

## Search for quantitative trait loci affecting growth and carcass traits in a cross population of beef and dairy cattle

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### Abstract :

A genome scan to detect QTL influencing growth and carcass-related traits was conducted in a Charolais x Holstein crossbred cattle population. Phenotypic measurements related to growth and carcass traits were made on the 235 second-generation crossbred males of this herd (F2 and reciprocal backcrosses), which were born in 4 consecutive annual cohorts. Traits measured in vivo were related to birth dimensions, growth rates, and ultrasound measurements of fat and muscle depth. The animals were slaughtered near a target BW of 550 kg, and a wide range of postmortem traits were measured: visual assessment of carcass conformation and carcass fatness, estimated subcutaneous fat percentage, weights of kidney knob and channel fat, and weights of carcass components after commercial and full-tissue dissections. The whole population, including grandparents, parents, and the crossbred bulls, was genotyped initially for 139 genome-wide microsatellite markers. Twenty-six additional markers were subsequently analyzed to increase marker density on some of the chromosomes where QTL had been initially identified. The linear regression analyses based on the 165 markers revealed a total of 51 significant QTL at the suggestive level, 21 of which were highly significant ( $F$ -value  $\geq 9$ ; based on the genome-wide thresholds obtained in the initial scan). A large proportion of the highly significant associations were found on chromosomes 5 and 6. The most highly significant QTL was localized between markers DIK1054 and DIK082 on chromosome 6 and explained about 20% of the phenotypic variance for the total bone proportion estimated after the commercial dissection. In the adjacent marker interval on this chromosome, 2 other highly significant QTL were found that explain about 30% of the phenotypic variance for birth dimension traits (BW and body length at birth). On chromosome 5, the most significant association influenced the lean:bone ratio at the fore rib joint and was flanked by markers DIK4782 and BR2936. Other highly significant associations were detected on chromosomes 10 (estimated subcutaneous fat percentage), 11 (total saleable meat proportion), 16 (prehousing growth rate), and 22 (bone proportion at the leg joint). These results provide a useful starting point for the identification of the genes associated with traits of direct interest to the beef industry, using fine mapping or positional candidate gene approaches.

### Key Word :

carcass composition, cattle, growth trait, quantitative trait loci

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