influence traits (that are called causal mutations) it is expected to increase selection accuracy, especially across breeds. Identifying these causal mutations may also increase the understanding of the desired traits, which will further increase the accuracy of genomic predictions (the likelihood that the trait is passed down reliably to offspring).

In our study we combined different sources of information to identify genetic variants that may directly affect important traits in dairy cattle. We then evaluated the performance of these new markers through various tests.

What did we do?

Eighteen production and fertility traits including lifetime profitability, milk production, fat production, protein production, open days, non-return rate and age at first service were considered in Holstein dairy cattle.

Genotypes were obtained for 16,054 bulls and a GWAS was performed to identify markers associated with one or more of the desired traits. These associations indicate that variations in genes located near the marker are affecting the traits. Next, various software tools and databases were used to predict which of the nearby genes and variants (mainly in the form of SNP markers) within those genes is most likely affecting the traits. Finally, a custom genotyping panel consisting of around 135,000 markers was designed so that the variants we selected could be evaluated as a new source of information for predicting breeding values.

GWAS: genome-wide association analysis – scans markers across the whole genome to determine associations to important traits. Associations are used to increase prediction accuracy

What did we find?

Breeding values were calculated using GBLUP, the genomic evaluation method in current use in Canada. We found that adding the new variants (custom panel) to the DNA markers slightly increased the accuracy of breeding values for eighteen production and fertility traits. The increase was small in most cases, 0.48% on average across all traits. However, it was larger for some traits such as fat deviation, protein deviation and age at first service.

GBLUP: genomic best linear unbiased prediction – estimator of genomic breeding values

Genetic evaluations for these traits were provided by the Canadian Dairy Network (CDN).

What does it mean?

Through the use of sequencing and genotyping technologies we were able to discover millions of previously unknown genetic variants, some of which are linked with important traits in Holstein dairy cattle. The increase in accuracy of genomic breeding values we obtained for traits such as protein deviation or age at first service suggests that we were able to identify some genes and variants that directly affect or that are more strongly related with these traits.

Therefore, this work will serve as a base for future efforts aimed at developing more effective genotyping panels, and thus could help enhance the efficiency and accuracy of genomic selection in dairy cattle in the future.

Summary Points

- Genomic prediction was done to identify markers that directly affect important traits
- Several genes and many new variants with a strong association with milk production and fertility identified
- The increased accuracy was highest for fat deviation, protein deviation and age at first service
- This approach and the new variants found may be useful in future genotyping tools used in the dairy industry

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