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BEEF CATTLE RESEARCH COUNCIL

RESEARCH FACTS

RESEARCH & TECHNOLOGY DEVELOPMENT FOR THE CANADIAN BEEF INDUSTRY

IN PROGRESS

Identifying causal mutations associated with bull and cow fertility and how they link to feed efficiency

Project Title:

Identification of causal mutations located in distortion regions in beef cattle genome associated with bull and cow fertility and its links to feed efficiency

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Project Code:

FDE.13.17

Completed:

*In Progress.
Results
expected in
March 2021.*

Background:

Cattle have two copies of each gene, with one coming from each parent. In theory, each parent is equally likely to pass either one of its copies to each one of its offspring, but sometimes one form of the gene is more likely to show up in the offspring than the other form, especially when one form of the gene is associated with embryonic death. This is called transmission ratio distortion (TRD). An earlier study looked for regions of the genome that are affected by TRD, for single nucleotide polymorphisms (SNPs) in those regions. This study will examine whether these SNPs are associated with fertility and feed efficiency in beef cattle.

Objectives:

Develop a new methodology/software to identify TRD regions using haplotypes approach and validate the results across 9 beef breeds. Researchers will also identify causal mutations associated with fertility and feed efficiency of the most promising genes found from commercial herds and correlate between feed efficiency traits and fertility traits in young bulls.

What They Will Do:

This team will analyze genotypes from Angus (225,984), Beefbooster (997), Charolais (863), Gelbvieh (927), Hereford (1,077), Limousin (717), Simmental (827), and composite cattle from Alberta (747) and Ontario (1596) as well as additional cow genotypes (600) from the University of Guelph. Data includes age at first service, first service to conception interval, calving to first service interval, days open, non-return rate, calving ease, sire conception rate, and semen quality traits. Researchers will key regulator genes and causative mutations related to fertility and its correlation with feed efficiency.

They will also look for groups of linked SNPs (haplotypes), and compare the 75 best and 75 worst phenotypes out of a population of commercial cattle to determine whether the SNPs and haplotypes are in a gene with a function. Functional genes will be mapped to chromosomes.

Implications:

This project will identify genes associated with reproductive failure to ensure that efforts to genetically improve feed efficiency do not cause severely negative unintended economic consequences by impairing fertility in Canadian beef cattle.

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