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Section E: Associations between Markers and Traits

E028

Detection of QTL for birth weight in Charolais within the SEGFAM resource population

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To investigate the genetic and physiological background of divergent nutrient transformation for growth and lactation in dairy and meat type cattle a resource population (SEGFAM) is established in the Research Institute for the Biology of Farm Animals. In SEGFAM the Charolais and the German Holstein breed serve as representatives of the accretion and secretion metabolic type, respectively. Substantial differences between those breeds exist for a variety of physiological traits. However, there was indication, that unlike the situation in inbred lines of model organisms QTL with effect on these traits still segregate within selected cattle breeds. This hypothesis of segregating QTL within a phenotypically extreme breed was tested for the trait birth weight by a whole genome scan in a half sib design originating from the Charolais founder sires of the SEGFAM population. Five families each consisting of a Charolais sire, which was mated to Charolais and German Holstein cows, as well as dams and offspring were genotyped with 198 microsatellite markers distributed across all chromosomes. Variance analysis indicated putative QTL for birth weight on chromosomes 4, 5, 6, 14, 15, 16, 19, und 23. For the QTL positions on BTA4, 5, 6, 19, and 23 corresponding results for birth weight or related traits have been found in other populations. Our results indicate, that in spite of extreme phenotype segregating QTL for the respective traits can be detected within high selection cattle breeds.