1999

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Abstract
Source and Description of Primers. Primers were designed from published sheep epidermal growth factor (EGF) sequence (GenBank accession no. U36428) and were used to amplify across intron 3 of the EGF gene from porcine genomic DNA. Of sequences produced, 84 bp showed 82.1% identity to sheep EGF exon 3 and 81.0% to human EFG exon 3. For exon 4, the 75 bp showed 82.3% identity to sheep EGF exon 4 and 77.3% identity to human EGF exon 4. These sequences were further used to design pigspecific primers and have been submitted to GenBank (accession nos. AF079768 and AF079769).

Keywords
Epidermal Growth Factor, Pigs, Genes

Comments
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Rapid Communication: *Epidermal Growth Factor* Maps to Pig Chromosome 8[1]

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Primer Sequences. Forward primer: 5′-CAACAGGAAGGAATCATTACAGTA-3′; reverse primer: 5′-CCAAAACAGCCGCTTATCAAG-3′. Pig-specific forward primer: 5′-GAAACAATTCCCGTGTTCTCT-3′; reverse primer: 5′-TCACTTCCACACCTGTAACATCT-3′.

Method of Detection. A PCR amplification was performed using 50 ng of genomic DNA, 1× PCR buffer (Promega), 2.0 m*M* $MgCl_2$, 200 μM each of dNTP, 1 unit of *Taq* polymerase (Promega), and 300 n*M* of each primer in a 30-μL reaction volume. A PCR amplification on a porcine-rodent somatic cell hybrid panel used 10 ng of genomic DNA in a 15-μL reaction. The PCR cycling conditions included an initial denaturation of 2 min at 94°C followed by 35 cycles of 30 s at 94°C, 1 min and 30 s at 54°C, and 2 min at 72°C, with a final 5-min extension at 72°C. The PCR products were separated by electrophoresis on 1% agarose gels. No PCR products were obtained from mouse or Chinese hamster genomic DNA under these reaction conditions.

Description of Polymorphism. The PCR amplification produced a PCR length polymorphism with one or two major bands: 1,527 bp (A allele) and 652 bp (B allele). Both PCR products were sequenced in their entirety to confirm an *EGF* product.

Inheritance Pattern. Autosomal Mendelian segregation of the polymorphic products was observed in two three-generation families.

Frequency. Analysis of 71 unrelated animals representing a total of eight breeds indicated allelic frequencies of .65 for the 652-bp B allele and .35 for the 1,527-bp A allele (Table 1).

Chromosomal Location. Two-point linkage analysis using data obtained from individuals of the PiGMaP families (Archibald et al., 1995) localized *EGF* to porcine chromosome 8. The most closely linked markers (centimorgans, log of the odds) are IL2 (.00, 3.01), S0086 (.17, 6.20), S0069 (.15, 5.31), S0017 (.21, 3.44), S0144 (.04, 12.90), S0225 (.00, 12.64), Alb-1 (.22, 3.42), and UCP1 (.09, 5.76).

Physical Mapping Chromosomal Location. Analysis of 27 porcine-rodent somatic cell hybrids (Yerle et al., 1996) allowed regional assignment of *EGF* to porcine chromosome 8q23–q27 with 100% concordance (Chevalet et al., 1997) (Figure 1).

Comments. Epidermal growth factor is a single polypeptide of 53 amino acid residues that is involved in the regulation of cell growth and cell differentiation

Table 1. Frequency of *Epidermal Growth Factor* (*EGF*) genotypes in several breeds

		Frequency of pigs with indicated genotype[a]		
Breed	No.	AA	AB	BB
Yorkshire	10	0	.30	.70
Chester White	10	0	0	1
Duroc	21	.14	.38	.48
Hampshire	11	0	.36	.64
Landrace	4	0	.75	.25
Minzhu	3	.33	.33	.33
Meishan	9	1	0	0
Pietrain	3	.33	.67	0
Total	71			

[a]A = 1,527-bp product; B = 652-bp product.

[1]The authors express their appreciation to S. Marklund for his technical support and to J. Helm and J. Newton for DNA collection and isolation. Contribution of PiGMaP DNA by PiGMaP laboratories is appreciated. This work was supported in part by the EC Bridge "PiGMaP" program. Journal Paper No. J-18018 of the Iowa Agric. and Home Econ. Exp. Sta., Ames, Project No. 3184, and supported by Hatch Act and State of Iowa funds.

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Received July 30, 1998.

Accepted November 4, 1998.

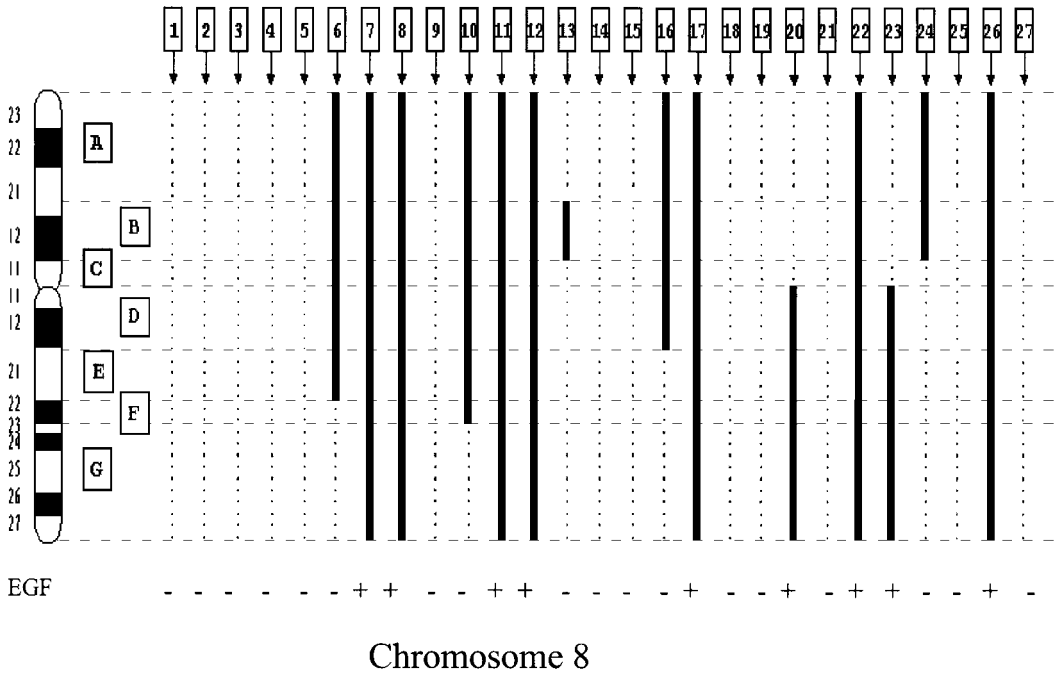

Figure 1. Diagram representing the presence of fragments of porcine chromosome 8 in each hybrid clone. Positive hybrids for *Epidermal Growth Factor* (*EGF*) are shown at the bottom of the figure and indicate that *EGF* maps to Region G. Results of chromosomal painting analysis support localization of this gene to Region G because *EGF* maps to a homologous segment of human chromosome 4.

(Boonstra et al., 1995). The PCR length polymorphism is a result of an 875-bp insertion containing portions of a porcine L1 nucleotide element and sequences similar to a part of a porcine cytochrome P450 aromatase gene. The localization of *EGF* to pig chromosome 8q23–q27 is in agreement with the assignment of this gene to human chromosome 4q25 and adds to the comparative map.

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