production indicated that including 10% of shea nut cake in finishing feedlot *Bos taurus* diets reduced 24-h in vitro methane production by approximately 20% without any significant reduction in total and individual VFA production. Methane output was also reduced during in vitro ruminal fermentation of *Brachiaria ruziziensis* when the in vitro mixture was supplemented with 20% of leaves of the browse plant *Securinega virosa*. Different fractions of Napier grass were evaluated in Ghana for methane production using a hand-held methane analyzer. The stem fraction was 2.5 times higher than that of the leaves, and as the grass advanced in age, the methane production increased. Emissions directly associated with animal production have globally increased partly because of the high demand for animal products. It is envisaged that emission intensity from animal agriculture in the West African subregion will increase due to the nature of feed they feed on. In an attempt to reduce emissions from animals, scientists adopt in vitro method of screening and selection of feed for ruminants. This, however, fails to estimate emission per feed intake, making it impossible to advance the best practices that result in GHG mitigation without any adverse effect on animal productivity. Although the global research alliance suggests to its member countries, of which Ghana is one, to focus on activities that reduce emissions intensity of livestock while increasing productivity, little is seen in terms of investment in developing research activities that reduces emissions. Several agro-byproducts including palm kennel cake and other cakes of leguminous crop exist in the subregion. Owing to their high lipids content, when supplemented to the high fibrous diet consumed by ruminants, it is certain that not only will methane emissions be reduced but that productivity will also increase.

Key Words: methane, mitigation, Africa

0690 Effects of native and tame grassland species reintroduction on carbon sequestration potential on the Canadian Prairies. A. D. Iwaasa*, B. McConkey, and H. Wang, *Agriculture and Agri-Food Canada, Swift Current, SK, Canada*.

Rising concentration of carbon dioxide in the atmosphere has prompted interest in implementing improved grassland management practices that could lead to a net accumulation of carbon in grassland soils. Converting cropland into native or tame perennial grasslands may result in substantial increase in soil C sequestration. Two studies were started in southern Saskatchewan where semiarid cropland was converted to perennial grasslands: Study 1 (2000–2014) seeded two different native pasture mixes (Simple, 7 species, and Diverse, 12 species) and Study 2 (2006–2011) seeded four different pasture types (meadow bromegrass + alfalfa [A], native grass mix [NG], NG + A, and NG + native legume). The objective of the studies was to determine the change in soil organic carbon (SOC) levels as affected by type of forage pasture mix and form of disturbance (grazing and nongrazing). In Study 1, the disturbance treatments were continuous, rotational, and nongrazing and the stocking rates were 0.8 and 1.9 animal unit (AU) ha^{-1}, respectively. In Study 2, continuous grazing occurred and the stocking rate ranged from 2.0 to 4.0 AU ha^{-1} depending on which pasture treatment was used. All pastures were grazed to a utilization rate of 50 to 60%. Soil samples from each pasture were collected from three locations and at each location, a five radial (star pattern) sampling pattern occurred. From each of the five microsites, core samples were taken at five depths (0–7.5, 7.5–15, 15–30, 30–45, and 45–60 cm). Soil sampling for study 1 occurred in 2000, 2004, 2008, 2011, and 2014, whereas in study 2, it occurred in 2008 and 2011. In study 1, no SOC level (0–15 cm) differences were observed between disturbance and pasture mix combinations and interaction after 14 production years. Soil organic C levels were affected by year ($P < 0.0001$), which was expected with the different environmental conditions experienced among the different soil sampling years. In study 2, no SOC level (0–15 cm) differences were observed for interaction or main effects after three production years. Our studies did not support our hypothesis that a more diverse native mix (higher species richness) and tame grass + alfalfa would have higher SOC level than other treatments. Detecting small SOC change is difficult due to spatial heterogeneity in initial SOC, soil texture, bulk density, and plant productivity. Using our results, we develop criteria for measurement systems to detect changes design to detect SOC change.

Key Words: grazing, soil organic carbon, native and tame forages

GENOMICS SYMPOSIUM: TRANSLATIONAL GENOMICS TO IMPROVE FERTILITY OF ANIMALS

0691 Translational genomics for improving sow reproductive longevity. D. C. Ciobanu*[1], S. D. Kachman[1], S. Olson[1], M. L. Spangler[1], M. D. Trenhaile[1], H. Wijesena[1], P. S. Miller[1], J. J. Riethoven[1], C. A. Lents[2], J. F. Thorson[2], R. Massey[3], and T. J. Safranski[3], *[1]University of Nebraska – Lincoln, Lincoln, [2]USDA, ARS, U.S. Meat Animal Research Center, Clay Center, NE, [3]University of Missouri, Columbia*.

Approximately 50% of sows are culled annually with more than one-third due to poor fertility. Age at puberty, the earliest prebreeding indicator of reproductive longevity, can be measured early in life and has a moderate heritability. Selection for age at puberty is challenging due to labor-intensive phenotyping. Genomic selection for this trait would be a more viable option because it could increase accuracy and selection response. This study aims to identify DNA markers that

will predict, at weaning, gilts with early age at puberty and superior reproductive longevity. Our hypothesis is that genetic sources that affect age at puberty also explain variation in sow reproductive longevity. To test the hypothesis, data and tissues from a UNL resource population (n > 1,700 gilts) were integrated with genomewide association analyses, genome/RNA sequencing, and polymorphism discovery to uncover DNA variants that could predict age at puberty and reproductive longevity. A BeadArray panel of 56,424 SNP explained 25.2% of the phenotypic variation in age at puberty in a training set (n = 820). In an evaluation data set consisting of subsequent batches of similar genetics (n = 412), we compared a model based on all SNP from major 1-Mb windows with one based on SNP with the largest estimated effect. The model based on all SNP from the major windows explained more of the phenotypic variance compared with the model based on large effect SNP (12.3 to 36.8% vs. 6.5 to 23.7%). One major pleiotropic region included AVPR1A, for which the favorable genotype was associated with higher probability of the gilts to produce the first parity compared with the other genotypes (P < 0.05). Genome sequencing of 20 sires using Proton technology provided sources of genetic variation outside the limited capability of the BeadArray. Sequencing reads averaged 165 bp with a depth that varied from 16.2x to 29.7x. A substantial proportion (38%) of the total SNP discovered (140,000) were located in known genes. Transcriptome profile was evaluated by RNA sequencing of the microdissected arcuate nucleus (ARC) in pre-/postpubertal gilts (n = 12) subjected to different dietary treatments. Using a combination of Tophat and local Bowtie, the majority of the reads were aligned to the reference genome/transcriptome (>93%). This integrated knowledge accompanied by economic modeling will be evaluated in commercial populations to understand and improve expression of puberty and sow reproductive potential through genomic selection. This project is supported by Agriculture and Food Research Initiative Competitive Grant number 2013-68004-20370 from the USDA–National Institute of Food and Agriculture. The USDA is an equal opportunity provider and employer.

Key Words: age at puberty, genomic selection, reproductive longevity.

0692 Detection and selection against early embryonic lethals in United States beef breeds. J. F. Taylor*[1], R. D. Schnabel[1], B. Simpson[2], J. E. Decker[1], M. Rolf[3], B. P. Kinghorn[4], A. Van Eenennaam[5], M. D. MacNeil[6], D. S. Brown[1], M. F. Smith[1], and D. J. Patterson[1], *[1]University of Missouri, Columbia, [2]GeneSeek, a Neogen Company, Lincoln, NE, [3]Oklahoma State University, Stillwater, [4]University of New England, Armidale, Australia, [5]University of California, Davis, [6]Delta G, Miles City, MT.*

More than 3,000 bovine genomes have now been sequenced worldwide, and much of the variation within the genome of cattle has been discovered. Many variants likely to have functional effects due to their locations within annotated coding regions have been identified. However, the lack of complete annotation leads to our inability to identify variants that lie within regulatory regions, and furthermore, the phenotypic effects caused by coding variants are not well understood. Among these are the class of loss of function variants within genes that are essential for life—a gene set that is largely conserved in identity among mammals. Based on marker haplotype analyses performed primarily in dairy breeds, we postulate that several lethal variants segregate within most cattle breeds and that these variants tend to be breed specific in their identity. To identify these variants, we have designed the first generation of a bovine functional assay, the GGP-F250, to contain 34,000 common variants present on many of the genotyping assays currently used by the cattle industry and 199,000 predicted genic functional variants. The assay is publicly available from GeneSeek. These variants were discovered by analyzing whole genome sequence data for 297 cattle from 17 breeds and RNA-seq data for 159 animals and were confirmed using data from the 1000 Bull Genomes Project and dbSNP. We have genotyped 18,300 animals with this assay representing Holstein and 9 U.S. beef breeds including over 11,000 Angus animals, and these data are being used to fine map QTL underlying susceptibility to respiratory disease and feed efficiency. Data from Angus are being used to sequentially test each putative functional variant for a deficiency of homozygotes and fully penetrant lethals will manifest with a complete lack of homozygotes. Candidate lethal alleles will be migrated to assays commonly used in the beef industry such as the GGP-LD and GGP-HD platforms to genotype hundreds of thousands of animals and validate the lack of homozygotes. Mate selection software is being developed as part of the USDA National Institute of Food and Agriculture grant number 2013-68004-20364 “Identification and management of alleles impairing heifer fertility while optimizing genetic gain in Angus cattle” project to assist breeders with mating decisions based on each animal’s carrier status for defects and embryonic lethals.

Key Words: GGP-F250, fertility, embryonic lethal

-693 Genomic selection for improved fertility of dairy cows with emphasis on cyclicity and pregnancy.

G. J. M. Rosa*[1], P. J. Pinedo[2], J. E. P. Santos[3], R. C. Bicalho[4], G. Schuenemann[5], R. Chebel[6], K. N. Galvão[3], R. O. Gilbert[7], S. L. Rodrigez-Zas[8], C. M. Seabury[9], J. Fetrow[6], and W. W. Thatcher[10], *[1]University of Wisconsin, Madison, WI, [2]Colorado State University, Fort Collins, CO, [3]University of Florida, Gainesville, FL, [4]Cornell University, Ithaca, NY, [5]The Ohio State University, Columbus, OH, [6]University of Minnesota, Saint Paul, MN, [7]Cornell University College of Veterinary Medicine, Department of Clinical Sciences, Ithaca, NY, [8]University of Illinois, Urbana-Champaign, IL, [9]College of Veterinary Medicine, Texas A&M University, College Station, TX, [10]Department of Animal Sciences, University of Florida, Gainesville, FL*

The overall goal of this ongoing integrated project (research, extension, and education) is to make use of advanced genomic technologies to improve dairy cattle fertility, with emphasis on cyclicity and pregnancy. The specific aims are 1) development of a fertility database with genotypes and phenotypes based on objective and direct measures of fertility in Holstein dairy cows, 2) identification of genome regions associated with fertility traits and use of this information on prediction models that can be applied in selection of dairy cattle for improved fertility, 3) development and implementation of a comprehensive extension program on best management and genomic selection practices to improve fertility of dairy herds, and 4) development of an education component targeting the general public as well as students in animal and veterinary sciences. In this presentation we will describe the development and outcomes on Specific Aim 1 as well as some preliminary analyses and results related to Specific Aim 2. A total of 12,000 Holsteins cows from 7 states (New York, Minnesota, Wisconsin, Texas, California, Florida, and Ohio), comprising 2 to 3 farms per state, were enrolled at calving and monitored weekly until pregnancy. Main events were uterine health, metabolic disorders, cyclicity, estrus, pregnancy per AI, and pregnancy loss, together with milk yield until 305 DIM. A reproductive index, calculating the predicted probability of pregnancy at first AI after calving, was generated using a logistic regression model that included cow-level variables such as diseases incidence, anovulation, BCS, and milk yield. Within each farm, cows were stratified as pregnant on d 60 after the first AI (high-fertility population) and as nonpregnant on d 60 after 2 AI (low-fertility population). A selective genotyping approach was implemented using the reproductive index developed, with selected cows from the high-fertility pregnant (850 cows) and the low-fertility nonpregnant (1,750 cows) groups. Preliminary analyses of the phenotypic data have been implemented, including the estimation of genetic parameters of cyclicity and other fertility indicators as well as the impact of postpartum diseases on lactation curves. Heritability estimates ranged from 0.03 to 0.12 for the various traits, and many factors influencing the lactation curve have been detected. The next step of the project will include multitrait and network analyses of the fertility indicators as well as genomewide association and gene-set enrichment analyses for detection of genomic regions and sets of genes affecting fertility traits in dairy cattle.

Key Words: genomics, fertility, dairy

0694 Improving fertility of dairy cattle using translational genomics.

T. E. Spencer*[1], H. L. Neibergs[2], P. J. Hansen[3], J. B. Cole[4], J. Dalton[5], D. A. Moore[6], M. Chahine[7], and A. De Vries[3], *[1]Division of Animal Sciences, University of Missouri, Columbia, [2]Department of Animal Sciences, Washington State University, Pullman, [3]Department of Animal Sciences, University of Florida, Gainesville, [4]Animal Genomics and Improvement Laboratory, ARS, USDA, Beltsville, MD, [5]University of Idaho, Caldwell, ID, [6]Department of Veterinary Clinical Sciences, Washington State University, Pullman, [7]Department of Animal and Veterinary Sciences, University of Idaho, Twin Falls*.

Selection for higher milk production in United States dairy cattle has been very successful during the past 50 yr; however, today's lactating dairy cows exhibit a high incidence of subfertility and infertility with a national pregnancy rate of only 15%. An integrated approach is being used to improve reproductive performance and profitability of dairy cattle using recent advances in animal genomics and improved understanding of fertility. The overarching hypothesis is that lactating cow fertility can be increased through genetic selection for maternal fertility in heifers and cows and use of sires with high daughter pregnancy rate (DPR), resulting in a significant, sustainable, and profitable increase in overall herd fertility. Objectives are to 1) identify genomic loci associated with fertility in dairy heifers and cows, 2) identify functional SNP associated with DPR and early embryo development, (3) evaluate the efficiency and profitability of increasing fertility in dairy cattle using genetic selection tools, and 4) engage in technology transfer regarding novel approaches for improving fertility using genetic selection tools to dairy farmers, dairy farm personnel, and their advisors in English and Spanish using DAIReXNET and extension road shows. Each objective involves an integrated team of scientists working in animal reproduction, genomics, breeding, and extension toward a common goal. The expected outcome and impact of meeting our goal is increased sustainability, profitability and international competitiveness of the U.S. dairy industry. This project was supported by Agriculture and Food Research Initiative Competitive Grant number 2013-68004-20365 from the USDA

National Institute of Food and Agriculture.

Key Words: dairy cattle, fertility, genomics

ADSA–ASAS NORTHEAST SECTION GRADUATE STUDENT ORAL COMPETITION

0695 Survival and growth of *Listeria monocytogenes* on queso fresco cheese stored under modified atmospheres. S. R. Barnes* and D. J. D'Amico, *University of Connecticut, Storrs*.

Cheese varieties characterized by high moisture and low acidity, such as queso fresco (QF), have been shown to support the growth of *Listeria monocytogenes* to very high levels during refrigerated storage. In addition to improving quality and extending shelf life, modified atmosphere packaging (MAP) has been used to control the growth of pathogenic microorganisms in various foods. The objective of this research was to determine the effect of five MAP conditions on the survival and growth of *L. monocytogenes* as postprocessing contaminants on QF during refrigerated storage at 7°C. To test the hypothesis that MAP affects *L. monocytogenes* growth on QF during storage when compared with conventional methods of packaging (i.e., vacuum), 25-g samples of QF were surface inoculated with an eight-strain cocktail of *L. monocytogenes* to achieve 4 log cfu/g. Following microbial attachment, individual cheeses were placed in 75-µm high barrier pouches (nylon/ethylene vinyl alcohol/polyethylene), packaged under one of seven conditions (air, vacuum, 100% carbon dioxide [CO_2], 70% CO_2/30% nitrogen [N_2], 50% CO_2/50% N_2, 30% CO_2/70% N_2, or 100% N_2), and stored at 7°C. Samples were removed weekly through 28 d of storage for enumeration of *L. monocytogenes*. Data were analyzed using one-way ANOVA. Analyses identified overall effects of time and packaging treatment on the change in *L. monocytogenes* counts over 28 d ($P < 0.001$). *Listeria monocytogenes* populations increased rapidly on cheese packaged under air, vacuum, and 100% N_2, with counts significantly differing ($P < 0.001$) from the initial inoculum by Day 7. Changes in counts over time and counts on individual days did not differ between these treatments, with means exceeding 7 log cfu/g on Day 14 and stabilizing at >8 log cfu/g through Day 28. Treatments that incorporated CO_2 at any percentage significantly limited pathogen growth over time compared with treatments without CO_2, including air and vacuum controls ($P < 0.001$). Although pathogen growth was limited, the change in counts over 28 d in CO_2 treatments was significant ($P < 0.05$), reaching a mean of 5.0 log cfu/g. Pathogen growth during storage did not significantly differ between treatments with varying percentages of CO_2. These data demonstrate that vacuum packaging and conditions containing 100% N_2 do not impede the growth of *L. monocytogenes* on QF. However, packaging under anaerobic modified atmospheres containing CO_2 may be a promising control for limiting *L. monocytogenes* growth on QF and other high-moisture, low-acid cheeses during cold storage.

Key Words: packaging, *Listeria monocytogenes*, cheese

0696 The effects of poor maternal nutrition on dam and offspring inflammatory status throughout gestation. A. K. Jones*, S. M. Pillai, M. L. Hoffman, K. K. McFadden, K. E. Govoni, S. A. Zinn, and S. A. Reed, *Department of Animal Science, University of Connecticut, Storrs*.

We hypothesized that poor maternal nutrition during gestation exaggerates the inflammatory status of ewes throughout gestation and that this would be reflected in the immune profile of offspring during late gestation and at parturition. Pregnant western white-faced ewes ($n = 78$) were individually housed and fed 100 (CON), 60 (RES), or 140% (OVER) of NRC requirements for TDN beginning at d 30.2 ± 0.2 of gestation. Whole blood was collected from a subset of ewes at d 24.0 ± 0.9 and 135.0 ± 0.3 of gestation ($n = 4$ ewes per diet per day) and from 3 to 4 offspring per diet euthanized at d 135 of gestation or within 24 h of parturition. Whole blood RNA was isolated, and expression of 84 genes mediating inflammation was profiled using a real-time PCR array. Data were analyzed using PROC MIXED in SAS for main effects and interaction of diet and day of gestation for ewes and main effect of maternal diet for offspring with the PDIFF option for mean comparisons. In ewes, regardless of diet, relative to d 24, *interleukin* (*IL*) *17β*; receptors for *IL1*, *IL6*, *IL8*, *IL10α*, and *IL10β*; *colony stimulating factor* (*CSF*) *2*; *CSF3*; *tumor necrosis factor superfamily member* (*TNFSF*) *13*; *TNFSF13β*; *chemokine ligand 17*; *chemokine receptor 1*; *vascular endothelial growth factor A*; and *platelet factor 4* increased 3.8-, 1.7-, 2.1-, 2.4-, 1.5-, 1.3-, 1.9-, 2.0-, 1.6-, 1.9-, 3.7-, 1.7-, 1.7-, and 2.5-fold at d 135 of gestation, respectively ($P \leq 0.05$). In contrast, *chemokine ligand 10* decreased 4.1-fold at d 135 relative to d 24 in ewes, regardless of diet ($P = 0.02$). In OVER ewes, *TNFSF4* decreased 1.5-fold compared with CON ewes ($P \leq 0.05$). *Interleukin 1 receptor antagonist* (*IL1RN*) increased 1.8-fold in RES ewes at d 135 compared with CON ewes at d 24 ($P \leq 0.04$). In offspring, *chemokine ligand 22* increased 2.8-fold in OVER ewes compared with CON ewes at d 135 ($P \leq 0.05$). At parturition, *interferon γ* decreased 3.0- and 3.8-fold in OVER and RES ewes, respectively, compared with CON ewes ($P \leq 0.006$). In conclusion, inflammatory progression is characteristic of advancing gestation and the increased expression of *IL1RN*, an antagonist of *IL1α* and *IL1β*, in RES ewes at d 135 may be a protective mechanism suppressing proinflammatory signaling. The inflammatory profile of offspring was altered by poor maternal nutrition, which may negatively affect growth and health if persistent postnatally, thereby reducing offspring productivity.

Key Words: inflammation, maternal nutrition, sheep