



Improving the history of health and fertility traits in dairy cows

Duration: 2016-2018

Highlights

- Dairy cattle productivity is influenced by the ways in which the animals are managed and their genetic potential. Through genetic improvement (traditional and genomic), we aim to improve performance by selecting the highest-performing versions of the genes. The traditional approach is to mate the highest-producing animals without taking DNA into account, while genomics aims to select the DNA sequences that are associated with animals exhibiting the highest productivity levels.
- The general model involves having two copies of the best version of the gene, representing the best genetic combination. However, it has been found that certain traits react better to the cross-breeding of different species, most notably traits associated with health and fertility. This means that, for certain traits, the best combination is to have two different versions.
- Dairy production in Quebec and Canada is not based on the cross-breeding of species to promote genetic heterogeneity. Furthermore, it is contraindicated to aim for genome-wide diversification (all of the DNA that is found in each cell) because this would counter the genetic gains made in the last 40 years.
- The project aimed to develop a genomic analysis tool that would leverage the genetic variability present in the Holstein breed to diversify specific regions of the genome that are known to be involved in health and fertility traits.

Objectives

Our hypothesis is that the diversification of specific regions of the genome will help improve health and fertility traits.

The objectives are to develop a genomic analysis tool that will allow us to generate a genetic diversity score, which we can then apply in the assessment of an animal's genetic heritage or to estimate diversification potential through mating. To do so, we must:

- 1) Identify the regions known to influence the health and fertility of dairy cattle;
- 2) Choose targets;
- 3) Develop a genome analysis tool;
- 4) Program the interface to make it easy to use;
- 5) Test the tool with genomic data.

Results and potential benefits

Canada has an excellent reputation in regards to the genetic quality of its dairy herds. The driving force of this efficiency in genetic improvement is the result of the amount and precision of performance data collected on farms. Since 2009, genomic selection has complemented traditional genetics. The current model focuses on concentrating the good versions of genes, which decreases genetic diversity. A decrease in the number of bulls also greatly affects the breeds and has led to an uptick in inbreeding rates. It is known that it is more difficult to improve health and fertility traits. This is possibly because these traits are greatly influenced by the environment, in addition to involving a large number of genes that, individually, have very little influence. All dairy genetic selection has turned to genomics and, currently, rising above the rest is difficult because everyone is focusing on the same genetic combination. We believe that we can make a difference in the improvement of health and fertility traits by attempting to diversify regions of the genome that are known to be involved in these traits. By leveraging the species' existing genetic diversity, we will avoid the unfavourable case of interbreeding animals of different species. Given equal genetic values, an animal with a higher genetic diversity score will be better suited for production. Based on sperm samples, the team genotyped 200 bulls and identified over 900 zones of interest in their genome. They then tested an additional lot of 1,000 dairy cows to validate the regions of the genome related to health and fertility. Their work has demonstrated that it is possible to increase the diversity of genes related to these traits without neglecting other traits such as milk production. The next step is to make the process more robust by applying it to a larger number of genotyped animals. Ultimately, farmers will be able to use a tool to select bulls in an effort to improve their health and fertility traits through increased genetic diversity.



Innovative aspects

- Non-traditional genetics approach that consists of using the genetic variability present in the Holstein breed to diversify certain regions of the genome responsible for health and fertility characteristics.
- Prototype of customized tool for selecting bulls in order to optimize the health and fertility characteristics of a given cow.

Professional trained

One Master's student was trained under this project, namely **Alexandra Carrier**.

For further information

The project's target audience is mainly those who work in the field of genetic selection as well as dairy farmers. The results will be presented at the CRAAQ's Dairy Cattle Symposium (Symposium des bovins laitiers) and Novalait's Forum Techno; additionally, an article has been written for the journal *Le producteur de lait québécois*. A follow-up study is being prepared to validate the project results using a larger sample size.

- Revue *Le producteur de lait québécois*, Décembre 2018, Un outil de sélection personnalisé. Pages 26-27.

Financial contributions

Partnership for innovation in dairy production and dairy processing (EPI 2015-2019):

- Fonds de recherche du Québec – Nature et technologies
- Consortium de recherche et innovation en bioprocédés industriels au Québec
- Novalait

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