and 83.3% in MAO-MET and MAO-FGFR2 conceptuses, respectively. Interestingly, phosphorylation of TSC2 was decreased ($P < 0.01$) by 79.2% in Tr of MAO-MET compared with MAO control but was no different ($P > 0.05$) between MAO-FGFR2 and MAO control conceptuses. Collectively, these results demonstrate critical roles for progestamedins (i.e., HGF, FGF7, and FGF10) in ovine conceptuses that are mediated via their receptors (MET and FGFR2) and activation of MAPK and MTOR pathways and that translational knockdown of *MET* and *FGFR2* mRNA increased apoptosis and retarded conceptus development during early pregnancy.

Key Words: progestamedin, trophectoderm, MTOR, MAPK, sheep

GROWTH AND DEVELOPMENT SYMPOSIUM: NEW -OMICS TECHNOLOGIES TO UNDERSTANDING THE BIOLOGICAL PROCESSES AND NETWORK PATHWAYS ASSOCIATED WITH CATTLE GROWTH AND HEALTH

0783 Objective-oriented genomic relationship matrices.

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The advent of affordable high-density SNP genotyping platforms has boosted the implementation of genomic selection program in many livestock species. However, large reference populations are required to accurately compute genomic predictions of breeding value (GEBV). Combining information from (seemingly independent) separate populations has been highlighted as a beneficial strategy and methods to adjust the realized genomic relationship matrix (GRM) to accommodate the heterogeneity in allele frequencies have been proposed. Simulation studies based on real sequence data have shown the importance of using only variants as close as possible or identical to the causative mutations. Recently, we showed that data from reference populations from two distinct breeds can be merged to generate GEBV, provided the SNP used to build the GRM are carefully selected based on their significance and direction of the effect associated to the phenotype. We show that this approach can optimize the genomic correlation for the phenotype of interest in the two populations. We further show how a "hybrid" GRM permits the linking of genotypic data of pooled DNA samples of commercial cattle pooled according to phenotype with individual DNA samples from animals available for selection. Our examples are concerned with beef cattle raised extensively in tropical and subtropical regions of Australia. We anticipate that the use of traditional "one size fits all" relationship matrices, based on pedigree information only, is coming to an end and predict the time has come for "objective-oriented" GRM purpose built for a specific breeding objective.

Key Words: genomic selection, genomic predictions, genomic relationship matrix

0784 Multi-omics data resources and use in genetic improvement of cattle growth and health.

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Interactions of growth and health influence the progression of cattle to maturity. Growth and carcass traits typically have moderate to high heritability ($h^2 = 0.2–0.5$), whereas pathogen-disease related health traits tend to have low heritability ($h^2 \leq 0.2$). Genetic improvement in beef cattle involves selection with EPD predicted from multitrait, and often multibreed, models that incorporate genomic data derived from SNP chips. Available genotyping platforms have genomewide distance gaps of 49.4 (BovineSNP50) and 3 kb (BovineSNPHD). Genetic prediction accuracy can be improved with use of genomic data; however, process varies greatly depending on trait heritability and quality–quantity of data. Because most economically relevant traits are polygenic and single SNP within a positional-candidate gene explain limited variation, there is great interest in discovery and use large numbers of causal-mutation SNP in genetic prediction. These SNP will likely be located within nodes and hubs of gene networks and can be added to the current chips to improve their effect. Various "omics" tools evaluating transcriptome, proteome, and metabolome assist with discovery of coding and tag SNP. Differentially expressed targets from the latter two tools reveal gene products closely associated with an animal's physiologic phenotype, which can correlate with gene expression levels observed in RNA. Concordant results and enrichment analyses from these tools yield confidence to analyze target sequence, either DNA or RNA, to discover functional SNP. However, transcript splicing, peptide processing, and post-translational modifications complicate comparing results from the various approaches. The animal's epigenome and microbiome also influence phenotype. To identify functional SNP, RNA must be harvested from tissues of animal models designed to be informative for a trait collected from large breeding populations. Case versus control or comparisons of cattle from the tails of the quantitative trait distribution curves have proven useful strategies in several multi-omics growth and health studies of which pulmonary arterial pressure (PAP; $h^2 = 0.2–0.4$), an indicator of hypoxia-induced pulmonary hypertension, is an example. Here, cardiopulmonary tissues were collected from high- and low-PAP Angus steers ($n = 10$/group) with sire-pedigree diversity to growing seed stock bulls. Transcript abundance was assessed and differential expression results were obtained and are being merged with QTL and whole-genome sequence information to discover SNP genotypes for incorporation into a PAP EPD, a tool for selecting cattle for high elevation tolerance. Therefore,

strategic application of multi-omic resources to discover functional SNP and obtain population-level genotype data provides opportunity to enhance EPD accuracy.

Key Words: cattle, growth, health, omics

TRIENNIAL GROWTH AND DEVELOPMENT SYMPOSIUM

0785 Muscle gene expression patterns associated with differential intramuscular fat in cattle and markers for skeletal muscle growth rate and major cell types. B. P. Dalrymple*, *CSIRO Agriculture, Brisbane, Australia*.

Growth rate, intramuscular fat content (IMF%), and IMF composition influence the value of individual animals. However, for IMF, there are many different pathways to the final common process of triacylglyceride (TAG) synthesis and storage in intramuscular adipocytes. Gene expression data from a number of cattle and sheep experiments was used to identify the pathways involved in the synthesis of IMF and the genes correlated with growth rate and as markers of cell populations. The data sets were from a time course of longissimus muscle (LM) development in Piedmontese (PxH) and Wagyu cross Hereford (WxH) cattle, from the LM of a group of 48 Brahman cattle of similar age and from the LM of a group of 20 sheep of similar age. The differential expression of genes between WxH (high marbling) and PxH (high muscling) cattle and the correlation of gene expression with measured IMF in the Brahman and sheep data sets was integrated with known biochemical pathways. Expression of genes encoding proteins involved in the synthesis and deposition of TAG was most correlated with IMF%. In well-fed immature animals, TAG deposition rate (estimated by TAG gene expression) was proportional to current IMF%. By comparing TAG gene expression and IMF%, we identified a small number of animals with unexpectedly low or high rates of IMF deposition for their IMF%. The genes in the fatty acid synthesis pathway were less correlated with IMF%, presumably as IMF TAG can contain preformed fatty acids from circulation as well as those synthesized de novo by intramuscular adipocytes. By comparing changes in expression of the TAG and fatty acid genes, we estimated the relative contributions of synthesized and preformed fatty acids to IMF deposition on different diets. The expression of two groups of genes in the LM of the Brahman steers, significantly enriched for "cell cycle" and "ECM (extracellular matrix) organization" GO terms, was correlated with ADG per kilogram liveweight. However, expression of the same genes was only partly related to growth rate across the development time course in (PxH and WxH). *K*-means clustering of genes with similar expression profiles to the ECM genes was undertaken. Analysis of the clusters and published markers of different cell types in muscle suggested that the "cell cycle" and "ECM" signals were from the fibro/adipogenic lineage. The increase in ECM remodeling required for increased IMF deposition probably altered the relationship between the expression of these genes and animal growth rate.

Key Words: cattle, lipid

0786 Factors influencing bovine intramuscular adipose tissue development and cellularity. E. Albrecht*[1], L. Schering[1], Y. Liu[1], K. Komolka[1], C. Kühn[2], K. Wimmers[3], and S. Maak[1], *[1]Muscle Biology and Growth, Leibniz Institute for Farm Animal Biology (FBN), Dummerstorf, Germany, [2]Leibniz Institute for Farm Animal Biology (FBN), Dummerstorf, Germany, [3]Genome Biology, Leibniz Institute for Farm Animal Biology (FBN), Dummerstorf, Germany*.

Appearance, distribution and amount of intramuscular fat (IMF) or marbling are highly variable depending on nutrition, gender, and environmental and genetic factors. On the molecular level, the concerted action of several factors, including hormones, receptors, transcription factors, etc., determines where clusters of adipocytes arise. Therefore, the aim remains to identify biological markers of IMF to increase the ability to identify animals that deposit IMF early in age to ensure the competitiveness of meat products and increase efficiency of high-quality meat production. In an attempt to unravel the cellular development of marbling, we investigated on the one hand the abundance of markers for adipogenic differentiation during fattening of cattle and on the other hand the transcriptome of muscle and dissected IMF from different breeds. Markers of different stages of adipogenic differentiation are well known from cell culture experiments. However, early markers are transiently expressed and late markers may reflect the number of mature adipocytes in the sample rather than gene activity in a tissue. On the cellular level, the development of marbling requires recruitment, proliferation, and differentiation of adipogenic cells. Hypertrophy of adipocytes is limited and hyperplasia occurs to store excess energy in the form of lipids in new cells. Within muscles, hyperplasia and hypertrophy of adipocytes can be observed throughout life. In a recent study, we investigated the localization and abundance of delta-like homolog 1 (DLK1) and CCAAT/enhancer-binding protein β (CEBPB), early markers of adipogenic differentiation, in bovine muscle tissue. Cell culture models demonstrated high expression of DLK1 in preadipocytes and complete disappearance during differentiation to adipocytes. Accordingly, we could demonstrate an inverse relationship between IMF content and number of DLK1 positive cells in bovine muscle. Considering the cellular environment of differentiating adipocytes in muscle and accepting mature adipocytes and myocytes as secretory cells, it becomes obvious that cross talk between cells via adipokines and myokines may be important