Rapid Communication: Genetic Linkage and Physical Mapping of the Porcine Androgen Receptor (AR) Gene


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Source and Description of Primers. Primers were designed from published bovine and human androgen receptor (AR) sequences (GenBank accession number Z75315 and M27430, respectively). These primers were used to obtain a porcine sequence (submitted to GenBank: accession number AF079783). A total of 247 bp out of the entire 793-bp PCR product shared 90.3% identity with sections of exons 7 and 8 of the human AR gene. Porcine specific primers (AR-3 and AR-4) were then designed to amplify a 160-bp fragment in intron 7 of the AR gene region from porcine genomic DNA.


Method of Detection. Polymerase chain reaction was conducted utilizing primers AR-3 and AR-4. Each reaction (10 μL total volume) contained 1 μL of genomic DNA (12.5 ng/μL), 5 pmol of each primer, .25 mM of each dNTP, .75 U of Taq polymerase (Promega), 1.5 mM MgCl₂, and 1 × PCR buffer (Promega). An MJ Research model PTC-100 (Watertown, MA) was used for thermocycling as follows: 4 min at 94°C, followed by 33 cycles of 45 s at 92°C, 1 min at 58°C, and 1 min at 72°C, with a final 5-min extension at 72°C. After amplification, the products were electrophoresed on an 8% acrylamide gel and then visualized by ethidium bromide staining for 15 to 20 min. Physical mapping of the marker was completed by genotyping the Somatic Cell Hybrid Panel containing 27 hybrid lines (Yerle et al., 1996) and comparing the results with the established regional assignment (http://www.toulouse.inra.fr/dc/pig/hybrid/chromo19/ chromo19.htm). Linkage mapping of AR was accomplished using CRIMAP (version 2.4, Green et al., 1990) and the existing USDA-MARC porcine linkage map (Rohrer et al., 1996).

Description of Polymorphism. A microsatellite polymorphism was recognized in the intron between exon 7 and exon 8. The sequenced products from a Meishan and a Yorkshire pig displayed a compound dinucleotide repetitive sequence: (GT)₈(GC)(GT)₂(GC)₄(GC)₂₃(GT)₁₆(GA)₈. Primers were designed flanking a 160-bp region containing a group of these repeats within the intron. Genotyping of the USDA-MARC mapping reference families revealed four alleles. Alleles 1 to 4 were 160 bp, 158 bp, 156 bp, and 154 bp, respectively.

Pattern of Inheritance. Sex-linked segregation was observed in eight two-generation USDA-MARC reference families (Rohrer et al., 1996).

Allelic Frequency. Allele frequencies were determined in 55 unrelated animals representing five breeds from Iowa State University. Allele 1 occurred with a frequency of .11 in Duroc (n = 8) and .15 in Hampshire (n = 11). Allele 2 occurred with a frequency of .22 in Duroc, .44 in Chester White (n = 10), .33 in Yorkshire (n = 9), .75 in Landrace (n = 10), and .69 in Hampshire. Allele 3 occurred with a frequency of .67 in Duroc, .56 in Chester White, .5 in Yorkshire, .16 in Landrace, and .15 in Hampshire. Allele 4 occurred with a frequency of .16 in Yorkshire and .08 in Landrace.

Chromosomal Location. The AR gene was physically mapped to the porcine X chromosome (SSCX) q13 (Figure 1) with a correlation coefficient of .86 and an error risk of less than .1%. Based on the linkage analysis with the USDA-MARC pig linkage map (Rohrer et al., 1996), the AR gene was confirmed to be on SSCX and closely linked to several previously mapped markers. Linked markers and their 2-point LOD scores (in parenthesis) were SW2470 (27.98), SW1861 (28.08), and SW2476 (28.00), SW1943 (23.66), HPRT1 (12.11), and SW2453 (21.61).

Comments. The AR is a member of the steroid receptor family and serves as a receptor for dihydrotestosterone, which controls differentiation of...