

Pregnancy loss directly impairs reproductive performance in dairy cattle. Early pregnancy losses (before 30 d after AI) cannot be detected and are indistinguishable from conception failure. Here, we evaluated the loss of pregnancy following accurate detection of a viable embryo. As such, our objectives were to assess alternative models for genetic analysis of presence (BIN) or number (NUM) of pregnancy losses in US Holstein cows. Linear and Probit models were fitted for BIN, whereas linear and Poisson models were used for NUM. Data consisted of 14k confirmed pregnancy/abortion records on 8k Holstein cows distributed over the first 2 lactations. All models included days in milk, year-season, and types of service (insemination or embryo transfer) as fixed effects, and animal and service sire as random effects. The alternative models were compared with respect to goodness-of-fit, ranking of sires, and predictive ability in 5-fold cross-validation. Estimates of heritability ranged from 1% to 8% for BIN and 1% to 9% for NUM. Nonlinear models (Probit and Poisson) showed better goodness-of-fit than their counterpart linear models. From a breeder's perspective, an important question is whether these models yield different breeding decisions. The Spearman rank correlations between bulls' breeding values were high, from 0.84 to 0.97, suggesting a minor re-ranking. All the models exhibited similar predictive ability. Indeed, for BIN models, the mean-squared error of prediction (MSEP) ranged from 0.16 to 0.18, whereas for NUM models, MSEP values ranged from 0.14 to 0.16. Overall, our results suggest that pregnancy loss is a heritable trait, and hence, genetic selection for reduced risk of abortion is feasible. In addition, the use of nonlinear models seems a reasonable choice for analyzing pregnancy losses.

Key Words: heritability, non-linear models, reproductive performance

127 Targeted sequencing reveals deleterious mutations affecting dairy bull fertility. R. Abdollahi-Arpanahi*, H. A. Pacheco, and F. Peñagaricano, *University of Florida, Gainesville, FL.*

Bull fertility is often overlooked as a potential cause of reproductive inefficiency in dairy cattle. However, semen from one bull is used to inseminate hundreds of cows, and hence, one subfertile bull could have a major impact on herd reproductive performance. We previously identified 5 genomic regions, located on BTA8 (72.2 Mb), BTA9 (43.7 Mb), BTA13 (60.2 Mb), BTA17 (63.3 Mb), and BTA27 (34.7 Mb), that show very significant dominance effects on dairy bull fertility. Each of these regions explains about 5–8% of the observed differences in sire conception rate between bulls. Here, we aimed to identify the causal variants responsible for this variation using targeted sequencing (10Mb per region). For each genomic region, 2 DNA pools were constructed from high-fertility and low-fertility Holstein bulls. The DNA Sequencing analysis included reads quality control (using FastQC), genome alignment (using BWA and ARS-UCD1.2), variant calling (using GATK) and variant annotation (using Ensembl). The sequencing depth per pool varied from 39X to 51X. We identified 7,144 SNPs with opposing homozygous genotypes between low- and high-fertility pools. Notably, 74 of these SNPs were annotated as missense mutations, and at least 5 of them were classified as strong candidate causal variants, i.e., missense mutations with deleterious effects located on genes exclusively/highly expressed in testis or actively involved in the fertilization process. These candidate causal mutations are located in genes *ADAM28*, *TLL9*, *TCHP*, *FOXN4* and *ADAM2*. This work is the foundation for the development of novel genomic tools for improving dairy bull fertility, these causal mutations will allow the early detection and culling of subfertile bull calves or young genomic bulls.

Key Words: causal variants, DNA sequencing, sire conception rate

128 Multiparous Holstein cow vaginal microbiome near parturition associated with neonatal fecal microbiome. C. E. Owens*, H. G. Huffard, A. I. Nin-Velez, A. J. Duncan, C. L. Teets, K. M. Daniels, K. F. Knowlton, and R. R. Cockrum, *Virginia Polytechnic Institute and State University, Blacksburg, VA.*

Initial microbial inoculation of the calf gut is thought to stem from the dam's birth canal and colostrum; the objective of this study was to identify interrelationships between dam reproductive, colostrum, and calf fecal microbiomes. Multiparous Holstein cows ($n = 6$) were enrolled at 14 d before expected calving. At 10 d before expected calving, a calving alert system was placed on cows. Flocked swabs of the posterior vagina were collected within 24 h before calving. At birth, calves ($n = 6$; heifers = 3, bulls = 3) were immediately isolated and meconium samples were collected. Representative colostrum samples were collected within 1 h of calving and representative placenta samples were collected within 6 h of calving. Calf fecal samples were collected at 24 h and 7 d of age. Bacterial DNA was isolated from all samples and 16S rDNA amplicons underwent 2×300 paired end sequencing on the Illumina MiSeq platform. Sequences were aligned to the 97% Greengenes reference database in CLC Genomics Workbench. Alpha diversity was calculated using phylogenetic diversity and β diversity was calculated using weighted unifracs distances. Spearman's rank correlations were performed based on genera relative abundance in the placenta, vagina, and colostrum of a dam and its calf's meconium and fecal samples. Proteobacteria were the most abundant phylum in the placenta (48%), vagina (58%), colostrum (96%), and 24 h calf feces (85%), while Bacteroidetes were the most abundant phylum in meconium (43%) and 7 d calf feces (43%). Colostrum and placenta samples had the least phylogenetic diversity within each sample, but had a high similarity between samples. Genera in the vagina had a moderate correlation with genera in meconium ($r_s = 0.45 \pm 0.03$). Genera in colostrum had a low correlation with 24 h calf feces ($r_s = 0.10 \pm 0.04$). Dam vaginal microbiota could be used to predict calf gut composition. Further research on understanding these relationships could lead to discovery of core microbes that are the most influential on microbial composition.

Key Words: microbiome, calf, reproduction

129 Investigating conception rate for beef service sires bred to dairy cows. T. M. McWhorter*, J. L. Hutchison², H. D. Norman³, J. B. Cole², G. C. Fok³, D. A. L. Lourenco¹, and P. M. VanRaden², ¹Department of Animal and Dairy Science, University of Georgia, Athens, GA, ²USDA Animal Genomics and Improvement Laboratory, Beltsville, MD, ³Council on Dairy Cattle Breeding, Bowie, MD.

The widespread use of sexed semen on US dairy cows has led to an excess of replacement heifers' calves, and the sale prices for those calves are much lower than in the past. Cows not selected to produce the next generation of replacement heifers are increasingly being bred to beef bulls to produce crossbred calves for beef production. The purpose of this study was to investigate the use of beef service sires bred to dairy cows and heifers and to provide a tool for dairy producers to evaluate beef service sires' conception. Sire conception rate (SCR) is a phenotypic evaluation of service sire fertility that is routinely calculated for US dairy bulls. A total of 268,174 breedings were available which included 36 recognized beef breeds and 7 dairy breeds. Most of the beef-on-dairy inseminations (95.4%) were to Angus (AN) bulls; therefore, final evaluations were restricted to AN service sires bred to Holstein (HO) cows. Pedigree data for AN bulls was unavailable. There were 233,379 breedings from 1,344 AN service-sire to 163,919 HO cows. A mean (SD) conception rate of 33.8% (47.3%) was observed compared with 34.3% (47.5%) for breedings with HO sires mated to HO cows. Mean SCR reliability was 64.5% for 116 publishable bulls, with a maximum reliability 99% based on 25,217 breedings. Average SCR was near 0 (on AN base) with a range of -5.1 to 4.4. Breedings to HO heifers were also examined which included 19,437 breedings (443 AN service sire and 15,971 HO heifers). A mean (SD) conception rate of 53.0% (49.9%) was observed, compared with 55.3% (49.7%) for breedings with a HO sire mated to a HO heifer. Beef sires were used more frequently in cows known to be problem breeders, which explains some of the difference in CR. Mean service number was 1.92 and 2.87 for HO heifers,

and 2.13 and 3.04 for HO cows mated to HO and AN sires, respectively. Mating dairy cows to beef bulls may be profitable if calf prices are higher, fertility is improved, or if practices such as sexed semen, genomic testing, and improved cow productive life allow herd owners to produce both higher quality dairy replacement and increased income from market calves.

Key Words: sire conception rate, beef-on-dairy, beef bull fertility

130 Across-country genomic prediction of bull fertility in Jersey dairy cattle. F. M. Rezende*¹, M. Haile-Mariam², J. E. Pryce², and F. Peñagaricano¹, ¹*University of Florida, Gainesville, FL*, ²*Agriculture Victoria Research, Bundoora, VIC, Australia*.

The use of information across populations is an attractive approach to increase the accuracy of genomic predictions for numerically small breeds and traits that are time-consuming and difficult to measure, such as male fertility in cattle. This study was conducted to evaluate genomic prediction of Jersey bull fertility using an across-country reference population combining records from United States (US) and Australia (AU). Data set consisted of 1.5k US Jersey bulls with sire conception rate (SCR) records, 603 AU Jersey bulls with semen fertility value (SFV) records and roughly 90k SNP genotypes. Both SCR and SFV are evaluations of

service sire fertility based on cow field data, and both are intended as phenotypic evaluations because the estimates include genetic and non-genetic effects. Within and across-country genomic predictions were evaluated using univariate and bivariate GBLUP models. Predictive ability was assessed in 5-fold cross-validation using the correlation between observed and predicted fertility values. Genomic predictions within-country exhibited predictive correlations around 0.30 and 0.02 for US and AU, respectively. The AU Jersey population is genetically diverse, so careful selection of the reference population by including only closely related animals (e.g., excluding New Zealand bulls) allowed to increase the predictive correlations up to 0.20. Notably, the use of bivariate models fitting all US Jersey records and the optimized AU population allowed to achieve predictive correlations around 0.24 for SFV values, which is a gaining in predictive ability of 20%. Conversely, for predicting SCR values, the use of an across-country reference population did not outperform the standard approach using a pure US Jersey reference data set. Overall, our findings indicate that genomic prediction of male fertility in cattle is feasible, and the use of an across-country reference population would be beneficial when local populations are small and genetically diverse.

Key Words: multi-country reference population, semen fertility value, sire conception rate