

## Potential Impacts of Maternal Nutrition and Selection for Residual Feed Intake on Metabolism and Fertility Parameters in Angus Bulls

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**Abstract :** Maximizing efficiency and growth potential of beef cattle requires not only genetic selection (i.e. residual feed intake (RFI)) but also adequate nutrition throughout all stages of growth and development. Nutrient restriction during gestation has been shown to negatively affect post-natal growth and development as well as fertility of the offspring. This, when combined with RFI may affect progeny traits. This study aims to investigate the impact of selection for divergent genetic potential for RFI and maternal nutrition during early- to mid-gestation, on bull calf traits such as fertility and muscle development using multiple 'omics' approaches. Comparisons were made between High-diet vs. Low-diet and between High-RFI vs. Low-RFI animals. An epigenetics experiment on semen samples identified 891 biomarkers associated with growth and development. A gene expression study on Longissimus thoracis muscle, semimembranosus muscle, liver, and testis identified 4 genes associated with muscle development and immunity of which Myocyte enhancer factor 2A [MEF2A; induces myogenesis and control muscle differentiation] was the only differentially expressed gene identified in all four tissues. An initial metabolomics experiment on serum samples using nuclear magnetic resonance (NMR) identified 4 metabolite biomarkers related to energy and protein metabolism. Once all the biomarkers are identified, bioinformatics approaches will be used to create a database covering all the 'omics' data collected from this project. This database will be broadened by adding other information obtained from relevant literature reviews. Association analyses with these data sets will be performed to reveal key biological pathways affected by RFI and maternal nutrition. Through these association studies between the genome and metabolome, it is expected that candidate biomarker genes and metabolites for feed efficiency, fertility, and/or muscle development are identified. If these gene/metabolite biomarkers are validated in a larger animal population, they could potentially be used in breeding programs to select superior animals. It is also expected that this work will lead to the development of an online tool that could be used to predict future traits of interest in an animal given its measurable 'omics' traits.

**Keywords :** biomarker, maternal nutrition, omics, residual feed intake

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