



Validation of somatic cell score-associated SNPs from Holstein cattle in Sudanese Butana and Butana × Holstein crossbred cattle

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Abstract

The *Bos indicus* zebu cattle Butana is the most commonly used indigenous dairy cattle breed in Sudan. In the last years, high-yielding Holstein dairy cattle were introgressed into Butana cattle to improve their milk yield and simultaneously keep their good adaption to extreme environmental conditions. With the focus on the improvement of milk production, other problems arose such as an increased susceptibility to mastitis. Thus, genetic selection for mastitis resistance should be considered to maintain healthy and productive cows. In this study, we tested 10 single nucleotide polymorphisms (SNPs) which had been associated with somatic cell score (SCS) in Holstein cattle for association with SCS in 37 purebred Butana and 203 Butana × Holstein crossbred cattle from Sudan. Animals were genotyped by competitive allele-specific PCR assays and association analysis was performed using a linear mixed model. All 10 SNPs were segregating in the crossbred Butana × Holstein populations, but only 8 SNPs in Sudanese purebred Butana cattle. The SNP on chromosome 13 was suggestively associated with SCS in the Butana × Holstein crossbred population (rs109441194, 13:79,365,467, $P_{BF}=0.054$) and the SNP on chromosome 19 was significantly associated with SCS in both populations (rs41257403, 19:50,027,458, Butana: $P_{BF}=0.003$, Butana × Holstein: $P_{BF}=6.2 \times 10^{-16}$). The minor allele of both SNPs showed an increase in SCS. Therefore, selection against the disadvantageous minor allele could be used for genetic improvement of mastitis resistance in the studied populations. However, investigations in a bigger population and across the whole genome are needed to identify additional genomic loci.

Keywords Association analysis · *Bos indicus* · Genotyping · Mastitis · SNPs