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# Rapid Communication: The Progesterone Receptor (PGR) Gene Maps to Porcine Chromosome 9p13-p11 by a Rodent-Porcine Somatic Cell Hybrid Panel

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**Abstract**

Genus and Species. Sus scrofa. Locus. Pig Progesterone Receptor ( PGR) gene. Source and Description of Primers. Oligonucleotide primers were designed from a partial pig PGR cDNA sequence (Genbank accession no. S49016) with inferred intron-exon boundary information from humans (Misrahi et al., 1993). The primers were designed to span the intron between exons 7 and 8 of the PGR gene.

**Keywords**

Progesterone, Somatic Hybridization, Pigs, Chromosomes, Gene Mapping



**Comments**

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# Rapid Communication: The *Progesterone Receptor (PGR)* Gene Maps to Porcine Chromosome 9p13-p11 by a Rodent-Porcine Somatic Cell Hybrid Panel[1]

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*Genus and Species.* *Sus scrofa.*

*Locus.* Pig *Progesterone Receptor* (*PGR*) gene.

*Source and Description of Primers.* Oligonucleotide primers were designed from a partial pig *PGR* cDNA sequence (Genbank accession no. S49016) with inferred intron-exon boundary information from humans (Misrahi et al., 1993). The primers were designed to span the intron between exons 7 and 8 of the *PGR* gene.

*Primer Sequences.* Forward primer: 5′-TGA AGA GAT GAG ATC AAG-3′; reverse primer: 5′-CAA GCA GTA CAG ATG AAG-3′.

*Method of Detection.* A polymerase chain reaction was used to amplify the genomic region between exons 7 and 8 of the porcine *PGR* gene in a 20-$\mu$L reaction volume comprising 1× PCR buffer, 1.75 m*M* $MgCl_2$, 2 pmol of each primer, .2 m*M* of each dNTP, .5 unit of *Taq* polymerase (Boehringer Mannheim, Indianapolis, IN), and 25 ng of porcine genomic DNA. A hot start was used to initiate a PCR profile on a PTC-100 Thermocycler (MJ Research, Watertown, MA): initial denaturation at 94°C for 4 min, 10 cycles of 92°C for 30 s, 60°C for 50 s, and 68°C for 3 min; followed by 20 cycles of 92°C for 30 s, 60°C for 50 s, 68°C for 3 min, with 20 s of extension time added for each cycle, and ended with a final 72°C for 7 min. The PCR products were examined using 1% agarose gel electrophoresis at 95 V for 50 min with a 1-kb ladder (Gibco BRL, Gaithersburg, MD) as a size reference. The same PCR protocol was used to type a pig-rodent somatic cell hybrid panel (Yerle et al., 1996).

*Results.* A genomic region of approximately 3 kb between exons 7 and 8 of the porcine *PGR* gene was amplified with PCR. The PCR product was confirmed with 100% identity by matching the 110 bp of the 5′ end of the sequence with exon 7, and 11 bp of the 3′ end of the sequence (excluding the primer sequence) with exon 8 of the porcine *PGR* gene. Analysis of 27 porcine-rodent somatic cell hybrids allowed regional assignment of the *PGR* gene to porcine chromosome 9p13 proximal to 9p11 region with 100% concordancy (Figure 1). No discordancy was observed, and the estimated error risk was lower than .1% (Chevalet et al., 1997; estimated with a web tool at http://www.toulouse.inra.fr/lgc/pig/pcr/pcr.htm).

*Chromosomal Location.* 9p13 proximal region-9p11.

*Comments.* Progesterone receptor belongs to the steroid-thyroid-retinoic acid receptor super family and has been mapped to human chromosome 11q22.1-22.3 with somatic hybrid panel and in situ hybridization, respectively (Rousseau-Merck et al., 1987; Mattei et al., 1988). Our results in mapping the *PGR* gene to porcine chromosome 9p13-p11 are in agreement with the bidirectional chromosomal painting results (Goureau et al., 1996) that showed conserved synteny between HSA11q14-qter and SSC9pter-p11, where genes for apolipoprotein AI (*ApoAI*), CIII (*ApoCIII*), tyrosinase (*TYR*), and *PGR* are located (Charmley et al., 1991; Fronicke et al., 1996).

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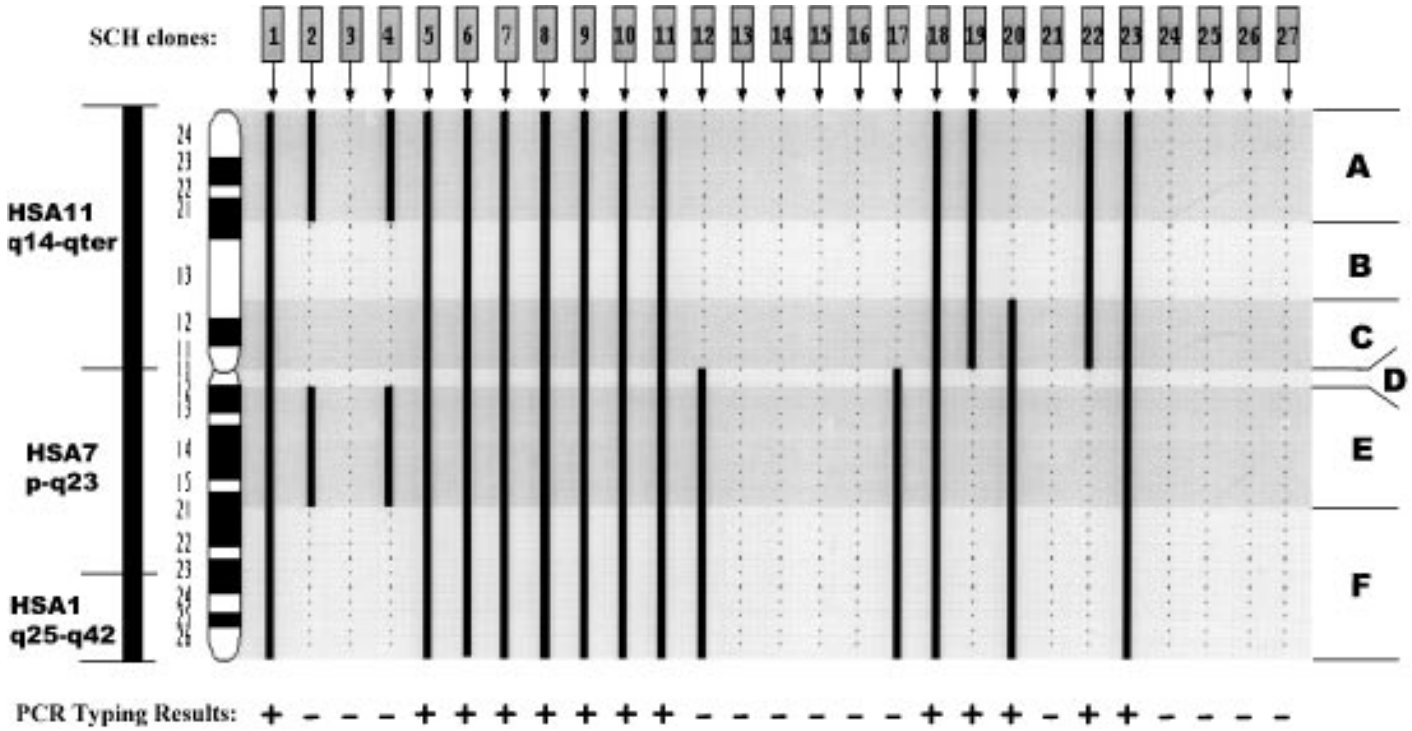


Figure 1. Diagram representing the presence of fragments of porcine chromosome 9 in each of the 27 somatic cell hybrid (SCH) clones. The porcine chromosome fragments are shown as vertical solid bars that span the length of the fragment as detected positive in the clone (Chevalet et al., 1997; http://www.toulouse.inra.fr/lgc/pig/cyto/gene/chromo/SSCG9.htm). The presence of various chromosome 9 fragments enables the definition of regions identified with capital letters A, B, C, D, E, and F, shown on the right. Corresponding human syntenic chromosomal fragments are shown on the left (HSA11q14-qter, HSA7p-q23, and HSA1q25-q42). Positive clones for *PGR* are shown at the bottom of the figure, which clearly indicate that the porcine *PGR* maps to region C with correlation coefficient = 1 and probability = .899 (estimated with a web tool at http://www.toulouse.inra.fr/lgc/pig/pcr/pcr.htm).

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