COMPARING BREEDING VALUES OF PIGS FROM DIFFERENT FARMS

G.M. MACBETH

Animal Research Institute, 665 Fairfield Rd, Yeerongpilly, Qld. 4105

Traditionally genetic improvement carried out by the Australian pig industry has been confined to within herd selection with across herd evaluations limited to the throughput of central test stations. A more flexible breeding structure is being established with the application of Best Linear Unbiased Prediction (BLUP) procedures to estimate breeding values. Using this methodology, breeding values of animals can be directly compared between farms which share common breeding animals. This allows the potential for higher selection pressures than was traditionally possible and the increased ability to select traits of low heritability. This study shows that there are genetic differences between herds in economically important traits.

Breeding values for number born alive (NBA), P2 fat (P2) and daily gain (DG) were predicted from 7 Large White herds and 1 central test station. The size of these herds ranged from 25 to 400 sows with the throughput of the test station being 250 Large White boars annually. All herds had pedigree and performance data from 1991 through to 1995 with the earliest records dating back to 198 1. Since 199 1 each herd had at least 5% its sires in common to those in other herds with each herd linked to at least four other herds from these sires. In total 43,682 performance and 12, 431 reproductive records were used to calculate breeding values with PEST (Groeneveld 1992). Genetic variance components were calculated using MTDFREML (Boldman *et al.* 1993) giving farm heritability estimates for NBA, P2 and DG of 0.11, 0.53 and 0.18 respectively.

The boar with the most profitable breeding value had a genetic advantage above the average of all animals born in 1991 for NBA, P2 and DG of 0.64 pigs, -3.29mm and 67g/day respectively. Herds with this economic advantage will be better off by $339/sow/year (CP McPhee, pers comm). Breeding value averages of each herd mean were calculated for each trait from animals born in 199 1 through to 1995. The best performing and most improved herds are also shown (Table 1). There was a significant difference between herds, apparently due to different selection histories. Identification of superior animals within these herds will make for rapid genetic gains from selection. Artificial insemination centres are now choosing sires from these BLUP evaluations. Extensive use of these sires will increase genetic linkages and further improve the accuracy of determination of breeding values across herds.

Table 1. Estimated breeding values of number born alive (NBA), P2 fat (P2) and daily gain (DG)

YEAR		1991	1992	1993	1994	1995	(1991-1995) $\pm$ SE
NBA	Herd average	-0.19	-0.18	-0.09	-0.09	-0.02	0.17 $\pm$ 0.01
	Best herd	0.21	0.25	0.32	0.39	0.39	0.18 $\pm$ 0.02
	Most improved	-0.23	-0.15	0.06	0.07	0.24	0.47 $\pm$ 0.04
P2 (mm)	Herd average	0.25	0.13	0.09	-0.18	-0.48	-0.73 $\pm$ 0.02
	Best herd	-0.66	-0.84	-1.05	-1.27	-1.49	-0.83 $\pm$ 0.07
	Most improved	0.91	0.44	-0.12	-0.36	-0.70	-1.61 $\pm$ 0.13
DG (g/day)	Herd average	-14	-14	-10	-8	-4	10 $\pm$ 0.4
	Best herd	16	23	26	32	33	17 $\pm$ 0.6
	Most improved	16	23	26	32	33	17 $\pm$ 0.6

BOLDMAN, K.G., KRIESE, L.A., VAN VLECK, L.D. and KACHMAN, S.D. (1993). "A Manual for Use of MTDFREML". U.S. Dept. of Agriculture, Agricultural Research Service.
GROENEVELD, E. and KOVAK, M. (1992). *Livest. Prod. Sci.* **30:** 319-31.