Public Abstract

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Title:COMPARISON OF METHODS FOR PARTITIONING TRAINING AND VALIDATION POPULATIONS TO OPTIMIZE PREDICTION ACCURACY AND ENABLE ACROSS-BREED GENOMIC SELECTION IN BEEF CATTLE

Across-breed genomic selection practices have the potential to revolutionize national genetic evaluation systems in the United States by including commerical cattle and increasing prediction power for hybrid animals. We used a population of 3,240 animals from the Carcass Merit Project to build across-breed genomic selection models for six carcass and four sensory panel traits across five breeds of commercially relevant beef cattle. Realized accuracies in these populations showed that the prediction models were very effective when used on animals within the same project and short time span. When used in an external validation in animals separated by approximately 10 years, prediction accuracies showed severe reductions, indicating that retraining of prediction models will have to be done frequently (possibly annually) in commercial populations. We also identified numerous regions of the genome which showed evidence of harboring causal mutations for these traits of economic importance. These regions will serve as independent validations in the literature as well as a guidepost for researchers looking for causal mutations within the bovine genome.