Rapid communication: Linkage and physical mapping of the porcine basic fibroblast growth factor (FGF2) gene

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Genus and species. Sus scrofa.

Locus. Pig Fibroblast Growth Factor 2 (FGF2) gene.

Source and Description of Primers. Primers were designed from human sequence (GenBank accession no. J04513.1) to amplify a 167-bp fragment within exon 1 of FGF2 from pig genomic DNA. This fragment was identified as FGF2 with 93% homology to the human FGF2 sequence.

Primer Sequences. Primers designed from human sequence were as follows: forward primer: 5′ GCA GCC GGG AGC ATC ACC AC 3′; reverse primer: 5′ TCG CTC TTC TCC CGG ACC C 3′. Pig-specific primers were as follows: forward primer: 5′ TGA ATA TAA AAA ATC CTA AGC GTG TGC ACT 3′; reverse primer 5′ CGC TCT TCT CCC GGA CCC 3′.

Method of Detection. The PCR reaction using the pig-specific primers was performed using 12.5 ng of porcine genomic DNA, 1× PCR buffer, 1.5 mM MgCl2, 100 μM dNTP, 2.5 μM of each primer, and 0.35 units of Taq DNA polymerase (Promega, Madison, WI) in a final volume of 10 μL. The PCR program consisted of an initial 4 min 94°C denaturing, 35 cycles of 45 sec at 94°C, 45 sec at 57°C, 45 sec at 72°C, and a final 5-min extension at 72°C in a MJ PTC-100 thermocycler (MJ Research, Watertown, MA). The PCR product was digested with BtsI at 37°C overnight and fragments were separated by electrophoresis on a 4% Nusieve agarose gel. The 99-bp and 73-bp fragments represent alleles 1 and 2, respectively (26-bp fragment not shown).

Description of Polymorphism. A single nucleotide polymorphism (SNP), C/T base pair change (silent mutation), was detected in the pig sequence at the human FGF2 nucleotide position 568 (GenBank accession no. J04513.1). A BtsI RFLP test was developed for this exon 1 SNP by designing pig-specific primers to amplify a 99-bp fragment and incorporate a BtsI restriction enzyme site. The BtsI digestion of the 99-bp exon 1 PCR fragment produced the following genotypes: homozygous 1/1 had a 99-bp fragment, heterozygous 1/2 genotype had 99-, 73-, and 26-bp fragments, and the 2/2 homozygous genotype had 73- and 26-bp fragments (Figure 1).

Pattern of Inheritance. Mendelian inheritance was observed in the three-generation Swedish family of the European PiGMaP family (Archibald et al., 1995).

Allele Frequencies. Allele 1 was identified in only 2 (one homozygous and one heterozygous individuals) of the 22 grandparents of the European PiGMaP families. A total of 312 unrelated animals from five breeds (Duroc, Hampshire, Meishan, Landrace, and Large White) were also genotyped and the combined gene frequency for allele 1 was 0.013.

Chromosomal Location. The FGF2 gene was physically mapped to porcine chromosome 8 (SSC8) q23–27 using the pig/rodent somatic cell hybrid panel (Yerle et al., 1996). Two-point and multipoint linkage analysis were performed on PiGMaP family FGF2 BtsI genotypes using the CRI-MAP program (Green et al., 1990). The FGF2 gene was most closely linked to IL2, S0225, S0442, and S0447 with equal recombination fractions of 0.05 and LOD scores of 4.3, 4.3, 4.3 and 4.02, respectively. The most probable order of FGF2 between linked markers (in Kosambi centimorgans) is S0069(9.0)–S0225(21.8)–S0144(26)–S0442(32.6)–S0447(32.6)–FGF2(37.7)–SW61(57.0)–SPP1(68.8).

Comments. The FGF2 gene is multifunctional and has been associated with mitogenesis and angiogenesis (Florkiewicz et al., 1991). Mutations within FGF2 could have strong implications in cell growth regulation and tissue repair (Abraham et al., 1986), making it a poten-

Figure 1. FGF2 BtsI PCR-RFLP allelic fragments are shown on a 4% Nusieve agarose gel. The 99-bp and 73-bp fragments represent alleles 1 and 2, respectively (26-bp fragment not shown).
tially important gene in muscle development association studies.

**Literature Cited**


Green, P., K. Falls, and S. Crooks. 1990. Documentation for CRIMAP, version 2.4. Washington Univ. School of Medicine, St. Louis, MO.


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