1496V Functional annotation of regulatory elements in cattle genome during rumen development. G. Liu*, *Animal Genomics and Improvement Laboratory, Henry A. Wallace Beltsville Agricultural Research Center, Agricultural Research Service, USDA, Beltsville, MD.*

Mapping epigenomic marks and chromatin accessibility have developed as a robust process to annotate genomes, identify putative regulatory elements, and study their changing activity across different cell types, developmental stages, and complex phenotypes. Two Holstein bull calves were chosen: one calf (before weaning) was fed with milk replacer only for 2 weeks; while the other (after weaning) was fed with milk replacer only for 6 weeks, followed by a combination of milk replacer and grain-based diet for 4 weeks. We then performed the ATAC-seq and ChIP-seq of H3K27ac, H3K27m3, H3K4m1, H3K4m3, and CTCF using their rumen tissues after euthanasia. We profiled landscapes of bovine regulatory elements and explored dynamic changes of chromatin states in rumen development during weaning. The regulatory elements (15 chromatin states) and their coordinated activities in cattle were defined through genome-wide profiling of 4 histone modifications, CTCF-binding, DNA accessibility, DNA methylation, and transcriptome in rumen epithelial tissues. Each chromatin state presented specific enrichment for sequence ontology, methylation, trait-associated variants, transcription, gene expression-associated variants, selection signatures, and evolutionarily conserved elements. During weaning, weak enhancers and flanking active transcriptional start sites (TSS) were the most dynamic chromatin states and occurred in tandem with significant variations in gene expression and DNA methylation, significantly associated with stature, production, and reproduction economic traits. By comparing with in vitro cultured epithelial cells and in vivo rumen tissues, we showed the commonness and uniqueness of these results, especially the roles of cell interactions and mitochondrial activities in tissue development. Overall, our data indicated that epigenomic landscapes and chromatin states in both rumen tissues and primary rumen epithelial cells could change dynamically induced by butyrate or weaning, resulting in specific gene expression changes and influencing rumen development.

Key Words: cattle genome annotation, rumen development, cell interaction

1497V Innovative consortium building allowing the creation of common models for milk mid-infrared spectra-based predictions. N. Gengler*[1], F. Dehareng[2], H. Soyeurt[1], C. Grelet[2], and A. Vanlierde[2], [1]*ULiège-GxABT, Gembloux, Belgium,* [2]*Walloon Agricultural Research Center, Gembloux, Belgium.*

Currently many researchers develop novel traits addressing sustainability, environmental efficiency, and animal health. The use of predictors based on milk mid-infrared (MIR) spectra is a promising approach. The calibration process needs to cover the largest possible and, during the later application of the equation, expected variability and this for both, the reference phenotypes but also the MIR data. Therefore, for model building purposes, assembling reference values across different data sets is needed. However, this data across different contexts generates many other challenges that are not always properly addressed. This talk describes the different steps, taking MIR based prediction of CH_4 as an example. First, standardized spectral data will be needed to allow the combination of spectra across brands and apparatuses, both during the model building but also the application of the developed prediction equation. A procedure was developed and will be illustrated which consists in 2 steps based on the use of the same reference milk across the whole standardization network. First, spectra taken in different ranges of wavelength are transformed to a common range. Then bias and slope corrections, based on spectra obtained using the same reference milk, are applied for each wavelength. This second step is crucial, even in the context of genetic evaluations when mean shifts may be compensated by common measurement group based fixed effects. The reason is that variable slopes according to apparatuses, when not corrected, will lead to the generation of heteroscedasticity issues that are not easy to address in genetic evaluation using directly or indirectly the MIR data. The use of the standardization procedure also facilitates the calibration process as developped equations are not linked to a specific brand or even type of apparatuses but can be deployed across a whole network of partners, even if they have very diverse material. For this reason, this open innovative consortium building strategy was a success, and is in the process to allow the development of continuously improved MIR based predictions.

Key Words: CH_4 predictions, open consortium, sustainability

1498V Flexible testing and use of milk-only records. P. M. VanRaden*[1], G. C. Fok[1], L. R. Bacheller[2], G. B. Jansen[2], and J. A. Carrillo[2], [1]*USDA Animal Genmics and Improvement Lab, Beltsville, MD,* [2]*Council on Dairy Cattle Breeding, Bowie, MD.*

National genetic evaluation software assumed that fat yield was always recorded and excluded milk-only records. Milking systems often can accurately measure and record milk volume, but inline estimation of milk components is more difficult. Edit programs were revised to begin using milk-only records in April 2022 in the multi-trait evaluation of yield traits. Other trait groups such as cow fertility and health also will have more usable records because edits for those traits require having usable yield records. Herd variance ratios had been estimated from 1 trait (milk yield since 1992 and then fat yield since 2007) and applied to adjust all 3 traits (milk, fat, and protein). Since 1998 when data collection ratings (DCR) were introduced, milk and fat received the same weight calculated as an average of the DCR values for milk and components instead of separate weights because of software limitations. Programs were revised to use trait-specific variance adjustments and weights, to include milk-only records, and to remove much obsolete code. Most milk-only records are unsupervised and therefore get the same reduced weights and extra edits for percent milk shipped and percentage of valid ID as other owner-sampler herds. Lactation weights for milk, fat, and protein now use 3 separate DCR based on the testing patterns and correlations among test-days within lactations. New and official genetic evaluations were compared from December 2020 data. Numbers of usable lactation records were 98,269,605 for milk, 97,393,419 for fat, and 78,044,073 for protein, indicating that 876,186 milk-only records were added. Correlations of new with previous PTA were >0.9995 across all bulls for all 3 traits and were >0.997 for bulls born since 2007 with >50% reliability. The SD of PTA increased slightly by 2.4% for milk, 0.1% for fat, and 0.4% for protein but reliability also increased a little from the extra records. Further research could help adapt to more flexible testing options and automated data collection that continue to increase in popularity.

Key Words: milk recording, component testing, genetic evaluation