

Mapping of the bovine growth hormone secretagogue receptor (GHS-R) and polymorphism study in cattle.

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A third control pathway of the Growth Hormone (GH) secretion has come into picture since the development of synthetic compounds known as Growth Hormone Secretagogues (GHSs). The GHS Receptor (GHS-R) and its subtype are abundantly located in the hypothalamus-pituitary unit, but are also distributed in other central areas and peripheral tissues. The GHS-R belongs to the G-protein coupled receptor family with seven transmembrane domain architecture.

In order to determine the GHS-R gene sequence, total mRNA was extracted from abomasum and two types of GHS-R cDNA were identified. These two types are transcript variants (1a and 1b) of the same GHS-R gene. The gene encompasses two exons and a single intron.

Using a 3000 Rad hybrid panel, the GHS-R gene was mapped to *Bos taurus* autosome 1 (BTA 1). This localization on BTA 1 agrees totally with comparative data between cattle and human since BTA 1 corresponds to part of human chromosome 3 where human GHSR is also mapped. By two-point analysis, most significantly linked marker are BL26 and BMS4031 (both LOD score : 5,66). Some studies detected different QTLs near these markers like for growth rate, carcass yield, milk protein and milk yield.

In the cattle industry, it is of economical importance to increase plasma GH secretion because it is associated with faster growth, less fat stores and improved milk production. Being of economical importance and the detected QTLs near the GHS-R gene, it would be interesting to study the polymorphism on the bovine GHS-R gene. Screening for polymorphisms in the two exons on ten Belgian Blue bulls, ten Holsteins bulls and ten Limousin bulls revealed a total of four single nucleotide polymorphisms (SNPs): three SNPs are in the first exon and one SNP in the second exon. In order to evaluate if GHS-R could be involved in genetic variation for growth rate, carcass yield, milk protein and milk yield, an association study between SNPs on GHS-R gene and these traits could be performed in a major cattle population.

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