Breeding and Genetics: Application and methods—Dairy II

748 The "it factor" for long-lived, high-producing dairy cows. Roger D. Shanks*[1,2] and Robert Miller[3], *[1]Holstein Association USA, Brattleboro, VT, [2]University of Illinois, Urbana, IL, [3]Mil-R-Mor Dairy, Orangeville, IL.*

Holstein cows that dairyman love live a long time and produce lots of milk. What is unique about these high-producing, long-lived cows? Obviously, these cows have received good management and avoided major health issues. Are the 50K genetics of these elite cows different from other Holsteins? Elite cows were defined phenotypically as having produced over 68,039 kg (150,000 lb) of milk during their lifetime and were classified as very good (VG) or excellent (EX). Elite cows were born in the decade before 2008. For a control, females born in the decade before 2008 with a 50K Holstein genome evaluation were chosen. Control females either had not produced 68,039 kg of milk during their lifetime or were not classified VG or EX. Genomes (50K or 77K) were available on 823 elite cows and 1,589 control females. Defining elite or control as binomial allowed detection of almost 200 markers that were different in allele frequency between elite cows and control females. The most significant chi-squared for differences in allele frequency between elite cows and control females identified a marker on chromosome 5, which had the largest difference in minor allele frequency of 0.17 between elite and control groups. Basing significance on chi-squared $-\log_{10} P$ of 8.000 as a threshold, 199 markers were significant and were distributed across all bovine chromosomes. Minor allele frequencies of elite cows were greater for 140 of these markers and minor allele frequencies of control females were greater for 59 markers. As interpretation, minor allele frequencies define uniqueness. The uniqueness of elite cows was supported by more positive changes in minor allele frequencies for the elite cows. A single "it factor" is insufficient to identify uniqueness of elite cows, but many markers are candidates to contribute to the uniqueness. Because allele frequency differences were found across all chromosomes, balance continues to be important in striving to increase the number of elite cows in the breed.

Key Words: genome, milk production, longevity

749 Identification of gene networks underlying dystocia in dairy cattle. Maria Arceo*[1], Francesco Tiezzi[1], John Cole[2], and Christian Maltecca[1], *[1]North Carolina State University, Raleigh, NC, [2]Animal Genomics and Improvement Laboratory, ARS, USDA, Beltsville, MD.*

Dystocia is a trait with high impact in the dairy industry. Among its risk factors are calf weight, gestation length, breed and conformation. Biological networks have been proposed to capture the genetic architecture of complex traits, where GWAS show limitations. Our objective was to identify gene networks in Brown Swiss (BS), Holstein (HO) and Jersey (JE) cattle related to dystocia. De-regressed PTA (dPTA) for calving ease, gestation length, stature, strength and rump width of 8780 HO, 505 BS, and 1818 JE bulls were used in the analysis. A total of 45188 genotypes were available for all bulls. A single trait Bayes B GWAS was performed within breed with $\pi = 0.9$. The proportion of genetic variance (PV_g) explained by each SNP was $(2pq\tilde{a}^2)/\sum^{45188}(2pq\tilde{a}^2)$, with $\tilde{a}$ = posterior mean of the allelic effect. SNP with $VP_g \geq$ 75th percentile of the sample were ruled significant. Relevant SNP (rSNP) were defined as: significant in all traits, significant in all functional traits, or significant in all type traits. An association weight matrix (AWM) was constructed with rSNP in rows and traits in columns. Cells of the AWM corresponded to rSNP normalized effect size. These were mapped to genes with a 5′ or 3′ maximum distance of 2500 bp, rows in the AWM were indexed with genes. Genes were used to search for enriched functional annotation (FDR ≤ 0.15 HO, JE; FDR ≤ 0.3 BS). AWM row-wise partial correlations were computed. Significant correlations were interpreted as gene-gene interactions, resulting in a gene network. Networks included 1454 (BS), 1272 (HO) and 1455 (JE) genes. Their number of connections ranged between 1 and 15 (BS), 80 (HO), 13 (JE). A total of 13 (BS), 152 (HO), 108 (JE) genes in the networks were within reported dystocia QTL. Top enriched terms were cell adhesion (HO, JE), regulation of purine nucleotide metabolic process (BS). Most connected genes in the networks, enriching GO terms and within dystocia QTL were: FLOT1 (BS, 9 interactions), RASA1 (HO, 77) and ADRBK2 (JE, 12). Integrating knowledge from annotation tools to identify the functional biology of dystocia in dairy cattle can potentially improve genomic predictions that could result in increasing profitability of the dairy industry.

Key Words: dystocia, gene network, dairy cattle

750 Distribution of runs of homozygosity and its association with inbreeding depression in United States and Australia Jersey cattle. Jeremy T. Howard*[1], Christian Maltecca[1], Mekonnen Haile-Mariam[2,3], Ben J. Hayes[2,3], and Jennie E. Pryce[2,3], *[1]North Carolina State University, Raleigh, NC, [2]Dairy Futures Cooperative Research Centre, Bundoora, Victoria, Australia, [3]La Trobe University, Bundoora, Victoria, Australia, [4]Biosciences Research Division, Bundoora, Victoria, Australia.*

Differences in environment, management practices or selection objectives have led to a variety of choices being made in the use of dairy sires between countries. This may result in variation in selection intensity across the genome and could result in detectable differences in patterns of genome-level homozygosity between populations and consequently affect inbreeding depression differently across populations. The objective of the study was to characterize the frequency of homozygosity and its relationship with regions associated with inbreeding depression in Jersey dairy cattle from the United States (US) and Australia (AU). Genotyped cows with phenotypes on milk, fat and protein yield (n = 6,751 US; n = 3,974 AU) and calving interval (n = 5,816 US; n = 3,905 AU) were utilized in a 2-stage analysis. A run of homozygosity statistic (ROH4Mb), counting the frequency of a SNP being in a ROH of at least 4 Mb, was calculated across the genome. In the first stage residuals were obtained from a model that accounted for the additive genetic as wells as fixed effects. In the second stage these residuals were regressed on ROH4Mb using a single marker regression model or a machine-learning tree based regression algorithm (gradient boosted machine). The relationship between ROH4Mb and the SNP effect of a region for each trait was further characterized based on sliding window (500kb) direct genomic value (DGV) derived from a Bayesian LASSO analysis. The ROH4Mb effects were estimated by regressing residuals from the 2-stage approach on ROH4Mb and SNP effects estimated by regressing residual deviations from a model including only fixed effects on SNP markers. Genomic regions across multiple traits were found to be associated with ROH4Mb on BTA13, BTA23 and BTA25 for the US population and BTA3, BTA7, BTA17 for the AU population. Furthermore, multiple potential epistatic interactions were characterized. Lastly, the covariance between ROH4Mb and the SNP effect of