

ABSTRACT

A Limousin specific myostatin allele affects longissimus muscle area and fatty acid profiles in a Wagyu-Limousin F₂ population^{1,2}

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A microsatellite-based genome scan of a Wagyu × Limousin F₂ cross population previously demonstrated QTL affecting LM area and fatty acid composition were present in regions near the centromere of BTA2. In this study, we used 70 SNP markers to examine the centromeric 24 megabases (Mb) of BTA2, including the Limousin-specific *F94L* myostatin allele (AB076403.1; 415C > A) located at approximately 6 Mb on the draft genome sequence of BTA2. A significant effect of the *F94L* marker was observed ($F = 60.17$) for LM area, which indicated that myostatin is most likely responsible for the effect. This is consistent with previous reports that the substitution of Leu for Phe at AA 94 of myostatin (caused by the 415C > A transversion) is associated with increased muscle growth. Surprisingly, several fatty acid trait QTL, which affected the amount of unsaturated fats, also mapped to or very near the myostatin marker, including the ratio of C16:1 MUFA to C16:0 saturated fat ($F = 16.72$), C18:1 to C18:0 ($F = 18.88$), and total content of MUFA ($F = 17.12$). In addition, QTL for extent of marbling ($F = 14.73$) approached significance ($P = 0.05$), and CLA concentration ($F = 9.22$) was marginally significant ($P = 0.18$). We also observed associations of SNP located at 16.3 Mb with KPH ($F = 15.00$) and for the amount of SFA ($F = 12.01$). These results provide insight into genetic differences between the Wagyu and Limousin breeds and may lead to a better tasting and healthier product for consumers through improved selection for lipid content of beef.

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