

reduced. The objective of this study was to investigate if loci associated with pregnancy at first service were shared with loci associated with pregnancy at ≥ 4 services in Holstein heifers and cows. Nine hundred 2 heifers and 1032 primiparous cows were bred by artificial insemination during observed estrus for up to 5 consecutive estrus cycles for heifers and up to 13 cycles for cows. Pregnancy was determined via palpation on d 35 for heifers and cows not returning to estrus. Heifers and cows were genotyped using the Illumina BovineHD BeadChip (777,962 SNPs) and a genome-wide association study (GWAS) was conducted with a significance threshold of $P < 5 \times 10^{-8}$ to identify individual associations and $P < 1 \times 10^{-5}$ to identify shared associations. The GWAS identified 65 SNPs associated with pregnancy to first service in heifers and 138 SNPs associated with pregnancy to first service in cows. Eleven SNPs associated with pregnancy to first service were shared among heifers and cows. One hundred 64 SNPs were associated with the number of times bred (1, 4 or 5 times) required for pregnancy at d 35 in heifers, 79 SNPs were associated with times bred (1, 4–13 times) in cows and 7 SNPs were shared among Holstein heifers and cows. Two loci were associated with all phenotypes in heifers and cows. These results indicate that although most loci associated with pregnancy per artificial insemination in heifers and primiparous cows are unique, there are shared loci that are important in achieving pregnancy in both groups that could be used for genomic selection. *This project was supported by Agriculture and Food Research Initiative Competitive Grant no. 2013-68004-20365 and 2018-67015-27577 from the USDA National Institute of Food and Agriculture.*

Key Words: genome-wide association study (GWAS), dairy heifer, loci

277 Big data genomic investigation of dairy fertility and related traits with imputed sequences of 27K Holstein bulls. J. Jiang¹, P. VanRaden², J. Cole², Y. Da³, and L. Ma^{*1}, ¹University of Maryland, College Park, MD, ²Animal Genomics and Improvement Laboratory, Beltsville, MD, ³University of Minnesota, St Paul, MN.

Imputation has been routinely applied to ascertain sequence variants in large genotyped populations based on reference populations of sequenced animals. With the implementation of the 1000 Bull Genomes Project and increasing numbers of animals sequenced, fine-mapping of causal variants is becoming feasible for complex traits in cattle. Using the 1000 Bull Genomes data, we imputed 3 million selected sequence variants to 27,000 Holstein bulls after quality control edits and LD pruning. These bulls were selected to have highly reliable breeding values (PTAs) for 35 production, reproduction, and body conformation traits. We first performed whole-genome single-marker scan for the 35 traits using the mixed-model based association test in MMAP (<https://mmap.github.io>). The single-trait association statistics were then merged in multi-trait analyses of 3 groups of traits, production, reproduction, and body conformation, respectively. Candidate genomic regions 2 Mb long,

were selected based on the multi-trait analyses and used in fine-mapping studies. We implemented a state-of-art fine-mapping procedure with a Bayesian method that can assign a posterior probability of causality to each variant and for each independent association signal generate a minimum set of associated variants whose total posterior probability of causality exceeds a threshold (e.g., 95%). Our fine-mapping identified 36 candidate genes for production traits, 48 for reproduction traits, and 29 for body conformation traits, respectively, including some previously reported causal variants, e.g., Chr6:38027010 in ABCG2 for production traits and Chr7:93244933 in ARRDC3 for reproduction and body conformation traits. The candidate variant list may facilitate follow-up functional validation and expand our understanding of complex traits in dairy cattle. Additionally, our method can be readily applied to other species where large-scale sequence genotypes are available.

Key Words: genomics, reproduction, dairy

278 Genetic cues from fertilization to pregnancy establishment. M. S. Ortega^{*1}, J. B. Cole², T. E. Spencer¹, and P. J. Hansen³, ¹University of Missouri, Columbia, MO, ²Animal Genomics and Improvement Laboratory, ARS, USDA, Beltsville, MD, ³University of Florida, Gainesville, FL.

One approach to improve genetic selection for reproductive traits is to identify SNP in genes linked to reproductive processes. Genes in which these SNP reside represent targets for physiological intervention to improve fertility. Sixty-eight SNP previously associated with genetic merit for fertility and production were tested for association with daughter pregnancy rate (DPR) and other fertility traits in an independent population of Holsteins. There were 22 SNP in genes associated with genotypic estimates of fertility in the 2 Holstein populations; moreover, animals carrying allelic variants associated with higher genetic merit for fertility also exhibit more favorable phenotypic measurements of fertility. DPR reflects days open, which entails many physiological events including the ovulation of a competent oocyte, adequate sperm transport in the reproductive tract, successful fertilization in the oviduct, and development and implantation in the uterus. Genes containing SNP repeatedly associated with reproductive traits provides an indication of physiological processes important for variation among cows in reproductive function. Among the genes associated with fertility traits in both populations 14 genes were regulated by steroids, there were also genes involved in processes including oocyte quality (*COQ9*), fertilization (*BSP3*), trophoctoderm formation (*WBPI*), and lipid biosynthesis (*ACAT2*, *HSD17B7*, and *HSD17B12*). Future directions should include functional studies involving genome engineering to understand the biological role of genetic variants in the tight regulation of reproductive function in cattle.

Key Words: fertility, embryonic development, pregnancy establishment