

Genome wide association study and whole genome selection for resistance to bovine respiratory disease in pre-weaned Holstein calves using thoracic ultrasonography

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Bovine respiratory disease (BRD) is one of the leading causes of morbidity and mortality in dairy calves. The objective of this study was to establish a protocol for objective and efficient assessment of BRD phenotypes in dairy calves to identify markers associated with BRD in a genome wide association study (GWAS) and build a reference population for whole genome selection (WGS). Trained evaluators assessed 1107 calves on 6 Wisconsin dairy farms at 3 and 6 weeks of age. Clinical scores were assigned by visual appraisal of eyes, nose, ears, attitude, cough, and temperature, and subclinical scores were assigned by measurement of lung lesions using thoracic ultrasonography. Overall BRD scores were computed as the interaction of clinical and subclinical assessments. Single nucleotide polymorphism (SNP) genotypes were available for 1016 calves, and after quality control and imputation data from 28,696 SNPs and 1014 individuals remained. A linear mixed model as used GWAS analysis, with SNP genotype as a fixed effect and polygenic background of the animal as a random effect. Phenotypes at 3 and 6 weeks of age were analyzed separately, and BRD scores were considered as binary (healthy or affected) or ordinal (six levels with increasing severity). At 3 weeks of age, 8 and 6 significant SNPs ($P < 0.00005$) were detected in the binary and ordinal analyses, respectively, with common SNPs on chromosomes 1, 7, 17, and 18. At 6 weeks of age, 3 significant SNPs were detected in each of the binary and ordinal analyses, with common SNPs on chromosomes 8 and 9. Assessment of BRD using visual (clinical) and ultrasound (subclinical) scores allows objective and efficient measurement of BRD for identifying important SNPs by GWAS or implementing WGS. Further analysis is needed to identify putative genes affecting BRD and to assess the reliability of whole genome predictions.

Key words: genome wide association study, bovine respiratory disease, whole genome selection