Rapid communication: Linkage mapping of the Mahogany (attractin) locus in cattle and pigs[1]

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Polymorphism. Restriction fragment length polymorphisms (RFLP) were detected within PCR amplification products of the porcine and bovine Mahogany (*attractin*; ***ATRN***) genes using the restriction enzymes *Taq*I and *Msp*I, respectively.

Primer Description. The common (porcine and bovine) forward and reverse primers were designed based on homologous regions of human and mouse *ATRN* cDNA sequences (GenBank accession no. AB011120 and AF120318, respectively). These primers amplified a region of the porcine and bovine *ATRN* gene spanning from exon 5 to the 3′ untranslated region.

Primer Sequences. Forward primer: 5′-GTGTACAAGGAGAAGTCAGGAG-3′; reverse primer: 5′-GATCTATT(C/T)AAAGTCTAGGCAC-3′.

Method of Detection. PCR amplification was performed using 50 ng of genomic DNA and 1 U of *Taq* Gold polymerase (Perkin Elmer, Foster City, CA) with the supplied buffer (final concentration of 1.5 m*M* $MgCl_2$). "Touchdown" thermal cycling used 10 cycles of amplification with annealing temperatures beginning at 65°C and decreasing 1°C per cycle, followed by 30 cycles with an annealing temperature of 55°C. Each cycle had an extension time of 2.5 min. Digestion of the resulting porcine ~980-bp product with *Taq*I revealed a polymorphism with two alleles (Figure 1). An 800-bp band is present in Allele A, with band sizes of 500 and 300 bp characterizing Allele B. Additional smaller bands were not visualized on the 4% metaphor (FMC BioProducts, Rockland, ME) gel. Digestion of the resulting bovine ~980-bp product with *Msp*I revealed a polymorphism with two alleles (Figure 1) characterized by bands of 550 and 250 bp (A allele) or 550 and 220 and 30 bp (B allele). Additional smaller bands were not visualized on the 4% metaphor gel. Confirmation of the identities of the porcine and bovine *ATRN* PCR amplification products was obtained by terminal end sequencing (GenBank accession no. AF194961 and AF194962, respectively).

Mendelian Inheritance. Mendelian segregation of porcine *ATRN* was confirmed in eight full-sib families (91 offspring). Mendelian inheritance of bovine *ATRN* was confirmed in 17 full-sib families (175 offspring).

Chromosomal Location. In a sex-averaged analysis using the three-generation PiGMaP reference families (Archibald et al., 1995), *ATRN* was linked to several microsatellite markers on chromosome 17 (SSC17), including *S0292*, *SW1031*, and *S0359* with recombination frequencies of 0.09, 0.20, and 0.17 and LOD scores of 5.27, 4.17, and 5.58, respectively. In addition, *ATRN* was linked to a marker within the *ENDO* locus (.06, 5.81) on SSC17.