M103 Genome-wide copy number variant analysis in Holstein cattle reveals variants associated with 10 production traits including residual feed intake and dry matter intake. E. E. Connor*[1], Y. Zhou[1,3], G. R. Wiggans[1], Y. Lu[2], R. J. Tempelman[2], S. G. Schroeder[1], H. Chen[3], and G. Liu[1], [1]*USDA-ARS, Animal Genomics and Improvement Laboratory, Beltsville, MD,* [2]*Michigan State University, East Lansing, MI,* [3]*Northwest A&F University, Yangling, Shaanxi, China.*

Copy number variation (CNV) is an important type of genetic variation contributing to phenotypic differences among mammals and may serve as an alternative molecular marker to single nucleotide polymorphism (SNP) for genome-wide association study (GWAS). Recently, GWAS analysis using CNV has been applied in livestock, although few studies have focused on Holstein cattle. Here, we describe 191 CNV of high confidence that were detected using SNP genotypes generated with the BovineHD Genotyping BeadChip (Illumina, San Diego, CA) among 528 Holstein cows. The CNV were used for GWAS analysis of 10 important production traits of cattle related to feed intake, milk quality, and female fertility, as well as 2 composite traits of net merit and productive life. In total, we detected 57 CNV associated ($P < 0.05$ after false discovery rate correction) with at least one of the 10 phenotypes. Focusing on feed efficiency and intake-related phenotypes of residual feed intake and dry matter intake, we detected a single CNV (CNV1) associated with both traits which overlaps predicted olfactory receptor gene *OR2A2* (*LOC787786*). Additionally, 2 CNV (CNV32 and CNV66) within the *RXFP4* and 2 additional olfactory receptor gene regions, respectively, were associated with residual feed intake. The *RXFP4* gene encodes a receptor for an orexigenic peptide, insulin-like peptide 5 produced by intestinal L cells, which is expressed by enteric neurons. Olfactory receptors are critical for transmitting the effects of odorants, contributing to the sense of smell, and have been implicated in participating in appetite regulation. Our results identify CNV for genomic evaluation in Holstein cattle, and provide candidate genes contributing to variation in feed efficiency and feed intake-related traits.

Key Words: dairy cow, genome-wide association study, copy number variation

M104 Association of residual feed intake with disease indicator traits in Holsteins. D. Hailemariam*[1], G. Manafiazar[1], J. Basarab[1,2], F. Miglior[3,4], G. Plastow[1], and Z. Wang[1], [1]*Department of Agricultural, Food and Nutritional Science, University of Alberta, Edmonton, AB, Canada,* [2]*Alberta Agriculture and Forestry, Lacombe Research Centre, Lacombe, AB, Canada,* [3]*Canadian Dairy Network, Guelph, ON, Canada,* [4]*CGIL Department of Animal Biosciences, University of Guelph, Guelph, ON, Canada.*

The objective of this study was to investigate the association of residual feed intake (RFI) with routinely measured milk components that are indicators of subclinical mastitis and ketosis. Milk somatic cell count (SCC, 10^3 cells/mL) is commonly used to diagnose subclinical mastitis while β-hydroxybutyrate (BHB, mmol/L) and acetone (ACT, mmol/L) are indicators of ketosis. RFI was phenotyped in 71 lactating Holstein dairy cows at the Dairy Research and Technology Center–University of Alberta with components of metabolic body weight, empty body weight change, and milk production energy requirements over 255 d in milk using random regression and multiple linear regression models. Correspondingly, test-day milk samples were collected twice a week and analyzed at DHI lab by a MIR spectrometer (MilkoScan FT+, Foss, Hillerød, Denmark) during the same period as for RFI prediction. A total of 3,810 test day records for each of the traits; SCC, BHB and ACT were obtained from April to August 2016. The data were analyzed using a MIXED model procedure of SAS with fixed effects of RFI (-RFI and +RFI), lactation number (1, 2 and 3+), milking time (AM and PM), interactions of RFI x lactation, RFI x milking time and random effects of cow. Days in milk was included in the model as a covariate. The result indicated that -RFI and +RFI groups did not differ in SCC (381.01 ± 55.77 vs. 359.47 ± 47.14; $P = 0.76$), BHB (0.53 ± 0.07 vs. 0.64 ± 0.05; $P = 0.25$) and ACT (0.30 ± 0.06 vs. 0.32 ± 0.04; $P = 0.75$). The correlation analysis also showed no evidence of RFI association with SCC ($r = 0.01$; $P = 0.91$), BHB ($r = 0.17$; $P = 0.17$) and ACT ($r = -0.042$; $P = 0.72$). The result suggests that selection for RFI may not be negatively correlated with incidence of subclinical mastitis or ketosis in dairy cattle. Estimation of the genetic correlations of RFI with SCC, BHB, and ACT in a larger sample is warranted to confirm these preliminary results.

Key Words: RFI, mastitis, ketosis

M105 Use of RNA-Sequencing technology for detection of microbial species. S. Lam*[1], F. Miglior[1,2], L. L. Guan[3], A. Islas-Trejo[4], D. Seymour[1], V. Asselstine[1], L. F. Brito[1], J. F. Medrano[4], and A. Cánovas[1], [1]*Centre for Genetic Improvement of Livestock, University of Guelph, Guelph, ON, Canada,* [2]*Canadian Dairy Network,, Guelph, ON, Canada,* [3]*Department of Agricultural, Food and Nutritional Science, University of Alberta,, Edmonton, AB, Canada.,* [4]*Department of Animal Science, University of California-Davis, Davis, CA.*

Evaluation of the bovine transcriptome using RNA-Sequencing (RNA-Seq) has made substantial impact in assessing functional and structural genomes in cattle. A preliminary study evaluated the metatranscriptome of bovine milk to determine the composition and structure of bacterial populations influencing subclinical mastitis. Differences in bacterial presence in milk between healthy and mastitic quarters were found in Holstein cows using RNA-Seq technology. The objective of this study is to further evaluate the use of RNA-Seq technology to assess the non-mapped milk bacteria genome in dairy cattle. Transcriptomic and metagenomic analysis were performed using RNA-Seq technology and 16S ribosome sequencing on milk collected from 4 quarters of healthy (n = 4) and mastitic (n = 4) dairy cows. Milk samples were collected 3 h after morning milking to obtain a high percentage of epithelial cells. Cow teats were cleaned with gauze (70% isopropanol) and milk was collected by hand milking directly into sterile 50 mL Falcon tubes or using a 3 cm plastic cannula to collect milk within the teat canal to avoid external contamination. Total RNA was extracted from somatic cells (SC) and milk fat globule (MFG) membrane from both hand milking and cannula milk samples. Using a RNA-seq analysis pipeline, preliminary results revealed that 60 to 75% of reads were categorized as mapped to the bovine reference sequence. All reads not mapping to the bovine genome were annotated for MFG (32% hand milking, 20% cannula) and SC (25% hand milking, 12% cannula). Analysis of SC non-mapped reads identified differences in microbial species present in healthy and mastitic milk. Further analysis will lead to more precise mapping of sequence data and improved understanding of bacterial gene expression, integrating data generated from RNA-Seq and 16S sequencing. Future assessment of the non-mapped reads using RNA-Seq will be performed to study the ability of RNA-Seq technology to capture invasive pathogens in milk and their association to genes differentially expressed in healthy and mastitic quarters. This assessment may lead to a comparative approach to examine the immune response to infection in dairy cattle.

Key Words: genome/host, transcriptomics/metatranscriptomics, RNA-sequencing technology