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

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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.

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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

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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