



Identification of SNPs located on BTA 6 and BTA 20 significantly associated with bovine respiratory disease in crossbred cattle

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ABSTRACT. The objective of the present study was to evaluate single nucleotide polymorphisms (SNPs) located in two quantitative trait locus (QTL) regions (BTA 6 and BTA 20) that are associated with bovine respiratory disease (BRD). A population of 323 crossbred steers sired by five purebred sire breeds during 2010-2013 (Angus, Braford, Braunvieh, Charolais, and Simmental) were evaluated for BRD susceptibility during the finishing process at a commercial feedlot. A total of 21 animals representing all sire breeds were affected with BRD at some time during the finishing process over the 4-year period. Although multiple sire breeds were evaluated in the present study, no sire breed effects were detected. A total of 82 SNPs were evaluated (58 on BTA 6 and 24 on BTA 20) in the present study for

potential associations with BRD incidence. When evaluating the previously described QTL regions on BTA 6, three SNPs (rs42968895, rs42823614, and rs43448463) were significantly ($P < 0.05$) associated with BRD incidence. Another three SNPs (rs42477340, rs42512588, and rs42524468) were identified as significantly associated with BRD on the previously described BTA 6 QTL region. For both of these regions, animals inheriting different genotypes differed in BRD incidence during the finishing period. Although multiple SNPs were identified as being significantly associated with BRD incidence in the present study, these SNP associations should be validated in larger and more diverse populations.

Key words: SNP; Bovine respiratory disease; Feedlot; Finishing