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RESEARCH FACTS

RESEARCH & TECHNOLOGY DEVELOPMENT FOR THE CANADIAN BEEF INDUSTRY

Beef Science Cluster



Developing a Better DNA Test for Tenderness

Project Title:

Genomic testing for tenderness in Canadian beef

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Background:

Beef tenderness is a common quality concern among consumers. Tenderness is influenced by many contributing factors, including a significant genetic component. Because tenderness cannot be measured in live cattle, it is difficult to select breeding stock with optimal tenderness, or to cull those with poor tenderness. Progeny testing for tenderness is difficult, costly and slow.

New DNA tests may help to overcome these challenges, if cost-effective DNA tests can be developed for beef tenderness. This would allow Canadian breeders to improve the genetic profile for tenderness in their herds, and perpetuate those genetics through the commercial cow-calf, feedlot, packing and retail sectors. In addition to improving overall consumer satisfaction with Canadian beef, this could create further opportunity for premium branded beef products with guaranteed beef tenderness.

Objective:

Develop and validate a DNA test that explains a significant proportion of the genetic variation in beef tenderness in Canadian beef cattle.

What They Did:

1. Whole Genome Scan: This step used DNA from cattle from Ontario, Alberta, Australia and U.S. research herds that also had ribeye tenderness measurements. Panels (known as SNP chips) that contained up to 650,000 individual DNA tests were used to identify DNA markers that appeared to influence tenderness.
2. Discovery Genotyping: The best 6,000 markers from step 1 were then combined into a smaller panel that was tested on 1032 animals from the University of Guelph population, including influential purebred sires.
3. Imputation: The 6,000 markers from step 2 were tested on 960 crossbred cattle with ribeye tenderness measurements. A

statistical test known as “imputation” was used to predict the DNA scores at the other 600,000 plus DNA sites.

4. Genomic prediction: Actual and imputed genotypes were determined in 860 more cattle with ribeye tenderness measurements. A statistical technique known as genomic prediction was used to convert the 600,000 plus DNA scores into an overall genetic value for each animal. DNA samples were then collected from 100 commercial cattle, their genomic predictions were calculated, and compared to their ribeye tenderness measurements.

What They Learned:

The whole genome scan confirmed that ribeye tenderness (like most other traits), is influenced by many genes that each have relatively small effects. The 6,000 markers that seemed to be the most important were dominated by 16 markers that were highly associated with ribeye tenderness. Based on the DNA scores at these 6,000 markers, the other 600,000 plus DNA scores could be predicted with 95% accuracy. Using all of the available DNA information to produce a genomic prediction explained about 36% of the genetic variation in tenderness. Overall, genetic factors accounted for approximately 22% of actual tenderness; environmental and management factors accounted for the other 78%. When all this was considered, the genomic prediction explained (36% x 22%) 8% of the variation in ribeye tenderness.

What it Means:

Further validation work is required to confirm these results. Successful validation in unrelated cattle would provide Canadian seedstock producers with a new, Canadian-made tool to improve beef tenderness more quickly and cost-effectively than ever before.

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