

# Designing a reference population to accelerate genetic gains for novel traits in Canadian Holstein

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## Abstract

Genomic selection has played a major role in Canadian dairy cattle breeding programs and has substantially increased the industry competitiveness worldwide. The development of the national health-recording program and various ongoing research projects funded by Canadian and international organizations have led to the collection of a large number of phenotypes for novel traits. In order to remain a world leader in the competitive international market, it is key to include those traits in future breeding programs. Some novel traits (e.g. mastitis and metabolic diseases) have been recently included in the national genetic evaluation, while other traits such as digital dermatitis, feed efficiency, immune response, methane emission, and fertility disorders are expected to be included in the near future. The size of the reference population (phenotyped and genotyped for the trait of interest) for these traits has a major impact on the accuracies of genomic estimated breeding values (GEBVs), and is presently the greatest limitation. We estimate that our current potential female reference population amounts to 20,000 cows for health traits, with an increase of approximately 4,000 cows per year. The number of genotyped cows with hoof health records is much smaller (below 5,000 cows). Therefore, the main goal of this project is to maximize the rate of genetic progress for novel traits by enlarging the size of the female reference population for a variety of novel traits. The most cost effective strategy is to select cows that already have phenotypic records for the novel traits (as well as the traditional traits), have not been under intense selection pressure, and are from herds which do not have any genotyped animals or are already partially genotyped. Thus, in addition to increasing the size of the reference population, it is key to design it in an efficient way by genotyping unselected cows and individuals from herds that do not routinely genotype their animals but do collect phenotypes for traits of interest. A new genotyping strategy will be developed to maximize the imputation accuracy from low to medium density SNP panels, by integrating the right balance of low density and medium density genotyping within a given herd. The newly genotyped cows, in addition to the current reference population based on proven bulls, will allow more accurate estimation of genomic evaluations. A single step genomic evaluation is the proper methodology for those novel traits with limited recorded populations. By improving the accuracy of GEBVs, the rates of genetic progress will be accelerated, thereby reducing the economic concerns and bringing more health, production efficiency, and welfare into Canadian dairy herds.

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