for all the spectral wavenumbers showed a similar pattern as found in literature. The second step involved fitting a model with the additive genetic and environmental effects, using calculated herd-year-season daughter-yield-deviations for milk yield and somatic cell score as dependent variables (n = 16,981). The additive genetic effect was modeled through a genomic relationship matrix, containing 483 sires. The environmental effect was modeled as an uncorrelated random effect or with the inclusion of an environmental covariance matrix (i.e., Kernel). The environmental effect included 3,316 herd-year season classes from 406 herds. The environmental kernels were built on BLUE solutions for the herd-year-season effect for different groups of wavenumbers as well as for milk yield and somatic cell score, as obtained from the first step. Results were split between predictions to new or known environments. The inclusion of the spectral-informed environmental effect allowed to outperform the other models in predicting performance to new environments, while prediction accuracy showed a slight decrease when predicting known environments. Fourier-transformed infrared spectral data can be used as a source of information for the calculation of the 'environmental coordinates' of a given farm in a given time, extrapolating genomic predictions to new environments.

Key Words: genomic selection, infrared spectra, kernel regression

306   Underlying genetic architecture of mastitis: A systematic review, meta-enrichment, and gene prioritization analysis of genome-wide association study results. S. G. Narayana*[1,2], E. de Jong[1], P. A. S. Fonseca[2], F. S. Schenkel[2], T. C. S. Chud[2], D. Powel[1], G. Wachoski-Dark[1], P. Ronskley[3], F. Miglior[2], K. Orsel[1], and H. W. Barkema[1,3], [1]*Department of Production Animal Health, Faculty of Veterinary Medicine, University of Calgary, Calgary, AB, Canada,* [2]*Center for Genetic Improvement of Livestock, Department of Animal Biosciences, University of Guelph, Guelph, ON, Canada,* [3]*Department of Community Health Sciences, Cumming School of Medicine, University of Calgary, Calgary, AB, Canada.*

Genome-wide association studies (GWAS) have been widely used to identify genomic variants associated with complex traits, such as mastitis, aiming to understand the underlying genetic architecture of the trait. However, no systematic review and gene prioritization analysis have been conducted to date on GWAS results for mastitis. Hence, the objective of this study was to perform a systematic review, meta-enrichment and gene prioritization analysis of GWAS studies to identify key genetic markers and genes associated with mastitis-related traits in dairy cattle. The systematic review was guided using the PPO framework (population: dairy cattle; prognostic tool: GWAS; outcome: mastitis/SCS). Four electronic databases and gray literature were searched and data were extracted from suitable articles. Meta-enrichment analysis was conducted using GALLO package. Gene prioritization analysis was performed using GUILDify and ToppGene. Out of 53 full-text articles identified from systematic review, 40 articles were used for meta-enrichment analysis. Gene and QTL annotation resulted in 9,125 and 43,646 unique genes and QTL, respectively. Nearly 7% of annotated QTL were related to "health" QTL class. Seventy-four genes were found to be common to Holstein, Jersey and Ayrshire breeds. The prioritization analysis resulted in 45 significant genes after Bonferroni correction. These genes were mainly associated with immune response, regulation of secretion and locomotion, and reproduction. Therefore, this study provides a fine mapping of the previously identified genomic regions associated with mastitis and pinpoints key candidate genes for mastitis.

Key Words: mastitis, gene prioritization, meta-enrichment

307   A comprehensive catalog of regulatory variants in the cattle transcriptome - a prototype for the FarmGTEx Project. G. Liu*, *Animal Genomics and Improvement Laboratory, Henry A. Wallace Beltsville Agricultural Research Center, Agricultural Research Service, USDA, Beltsville, MD.*

The systematic characterization of genetic regulatory variants on the transcriptome of livestock is essential for interpreting the molecular mechanisms underlying traits of economic value, and to increase the rate of genetic gain through artificial selection. The Farm Animal Genotype-Tissue Expression (FarmGTEx) Consortium is a collaborative endeavor to provide a comprehensive atlas of tissue-specific gene expression and genetic regulation in livestock species. In its pilot phase, by uniformly analyzing publicly available sequence data using our newly developed transcriptome pipeline as described in the cattle GTEx preprint (https://www.biorxiv.org/content/10.1101/2020.12.01.406280v1), we build a cattle Genotype-Tissue Expression atlas (cGTEx, http://cgtex.roslin.ed.ac.uk/) for the research community, based on 11,642 RNA-seq data sets from over 100 cattle tissues. We describe the landscape of bovine transcriptome across tissues and report thousands of *cis* and *trans* genetic variants (like expression QTL, or eQTL), associated with gene expression and alternative splicing for 24 tissues. We evaluate the specificity/similarity of these genetic regulatory effects across tissues, and functionally annotate them using a combination of multi-omics data. Finally, we link gene expression in different tissues to 43 economically important traits using a large transcriptome-wide association (TWAS) study to provide novel biological insights into the molecular regulatory mechanisms underpinning agronomic traits in cattle. This study provides a prototype for the FarmGTEx Project in other major farm animal species including pigs, chicken, sheep, and goats. This is a presentation about Cattle Genotype-Tissue Expression Atlas from the FarmGTEx Project Pilot phase. The contributors include Shuli Liu, Yahui Gao, Oriol Canela-Xandri, Sheng Wang, Ying Yu, Wentao Cai, Bingjie Li, Erola Pairo-Castineira, Kenton D'Mellow, Konrad Rawlik, Charley Xia, Yuelin Yao, Xiujin Li, Ze Yan, Congjun Li, Benjamin D. Rosen, Curtis P. Van Tassell, Paul M. Vanraden, Shengli Zhang, Li Ma, John B. Cole, George E. Liu, Albert Tenesa, and Lingzhao Fang from multiple international institutions.

Key Words: expression QTL, transcriptome-wide association (TWAS), RNA-seq

308   Signatures of selection as a tool to identify past selection criteria in Holstein cattle. F. J. Ruiz-Lopez*, A. Garcia-Ruiz, and J. G. Cortes-Hernandez, *CENIDFyMA-INIFAP, Queretaro, México.*

The small holder dairy production system in Mexico does not have an established genetic improvement program and therefore the selection criteria used by farmers to identify the genetic material to use in their dairies are unknown. Signatures of selection are regions conserved in the genome for generations due to selection processes, and one method to identify them is through runs of homozygosity (ROH). The aim of the present study was to investigate which characteristics have been improved over the years by farmers' mating decisions through signatures of selection in the genome of Holstein cattle in the small holder system in Mexico. After quality controls the study included 214 GeneSeek Genomic Profiler Bovine GGP 50K chip genotypes of Holstein cows from 4 small holder dairy herds located in the region of Tepatitlán Jalisco, Mexico. Only runs of homozygosity that had a minimum length of 500 kb and a minimum number of 25 SNPs were included, allowing up to 1 heterozygous SNP and 5 lost genotypes per run. The analyses were carried out with the bioinformatics platform SNP & Variation Suite v7.6.8.