A consistent and adequate supply of nitrogen to ruminal microbes is essential for the efficient conversion of feed to ruminant products. Data exist that suggest there are substantial differences between genotypes in their ability to supply adequate levels of ruminal nitrogen. Additionally, observations have been made suggesting that the deposition of amino acids, both dietary and microbial sources, into tissue or milk is different between genotypes. Quantification of the genes that influence ruminal nitrogen supply or control the deposition of amino acids would increase our ability to select livestock capable of the highest level of performance.

Understanding the differences in genotypes and their respective nitrogen requirements would enable us to more precisely formulate diets to meet nutritional requirements and prevent overfortification of ruminant diets. While the possible improvements in performance and profitability provide sufficient justification for exploring the relationship between nitrogen metabolism and genotype, increasing environmental regulations and the need to reduce the environmental footprint of ruminant production serve as an additional impetus for pursuing this management tool.

Process
- Confirm the existence of substantial differences in nitrogen and amino acid metabolism between cattle of divergent genotypes.
- Quantify the response surface available for targeted selection and the impacts of targeted selection for other traits of economic importance.
- Commercial application of the genetic markers for nitrogen and amino acid metabolism.

Outcomes
- A detailed understanding of the differences in ruminal nitrogen and whole-animal amino acid metabolism in divergent genotypes
- A commercially viable application of genetic markers that allows the selection of cattle with improved nitrogen metabolism specific for different production scenarios