**38 Genetic background influences pig growth rate responses to porcine circovirus type 2 (PCV2) vaccines.** M. L. Potter*[1], L. M. Tokach[2], S. S. Dritz[1], S. C. Henry[2], J. M. DeRouchey[1], M. D. Tokach[1], R. D. Goodband[1], J. L. Nelssen[1], R. R. R. Rowland[1], and R. A. Hesse[1], [1]*Kansas State University, Manhattan*, [2]*Abilene Animal Hospital, PA, Abilene, KS.*

Commercial porcine circovirus type 2 (PCV2) vaccines have become available as aids for the prevention and control of losses due to porcine circovirus disease (PCVD). Reports that genetic background affects severity of PCVD expression prompted this field study to compare PCV2 vaccine effects on growth rate across pigs from different genetic backgrounds. This 130 d study used 454 weaned pigs (21 d of age; 6.1 kg) in a PRRS and Mycoplasma negative multiplier farm. The presence of PCV2b virus in the herd was noted but clinical disease did not meet the epidemiological case definition for PCVD. Comparisons between vaccinate and unvaccinated control, genetic background, and gender (boars and gilts) were made in a 2 × 4 × 2 factorial treatment design. The 4 genetic backgrounds used were A×A (Duroc based sire and dam), B×B (Synthetic line for the sire and dam primarily derived from Duroc, Pietrain, and Large White), A×B, and B×A. Commercial PCV2 vaccine (Intervet) was administered according to label dose at weaning and again 2 weeks later. Pigs were individually weighed at weaning, end of the nursery phase (d 40) and off-test (d 130) to measure ADG. No significant three-way interactions were observed. There was a vaccine treatment by genetic interaction ($P=0.05$) for finisher ADG and off test weight. The ADG was 0.77±0.017, 0.87±0.018, 0.87±0.024, and 0.85±0.019 kg for control pigs and 0.86±0.018, 0.92±0.018, 0.91±0.025 and 0.88±0.019 kg for vaccinated pigs for A×A, A×B, B×A and B×B, respectively. This resulted in 9.0, 2.9, 4.7, and 2.3 kg heavier vaccinates compared to controls for each of the 4 genetic backgrounds. The vaccine was effective in increasing finisher growth rate while the magnitude of the weight difference was almost 4 times greater in the A×A pigs compared to the B×B pigs. These data indicate that the genetic background has an influence on the expression of PCVD or response to PCV2 vaccination.

**Key Words:** Growth, Circovirus, PCV2

**39 Analysis of incidence of Porcine Circovirus Associated Disease (PCVAD) in a Landrace/Large White composite population.** J. Bates*, R. Johnson, and A. Doster, *University of Nebraska, Lincoln.*

The objective was to determine the importance of genetic and environmental effects on the incidence of Porcine Circovirus Associated Disease (PCVAD) in pigs. 2,554 pigs from Generations 24-26 of two lines selected for increased reproduction and growth and two control lines were scored for symptoms of PCVAD. From 60 d of age pigs were grown in confined buildings or outside lots containing straw-bedded hoop structures. Scoring was on a scale of 0 (no symptoms), 1 (suspect), or 2 (positive) for symptoms of muscle wasting, growth retardation, rough hair coat, and diarrhea, and was done weekly from 70 to 180 d of age. 17.7% of the pigs received a score of 2. A sample of 37 pigs with a score of 2 were necropsied and lung, lymph node, tonsil, liver, kidney, thymus, spleen, ileum, and colon tissue were microscopically examined for lesions suggestive of PCVAD. Immunohistochemistry and RT-PCR were used to detect the presence of PCV-2 in collected tissues. All 37 pigs scored as a 2 were positive for PCV-2. PCVAD score was analyzed with ASREML using the Binomial and Probit functions to estimate genetic and environmental effects. Pigs receiving at least one score of 2 were considered positive for PCVAD; pigs scored only as 0 or 1 were considered negative. Direct and maternal heritabilities were 0.01 ± 0.001 and 0.11 ± 0.006, respectively, with a correlation of 0.61 between direct and maternal genetic effects. The proportions of variance due to common birth litter, common finishing pen, and common year/contemporary group/area were 0.11 ± 0.032, 0.05 ± 0.035, and 0.06 ± 0.035, respectively. Males had a significantly higher probability of PCVAD score than females ($P<0.025$). Significant differences ($P<0.05$) in weight between PCVAD pigs scored as positive or negative, estimated in ASREML, were -0.1 kg at birth, -0.52 kg at weaning, -4.35 kg at 60 d, and -20.17 kg at 180 d. Maternal genetic and common litter effects, as well as sex, environmental effects of finishing pen and year/contemporary group/area, affect incidence of PCVAD.

**Key Words:** Genetic variation, PCVAD, Immunity

**40 Genetics relationships among breeds of beef cattle.** Y. Huang*[1], M. D. MacNeil[2], L. J. Alexander[2], and J. P. Cassady[1], [1]*North Carolina State University, Raleigh*, [2]*USDA, Agricultural Research Service,, Miles City, MT.*

The objective was to estimate genetic distance among 16 populations of beef cattle from within the U.S. Thirty-three microsatellite markers representing 26 autosomes were used. MicroSatellite Analyzer 3.15 (MSA) was used to quantify number of alleles per marker, and observed and expected heterozygosity. Differentiation of allele frequencies among populations was also quantified with MSA. CONVERT 131 was used to prepare data for submission to PHYLIP 3.67 where Nei's unbiased genetic distance was estimated. Arlequin 2.0 was used to estimate within and among breed variation. The FST for these loci ranged from 0.05 to 0.22. On average, 11% of total genetic variation was between breeds. Unrooted neighbor-joining trees were constructed from Nei's unbiased genetic distance. Populations were roughly placed into five groups that were consistent with documented breed history and geographical origin. Angus, Red Angus, and Shorthorn were grouped as "Scottish A"; Highland and Hereford were grouped as "Scottish B"; Salers, Charolais, and Limousin were grouped as "French"; Texas Longhorn, Pineywoods, Florida Cracker, and Criollo were grouped as "Spanish"; and Braunvieh, Brown Swiss, Tarentaise, and Simmental were grouped as "Alpine". Min and max intra-group genetic distance are 0.12 ("French" and "Spanish") and 0.19 ("Alpine" and "Scottish A"). Angus and Red Angus diverged in the 1950s and Braunvieh and Brown Swiss diverged in the 1880's. As expected, Angus and Red Angus had the least genetic distance between them of any two populations. Surprisingly, shorter genetic distances were estimated between Braunvieh and Tarentaise (0.17), Braunvieh and Limousin (0.17), and Braunvieh and Charolais (0.15) then between Braunvieh and Brown Swiss (0.19). The greatest genetic distance was between Brown Swiss and Highland (0.44). Results may identify populations that would be expected to provide the greatest amount of hybrid-vigor when crossed, although we are unaware of experimental data with which to test this hypothesis.

**Key Words:** Cattle, Genetics, Diversity

**41 Identifying genes associated with bacterial shedding through transcriptional profiling.** J. J. Uthe*[1,2], Y. Wang[2], S. M. D. Bearson[1], A. M. O'Connor[2], J. McKean[2], D. Nettleton[2], J. C. Dekkers[2], and C. K. Tuggle[2], [1]*USDA, ARS, National Animal Disease Center, Ames, IA*, [2]*Iowa State University, Ames.*

Breeding animals with enhanced resistance to infection will reduce the use of antimicrobial agents during animal rearing without increasing