different, and *in silico* gene analyses indicated that selection has impacted different metabolic pathways in the LRFI and HRFI lines. These results provide new information on the genetic basis of feed efficiency in pigs.

PO0401:   Swine

Allele-Biased Expression and Histone Modification in Fetuses from Reciprocal Crosses of Divergent Pig Breeds

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Identifying genetic variants affecting gene expression by allele-biased expression (ABE) and epigenetic modification analyses is important for us to understand gene expression regulation. And hybrids of genetically divergent breeds maximize the potential of discovering genetic variants regulating gene expression. In this study, we performed both RNA-seq (4 tissues: brain, liver, muscle and placenta, two developmental stages, Day 30 of gestation (D30G) and Day 70 pf gestation(D70G)) and ChIP-seq (liver and muscle, D70G) to identify variants of allele-biased expression (ABE) and allele-biased histone modifications (ABHM), in F1 fetuses from reciprocal crosses of Meishan (MS) and White composite (WC) pigs. Using a robust pipeline for allele-biased analysis, we identified xx SNPs and yy SNPs showing allele-biased expression and histone modifications. Functional annotation of the genes with ABE and ABHM is undergoing. The sets of variants and their associated genes showing ABE and ABHM will provide a foundation for understanding gene regulation and the underlying phenotypic differences between MS and WC.

PE0402:   Swine

Whole Genome Analysis of Alentejano Pigs with Contrasting Meat Quality Phenotypes

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The Alentejano is a Mediterranean pig breed, found in southern Portugal, reared under extensive conditions and finished on grass and acorns during the fall and winter months. From these animals a variety of dry-cured meat products of great economic importance are generated. A total of 541 pigs were studied during the 2017 slaughter campaign. Phenotypic records for carcass and meat quality were collected and subsequently analyzed to identify the groups of animals that displayed the most contrasting phenotypes. Two groups comprising 13 animals each were selected, based on pH, water loss, total lipids, total protein, total collagen and pigments content. All samples were re-sequenced to a 23x coverage. The reads were aligned to the pig genome and SNPs and structural variants identified between the two groups of animals. A total of 13,418,254 SNPs were identified, of which 6,851,475 and 6,566,779 were located in the genic and intergenic genomic regions, respectively. The number of SNPs for which at least 25 samples were present comprised 88.7%. The set of genic SNPs included 43,405 exonic non-synonymous SNPs and 60,750 exonic synonymous SNPs. The remaining SNPs were located in introns and ncRNA regions. Interestingly, SNPs with markedly different allele frequencies between the groups were also identified (a total of 230 SNPs with allele frequency differences between the groups of at least 30% or 70%). This study represents the first major characterization of Alentejano pigs at the genome level, and identified a significant number of SNPs potentially associated with meat quality.

PO0403:   Swine

Differential Gene Expression across Developmental Stages in Swine Tissues

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