ABSTRACT

Bovine respiratory disease (BRD) is the leading natural cause of death in beef and dairy cattle. The objective of this study was to identify host loci associated with susceptibility to BRD in Holstein calves between d 10 and weaning (d 63 - 73). One day old Holstein calves transported to a calf ranch in Hanford, California were monitored 4d/week for signs of BRD using established calf-health scoring criteria (McGuirk, 2008). BRD affected calves scored ≥ 6, and controls scored <6. Controls were selected from hauls adjacent to cases. Over 200,000 calves were screened to obtain 1,003 cases and 969 controls over 1 year. Blood samples and diagnostic swabs (mid-nasal and 2 deep pharyngeal) were obtained for each calf. DNA was extracted from blood using the Qiagen DNA extraction kit, and genotyped using the Illumina BeadChip. Seventy-six animals were removed from the analysis due to a single nucleotide polymorphism (SNP) call rate of < 95%, and 28 were removed as outliers following principal component analysis (PCA). SNPs were discarded if their minor allele frequency was <1% (143,357, more than 10% failed (16,603), there was a difference in the proportion that failed between cases and controls (29), or they failed the Hardy-Weinberg Equilibrium test (490 SNPs p<1x10-69), thereby leaving 1665 calves for the genome wide association study (GWAS). SNPs were filtered using the Illumina SNP and Variation Suite (SVS) for moderate significance and the blue line represents the threshold for moderate P<0.3x10-6. The GWAS was conducted with PLINK and SNP and Variaton Suite (SVS), Multiple testing corrections were based on modified Wellcome Trust recommendations that accounted for array size. Strong evidence for an association was found on BTA27 (p=1.5x10-4) and moderate evidence for associations involving 155 SNPs were found across 33 genomic regions on bovine chromosomes. Bovine chromosomes 4, 11, 12, 17 and 18 possessed the vast majority of moderately associated SNPs, with the red line representing the threshold for strong significance.

MATERIALS AND METHODS

INTRODUCTION

BRD causes annual losses of more than one million animals and $692 million. Despite extensive use of vaccines and antimicrobials, morbidity and mortality rates have actually increased in some feedlot cattle. Typically, cattle with BRD have clinical symptoms including fever, rapid breathing, repetitive coughing, nasal and/or eye discharge, diarrhea, dehydration, and appetite depression. Animals are more likely to be affected by BRD when stressed by sudden changes in feed, crowding, temperature, transportation, and when clean air is contaminated. Ill cows with ammonia, dust and pathogens. Although the environment plays a major role in BRD infection rates, there is increasing evidence that resistance to BRD is under genetic control. Differences in BRD resistance have been found between cattle breeds and sire lines, and a heritability estimate of 0.48 on an underlying continuous scale was reported in unweaned beef calves. This suggests that selecting for BRD resistant cattle could have a substantial impact on BRD prevalence. A limited number of quantitative trait loci related to bovine health, including susceptibility to BRD, have been reported.

OBJECTIVE

The objective of this study was to identify host loci associated with susceptibility to bovine respiratory disease in pre-weaned Holstein calves.

MATERIALS AND METHODS

Samples:
• 2033 animals were identified as either a case or a control between d 10 and d 73 of life at a single operation based on a calf-health scoring system
• Deep pharyngeal and mid-nasal diagnostic samples were taken for identification of bacteria and viruses common to BRD
• Blood samples were used for DNA extraction
• 1972 animals were genotyped with the Illumina HD BeadChip

RESULTS

DISCUSSION

Several loci have, for the first time, been identified as being associated with susceptibility to BRD and 14 genomic regions on 6 chromosomes (Table 1) are represented by five or more associated SNPs. A region on BTA26, which has previously been identified as associated with BRD in beef cattle, showed moderate evidence for association in Holstein calves. These preliminary data will be validated in an independent population of Holstein calves and compared to ongoing studies in beef cattle. Loci associated with susceptibility to infection by specific BRD pathogens will also be investigated.

CONCLUSION

These results represent a preliminary analysis of ongoing work to identify loci associated with BRD and represents the first step in selection of cattle that are less susceptible to disease resulting in improved production and animal welfare, and increased profitability.

BIBLIOGRAPHY