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Rapid Communication: The Very-Long-Chain Acyl-CoA Dehydrogenase Gene Maps to Pig Chromosome 12

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Abstract

Source and Description of Primers. Primers for the very-long-chain acyl-CoA dehydrogenase (ACADVL) gene were designed from a bovine cDNA sequence (GenBank accession No. U30817) aligned with the human ACADVL gene (GenBank accession No. L46590). The forward primer was 5¢-TTT GGG GAG AAA ATT CAC AAC-3¢ and the reverse primer was 5¢-GCG GCC TCT ATC TGG AAG T-3¢. The amplification product was expected to span from exon 11 to exon 12 of the ACADVL gene. Exonic parts (103 bp) of the pig sequence were 91% identical at the nucleotide level with the human ACADVL sequence. The pig sequence produced here has been submitted to GenBank (accession no. AF022255).

Keywords

Pigs, Gene Mapping, Chromosome 12

Disciplines

Agriculture | Animal Sciences | Genetics and Genomics

Comments

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Rapid Communication: The Very-Long-Chain Acyl-CoA Dehydrogenase Gene Maps to Pig Chromosome 12[1]

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Method of Detection. The PCR amplification was performed using 12.5 ng porcine genomic DNA, 1× PCR buffer (Promega, Madison, WI), 1.5 m*M* $MgCl_2$, .125 m*M* dNTP, .3 μM of each primer, and .35 U *Taq* DNA polymerase (Promega, Madison, WI) in a 10-μL reaction volume. The PCR profile included 2 min at 94°C followed by 35 cycles of 30 s at 94°C, 1 min 30 s at 57°C, 2 min at 72°C, and a final extension of 5 min at 72°C in a Robocycler (Stratagene, La Jolla, CA).

Description of Polymorphism. The 563-bp PCR product was digested with *Stu*I and fragments of 451, and 112 bp were produced from allele 2; allele 1 did not contain a *Stu*I site. Fragments were separated by electrophoresis on 1.5% agarose gels (Figure 1).

Inheritance Pattern. Inheritance in accordance with Mendelian expectations was observed in four three-generation international reference families.

Allele Frequencies. Frequency of allele 1 was determined in Meishan (.28; n = 9), Large White (.95; n = 11), and wild boar (1.0; n = 2) grandparents from the PiGMaP families (Archibald et al., 1995). Additionally, the allele 1 frequency was 1.0 in Chester White (n = 7), .93 in Duroc (n = 7), .88 in Hampshire (n = 9), .81 in Landrace (n = 8), and .85 in Yorkshire (n = 10) from Iowa State University.

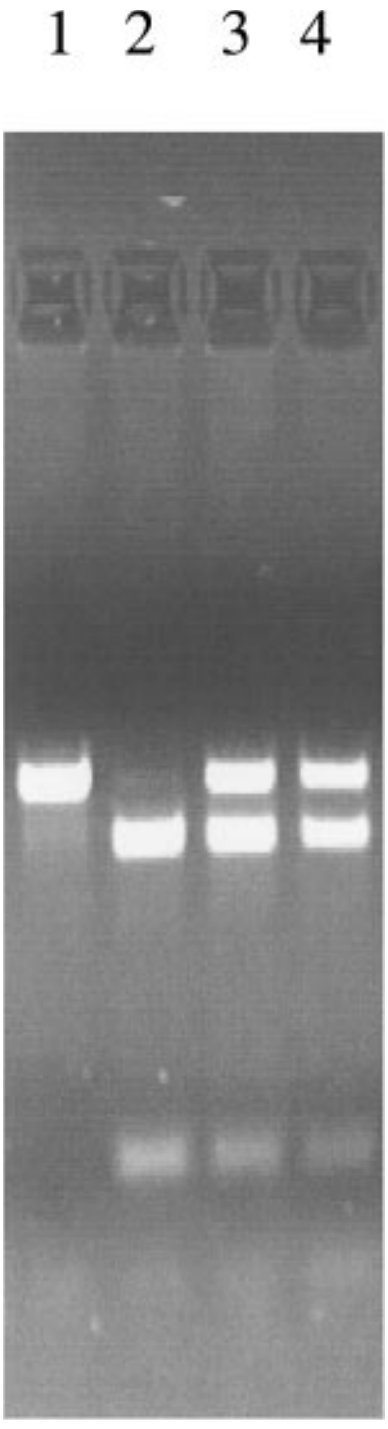

Figure 1. Parental animals (lanes 1, 2) and two offspring (lanes 3, 4) showing the ACADVL genotypes: 1/1 (lane 1), 1/2 (lanes 3, 4), and 2/2 (lane 2).

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Chromosomal Location. Two-point linkage analysis of the ACADVL gene was performed on genotypes from the European PiGMaP families (Archibald et al., 1995) using the CRI-MAP program (Green et al., 1990). Significant linkage was observed with S0090 at a recombination distance of 26 cM and a LOD score of 3.81 as well as with three polymorphisms in the ALOX12 gene at recombination distances of 1, 2, and 12 cM and LOD scores of 19.59, 14.38, and 5.33, respectively. Both of these markers have previously been mapped to pig chromosome 12, ALOX12 to the distal end of the linkage map (Archibald et al., 1995).

Comments. Very-long-chain acyl-CoA dehydrogenase is an enzyme that catalyzes the β-oxidation of long-chain fatty acids. In humans, a deficiency of this β-oxidation process due to a defective ACADVL gene has been linked to the occurrence of cardiomyopathy, severe lipid storage in body organs, liver dysfunction, skeletal myopathy, and sudden death during childhood. Close linkage of ACADVL with ALOX12 seems to be a conserved feature across species because both genes have been assigned to human chromosome 17p13 and mouse chromosome 11.

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