Breeding and Genetics: Genomic methods and application—Dairy

W79 Common copy number variation regions affecting dairy traits in Gyr cattle. Gerson A. Oliveira Junior*[1], Adriana S. Carmo[2], Adam T. H. Utsunomiya[3], Tatiane C. S. Chud[3], Fernando S. B. Rey[3], Jose Bento S. Ferraz[1], and Marcos Vinicicus G. B. da Silva[2], *[1]University of São Paulo, Pirassununga, São Paulo, Brazil, [2]Embrapa Dairy Cattle, Juiz de Fora, Minas Gerais, Brazil, [3]São Paulo State University, Jaboticabal, São Paulo, Brazil.*

The Gyr cattle (*Bos indicus*) is a very important dairy breed in tropical countries like Brazil, mainly due to its tolerance to heat stress and parasites infestations as well as their use in crossbreeding schemes with other specialized dairy breeds, such as Holstein. In addition to the single nucleotide polymorphism (SNP), genomic structural variants such as copy number variants (CNV) have been revealed to be a substantial source of genetic and phenotypic variation in cattle, being an alternative to explain the missing heritability of complex traits. The aim of this work was to investigate common CNV regions associated with dairy traits in Gyr cattle. The Log R ratio profiles of 481 Gyr animals were determined using a high density SNP chip (Illumina BovineHD BeadChip assay), and the phenotypes evaluated were: age at first calving (AFC), milk (MY), fat (FY), protein (PY) and total solids yields (TSY), and protein (PP), fat (FP) and total solids percentage (TSP). The Log R ratio, predicted from Genome Studio software, was used in Golden Helix SNP & Variation Suite (SVS) 8.1, and the copy number analysis module (CNAM – multivariate algorithm) was used to identify common CNVs among animals. Linear regression was employed to identify CNVs associated with each production trait with significance level of FDR >0.05. A total of 47 CNV regions were detected that affected at least one trait, with 22 regions affecting 3 or more traits where one of them, located at chromosome 7, affected all traits except MY. Under these 22 regions, 38 structural variation, 18 genes and one pseudo-gene annotated in bovine genome (Biomart tool of Ensembl) were observed. The Panther Classification System divided these genes into 10 biological process categories highlighting localization, immune system and metabolic processes. The results suggest that common CNV regions can be biologically involved with more than one dairy trait.

Key Words: structural variant, genomics, dairy cattle

W80 Genome-wide association study on conception rate, milk production, and SCS in different stages of lactation for first three parities in US Holsteins. Shogo Tsuruta*[1], Daniela A. L. Lourenco[1], Ignacio Aguilar[2], and Ignacy Misztal[1], *[1]University of Georgia, Athens, GA, [2]INIA, Las Brujas, Canelones, Uruguay.*

The objectives of this study were to conduct genome-wide association studies (GWAS) on conception rate (CR), production traits, and SCS for Holstein cows and determine if the genetic architecture of these traits is different in 3 stages of lactation for the first 3 parities in US Holsteins. Genome-wide association studies were conducted for conception rate (CR), test-day milk, fat and protein yields, and test-day SCS. The data were split into 3 sets: early (<14wk), middle (14wk ≤ DIM ≤ 29wk), and end (29wk <). Heritability estimates for CR were lowest (0.03) in the middle and highest (0.05 to 0.08) in the end of lactation in all parities. Genetic correlations of CR with other production traits were low and all negative (−0.1 to −0.5). The SNP marker effects were divided into equal segments of 30 SNP. A segment on chromosome 14 was associated with CR only in early and middle stages of lactation in the third parity; the proportion of the total genetic variance explained by this segment for CR were 2.7% and 2.5%, respectively. The proportions for test-day milk and fat yields were highest in the middle of lactation (7% for milk and 8% for fat) in all 3 parities, whereas the proportions for test-day protein and SCS were low (<2%). The results suggest that gene expression for CR and milk production traits is stronger in early and middle lactation stages and similar over the lactations.

Key Words: GWAS, conception rate, US Holsteins

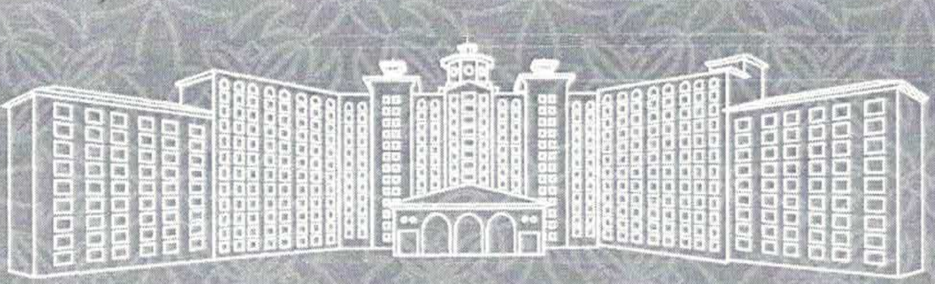
W81 Single nucleotide polymorphisms associated with thermoregulation in lactating dairy cows exposed to heat stress. Serdal Dikmen*[1,3], Xian-zhong Wang[2,3], and Peter J. Hansen[3], *[1]Department of Animal Science, Faculty of Veterinary Medicine, University of Uludag, Bursa, Turkey, [2]College of Animal Science and Technology, Southwest University, Chongqing, China, [3]Department of Animal Sciences, University of Florida, Gainesville, FL.*

Dairy cows with increased rectal temperature during heat stress experience lower milk yield and fertility. Given that rectal temperature during heat stress is heritable in dairy cattle, genetic selection for regulation of body temperature should reduce effects of heat stress on production. One goal of the study was to validate the relationship between genotype and heat tolerance for SNPs previously related to resistance to heat stress. A second goal was to identify new candidate gene SNPs related to resistance to heat stress. Thermotolerance was assessed in 625 lactating Holstein cows during the hottest part of the day in summer by measuring rectal temperature (a direct measurement of body temperature regulation), respiration rate (an indirect measurement body temperature regulation) and sweating rate (the major evaporative cooling mechanism in cattle). Specific genetic markers and candidate genes responsible for genetic variation in these variables were identified. For SNPs previously related to heat tolerance in genome-wide analysis, a region of BTA6 was related to rectal temperature and 3 closely-located genetic markers on BTA24 and another on BTA29 were associated with sweating rate. New candidate gene SNPs were identified for rectal temperature (n = 7), respiration rate (n = 9), and sweating rate (n = 6). The largest effect on rectal temperature was for *PGR*, which explained 2.1% of the phenotypic variation after adjustment for dry bulb temperature. This SNP could affect heat loss via cutaneous cooling because progesterone regulates vasodilation in the skin during local heating. *ACAT2* (involved in lipid metabolism) explained the largest variation in respiration rate (3.3%) and *SERPINE2*, which regulates the enzyme thrombin that regulates epithelial cells in sweat glands, explained the largest variation in sweating rate (2.1%). These genetic markers could prove useful in genetic selection for heat tolerance in Holstein cattle.

Key Words: heat stress, thermoregulation, SNP

W82 Multi-generational imputation of SNP genotypes and accuracy of genomic selection. Sajjad Toghiani* and Romdhane Rekaya, *The University of Georgia, Athens, GA.*

Superiority of genomic selection (GS) is possible only when high density single nucleotide polymorphism (SNP) panels are used to track QTLs affecting traits. Even with the continuous decrease in genotyping costs, only a small fraction of the population has been genotyped with these high-density panels. To reduce the cost of GS, it is often the case that a larger portion of the population is genotyped with low-density SNP panels and then imputed to a higher density. Accuracy of SNP genotype



JOINT ANNUAL MEETING

CONFERENCE INFORMATION AND SCIENTIFIC PROGRAM

2015
JAM
JOINT ANNUAL MEETING

ADSA®–ASAS
July 12–16 · Orlando, Florida

www.jtmtg.org/2015