Maximizing rates of genetic progress in Canadian dairy cattle by using alternate genomic methodologies

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Over the past decades, the Canadian dairy cattle industry has focused efforts on generating large amount of genotypic, phenotypic and pedigree data aiming to increase the rates of genetic gain for various economically important traits. Besides large amount of data, advancements in genomic evaluation methodologies are of similar importance and play a large role on the success of breeding programs. Considering this, two strategic projects were funded by the Dairy Cluster 2 Program: 1. "Development and testing of new methods for genomic evaluation in dairy cattle" and 2. "Canada's ten thousand cows' genome project". Alternatives to increase reliabilities of genomic estimated breeding values for functional traits, e.g., health, fertility and reproduction, which have lower reliability compared to production traits, were investigated. Different genomic prediction strategies were evaluated, such as the use of genotyped cows, alternative genomic evaluation models based on groups of genetic markers (haplotypes), and adoption of different methodologies, such as the simultaneous use of genotyped and non-genotyped animals, known as the single-step genomic BLUP (ssGBLUP), allowing for the incorporation of external MACE proofs. Furthermore, genome-wide association studies and functional analyses were performed for various fertility disorders and important candidate genes and metabolic pathways were unraveled. For traits expressed over time, such as milk, fat and protein yields, cows with a better shaped production curve (e.g., higher lactation persistence) bring economic, welfare and health benefits to the dairy industry. Therefore, it was also investigated whether the simultaneous incorporation of phenotypic, genotypic and pedigree information could be used to efficiently predict genomic lactation curves of young animals and perform more informed selection decisions. As part of this study, candidate genes affecting different stages of lactation were also identified.

Implications: These research projects provided valuable information on strategies to more accurately predict GEBV for functional and longitudinal traits in dairy cattle by adopting ssGBLUP and different sources of domestic and foreign information, which can largely contribute to enhance accuracy of selection decisions in the Canadian dairy cattle breeding programs.