

Livestock Metabolomics and the Livestock Metabolome Database

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Metabolomics has become an increasingly popular “omics” approach to assist with the robust phenotypic characterization of humans, plants and model organisms. However, livestock metabolomic research, specifically in sheep, is by far behind the potential it offers. To address this shortfall, we have attempted two major steps; experimental analysis to further describe the sheep metabolome, and systematically gather livestock metabolomic data (for 5 of the most common livestock species: cattle, sheep, goats, horses and pigs) in an open access online database (Livestock Metabolome Database [LMDB] available at www.lmdb.ca). The LMDB is expected to serve as a hub to support metabolomic studies in livestock by identifying where further metabolome coverage is needed. Three experimental projects to assess the metabolome associated with sheep feed efficiency and carcass merit, pregnancy and litter size, and parasitic infection are currently being conducted. The main objectives are to: 1) profile (identify and quantify) the blood metabolome of healthy sheep at different production levels, and 2) identify biomarkers that are predictive for productivity level, and pregnancy and/or parasite infection status. Our experimental results will be used to expand LMDB in addition to the 1070 metabolites already included from livestock publications, and to develop a “pen-side” device for biomarkers using a few drops of blood to improve sheep selection or management. Preliminary laboratory analyses using nuclear magnetic resonance (NMR) spectroscopy to evaluate serum samples (n=35) collected from lambs and ewes has been promising. We have identified candidate biomarkers that distinguish between high and low feed efficient lambs, open and pregnant ewes with a single fetus or multiple fetuses, and parasite-infected sheep. We are currently investigating a larger cohort of samples (n=1720) using 3 different analytical platforms (NMR, ICP-MS, DFI-MS) to validate initial results.