

ABSTRACT

Mapping of quantitative trait loci for carcass traits in a Japanese Black (Wagyu) cattle population

Y Mizoguchi¹, T Watanabe, K Fujinaka, E Iwamoto, Y Sugimoto

¹Shirakawa Institute of Animal Genetics, Odakura, Nishigo, Fukushima 961-8061, Japan.

To detect quantitative trait loci (QTL) that influence economically important traits in a purebred Japanese Black cattle population, we performed a preliminary genome-wide scan using 187 microsatellite markers across a paternal half-sib family composed of 258 offspring. We located six QTL at the 1% chromosome-wise level on bovine chromosomes (BTA) 4, 6, 13, 14 and 21. A second screen of these six QTL regions using 138 additional paternal offspring half-sib from the same sire, provided further support for five QTL: carcass weight on BTA14 (22–39 cM), one for rib thickness on BTA6 (27–58 cM) and three for beef marbling score (BMS) on BTA4 (59–67 cM), BTA6 (68–89 cM) and BTA21 (75–84 cM). The location of QTL for subcutaneous fat thickness on BTA13 was not supported by the second screen ($P > 0.05$). We determined that the combined contribution of the three QTLs for BMS was 10.1% of the total variance. The combined phenotypic average of these three Q was significantly different ($P < 0.001$) from those of other allele combinations. Analysis of additional half-sib families will be necessary to confirm these QTL.

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