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RESEARCH FACTS

RESEARCH & TECHNOLOGY DEVELOPMENT FOR THE CANADIAN BEEF INDUSTRY

Beef Science Cluster



Finding DNA markers for feed efficiency

Project Title:

Whole Genome Scan for Feed Efficiency

Researchers:

Project
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Background:

The largest cost of raising beef cattle is due to feed. Feed efficiency is heritable, meaning that feed efficient parents produce feed efficient offspring. However, feed efficiency has rarely been the subject of breeding efforts because of the time, expense, labor, pen space and specialized feeding equipment required to measure feed intake on individual animals. Individual feed intake is usually only measured in research situations or specialized bull test stations.

An animal's genetic potential is programmed in its DNA. Ongoing improvements in genomic tools are steadily increasing the number of DNA tests that can be done, while reducing testing costs. It is now possible to test animals at 50,000 different DNA markers at the same time. If several (or many) of these DNA markers on the "50K SNP chip" are strongly associated with feed intake, it may be possible to start pre-selecting animals based on an inexpensive DNA test instead of a requiring feed intake tests on every potential breeding animal.

Objective:

The objective of this study is to improve the reliability of DNA tests for feed efficiency.

What They Did:

These researchers used the 50K SNP chip to identify DNA markers associated with feed efficiency. They first did a DNA test on 2,000 animals from 3 different herds with different breed compositions. The main breeds represented included Angus, Chablais, Simmental, Hereford, Piedmontese, Gelbveih, Beef Booster, Galloway, as well as some cattle with dairy influence, primarily Holstein and Brown Swiss. All animals used had previously been tested for feed efficiency using Residual Feed Intake (RFI) to confirm which DNA markers were most strongly associated with feed efficiency. Once the most

informative markers were identified, researchers examined the surrounding DNA more closely to increase the chance of finding actual genes affecting feed efficiency. The DNA markers were then tested in a different population of cattle to determine how accurate they were at predicting feed efficiency.

What They Found:

In the 3 research herds measured, researchers found that there were 6767 markers that correlated to feed efficiency, but those markers were not the same in every herd. Only 2 of these markers were found to be significant in all 3 herds and 145 (2%) were found to work in more than one herd. Because of the low number of markers that worked across all herds when researchers went to test them in a different population, they were very inaccurate.

What it Means:

The low accuracy of prediction means that breed and individual cattle population play a major role in the ability to develop genetic predictions for feed efficiency. This means that at the moment, with current technologies, it will be difficult to develop robust across breed predictions. That being said, these results do suggest that developing genomic tests for feed efficiency within a breed is very feasible. This work does also add to the growing number of cattle analyzed for these traits which may lead to development of a DNA test that can be used across breeds in the future.

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