GRADUATE STUDENT ORAL COMPETITION: PhD ORAL II

093 **Stimulation of estrus and ovulation in lactating sows.**H. L. Frobose*, K. M. Gourley, M. D. Tokach, J. M. DeRouchey, S. S. Dritz, R. D. Goodband, J. L. Nelssen, D. L. Davis, *Kansas State University, Manhattan.*

Practical methods for inducing estrus and conception in lactating sows have been a goal of researchers since the 1950s. In this experiment, we used a modified litter separation and boar exposure treatment for inducing lactational estrus. A total of 36 multiparous and 17 primiparous sows were assigned to either control ($n = 25$) or altered sucking (ALT; $n = 28$) treatments. Litter size was equalized within parity (multiparous or primiparous) to 11.6 ± 1.2 pigs at d 2 postfarrowing. At d 18 of lactation (this and subsequent days are averages), sows were allotted to treatments and the ALT sows were penned in adjacent pairs within parity so that pigs could be moved between litters by temporarily lifting the divider between the two litters. On d 18, all but the 5 lightest pigs from each ALT litter were weaned. The 5 lightest pigs for each pair of litters formed a combined litter that nursed each sow of the pair 12 h/d from d 18 to 25. Therefore, pigs had nursing access 24 h/d, but each ALT sow was only suckled 12 h/d. Boar exposure was provided only to ALT sows for 15 min/d by moving sows to a pen outside the farrowing room. Control and ALT sows were weaned at d 21 and d 25, respectively. Sow weights and litter performance during lactation were similar between treatments although ALT sows had 16% greater total feed intake (138 vs. 116 kg; $P < 0.01$) due to the 4 d extended lactation period. Primiparous sows lost a greater percentage (7.4 vs. 3.4%) of BW and consumed less feed ($P < 0.01$) than multiparous sows. A total of 26 ALT sows (93%) were detected in estrus and inseminated in lactation. Although the interval from initiating ALT to estrus was greater ($P < 0.001$) than the wean-to-estrus interval for controls, ALT sows were in estrus earlier postfarrowing (23.0 vs. 24.6 d; $P < 0.001$) than controls. Primiparous sows exhibited estrus later (5.4 vs. 3.8 d; $P < 0.01$) than multiparous sows for both treatments. Pregnancy rate and subsequent reproductive performance were similar between treatments. The ALT treatment is unique in that nursing is by a combined litter of light-weight pigs. Whether this contributed to the high incidence of lactational estrus is not known; however, our results provide evidence that the ALT treatment can induce estrus in lactating sows at rates comparable to conventionally weaned sows and with similar reproductive performance.

Key Words: boar exposure, lactational estrus, split weaning

094 **Predicting swine MHC haplotypes from high-density SNP genotypes.**J. Dunkelberger*, *Iowa State University, Ames.*

The major histocompatibility complex (MHC) region in swine, the swine leukocyte antigen (SLA) complex, is rich in genes associated with disease resistance. Many of these genes have haplotype-specific expression. There are various ways to determine MHC haplotypes, including wet lab assays such as using PCR-sequence-specific primers (PCRSSP) for low-resolution (Lr) SLA haplotyping, which can be time intensive and costly. Alternatively, high-density single nucleotide polymorphism (SNP) panels can be used to infer haplotypes in a genomic region. The objective of this study was to determine whether SNP genotypes from a commercial high-density SNP chip can be used to predict haplotypes within the MHC region of the swine genome.

A total of 140 pigs from four PRRS Host Genetics Consortium trials were haplotyped using the PCRSSP method. Pigs were selected, in roughly equal numbers per trial, based on extreme (high/low) viremia and growth after inoculation with the NVSL 97–7985 PRRS strain.

All pigs were genotyped using the Illumina SNP60 BeadChip. Seventy-five SNPs located within the 23 through 27 Mb SLA I region and 64 SNPs within the 29 through 31 Mb SLA II region of chromosome 7 were used to analyze MHC class I and II, respectively. SNP genotypes in each region were phased into haplotypes using BEAGLE software. Resulting haplotypes in the 23 through 27 Mb window (the entire window used for phasing) or the 24 Mb window were analyzed for SLA class I. Similarly, SNP haplotypes in either the 29 through 31 Mb window or 29 Mb window were analyzed for SLA class II. Identical SNP haplotypes for a given window were grouped to determine which Lr SLA haplotype they shared. Accuracy of prediction was calculated as the percentage of SNP haplotypes that could be assigned to a Lr SLA haplotype.

When analyzing SNP haplotypes using the entire window used for phasing to group haplotypes, accuracy of prediction was 85% for class I and 88% for class II. Greater haplotype prediction accuracy was obtained when grouping SNP haplotypes using the 1 Mb approach (91 and 95% for class I and II, respectively).

In conclusion, BEAGLE software can be used to predict MHC haplotypes from high-density SNP genotype data with fairly high accuracy. These results indicate that the Illumina SNP60 BeadChip can be used to predict SLA haplotypes as an alternative to wet lab methods. This will enable us to investigate the role of SLA class I and II genes in PRRS resistance/susceptibility.

Key Words: swine leukocyte antigen