## ABSTRACTS

American Dairy Science Association American Society of Animal Science Canadian Society of Animal Science

## Sunday, July 12, 2009 SYMPOSIA AND ORAL SESSIONS

## Triennial Reproduction Symposium: Challenges and Opportunities Facing Livestock Reproduction in the 21st Century: Session 1: Global perspectives on animal health and livestock reproduction

**1 A global perspective on the evolution of animal agriculture.** R. D. Green\*, *Pfizer Animal Genetics, Sutton, NE.* 

As the end of the first decade of the new millennium approaches, the landscape of global animal agriculture appears to be changing more rapidly than ever. With the prediction that world demand for meat and dairy products is expected to increase by 40 to 50% by 2025, the challenges of the so-called Livestock Revolution to animal and dairy science cannot be understated. In previous generations, tremendous gains in the efficiency of production and product quality have been achieved through the advancement of the animal and dairy sciences across all disciplines. Most of these improvements came in the form of technologies that were developed based upon an improved understanding of farm animal biology and husbandry. However, the global animal agriculture of the future will require rapid science-based solutions to: 1) decrease the environmental footprint of livestock production including soil, range, water, and air quality; 2) reduce all aspects of energy utilization for production of animal products while increasing the efficiency of nutrient utilization; 3) capture energy from non-traditional sources for use in animal production systems; 4) enhance the well-being (as defined by a non-agrarian society) and adaptability of animals to efficient production environments; 5) improve the recycling of animal inputs and products; 6) enhance animal health and food safety in the face of a *smaller* planet; and 7) preserve and appropriately utilize plant and animal genetic resources. Additionally, while the trend of further consolidation, integration, and industrialization of animal agriculture is expected to continue in to the foreseeable future, there is also a growing differentiation toward small farms and production for local markets. Application of the new sciences of genomics and systems biology to address these challenges is a key strategy to meet the global needs for production of animal protein and by-products. Increasing reproductive efficiency and longevity, coupled with enhancing animal and human health in the face of greater disease challenge, are desired outcomes to meet the challenges which lie ahead.

Key Words: animal agriculture, global, technology

**2** Impact of animal health on endocrinology and reproduction in dairy cows. D. Wolfenson<sup>\*1</sup>, Y. Lavon<sup>1</sup>, R. Meidan<sup>1</sup>, Z. Roth<sup>1</sup>, and G. Leitner<sup>2</sup>, <sup>1</sup>The Hebrew University, Rehovot, Israel, <sup>2</sup>The Veterinary Institute, Bet-Dagan, Israel.

Mastitis is an important health issue in dairy production. Both shortterm clinical mastitis and chronic subclinical mastitis caused by Gram (+) or Gram (-) bacteria depress fertility. Yet, the detailed mechanisms underlying reproductive failure are not clear. In a series of studies, we examined the effects of subclinical, long-term mastitis, or short-term clinical mastitic events that ended weeks earlier, on ovarian follicle function. About 30% of mastitic (mainly subclinical) cows exhibited an extended (twice longer) estrus to ovulation interval than that of uninfected, or the remaining 70% of mastitic cows that exhibited a normal interval. This syndrome may lower fertilization rate. Delayed ovulation was associated with low follicular androgen and low follicular and circulating estradiol concentrations, resulting in low or delayed or no preovulatory LH surge. The one third of mastitic cows with low estradiol also exhibited low expression of steroidogenic genes in both theca and granulosa cell layers. The above syndrome is probably not related to attenuated pulsatile LH secretion, but rather to the direct disruptive effect of mastitis on follicle function. Delayed ovulation resulted, as expected, in a delayed rise of circulating progesterone. The factors affecting the variability in response among individual mastitic cows are unclear. In another study we found that the Gram-positive toxin (but not Gram-negative LPS), which is usually associated with subclinical mastitis, manifested a significant carryover disruptive effect on preovulatory steroid concentrations and steroidogenic gene expression. The disruptive effect of mastitis on oocyte competence was demonstrated in vitro. Blastocyst formation rate but not cleavage rate was significantly lower in oocytes obtained from mastitic cows. These studies indicate that mastitis has a profound disruptive effect on timing of ovulation, follicular steroidogenesis and oocyte competence, which may partially explain the low fertility of mastitic cows.

Key Words: mastitis, reproduction, cow

**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-toovulation 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<sup>\*1</sup>, F. W. Bazer<sup>1</sup>, G. A. Johnson<sup>1</sup>, S. W. Kim<sup>2</sup>, and T. E. Spencer<sup>1</sup>, <sup>1</sup>*Texas A&M University, College Station*, <sup>2</sup>*North 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