

3 Challenges in matching the physiology and productivity of the modern commercial sow. G. R. Foxcroft*, *University of Alberta, Edmonton, Alberta, Canada.*

Current management practices are failing to capture the extraordinary reproductive potential of the modern commercial sow. This is partly due to a failure to meet the nutritional demands of the gilt and sow throughout her productive lifetime. Inappropriate management of gilt development results in unacceptable variation in the weight of the gilt at breeding. Over-weight, rather than under-weight sows at the time of farrowing their first litter is an increasing risk factor for lack of retention in the breeding herd due to locomotor problems. Selection pressures placed on dam-line females has resulted in gradual improvements in overall productivity (pigs born or weaned/sow/year) and less variability in post-weaning fertility. However, although a very high percentage of weaned sows in well managed herds are expected to show post-weaning estrus and be bred immediately after weaning, the short weaning-to-ovulation intervals appear to place a limitation on subsequent litter size, linked to inadequate pre-ovulatory follicle development at the time of ovulation. Delaying breeding of the weaned sow for 14 to 21 days after first estrus, using either pharmacological suppression of estrus or skip-a-heat protocols, results in up to a two-pig increase in subsequent litter size, and a greater retention of sows in the breeding herd. Finally, biology of more prolific sow dam-lines appears to be associated with increasing variation in average litter birth weight as sows mature. In this sub-population of low litter weight-bearing sows, we hypothesize that high ovulation rates, associated with moderate to high embryonic survival to d 30 of gestation, results in extreme intra-uterine crowding, inadequate placental development and hence intra-uterine growth restriction due to an inability to compensate for inadequate placental growth in the peri-implantation period. Therefore, although some sows can show excellent lifetime performance in well managed breeding herds, genetic selection programs and management practices must address the increasing variability in the quality of the litters born.

Key Words: sow, fertility, management

4 The impact of amino acid nutrition on pregnancy outcome in pigs: mechanisms and implications for swine production. G. Wu*¹, F. W. Bazer¹, G. A. Johnson¹, S. W. Kim², and T. E. Spencer¹, ¹Texas A&M University, College Station, ²North Carolina State University, Raleigh.

Pigs suffer up to 50% embryonic/fetal loss during gestation and exhibit the most severe naturally occurring intrauterine growth retardation among livestock species. Placental insufficiency is a major factor contributing to suboptimal reproductive performance and low birth weights of piglets. We recently reported the unusual abundance of members of the arginine family of amino acids (e.g., arginine, ornithine, and glutamine) in porcine allantoic fluid during early gestation when placental growth is most rapid. Arginine is synthesized from glutamine and proline in swine and serves as the nitrogenous precursor for the synthesis of nitric oxide (a major vasodilator and angiogenic factor). Proline is the major substrate for placental synthesis of ornithine and polyamines (key regulators of protein synthesis and angiogenesis) in pigs, whereas branched-chain amino acids (BCAA) donate an amino group for glutamine production in placentae. Additionally, arginine, leucine and glutamine activate the mammalian target of rapamycin cell signaling pathway to enhance protein synthesis and cell proliferation in placentae. In support of a functional role for amino acids in improving pregnancy outcome, dietary supplementation with arginine to gilts fed a conventional diet beginning on d 30 of gestation to term increased the number and total litter weight of live-born piglets by 22% and 24%, respectively. In addition, formulating the diet for gestating gilts on the basis of optimal requirements of arginine and BCAA (relative to lysine) for fetal protein accretion decreased the oxidation of dietary amino acids, enhanced maternal tissue nitrogen balance, and reduced variation in piglet birth weight. We propose that amino acids, through the synthesis of nitric oxide and polyamines, stimulate placental angiogenesis and growth (including vascular growth), placental and uterine blood flow, and the transfer of nutrients from mother to fetus to promote fetal survival, growth and development. (Supported by USDA/NRI grants #2006-35203-17199 and 2008-35203-19120)

Key Words: amino acids, pigs, reproduction

Triennial Reproduction Symposium: Challenges and Opportunities Facing Livestock Reproduction in the 21st Century: Session 2: Genetic influences on animal reproduction

5 Application of genome based technologies for identifying genes and their expression that are important for livestock reproduction. J. F. Taylor*, S. D. McKay, J. E. Decker, D. Vasco, M. C. McClure, J. W. Kim, M. A. Rolf, T. Taxis, and R. D. Schnabel, *University of Missouri, Columbia.*

High-density single nucleotide polymorphism (SNP) genotyping platforms are beginning to revolutionize genetic improvement within the livestock industries. Because the effective population sizes of most breeds is small there are strong correlations between the alleles present at loci separated by hundreds of thousands of nucleotides. Consequently, even when unrelated animals are genotyped at high resolution, the presence of genes responsible for variation in a trait can be detected by associating individual SNPs with phenotypes. Genome-wide association (GWA) analyses using thousands of Holstein and Angus bulls have now been performed and have revealed that there are hundreds or thousands of loci contributing to phenotypic variation. However, the limiting factor in these studies is the availability of populations with a large number of high-quality phenotypes. We performed a GWA for

Heifer Pregnancy Rate (HPR) in 1721 registered Angus bulls, of which only 855 had EPDs for HPR. At genome-wide $P < 0.01$ we found only 13 regions on 9 chromosomes associated with HPR and none harbored the 'usual hormone suspects.' Variation within the gamma-aminobutyric acid A receptor cluster which is integral to gonadotropin production and release and therefore controls oocyte recruitment and ovulation was associated with variation in HPR. Unfortunately, variation within any of the four genes within this cluster may be causal for the detected HPR effect and technology does not yet exist to rapidly identify the causal mutations in genes/regulatory elements. This has led away from the concept of marker-assisted selection on casual mutations and towards a novel approach called genome-wide selection in which animals' breeding values are estimated from their high-density SNP genotype profiles. Genomic estimates of breeding value were officially incorporated into the USDA's genetic evaluation system in Spring 2009 and are currently under development for beef cattle.

Key Words: single nucleotide polymorphism, genome-wide association, genomic selection

6 Application of molecular and genetic tools for identification of reproductive traits to create and establish commercial lines of swine.

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Modern swine breeding programs seek to produce lines that optimize the efficiency of pork production systems. Pork production systems have increasingly utilized economic metrics that identify the key drivers of profitability for their operations. Providers of genetic material utilize these metrics to identify the phenotypes in pigs that contribute positively to the economic performance of customer businesses. Reproduction, and its numerous component traits, continues to be one of the main causes of success or failure in production systems. Improving these traits has been quite successful using quantitative genetic approaches (e.g., litter size, structure score) despite relatively low heritabilities. Application of molecular genetics holds the promise of increasing the rate of genetic improvement and permitting the inclusion of traits difficult to measure quantitatively on a routine basis. Two example traits, live pigs at five days of age and sow longevity, will be used to illustrate the research and development involved in generating new traits currently being used in a modern selection program. An example of pig survival will be used to demonstrate the combined impact of molecular and quantitative approaches to new trait development. The economic considerations of molecular and quantitative approaches will be discussed.

Key Words: trait development, pigs, marker-assisted selection

7 Epigenetics: A mechanism of adaptation to perinatal events. R. Lane*, R. McKnight, L. Joss-Moore, Q. Fu, and X. Ke, *Division of Neonatology, University of Utah Department of Pediatrics, Salt Lake City.*

Mammalian pregnancies have experienced threats throughout time from external environmental conditions and maternal pathophysiologies. These conditions and pathophysiologies threaten the life of the fetus. To survive, adaptations have arisen that increase the odds of survival in the fetus. Recent human epidemiological evidence and animal model studies suggest the price for these adaptations are postnatal morbidities such as diabetes. A molecular mechanism that links fetal adaptation to postnatal morbidities is epigenetics. Epigenetics are heritable changes in gene expression that occur in the absence of altered DNA sequence. Epigenetic determinants of gene expression are defined through modifications of chromatin structure, such as DNA methylation, covalent modifications of histones, and nucleosome repositioning. We have used multiple models of perinatal disease, ranging from intrauterine growth retardation (IUGR) to mechanical ventilation, to test the hypothesis that significant changes in the perinatal environment 1) modify chromatin structure of target relevant genes; 2) affect perinatal and postnatal gene expression of the same target genes; and 3) increase the risk of associated adult morbidities, such as diabetes. Relevant genes whose chromatin structure is known to be vulnerable to perinatal disease include insulin

growth factor 1 and peroxisomal proliferator activated receptor gamma. Our studies of these genes and others have led us to the following conclusions. First, epigenetics as a mechanism of perinatal adaptation is different from the traditional dogma of embryonic imprinting epigenetics, in which genes are turned either off or on. Within the context of a perinatal adaptation, epigenetics acts as a rheostat and/or alters mRNA variant expression. Second, epigenetic perinatal adaptations modify chromatin structure along the whole gene and do not necessarily concentrate at the 5 prime end of a gene. Third, epigenetic perinatal adaptations are tissue and gender specific events. A goal in the field will be to understand how to moderate the consequences of the epigenetic perinatal adaptations to minimize the predisposition towards postnatal morbidities.

Key Words: epigenetics, histone, chromatin

8 Impact of dam nutrition on subsequent growth and reproduction in beef heifers. R. N. Funston*, *University of Nebraska, West Central Research and Extension Center, North Platte.*

Maternal stimuli or an insult during a critical period of fetal development having long term implications for the offspring is the concept of fetal programming. Much of the evidence regarding how maternal nutrient restriction impacts prenatal physiological parameters was generated in laboratory animals. Few studies have evaluated effects of maternal nutrient restriction on post-natal growth and development in livestock species. Very few experiments have restricted specific diet components during pregnancy, such as protein, and evaluated offspring growth and performance. In recent studies at the University of Nebraska, calf birth weights were unaffected while calf weaning weights were greater from cows gestated on dormant winter range receiving protein supplementation during late gestation compared to unsupplemented cows. These studies demonstrated gestational treatments may augment physiologic parameters in production scenarios in contrast to data generated from laboratory-based studies. It is valuable to note protein supplementation enhanced growth after birth. Protein supplementation of the dam increased weaning weight of heifer calves, without a change in birth weight, and the change persisted through pregnancy diagnosis and subsequent calving. More interestingly, age at puberty was not greatly affected, yet protein supplementation of the dam increased heifer calf pregnancy rates. In a subsequent study, more heifers from protein-supplemented dams were pubertal before breeding, possibly affecting pregnancy rate. Heifers from protein-supplemented dams appear less feed efficient compared to heifers from unsupplemented dams. These data provide evidence that heifer fetuses exposed to nutritionally restricted environments (non-supplemented dams) during gestation become more efficient in later life. This body of research provides compelling evidence of a fetal programming response in female progeny to maternal nutrition in beef cattle.

Key Words: fetal programming, heifer progeny, supplementation