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Rapid communication: Mapping of the bovine stearoyl-coenzyme A desaturase (*SCD*) gene to BTA26[1]

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Genus and Species. *Bos indicus* and *Bos taurus*.

Locus Name. Bovine stearoyl-coenzyme A desaturase (*SCD*).

Source and Description of Primers. Primers were designed that amplified a 135-bp region in *SCD* exon 6. Sequences from human (GenBank accession number Y13647), rat (AB003357), mouse (M21285), and pig (Z97186) were aligned to identify a conserved region in which to design the primers. The forward primer was 5′ YGA GGG CTT CCA CAA CTA C 3′ and the reverse primer was 5′ ACT TTC TTC CGG TCA TAR GC 3′.

Method of Mapping. Primers were used to screen a bovine artificial chromosome (**BAC**) library (Cai et al., 1995), resulting in identification of a single clone. Screening the BAC library was performed by PCR containing 1× Taq buffer and 1.5 m*M* $MgCl_2$. Conditions for PCR were 35 cycles of 30-s denaturing at 94°C, 30-s annealing at 58°C, and 30-s extension at 72°C. The PCR product was sequenced to validate the identity of the clone. All reactions were performed on a Techne MW-2 (Techne, Princeton, NJ). The sequence aligned completely with bases 886 to 1,017 of the bovine stearoyl-coenzyme A desaturase cDNA (GenBank accession number AF188710) and was 91% homologous to the porcine (Z97186) and murine (NM_009127) *SCD1* cDNA.

A GT repeat was found when the BAC clone was digested with *Sau*3AI. Primers were designed to amplify a 178-bp segment encompassing this repeat. The forward microsatellite primer was 5′ TTC TGC TGT ATA TCG AAG TA 3′ and the reverse microsatellite primer was 5′ TTA TCA GAT GCA AGC TAT T 3′. For the microsatellite, reagents were the same as those for screening the BAC library, except the forward primer was end-labeled with [γ-^{32}P]ATP and the annealing temperature was 52°C.

The BAC clone that contained the *SCD* gene was mapped with the fluorescence in situ hybridization procedure described by Pinkel et al. (1986).

Inheritance Pattern. Seven alleles were found for the *SCD* microsatellite; the heterozygosity and PIC values were 0.8512 and 0.7723, respectively. Autosomal segregation, in accordance with Mendelian expections, was observed in the Texas A&M University Angleton population described by Yeh et al. (1996). There were 622 informative meioses.

Chromosomal Location. The BAC clone containing the *SCD* gene hybridized to 26q21. The microsatellite marker, SCD, was integrated into an existing linkage group of bovine chromosome 26 (BTA26) (Green et al., 1990). The two-point associations that placed *SCD* were (cM, LOD) HEL11 (3.7, 26.21) and BM1314 (2.2, 25.11). This linkage assignment was in agreement with the physical assignment and comparative map data.

Comments. Stearoyl-coenzyme A desaturase is responsible for the conversion of saturated fatty acids to Δ9-monounsaturated fatty acids. Inhibition of desaturase activity leads to an accumulation of stearic acid in bovine adipose tissue, which can cause a substantial increase in fat hardness (Smith et al., 1998; Yang et al., 1999). Tabor et al. (1998) mapped two stearoyl-coenzyme A desaturase genes, *SCD1* and *SCD2*, to mouse chromosome 19. Zhang et al. (1999) found two loci for *SCD* in humans, one on HSA10 and one on HSA17. However, only the locus on HSA10 produced a transcript, indicating that the HSA17 locus is most likely a psuedogene (Zhang et al. 1999). Bovine chromosome BTA26 is homologous with regions of MMU19 and HSA10 (Carver and Stubbs, 1997; Solinas-Toldo et al., 1995). Although two *SCD* genes have been identified in mice, only one was identified in sheep (Ward et al., 1998). The number of *SCD* genes in cattle currently is unknown.

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