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Abstract

Genus and Species. Sus scrofa. Locus Name. Peroxisome Proliferator Activated Receptor gamma (PPARγ). Source and Description of Primers. Primers were designed in exon 5 from a published porcine cDNA sequence (GenBank accession no. AJ006756). Forward primer: 5′ GAC ATG AAT TCC TTA ATG 3′; reverse primer: 5′ ACT TCA CAG CGA ACT CGA ACT T 3′.

Keywords

Gene Mapping, Linkage, Peroxisome Proliferator Activated Receptor Gamma, Porcine, PPARγ

Disciplines

Agriculture | Animal Sciences | Genetics and Genomics

Comments

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Rapid communication: Physical and genetic mapping of the *Peroxisome Proliferator Activated Receptor γ* (*PPARγ*) gene to porcine chromosome 13[1]

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Locus Name. Peroxisome Proliferator Activated Receptor gamma (*PPARγ*).

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Method of Mapping. The *PPARγ* gene was mapped both by physical mapping and linkage mapping. For physical mapping, PCR was performed on a somatic cell hybrid panel (Yerle et al., 1996) using 1 ng of genomic DNA in 10-μL reactions containing 1× PCR buffer, 1.5 m*M* $MgCl_2$, .125 m*M* dNTP, .3 μ*M* of each primer, and .35 U *Taq* DNA polymerase (Promega, Madison, WI). The PCR profile included an initial denaturation of 2 min at 94°C followed by 40 cycles of 30 s at 94°C, 30 s at 55°C, 30 s at 72°C, and a final extension of 72°C at 5 min. The PCR products were obtained from both mouse and hamster genomic DNA using these reaction conditions. The PCR product was sequenced and the exon 5 nucleotide sequence showed 93% similarity to human *PPARγ*. To make different restriction fragment lengths for pig, mouse, and hamster, the PCR product was digested with *Hin*fI, and fragments were separated by electrophoresis on a 2% agarose gel. For linkage mapping, a 370-bp fragment was PCR-amplified using 12.5 ng of porcine genomic DNA and the same PCR conditions as described above. The fragment sequence revealed a *Bsg*I site in exon 5, and therefore the 370-bp PCR product was digested with *Bsg*I and fragments were separated by electrophoresis on a 2% agarose gel. Meishan was the only breed without the *Bsg*I digestion site. The *Bsg*I digestion of the PCR product produced allelic fragments of 125 bp and 245 bp for allele 2, whereas allele 1 did not contain a *Bsg*I site (Figure 1).

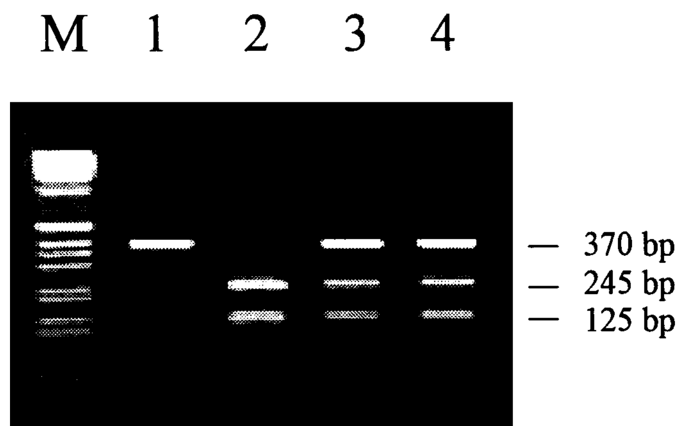

Figure 1. Parental animals (lanes 1 and 2) and two offspring (lanes 3 and 4) showing the *PPARγ* genotypes: 1/1 (lane 1), 2/2 (lane 2), and 1/2 (lanes 3 and 4). Lane M is a 1-kb molecular weight standard (Gibco, Gaithersburg, MD).

Inheritance Pattern. Autosomal segregation, in accordance with Mendelian expectations, was observed in four three-generation European PiGMaP families of Meishan × Large White pigs (Archibald et al., 1995).

Allele Frequencies. Allele frequencies were calculated using animals from several breeds kept at the Iowa State University swine breeding herd and PiGMaP grandparents. Allele 1 was observed only in the Meishan (.83, n = 9) grandparents from the PiGMaP families (Archibald et al., 1995), whereas the Large White (n = 15), Duroc (n = 11), Landrace (n = 10), Hampshire (n = 4), Wild Boar (n = 2), and Minzhu (n = 3) breeds were found to be monomorphic for allele 2.

Chromosomal Location. Analysis of 27 porcine-rodent somatic cell hybrids (Yerle et al., 1996) allowed regional assignment of *PPARγ* to porcine chromosome 13 with .98 probability and to region 13q23-q41 with .8 probability (Chevalet et al., 1997) (Figure 2). A two-point linkage analysis was performed in four of the PiGMaP families (Archibald et al., 1995) using the CRI-MAP program (Green et al., 1990), and close linkage was found between *PPARγ* and several markers (Figure 2) previously mapped on porcine chromosome 13. The most closely linked markers (centimorgans, LOD) were *S0222* (5.9 cM, 8.17), *S0021* (2.7 cM, 12.06), *S0223* (0 cM, 11.74), *Sw937* (2.2 cM, 12.52), *TF* (2.2 cM, 6.20), and *S0281* (4.0 cM, 11.76).

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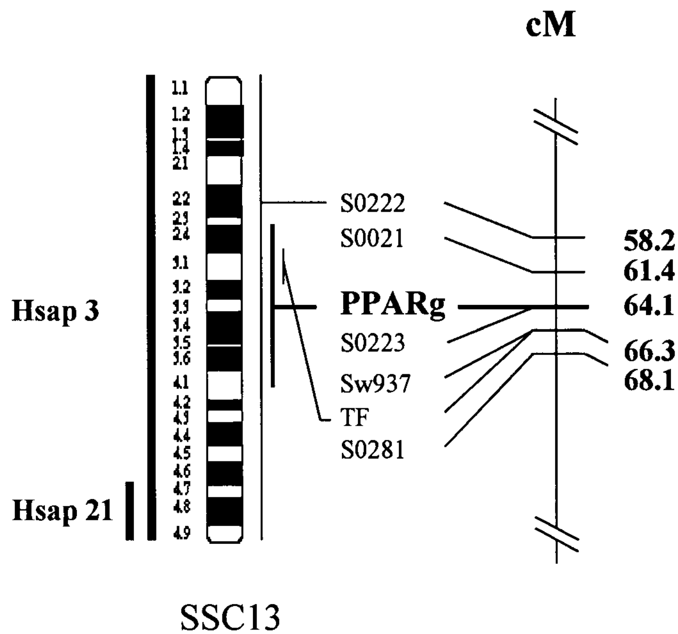

Figure 2. Summary of the physical and linkage maps of *PPAR*γ and other genetic markers on SSC13. Syntenic regions on corresponding human chromosomes are shown on the left (Sun et al., 1999).

Comments. The Peroxisome Proliferator-Activated Receptor (*PPAR*γ) is a member of the nuclear receptor superfamily and regulates the expression of several genes encoding proteins involved in adipocyte differentiation (Spiegelman et al., 1997; Yanase et al., 1997) and fat deposition (for review see Schoonjans et al., 1996). It has been shown that *PPAR*γ expression in porcine adipose tissues varies among different breeds and ages (Grindflek et al., 1998). Because intramuscular fat is positively correlated with meat quality (Wood et al., 1988), *PPAR*γ may have an effect on meat quality traits and is therefore interesting for a candidate gene approach.

Results from both the genetic linkage and physical mapping in this study are in agreement with each other. Chromosome painting analysis has demonstrated high correspondence between pig chromosome 13 and human chromosome 3 (Goureau et al., 1996; Sun et al., 1999). The localization of *PPAR*γ to porcine chromosome 13q23-q41 is also in agreement with the previous assignment of this gene to human chromosome 3p25 (Greene et al., 1995).

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