RESEARCH FACTS

UNIVERSITY OF SASKATCHEWAN
Livestock and Forage Centre of Excellence
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IN PROGRESS

The forage-efficient beef cow: investigating the underlying physiology

PROJECT TITLE

The forage-efficient beef cow: an investigation into the underlying physiology

In progress:

Results expected in August 2022

RESEARCHERS

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Background:

The overarching benefit of ruminants is the ability to use forage as the predominant source of nutrients. Efficient use of forage is therefore important from nutrition and cost of production perspectives. While feed-use efficiency has often been reported as gain:feed, this quantification is not a suitable measure of efficiency for extensively managed cows since they are no longer in an active growth phase. We propose a new definition of cow efficiency. In our definition, forage efficiency relates to the ability of cattle to perform (maintain or gain body condition score during the winter grazing season, calve early in the calving season, rebreed early in the breeding season and wean a healthy calf) on a forage-based diet under extensive conditions with minimal supplemental feed. This may or may not be related to dry matter intake (DMI) or other conventional definitions of feed efficiency and could be an early way to assess potential lifetime productivity.

Objectives:

- Assess phenotypic factors inlucing characterization of cows efficient at converting forage for maintenance and productive functions. This classification will be assessed through body weight and back and rump fat thickness change during the winter-feeding period. Conception in the following breeding season is a mandatory component to be ranked as efficient.
- Identify whether the microbiome differs between forage-efficient and inefficient cows.

- Evaluate underlying physiological causes determining forage efficient cattle. We hypothesize that forage-use efficiency is related to digestive characteristics (rumen volume and retention).
- The phenotypic data outlining differences between low- and high-efficient forage utilizers will be used to identify genomic markers and candidate genes to differentiate cows genetically.

What They Will Do:

Characterizing the forage-efficient phenotype

- In Year 1, heifers will be managed under extensive grazing conditions using stockpiled perennial forages and straw/chaff-based systems. At the start of the study, heifer body weight, rib and rump fat, frame measurements will be assessed. In addition, a blood sample will be collected from all cows and DNA will be extracted. Performance will be tracked throughout the winter-feeding period. At calving, body weight, rib and rump fat thickness and frame measurements will be assessed along with calf birth weight.
- Cow-calf pairs will be managed similarly throughout spring, summer, and into fall before being enrolled into this study. Those identified as being pregnant following their first calf will be enrolled into Year 2 of the study. Management and data collection in Year 2 will follow that described for Year 1. Data for cows with two winter feeding periods and two successful breeding seasons will be assessed. The primary measurement for ranking will be based on the change in back-fat thickness and body weight (conceptus corrected).

Determining underlying causes for forage-efficient cows

- Evaluation of Host Physiology: Cows with the least (n = 10) and greatest change (n = 10) in back-fat from the above-listed phenotypic assessment project will be selected. These cows will be fit with a ruminal cannula and will be used to determine whether differences in digestive physiology explain the forage-use efficiency phenotype. Each cow will be exposed to four diets differing in forage quality, particle size and energy density (chaff-based, straw-based, good quality hay-based, silage-based) to evaluate dry matter intake, ruminal volume, rumen digesta mass, total tract digestibility, and the passage rate of solids and liquids out of the rumen.
- Evaluation of Rumen Microbiology**:** The rumen microbiome will be examined in the same cannulated cows as above (n = 10 from each of the high and low forage efficiency cohorts). Samples of ruminal fluid will be collected while being fed the diets described above immediately prior to the host-physiology sampling approaches as described above. From the mixed digesta sample, DNA will be extracted. A PCR-free method of assessing the microbiome called CaptureSeq will be used to assess the microbiome. The two key advantages of CaptureSeq over conventional PCR-based approaches are that CaptureSeq covers all domains of life (e.g. Archaea, Bacteria and Fungi) simultaneously and provides highly accurate quantitative measures of microbial abundance. We intend to determine if microbial responses to diets change differently for the forage-efficient phenotypes, whether individual microbial communities can be determined, and the putative functional roles of microbes associated with the phenotypes.
- Evaluation of Host Genetics: After clear phenotypic evaluation has been completed, DNA will be extracted from the heifers using the original blood samples collected at the start of the study. A genome-wide association analysis (GWAS) will be conducted to identify regions of the cattle genome associated with high and low feed-use efficiency using the 10 cows with the greatest and least forage-efficiency (n=20) using a microarray of over 150K single nucleotide polymorphisms distributed across the entire cattle genome. Using genetic and genomic methods, we have designed a robust approach to identify potential candidate genes and their causative mutations related to forage use efficiency.

Implications:

This research represents a significant opportunity for cow-calf producers in Saskatchewan and western Canada and has the long-term potential to develop several technologies. Firstly, should there be the ability to easily identify forage-efficient cow based on physical characteristics, these criteria will be presented in a rubric and disseminated using fact sheets to enable rapid adoption by primary producers. The microbial assessment will enable identification of key species and activities and can be used to develop future strategies to improve forage-use efficiency in the long-term. This may include development of other products used to inoculate cattle to modulate the microbial community structure. Finally, should we identify a genotype or microbial community structure associated with improved forage-use efficiency, a commercial test will be developed and commercialization will be explored.

Proudly funded by:

CANADIAN AGRICULTURAL PARTNERSHIP

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