

A genome wide association study of twinning in Holstein cattle.

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Twinning is considered an undesirable trait by the dairy industry and identification of markers associated with twinning rate would facilitate selection for reduced incidence. The primary objective of this study was to conduct a Genome Wide Association Study (GWAS) of twinning rate in US Holstein cattle. Approximately 2.9 million calving records from 2010 to 2016 were obtained from Ag Source and edited for breed (Holstein), records per herd (≥ 100) and daughters per sire (≥ 100) leaving 1,444,540 calving records from 658,436 Holstein cows. A generalized linear mixed model considering affects of herd, year, season, parity for each daughter record was run to generate sire means for twinning rate corrected for fixed effects for 2,223 sires. Genotype data obtained from the Council for Dairy Cattle Breeding (CDCB) included 60,670 SNPs for 2,067 of the sires. GWAS analysis was conducted in R using the GenABEL package. SNPs with call rate $< 95\%$, minor allele frequency < 0.01 , or Hardy Weinberg Equilibrium test < 0.000001 were excluded. Samples with call rate $< 95\%$ were likewise excluded. The analysis was run on 58,119 SNPs and 2,061 individuals. False discovery rate (FDR) was calculated using R package qvalue. Preliminary results indicated 6 SNPs on chromosomes 5,13,15,22, and 29 that were significant at $P < 5 \times 10^{-5}$ and FDR of 0.5 to 0.05. Results will be validated in future work using independent Holstein data. Key words: genome wide association study, bovine respiratory disease, whole genome selection