1999

Rapid Communication: Mapping and Genetic Analysis of Porcine FOSB

J. M. Helm
Iowa State University

Z. Hu
Iowa State University

Max F. Rothschild
Iowa State University, mfrothsc@iastate.edu

Rapid Communication: Mapping and Genetic Analysis of Porcine FOSB

Abstract
Genus and Species. Sus scrofa. Locus. FBJ murine osteosarcoma viral oncogene homolog B (FOSB) gene. Source and Description of Primers. Primers were designed from a human and mouse FOSB consensus sequence and used for PCR amplification of the genomic region from Exons 2 to 3 of the porcine FOSB gene.

Keywords
Genes, Maternal Behavior, Pigs, Gene Mapping

Rapid Communication: Mapping and Genetic Analysis of Porcine *FOSB*[1]

J. M. Helm, Z. Hu, and M. F. Rothschild[2]

Department of Animal Science, Iowa State University, Ames 50011

Genus and Species. *Sus scrofa*.

Locus. FBJ murine osteosarcoma viral oncogene homolog B (*FOSB*) gene.

Source and Description of Primers. Primers were designed from a human and mouse *FOSB* consensus sequence and used for PCR amplification of the genomic region from Exons 2 to 3 of the porcine *FOSB* gene.

Primer Sequences. The forward primer was 5′ GCA ACC CAC CCT CAT CTC T 3′, and the reverse primer 5′ GTC AGC TCC CTC CGC CGG TTC 3′.

Method of Detection. A 567-bp fragment was amplified from genomic porcine DNA. Amplification products were obtained under the following conditions. A 25-μL reaction containing 1× PCR buffer (Promega; Madison, WI), 1.5 m*M* $MgCl_2$, 200 μM dNTP, 10 pmol of each primer, .2 U of *Taq* DNA polymerase (Promega), and 12.5 ng of porcine genomic DNA was placed in a Robocycler (Stratagene; La Jolla, CA) for a thermal cycling regimen of initial denaturation for 3 min at 93°C, 35 cycles of 45 s at 93°C, 45 s at 60°C, and 45 s at 72°C, and a final extension of 5 min at 72°C. The PCR products were detected on a 1% agarose gel.

Sequence Homology. The 567-bp amplified product was confirmed as the porcine *FOSB* gene through sequence comparison (primer sequences excluded) to mouse and human *FOSB* sequence. Exonic sequences had a 91 and 84% nucleotide identity to human and mouse *FOSB*, respectively. This porcine *FOSB* sequence has been submitted to GenBank (accession number AF120155).

Description of Polymorphism. A single nucleotide substitution was detected by sequence analysis in intron 2, and a *Nla*III PCR-RFLP assay was developed. Upon *Nla*III digestion, polymorphic allelic fragments, 355 bp (allele 1) or 340 and 15 bp (allele 2), and monomorphic fragments, 110, 72, and 30 bp, were seen (Figure 1). Fragments were resolved with electrophoresis using a 3.5% MetaPhor agarose gel (FMC BioProducts; Rochland, ME) for 550 Vh.

Pattern of Inheritance. The PCR-RFLP (*Nla*III) for the porcine *FOSB* gene showed autosomal Mendelian segregation in 3 three-generation Iowa State University (ISU) and 2 three-generation European PiGMaP swine reference families.

Allelic Frequencies. Analysis of allelic frequencies (Table 1) in eight swine breeds, 71 pigs in total, showed allele 2 to have a marginally, but not significantly, higher frequency in breeds traditionally associated with good maternal behavior (i.e., number

[1]The authors appreciate the technical advice and valuable discussions with Graham Plastow, Richard Wales, Stefan Marklund, Lena Marklund, and Zhiliang Hu. Project funding was kindly provided in part by PIC Group and the Iowa Agric. and Home Econ. Exp. Sta., Ames and Hatch Act and State Funds; Journal paper number, J-18227, project no. 3148.

[2]To whom correspondence should be addressed.

Received January 19, 1999.

Accepted May 10, 1999.

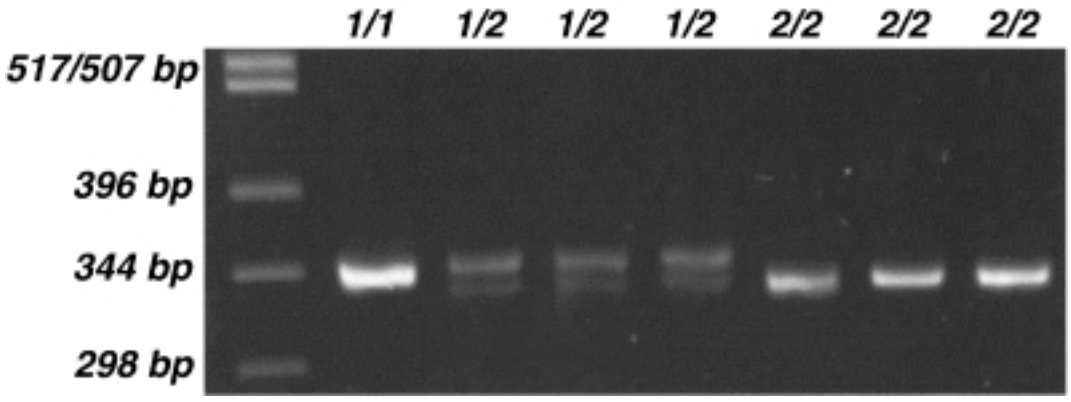

Figure 1. *FOSB Nla*III PCR-RFLP allelic fragments, 355 bp for Allele 1 and 340 bp for Allele 2, are illustrated. Not shown are a second band, 15 bp, for Allele 2 and three monomorphic bands.

Table 1. Allelic frequencies for the porcine *FOSB Nla*III PCR-RFLP in eight swine breeds

	Breed[a]							
Allele	Y n = 6	D n = 25	H n = 7	L n = 11	CW n = 8	Me n = 17	LW n = 11	WB n = 2
1	.42	.56	.21	.23	0	.31	.18	0
2	.58	.44	.79	.77	1.0	.69	.82	1.0

[a]Y = Yorkshire, D = Duroc, H = Hampshire, L = Landrace, CW = Chester White, Me = Meishan, LW = Large White, and WB = Wild Boar.

born and number weaned). Frequencies for allele 2 ranged from .44 in Duroc to 1.0 in Chester White and Wild Boar. In sire lines, allelic frequencies were mixed. In Hampshire, allele 2 had a frequency of .79, and in Duroc this allele had a lower frequency, .44, than allele 1.

Chromosomal Location. The *FOSB* was physically mapped to the distal part of SSC6q21 using a Swine-Rodent Somatic Cell Hybrid Panel (Yerle et al., 1996). Linkage mapping analysis (CRIMAP, v. 2.4; Green et al., 1990) using *FOSB Nla*III genotypes from a three-generation European PiGMaP family (Archibald et al., 1995) confirmed the placement of *FOSB* on chromosome 6. Two-point linkage analysis showed significant linkage (LOD = 4.82) between *FOSB* and *GPI* (glucose phosphate isomerase), which was previously mapped on swine chromosome 6. Multipoint linkage analysis indicated that *FOSB* is in close proximity to swine *GPI*, *CRC* (calcium release channel for skeletal muscle), and *EAH* (erythrocyte antigen H). Synteny between *FOSB*, *GPI*, *CRC*, and *EAH* has also been detected on human chromosome 19 (q13.3) and mouse chromosome 7.

Comments. The genetic components to behavioral traits have rarely been elucidated. However, the *FOSB* gene has been shown to directly control one specific behavior, maternal nurturing in mice (Brown et al., 1996). Recently other genes have also been linked to specific maternal behaviors (Bridges, 1998; Lefebvre et al., 1998). In swine, differences among breeds in sow behaviors related to the care of pigs, have long been noted by pork producers. We have made a preliminary investigation of the association between genetic differences with the *FOSB* gene by examining those swine breeds predominantly differentiated as sire and maternal breeds. No allelic association with breeds traditionally assigned as sire vs maternal breeds was noted. Further breed analysis is necessary to determine whether there is an obvious association between *FOSB* and differences in breed maternal performance.

Literature Cited

Archibald, A. L., C. S. Haley, J. F. Brown, S. Couperwhite, H. A. McQueen, D. Nicholson, W. Coppieters, A. Van de Weghe, A. K. Stratil, A. K. Winterø, M. Fredholm, N. J. Larsen, V. H. Nielsen, D. Milan, N. Woloszyn, A. Robic, M. Dalens, J. Riquet, J. Gellin, J.-C. Caritez, G. Burgaud, L. Ollivier, J.-P. Bidanel, M. Vaiman, C. Renard, H. Geldermann, R. Davoli, D. Ruyter, E.J.M. Verstege, M.A.M. Groenen, W. Davies, B. Høyheim, A. Keiserud, L. Andersson, H. Ellegren, M. Johansson, L. Marklund, J. R. Miller, D. V. Anderson Dear, E. Signer, A. J. Jeffreys, C. Moran, P. Le Tissier, Muladno, M. F. Rothschild, C. K. Tuggle, D. Vaske, J. Helm, H. C. Liu, A. Rahman, T.-P. Yu, R. G. Larson, C. B. Schmitz. 1995: The PiGMaP consortium linkage map of the pig (*Sus scrofa*). Mamm. Genome 6: 157–175.

Bridges, R. S. 1998. The genetics of motherhood. Nat. Genet. 20: 108–109.

Brown, J. R., H. Ye, R. T. Bronson, P. Dikkes, and M. E. Greenberg. 1996. A defect in nurturing in mice lacking the immediate early gene *fos*B. Cell 86:297–309.

Green, P., K. Falls, and S. Crooks. 1990. Documentation for CRIMAP, version 2.4. Washington Univ. School of Medicine, St. Louis, MO.

Lefebvre, L., S. Viville, S. C. Barton, F. Ishino, E. B. Keverne, and M. A. Surani. 1998. Abnormal maternal behaviour and growth retardation associated with loss of the imprinted gene *MEST*. Nat. Genet. 20:163–169.

Yerle, M., G. Echard, A. Robic, A. Mairal, C. Dubut-Fontana, J. Riquet, P. Pinton, D. Milan, Y. Lahbib-Mansais, and J. Gellin. 1996. A somatic cell hybrid panel for pig regional gene mapping characterized by molecular cytogenetics. Cytogenet. Cell Genet. 73(3):194–202.

Key Words: Genes, Maternal Behavior, Pigs, Gene Mapping