

LOCATING SOME QUANTITATIVE GENES IN THE PIG

C.P. McPhee

Queensland Department of Primary Industries, Animal Research Institute, Yeerongpilly, Qld. 4105.

Most economically important traits in pigs are under the control of quantitative genes. Locating these on the pig genome will facilitate genetic improvement in pig productivity. Substituting portions of the chromosome (haplotypes) with standard haplotypes containing marker genes and observing changes in a quantitative trait can help to locate genes affecting that trait, as was demonstrated in *Drosophila* by McPhee (1971). This study uses the same principle to locate haplotypes of the pig which appear to contain genes for appetite and growth rate. The effect on these traits of substituting haplotypes containing the halothane gene n was examined in a genetic line which had been selected for rapid lean growth then relaxed for 4 generations, and in an unselected line of the same origin. The n haplotype was segregating in both lines and its substitution effect was measured from $(nn - NN)/sd$ where nn and NN are the means of the halothane and normal homozygotes and sd is the line standard deviation of each trait. The least square mean growth rates, appetites and backfats of NN genotypes ($N = 50$) and substitution effects of the n haplotype are given in Table 1 for pigs from both lines grown to 90 kg on *ad libitum* feeding.

Table 1. Line means of NN genotypes and n gene substitution effects

Trait	Line means (NN)			Substitution effects		
	Selected	Unselected	Sign. ¹	Selected	Unselected	Sign. ¹
Growth rate (kg/d)	0.63±.01	0.55±.01	**	-2.2	-0.4	**
Feed intake (kg/d)	2.55±.05	2.37±.01	**	-2.0	-0.6	**
Backfat (mm)	14.0±.6	19.4±.5	**	-0.6	-0.4	NS

¹NS, non significant, $P > 0.05$; ** $P > 0.01$.

Compared with the unselected line, the selected line grew faster and had a higher appetite and less fat. Substitution of n for normal N gene containing haplotypes reduced all traits in both lines, the effect being much greater in the selected than in the unselected line for growth rate and appetite, but about the same for fat.

These observations are consistent with a model in which the halothane locus is the site of a series of normal haplotypes affecting growth rate and appetite (say N_1, N_2, N_3, N_4) in the unselected population. During selection, those with a neutral or negative effect on these traits (say N_3, N_4) are removed leaving N_1, N_2 in the selected line. The replacement of some of these N containing haplotypes with n haplotypes would be expected to have a much greater depressing effect on growth rate and appetite in the selected than in the unselected line, as was observed. In contrast, low fatness genes accumulated in the selected line seem to have been at loci away from the halothane locus since the substitution effect of the n haplotype on fat did not differ significantly between the lines. It is intended to explore other statistical techniques (eg; DFREML) to check for bias in estimating haplotype effects.

References

McPHEE, C.P. (1971). *Theoretical and Applied Genetics*. 41:25-30.