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Linkage mapping of the bovine bone morphogenetic protein receptor-1B (*BMPR1B*) to chromosome 6

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Source/description of primers: A mutation in the ovine bone-morphogenetic protein receptor-1B (*BMPR1B*) gene is associated with an increased ovulation rate phenotype in Booroola Merino sheep^{1–3}. Therefore, *BMPR1B* is considered as a candidate gene for ovulation rate in cattle. A cDNA was obtained for porcine *BMPR1B* and the gene was mapped in the porcine genome⁴. Comparison of the ovine and porcine *BMPR1B* cDNA sequences indicated that they are highly conserved. Therefore, a pair of primers derived from the porcine *BMPR1B* cDNA, which amplified across intron 8 in the pig, were used to amplify the bovine genomic DNA. The forward (NZ-F1)³ and reverse (exon9-R1) primers correspond to bases 1041–1064 and 1289–1265 of the porcine *BMPR1B* cDNA (GenBank accession no. AF432128), respectively. Agarose gel electrophoresis and sequencing of the polymerase chain reaction (PCR) amplicons of bovine genomic DNA indicated that the size of this product was 1253 bp (GenBank accession no. AY242067).

PCR primer sequences and a flanking sequence for a single nucleotide polymorphism: *BMPR1B* NZ-F1: GTCGCTATGGGGAAGTTTGG ATG

BMPR1B exon9-R1: GGTGGTGGACTTCAGTAATCATAG
 Sequence flanking polymorphism: GTGGTAAAGA(A/G)TCTA CCTGCC

PCR conditions: Polymerase chain reactions were carried out in a 25- μ l volume containing 100 ng genomic DNA, 1.5 mM MgCl₂, 20 pmol of each primer, 100 μ M dNTP and 0.35 U *Taq* polymerase. Amplification was performed under the following

PCR conditions: 2 min at 94 °C; 45 cycles of 30 s at 94 °C, annealing for 1 min at 61 °C, 1 min at 72 °C and a final extension of 5 min at 72 °C. Both strands of the amplified genomic DNAs were sequenced and evaluated for polymorphisms⁵ in four bulls from the Meat Animal Research Center (MARC) Bovine Reference Population⁶.

Polymorphism and chromosomal location: An A/G single nucleotide polymorphism was detected in intron 8 (GenBank accession no. AY242067), position 658 from the exon/intron boundary. This polymorphism was heterozygous in two of the four bulls from the MARC Bovine Reference Population⁶. An assay was designed to genotype this polymorphism using primer extension with analyte detection on a MALDI-TOF mass spectrometer (Sequenom Inc., San Diego, CA, USA). This marker generated 50 informative meioses (40 phases known) in the MARC Bovine Reference Population. The *BMPR1B* gene was mapped to chromosome 6 position 42.4 cM on the current MARC bovine chromosome 6 linkage map (<http://www.marc.usda.gov/>) using CRI-MAP near the quantitative trait locus for milk production⁷. The most significant two-point linkage detected was with *BMS2508* (LOD = 11.40) at 0.04 recombination. The *BMPR1B* gene in human is located on chromosome 4q22.3, which shares homology with bovine chromosome 6.

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Mutations in the *limbin* gene previously associated with dwarfism in Japanese brown cattle are not responsible for dwarfism in the American Angus breed

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Source/description: Bovine chondrodysplastic dwarfism in Japanese brown cattle has been mapped to the distal end of bovine chromosome 6 by linkage analysis. Disease-specific mutations in *limbin* were identified in affected dwarf calves¹. Disproportionate dwarfism has been reported in many cattle breeds including Dexter, Holstein, Aberdeen Angus, Hereford and Shorthorn breeds^{2,3}. Dwarfism in American Angus has not been reported since the 1970's until recently when

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