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Rapid Communication: Genetic Linkage Mapping of the Porcine Fibroblast Growth Factor 7 (FGF7) Gene

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Abstract

Source and Description of Primers. The forward primer was developed from a human fibroblast growth factor (FGF7) cDNA sequence (GenBank accession no. L06243), and the reverse primer was a published primer (Kelley et al., 1992). These primers were used to amplify a 1.3-kb fragment from porcine genomic DNA. This fragment included regions corresponding to exon 2, exon 3, and the intron flanked by these two exons. Sequences were obtained from both ends of the PCR fragment and compared with a human sequence showing 95.9% identity at the amino acid level in a 73-amino acid overlap. Sequences produced in this experiment have been submitted to GenBank (accession no. AF052657).

Keywords

Fibroblast Growth Factor, FGF7 Gene, Pigs, Polymerase Chain Reaction-Restriction Fragment Length Polymorphism, Mapping

Disciplines

Agriculture | Animal Sciences | Genetics and Genomics

Comments

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Rapid Communication: Genetic Linkage Mapping of the Porcine Fibroblast Growth Factor 7 (FGF7) Gene¹

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Source and Description of Primers. The forward primer was developed from a human fibroblast growth factor (*FGF7*) cDNA sequence (GenBank accession no. L06243), and the reverse primer was a published primer (Kelley et al., 1992). These primers were used to amplify a 1.3-kb fragment from porcine genomic DNA. This fragment included regions corresponding to exon 2, exon 3, and the intron flanked by these two exons. Sequences were obtained from both ends of the PCR fragment and compared with a human sequence showing 95.9% identity at the amino acid level in a 73-amino acid overlap. Sequences produced in this experiment have been submitted to GenBank (accession no. AF052657).

Primer Sequences. The forward primer was 5'-TGG AAT TGT GGC AAT CAA AG-3', and the reverse primer was 5'-AGT TAT TGC CAT AGG AAG AA-3'.

Method of Detection. A 1.3-kb fragment was produced by PCR-amplifying 12.5 ng of porcine genomic DNA using the *Taq* extender system (Stratagene, La Jolla, CA): 1× *Taq* extender buffer, .125-mM dNTP, .3-mM of each primer, and .35 U each of *Taq* extender and *Taq* DNA polymerase (Promega, Madison, WI) in a 10-μL reaction volume. The PCR profile included 2 min at 94°C, 35 cycles of 30 s at 94°C, 1 min 20 s at 54°C, 2 min at 72°C; and 5 min at 72°C in a Robocycler (Stratagene, La Jolla, CA). The PCR product was digested with *AluI*, and fragments were separated by electrophoresis in 2% agarose gels.

Description of Polymorphism. *AluI* digestion of the 1.3-kb PCR product produced allelic fragments of sizes 629 bp for allele 1 and 401 and 228 bp for allele 2. Constant fragments of sizes 236, 206, 119, and 89 bp were also produced (Figure 1).

Pattern of Inheritance. Autosomal Mendelian segregation was observed in three three-generation European PiGMAP families (Archibald et al., 1995).

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Allelic Frequency. Allele frequencies were determined in grandparental animals of the European PiGMAP families and in 47 unrelated animals from Iowa State University. Allele 1 occurred with a frequency of .14 in Chester White (n = 6), .07 in Landrace (n = 6), .94 in Meishan (n = 9), and .09 in Large White (n = 11). Allele 1 was not observed in Hampshire (n = 7), Duroc (n = 6), or Wild Boar (n = 2).

Chromosomal Location. Two-point linkage analysis was performed using data obtained from individuals from the PiGMAP families (Archibald et al., 1995) using the CRI-MAP program (Green et al., 1990). Based on this analysis, the *FGF7* gene was found to be closely linked to several other markers previously located on porcine chromosome 1 (SSC1) and resides between *S0122* and *S0082*. The most closely linked markers (cM, LOD) are *S0122* (10, 14.12), *CAPN3* (8, 9.59) (Larsen et al., 1998), and *S0082* (15, 10.53).

Comments. The *FGF7* gene was previously localized to human chromosome 15q13-q22 and to mouse chromosome 2. The *FGF7* gene, originally termed *keratinocyte growth factor (KGF)*, has potent mitogenic activity in keratinocytes of epithelial tissue. Primarily, *FGF7* is a paracrine effector of epithelial cell repair and has a direct association with development during embryogenesis and angiogenesis. The offset of delicate balances of *FGF7* in various tissues can lead to overproliferation of epithelial cells, possibly leading to cancer in humans (Werner et al., 1994).

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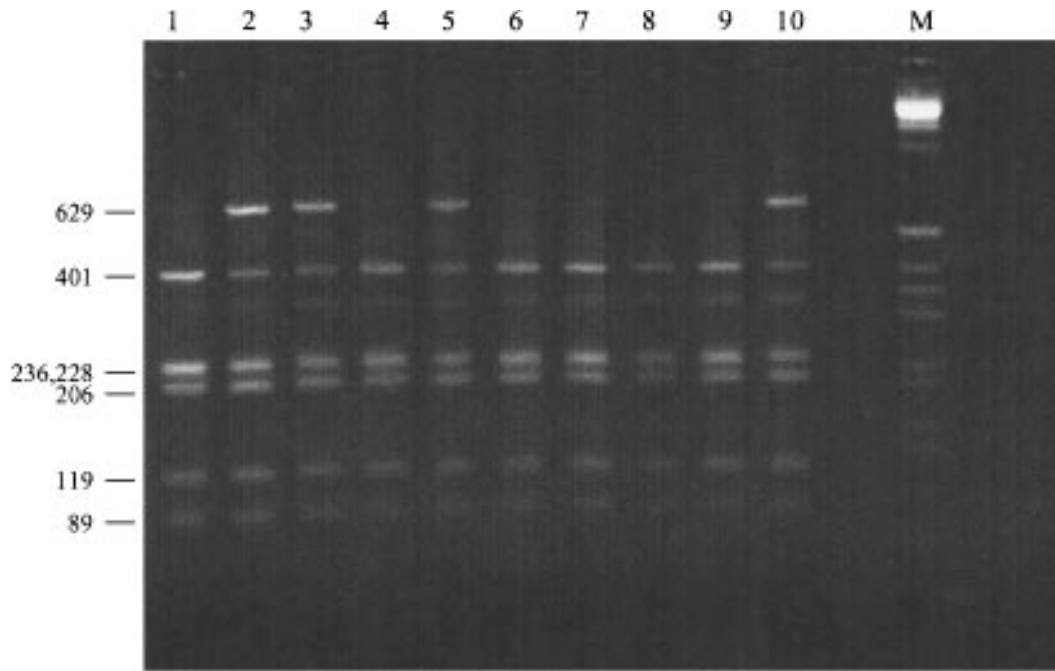


Figure 1. *FGF7-AluI* PCR-RFLP segregating in two parents (lanes 1 and 2) and eight offspring (lanes 3–10). Lane M is a 1-kb molecular weight standard (Gibco, Gaithersburg, MD). Fragments specific for allele 1 are located at approximately 629 bp and for allele 2 at 401 and 228 bp.

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