

ABSTRACT

**Bovine quantitative trait loci analysis for growth, carcass, and meat quality traits in an F<sub>2</sub> population from a cross between Japanese Black and Limousin**

*T. Abe,<sup>\*1</sup> J. Saburi,<sup>\*</sup> H. Hasebe,<sup>\*</sup> T. Nakagawa,<sup>\*</sup> T. Kawamura,<sup>†2</sup> K. Saito,<sup>‡3</sup> T. Nade,<sup>\*4</sup> S. Misumi,<sup>\*</sup> T. Okumura,<sup>\*5</sup> K. Kuchida,<sup>§</sup> T. Hayashi,<sup>#</sup> S. Nakane,<sup>\*6</sup> T. Mitsuhashi,<sup>\*7</sup> K. Nirasawa,<sup>\*7</sup> Y. Sugimoto,<sup>||</sup> and E. Kobayashi<sup>\*</sup>*

<sup>\*</sup>National Livestock Breeding Center, Nishigo, Fukushima 961-8511, Japan; <sup>†</sup>Tokachi Branch of National Livestock Breeding Center, Otofuke, Hokkaido 080-0572, Japan; <sup>‡</sup>Ohu Branch of National Livestock Breeding Center, Shichinohe, Aomori 039-2567, Japan; <sup>§</sup>Obihiro University of Agriculture and Veterinary Medicine, Obihiro, Hokkaido 080-8555, Japan; <sup>#</sup>National Institute of Agrobiological Sciences, Tsukuba, Ibaraki 305-8602, Japan; and <sup>||</sup>Shirakawa Institute of Animal Genetics, Nishigo, Fukushima 961-8061, Japan

A genome-wide scan for QTL affecting economically important traits in beef production was performed using an F<sub>2</sub> (2) resource family from a Japanese Black x Limousin cross, where 186 F<sub>2</sub> animals were measured for growth, carcass, and meat-quality traits. All family members were genotyped for 313 informative microsatellite markers that spanned 2,382 cM of bovine autosomes. The centromeric region of BTA2 contained significant QTL (i.e., exceeding the genome-wide 5% threshold) for 5 carcass grading traits [LM area, beef marbling standards (BMS) number, luster, quality grade, and firmness], 8 computer image analysis (CIA) traits [LM lean area, ratio of fat area (RFA) to LM area, LM area, RFA to musculus (M.) trapezius area, M. trapezius lean area, M. semispinalis lean area, RFA to M. semispinalis area, and RFA to M. semispinalis capitis area], and 5 meat quality traits (contents of CP, crude fat, moisture, C16:1, and C18:2 of LM). A significant QTL for withers height was detected at 80.3 cM on BTA5. We detected significant QTL for the C14:0 content in backfat and C14:0 and C14:1 content in intermuscular fat around the 62.3 to 71.0 cM region on BTA19 and for C14:0, C14:1, C18:1, and C16:0 content and ratio of total unsaturated fatty acid content to total SFA content in intramuscular fat at 2 different regions on BTA19 (41.1 cM for C14:1 and 62.3 cM for the other 4 traits). Overall, we identified 9 significant QTL regions controlling 27 traits with genome-wide significance of 5%; of these, 22 traits exceeded the 1% genome-wide threshold. Some of the QTL affecting meat quality traits detected in this study might be the same QTL as previously reported. The QTL we identified need to be validated in commercial Japanese Black cattle populations.

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