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Fine Mapping Of Tick Resistance QTL On BTA23 In Gyr X Holstein Population

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In tropical countries, losses caused by bovine tick *Rhipicephalus (Boophilus) microplus* infestation have a tremendous economic impact on cattle production systems. The identification of DNA markers linked to tick resistance would provide a better strategy for selecting resistant animals and could lead to the isolation of the genes underlying the resistance to ticks. Marker assisted selection could be used to pre-select young animals, shorten generation interval and increase genetic gain. The objective of this work was to fine map a QTL associated with tick resistance/susceptibility previously detected on BTA 23 in a Gyr x Holstein F2 population. In order to reduce the confidence interval of the QTL, four new microsatellite markers on BTA23 were genotyped. The same QTL was detected for the wet and dry seasons, located near to the telomeric region of the chromosome 23. The confidence interval dropped from 17 to 13 cM for wet season QTL and 12 to 9 cM for dry season QTL. With the additional markers, a new QTL for tick resistance in dry season was detected near to the centromeric region of the chromosome 23. The phenotypic variation explained by the dry season QTL was 5.6% and 6.4% for the wet season. The reduction of confidence interval facilitates validation and identification of candidate genes underlying these QTL.

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P.167