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J Anim Sci 1993. 71:2275.

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Rapid Communication: A *MspI* Restriction Fragment Length Polymorphism at the Swine *PIT-1* Locus¹

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Name of Marker. Swine PIT-1*2.

Source and Description of Clone. Probe used in RFLP analysis was a cDNA fragment encoding the swine PIT-1 POU-domain region (Tuggle et al., 1993). The 311-bp probe was isolated from the vector pCR1000 using *EcoRI* and *HindIII*.

Method of Detection. DNA was isolated from whole blood, digested with *MspI*, and transferred to charged nylon membranes. Hybridizations were at 65°C for 20 to 22 h in .5 M NaCl, .05 M Na-phosphate buffer, pH 6.5, 5 × Denhardt's reagent, 10% dextran sulfate, 1% SDS, and 50 µg/mL of sonicated, denatured salmon sperm DNA. Final washes were at 65°C with .5× SSC, .1% SDS for 10 to 15 min.

Description of Polymorphism. Two fragments are observed with this probe/enzyme combination (See Figure 1). Both 4.5-kb and 3.75-kb fragments are polymorphic. Swine *PIT-1* is not polymorphic in 21 unrelated animals using *TaqI*.

Inheritance Pattern. Autosomal Mendelian segregation of the 4.5- and 3.75-kb bands was observed in 39 animals in nine families.

Frequency. The frequency of the alleles in 73 unrelated pigs from eight breeds was .21 for the 4.5-kb allele and .79 for the 3.75-kb allele (Table 1).

Chromosomal Location. Not determined.

Probe Availability. Probe is available from C. K. Tuggle (Tuggle et al., 1993).

Comments. PIT-1 has been shown to control growth hormone and prolactin synthesis in the mammalian pituitary (Ingraham et al., 1990). Restriction fragment length polymorphisms in both mice and humans are associated with dwarf stature and hypopituitarism (Ingraham et al., 1990; Radovick et al., 1992). The authors thank R. G. Larson for providing swine DNA.

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Key Words: Pigs, Growth Hormone, RFLP, Genetic Markers

J. Anim. Sci. 1993. 71:2275

Table 1. PIT-1 polymorphism analysis

Breed (no.)	Percentage of animals with indicated genotype		
	4.5/4.5	4.5/3.75	3.75/3.75
Fengjing (6)	66	33	0
Meishan (9)	22	66	11
Minzhu (7)	28	43	28
C. White (9)	0	0	100
Duroc (12)	0	0	100
Hampshire (12)	0	0	100
Landrace (9)	0	0	100
Yorkshire (9)	0	33	66
Total: 73			

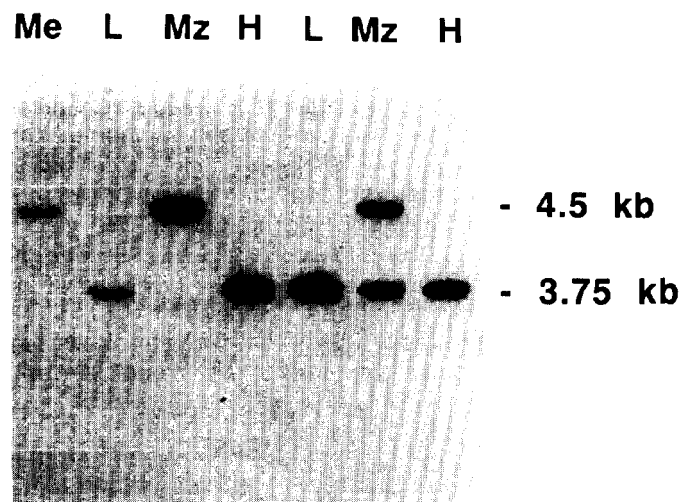


Figure 1. Swine PIT-1 *MspI* polymorphism analysis. Two allelic fragments of 4.5 kb and 3.75 kb are detected. Note that all three possible genotypes are represented (Me: Meishan; L: Landrace; Mz: Minzhu; H: Hampshire).

¹Journal paper no. J-15309 of the Iowa Agriculture Home Econ. Exp. Sta., Ames. Projects no. 3038 and 3085.

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Received April 14, 1993.

Accepted May 27, 1993.