match/mismatch oligonucleotide sets, to assess non-specific hybridization. Final statistical analyses of the PRRSV study are underway. These studies provide important support for our PRRS Host Genetic Consortium studies of neonatal pig resistance to infection that have just begun. Overall, these studies will reveal immune pathways and candidate genes involved in PRRSV resistance.

Poster 2096

Title: Arachnomelia in cattle: mode of inheritance and initial genetic mapping

Presenting Author: Dr. Johannes Buitkamp, Bavarian State Research Center for Agriculture, Institute of Animal Breeding 85580 Grub/Germany

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Abstract:
Arachnomelia is a congenital disease of cattle. It is characterized by malformed bones of the limbs, back and head. Sporadically, additional findings, like cerebral herniation or hydrocephalus externus and internus, are observed. It causes losses, not only since the calves are not viable, but, more importantly, because sires that carry the mutation are banned from breeding and cows are hurt during delivery. A rapid rise of arachnomelia cases was observed in the years 2005 and 2006 in German and Austrian Simmental cattle. A number of sires with high genetic merit were recognized carriers of the mutation. Therefore, appropriate control measures had to be rapidly developed to avoid further spread of the allele in the population. In a first step breeding management measures were applied. To avoid the final exclusion of important sire lines from breeding, we started the genetic mapping of the disease with the final goal to develop an indirect gene test. Data about the pedigree analysis and population frequency estimation of arachnomelia as well as the genetic mapping are presented.

Poster 2097

Title: Quantitative trait loci for milk-fat composition in Dutch Holstein Friesians

Presenting Author: Anke Schenninkg, Animal Breeding and Genomics Centre, Wageningen University, Wageningen, the Netherlands

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Abstract:
This study is part of the Dutch Milk Genomics Initiative and aims at the characterization of genes involved in milk-fat synthesis and milk-fat metabolism. Previous research has shown substantial genetic variation in milk-fat composition: heritabilities were high (0.42-0.71) for short- and medium-chain fatty acids (C4-C16) and moderate (0.22-0.42) for long-chain fatty acids (C18 and longer). To map QTL affecting milk-fat composition we conducted a whole-genome-scan. The mapping population consisted of 7 half-sib families containing 849 cows in a daughter design. A total of 1379 SNPs were typed covering all 29 autosomes. The phenotypes under study were 56 milk-fat composition traits, including saturated, mono-unsaturated, poly-unsaturated, and conjugated fatty acids, unsaturation indices and fat percentage. A regression interval mapping approach was used to estimate effects and positions of the QTL. QTL for short- and medium-chain fatty acids were detected on BTA6, 14, 19 and 26. QTL for long-chain fatty acids were detected on BTA14, 15, and 16. Our results will enable marker assisted differentiation and marker assisted selection, in order to optimize milk quality and to develop innovative dairy products. Fine mapping of the chromosomal locations is currently in progress.

Poster 2098

Title: Genomic signatures of artificial selection in U.S. Holstein cows

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Abstract:
Selection in Holstein cattle has achieved tremendous phenotypic changes over the past 40 years. However, it is unknown how selection has changed the Holstein genome and how those genome signatures of selection are associated with the phenotypic changes. To categorize genome regions either affected or unaffected by selection, we contrasted genome structure data between 148 contemporary Holsteins and 151 cows from an unselected line of Holsteins bred and maintained at the University of Minnesota since 1964. Marker genotypes from 46,231 SNP were analyzed for allele frequency differences and trait associations using Wright's Fst test and EPISNPmpi, respectively. Comparison of the most significant marker effects with Fst results revealed strong signatures of selection for production traits on chromosomes 1, 2, 3, 7, 8, 11, and 26. Chr 26 also had significant associations (16 markers; $p<1.0E-12$) with udder traits that co-localize with strong signatures of selection. Of the 31 SNPs with the most significant effects on both milk and daughter pregnancy rate, 29 had opposite effects on these traits providing strong evidence for the antagonistic effect of selection for production on fertility. These findings identify where selection has affected the genome and assist in searching for genes of large effect.

Poster 2100

Title: Global gene expression for cattle selection lines with low and high feed efficiency

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Abstract:
Feed efficiency is an economically important trait in beef cattle and it is affected by several physiological systems. The net feed efficiency measured as net feed intake (NFI) is the difference between the actual feed intake over a test period and its expected feed intake based on its size and growth. The objective of this project was to identify differentially expressed genes between animals with high and low NFI and pathways which contribute to the phenotype by global gene expression profiling using a 24K bovine long oligonucleotide array designed by the Bovine Oligonucleotide Microarray Consortium.

Liver tissue biopsies were taken from the top and bottom 30 tested bulls of Angus cattle divergently selected for low or high NFI and 44 animals were chosen for the microarray experiment. The microarray experiment was designed by ranking the animals based on NFI phenotypes and then pairing the top with the bottom animals using dye-swap.
Standard QC measures were performed and arrays were individually normalized using print-tip loess normalization after background correction. Differentially expressed genes were ranked based on the p-values of a moderated t-statistic after fitting a linear model. The differentially expressed genes were assessed with regard to gene ontology, biological function and known genetic pathways.

Poster 2101

Title: Comparative performance and efficiency of five methods used for genome wide selection in dairy cattle using high density SNP data

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Abstract:
Three commonly used methods (Least squares regression-LS, Kernel regression-SVM, Bayesian regression- BayesA) and two new approach (Partial least squares-PLS, PLS with SNP selection-PLSjack) were compared in a Genome Wide Selection (GWS) analysis for prediction of genetic merit in dairy cattle. The data included 1945 progeny tested Holstein Friesian sires and genome wide analysis with 7372 SNP. The accuracy (r) of predicting EBV based on SNP genotypes (MBV) was studied by cross-validation. When test subsets were randomly drawn form the data (mirror prediction), accuracies for Australian Profit Rank (APR), an index of 9 component traits, ranged from r=0.69-0.80 and r=0.57-0.68 for protein%. To asses accuracies of MBV for young animals (forward prediction), the data was partitioned in a training set of 1239 bulls born before 1998, and 5 single year cohorts (1998-2002) of young bull teams. For forward prediction a loss in accuracies of 45% to 75% for APR and 15% to 40% for prot% was observed as compared to mirror prediction. In mirror and forward prediction LS, and Bayes A performed worse than SVM or either PLS method. For GWS, PLS with SNP selection performed the best and most consistent across the 5 year cohorts, and was computationally highly efficient.