P4018 Use of a whole genome association study to characterize gene networks for pig reproduction traits

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A whole-genome association study (WGAS) utilizing commercial sows born over a 6 month period (n = 683) identified genetic markers (SNPs) associated with pig reproduction traits. These traits included total number born (TNB), number born alive (NBA), number still-born (SB), number of mummies and gestation length. Traits were recorded on all parity1 females and those 558 and 442 sows that went on to parities 2 and 3, respectively. The association analyses used a Bayes C model averaging approach, which fitted ~250-300 SNPs per iteration to predict individual genetic marker effects and consecutive five genetic marker window effects. Gene networks were constructed with PubGene software using genes located at the associated chromosomal regions for each trait among different parities. Many different chromosomal regions (and therefore genes e.g., *MEF2C* on SSC2, *PTX3* on SSC13 and *ITG6* on SSC15 for TNB in parities 1, 2 and 3, respectively) were associated with each trait in different parities. These results provide evidence of temporal gene effect trends on reproductive traits in different parities. Gene network analyses determined that genes within the associated genomic regions in different parities were related by pathways including TNF for TNB and NBA, BMP for SB, insulin for gestation length, and MAPK1, activin and the ubiquitin for the mummified fetuses. Studies focusing on additional gene/SNP discovery, haplotypes, epistasis and gene networks using high density SNP chips are recommended for further understanding of the complex genetic architecture of pig reproduction traits.

P4019 A novel resource population for mapping QTLs focusing on the weight ratio of thigh meat to live body weight in chickens

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Generally, breast meat is more popular than thigh meat because of its healthiness and cooking. In contrast, most Japanese people prefer thigh meat to breast meat. Accordingly, we developed a resource population to detect QTLs affecting the thigh meat weight ratio (%) to live body weight (TMR), relating the breast meat weight ratio (%) to live body weight (BMR), and other carcass traits. Among the 23 pairs of Satsumadori male and Nagoya female (Japanese native fowl), 2 pairs were selected to parent the resource population regarding their utility for QTL analysis. In total, 420 F2 birds were produced from 12 F1 birds (4 males and 8 females) with 16 hatcheries. Three hundred and eleven F2 birds were slaughtered at 140 days of age and 12 carcass traits were measured. The average TMRs of male and female birds were 23.4 ± 1.1 % (20.8–26.1 %) and 21.4 ± 1.0 % (19.4–24.3 %), respectively. Now we are collecting genotype data of microsatellite markers for QTL analysis. Prior to QTL analysis, the association of promising marker alleles with the carcass traits was analyzed. Alleles of some markers were significantly associated with TMR or BMR. For example, in marker ADL0019 (122 cM of Ch.1); the A allele was associated with higher TMR (p=0.014) and higher meat yield (p=0.029), the B allele with lower BMR (p=0.011) and the C allele with lower TMR (p=0.0002) and higher BMR (p=0.008).

P4020 Identification of genomic regions associated with backfat thickness in synthetic cattle

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Canchim is a synthetic beef cattle developed in Brazil which have good growth potential and tropical adaptation but suboptimal fat deposition. There are genomic regions associated with fat deposition already described, among them the centromeric region of BTA14. The scope of this work was to identify genomic regions associated with backfat thickness in Canchim (5/8 Charolais + 3/8 zebu) and MA (offspring of Charolais bulls and 1/2 Canchim + 1/2 Zebu cows) populations and to validate the association of haplotypes of the BTA14 with backfat thickness in this population. Thirty animals with extreme phenotypes were genotyped with the 54 K SNP chip, revealing 100 significant SNPs contained in chromosomes 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 14, 15, 17, 18, 19, 20, 21, 23, 24, 27, 28 and X. Thirty-four SNPs constituted seven chromosomal regions containing 3 or more SNPs located at intervals shorter than 9 Mb and, among these, ten SNPs in BTA 14 were selected for validation. Genotyping in the population was performed by the TaqMan method in families comprising more than 10 individuals with backfat thickness information at the age of 18 months (644 animals). Validation of the BTA14 SNPs revealed two haplotypes, one in the centromeric region and another in the middle region of BTA14, significantly associated with fat thickness, both with additive effects on backfat thickness. Genes located close to these two regions should be further studied to identify potential mutations involved in backfat deposition.

P4021 MicroRNA expression analysis in bovine blastocysts by Megaplex stem-loop primer Reverse Transcription

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Mammalian blastocyst formation is characterized by two segregation events, resulting in the formation of the trophectoderm, the epiblast and the hypoblast. These differentiation events are known to be regulated by lineage specific transcription factors, but it is more and more presumed that besides these totipotency and differentiation markers, miRNAs play an important role in the posttranscriptional regulation of differentiation events.

A stem-loop reverse transcription quantitative PCR with a human Megaplex primer pool was applied for the detection of miRNAs expressed in early bovine blastocysts (day 7 p.i.) and expanded/hatched bovine blastocysts (day 8 p.i.) and resulted in the detection of 93 different bovine miRNAs. Twelve out of the 93 miRNAs were differentially expressed between the day 7 and day 8 blastocysts. Eight Bta-miRs were significantly upregulated (P<0.05) in day 8 blastocysts, whereas 4 Bta-miRs were significantly downregulated in day 8 blastocysts compared to day 7 blastocysts. Target genes were predicted for these 12 miRNAs using the Targetscan 5.1 database. Next, gene functions and pathways enriched in these lists of predicted targets were calculated using the Ingenuity Pathway analysis software. Several pathways, such as the growth hormone, the TGF-β, the WNT/β-catening and the Notch signaling pathway were significantly enriched in these lists of predicted targets.

The results of this study confirm the presence and tight expression regulation of specific miRNAs in bovine blastocysts. Functional characterization of the identified