

## ACCOUNTING FOR DIFFERENCES IN GENETIC MERIT OF FOUNDATION ANIMALS AMONG HERDS IN AN ACROSS-HERD GENETIC EVALUATION

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### SUMMARY

Data from 3 pig breeds were analysed using different genetic grouping of base animals for an across herd evaluation system. Base animals were grouped by herd of first performance, time of entry into the evaluation system, and time within herd. BLUP estimates of group solutions and estimated breeding values for backfat and average daily gain, and comparisons among them using confidence intervals and correlations between the solutions were used to compare each grouping. It is concluded that grouping base animals by time within herd is the most appropriate method of genetic grouping.

**Keywords:** Across-herd evaluation, genetic groups, pigs, BLUP

### INTRODUCTION

Across-herd genetic evaluations often assume that the base populations across herds (the animals with unknown parents) have the same mean genetic value. If herds have developed separately with a different selection strategy in the past, then base animals from each herd may have different genetic levels. Lack of ties between herds together with different genetic levels among them are often considered obstacles to using BLUP for across herd evaluations (Groeneveld and Spilke 1998). Westell and Van Vleck (1987) presented a procedure for grouping base animals with different genetic background that has been widely adopted, using herd of precedence and the time they entered the population to form genetic groups. The aim of this study is to determine how best to assign base animals to genetic groups for 3 breeds of pigs in an across-herd evaluation system.

### MATERIALS AND METHODS

Data from the National Pig Improvement Program (NPIP) were analysed using ASREML (Gilmour *et al.* 1997). Animal solutions from different ways of grouping base animals were compared using Pearson correlations and confidence intervals. The data structure is summarized in Table 1 for the 3 breeds under consideration, namely Duroc (Du), Landrace (Lr), and Large White (Lw).

The traits considered were backfat (BF) and average daily gain (ADG). Univariate analyses fitting management group were performed within each breed. Management groups were formed as in PIGBLUP, i.e. the date of end of test for animals within herd, user recorded management group, and sex, should not be more than 9 weeks apart and/or the number of records should not be more than 50. The number of management groups formed in this way are presented in Table 1. Weight at end of test was used as a covariate in the analysis of BF.

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**Table 1. Number of animals, management groups per breed and percentage of base animals**

	Duroc (Du)	Landrace (Lr)	Large White (Lw)
Herds	9	9	11
Animals with Records	20,356	43,151	74,294
Base Animals	563	1,772	3,007
Total Animals	20,919	44,923	77,301
Management Groups	644	1,110	1,729
Base Parents (%)	35.78	47.09	47.13
Progeny from Base Parent (%)	21.84	25.00	26.60

On average, base parents accounted for 43 % of the parental populations (Table 1) and they contributed around 25 % of the progeny with records, which could be considered a significant contribution of genetic material. Thus, the groups of base animals were formed according to the herd and their year of entry into that herd as explained below. There were 4 groupings for each breed: 1) one base group across all herds and time units (called "1g"); 2) one group per herd (called "h"); 3) one group per time unit across herds (called "t"); and 4) one group per time unit within herds (called "ht").

For herd grouping, base animals were grouped according to the herd in which they first performed. The number of groups formed for Du, Lr, and Lw were 8, 9, and 11, respectively. Grouping by time followed the PIGBLUP procedure, i.e. the number of base sires should be greater than 5, the number of base sires plus base dams should be greater than 25 and the number of progeny coming from either base sires or base dams should be more than 400 (called 5-25-400). If the number of animals in a specific year did not meet these criteria, the year was "absorbed" into the current group until these conditions were met when another group was formed. Since this way of grouping depends on the number of animals in each breed, two additional time grouping strategies were tested, 5-25-200 and 5-10-20, the numbers meaning as above. For the time grouping "t", conditions were tested using the time period over all herds. Conditions were tested within each herd for the herd-time grouping "ht". The number of time groups ranged from 7 to 16, and herd-time groups from 9 to 48.

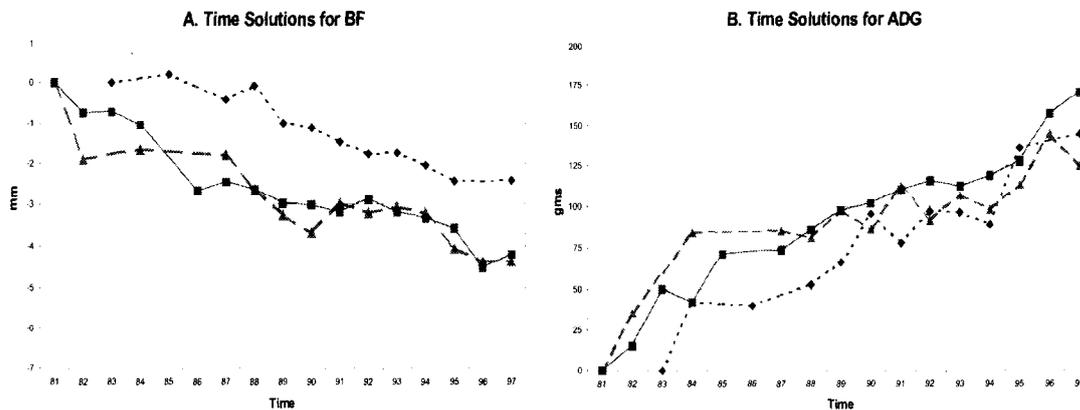
## RESULTS AND DISCUSSION

The solutions for BF and ADG when grouping by herd are shown in Table 2. It can be seen that BF had significant differences between herds in all breeds, while, for ADG, there were only differences in the Lw breed. The higher heritability of BF (estimated as 0.47, 0.56, and 0.52 with a SE of 0.02, for Du, Lr, and Lw, respectively) compared to ADG (0.38, 0.37, and 0.35 with a SE of 0.02) could have helped to detect herd differences. Solutions (and correlations) for the three grouping strategies, 5-25-400, 5-25-200, and 5-10-20, were very similar, so the results presented in this paper are only for the latter, since it had more group solutions to compare. There were significant differences between time periods, both across herds (Figures 1A and 1B) and within herds, for both traits. Trends due to time were as expected (BF going down, ADG going up). Table 3 shows the correlation between EBV's for BF and ADG for the different ways of grouping for all animals (All), only sires (Sires), only dams (Dams), and progeny born in the last year of evaluation (Prog. 97), which could be regarded as the current "active" animals. The genetic groups affected all breeds (Table 3). Du was

affected more so when herd was accounted for, giving a correlation as low as 0.62. Even for the more accurate estimates of only sires and dams (since their progeny contribute to their EBV's) the correlations with 1g were around 0.75. Assuming that a genetic group has to be formed, then just grouping by herd or by time would have different EBV's, as can be seen by the low correlations for h-t in Table 3, and both alternatives may be wrong. However, when grouping by time within herd (ht), higher correlations with either h or t were achieved, thus giving the best strategy for grouping.

**Table 2. Herd solutions ( $\pm$ SE) for BF and ADG for the three breeds under study. They are expressed relative to herd 1. Solutions within each column with different superscripts are significantly different ( $P<0.05$ ) based on confidence intervals**

Herd	Du		Lr		Lw	
	BF	ADG	BF	ADG	BF	ADG
1	0.00 <sup>A</sup> $\pm$ 0.35	0.00 <sup>A</sup> $\pm$ 32.43	0.00 <sup>A</sup> $\pm$ 0.32	0.00 <sup>A</sup> $\pm$ 12.86	0.00 <sup>A</sup> $\pm$ 0.34	0.00 <sup>A</sup> $\pm$ 10.87
2	-2.42 <sup>AB</sup> $\pm$ 1.18	54.96 <sup>A</sup> $\pm$ 46.28	-0.73 <sup>AD</sup> $\pm$ 0.45	43.47 <sup>A</sup> $\pm$ 13.53	-1.31 <sup>AB</sup> $\pm$ 0.43	60.03 <sup>BC</sup> $\pm$ 11.93
3	-2.15 <sup>AB</sup> $\pm$ 1.21	10.97 <sup>A</sup> $\pm$ 47.05	-1.70 <sup>ABCD</sup> $\pm$ 0.64	19.04 <sup>A</sup> $\pm$ 17.72	-1.46 <sup>AB</sup> $\pm$ 0.47	29.87 <sup>AB</sup> $\pm$ 11.89
4	-2.89 <sup>B</sup> $\pm$ 0.61	68.88 <sup>A</sup> $\pm$ 33.36	-1.34 <sup>ABCD</sup> $\pm$ 0.45	21.28 <sup>A</sup> $\pm$ 11.77	-1.31 <sup>AB</sup> $\pm$ 0.39	45.61 <sup>BC</sup> $\pm$ 9.63
5	-0.43 <sup>AB</sup> $\pm$ 1.02	-17.4 <sup>A</sup> $\pm$ 43.95	-2.79 <sup>BCD</sup> $\pm$ 0.51	36.78 <sup>A</sup> $\pm$ 56.01	-2.33 <sup>BC</sup> $\pm$ 0.43	68.9A <sup>BC</sup> $\pm$ 27.69
6	-1.30 <sup>AB</sup> $\pm$ 0.61	17.47 <sup>A</sup> $\pm$ 28.05	-1.46 <sup>ABCD</sup> $\pm$ 0.45	35.07 <sup>A</sup> $\pm$ 9.46	-2.09 <sup>BC</sup> $\pm$ 0.37	66.57 <sup>BC</sup> $\pm$ 6.95
7					-2.00 <sup>B</sup> $\pm$ 0.44	76.42 <sup>C</sup> $\pm$ 10.01
8	-0.42 <sup>AB</sup> $\pm$ 0.66	37.78 <sup>A</sup> $\pm$ 30.22			-3.51 <sup>C</sup> $\pm$ 0.51	80.82 <sup>C</sup> $\pm$ 11.66
9			-3.38 <sup>CD</sup> $\pm$ 0.71	21.17 <sup>A</sup> $\pm$ 19.14	-1.17 <sup>AB</sup> $\pm$ 0.48	79.26 <sup>C</sup> $\pm$ 12.36
10	-2.54 <sup>AB</sup> $\pm$ 1.16	68.28 <sup>A</sup> $\pm$ 45.65	-3.97 <sup>D</sup> $\pm$ 1.31	33.51 <sup>A</sup> $\pm$ 34.00	-2.70 <sup>BC</sup> $\pm$ 0.76	13.35 <sup>AB</sup> $\pm$ 20.45
11			-0.44 <sup>ABCD</sup> $\pm$ 1.43	-20.1 <sup>A</sup> $\pm$ 38.55	-1.33 <sup>AB</sup> $\pm$ 0.45	70.10 <sup>BC</sup> $\pm$ 11.09



**Figure 1. Time solutions for (A) BF and (B) ADG (Key:  $\blacklozenge$  Du  $\blacktriangle$  Lr  $\blacksquare$  Lw).**

In conclusion, these results suggest that there is a need to account for genetic groups in the NPIP and that grouping base animals by time within herds would give the best EBV's.

**Table 3. Correlations between EBV's for BF and ADG for the various ways of grouping**

		Du		Lr		Lw		Number of Animals		
		BF	ADG	BF	ADG	BF	ADG	Du	Lr	Lw
lg-h	All	0.77	0.79	0.90	0.97	0.92	0.84	20,919	44,923	77,301
	Sires	0.78	0.84	0.89	0.93	0.90	0.81	419	972	1,563
	Dams	0.71	0.79	0.87	0.95	0.89	0.78	1,232	3,000	5,188
	Prog. 97	0.62	0.80	0.91	1.00	0.98	0.93	1,939	5,043	9,612
lg-t	All	0.89	0.76	0.80	0.82	0.89	0.77	Same as above . . .		
	Sires	0.87	0.76	0.79	0.79	0.89	0.77			
	Dams	0.84	0.73	0.73	0.76	0.84	0.71			
	Prog. 97	0.87	0.84	0.96	0.99	0.98	0.96			
lg-ht	All	0.77	0.77	0.82	0.88	0.87	0.74	Same as above . . .		
	Sires	0.65	0.82	0.79	0.80	0.84	0.70			
	Dams	0.67	0.76	0.75	0.80	0.80	0.64			
	Prog. 97	0.66	0.78	0.90	0.99	0.97	0.88			
h-t	All	0.93	0.94	0.95	0.92	0.97	0.95	Same as above . . .		
	Sires	0.82	0.82	0.90	0.89	0.95	0.92			
	Dams	0.86	0.87	0.89	0.87	0.94	0.91			
	Prog. 97	0.90	0.96	0.94	0.99	0.99	0.92			
h-ht	All	0.98	0.99	0.97	0.96	0.98	0.97	Same as above . . .		
	Sires	0.90	0.95	0.94	0.94	0.97	0.94			
	Dams	0.95	0.97	0.94	0.93	0.96	0.94			
	Prog. 97	0.99	0.99	1.00	1.00	1.00	0.99			
t-ht	All	0.88	0.97	0.99	0.98	0.99	0.98	Same as above . . .		
	Sires	0.61	0.91	0.94	0.96	0.96	0.95			
	Dams	0.76	0.94	0.96	0.97	0.96	0.94			
	Prog. 97	0.90	0.97	0.94	0.99	0.99	0.90			

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#### REFERENCES

- Gilmour, A.R., Thompson, R., Cullis, B.R. and Welham, S.J. (1997) "ASREML" NSW Agriculture  
 Groeneveld, E. and Spilke, J. (1988) Proc. 6<sup>th</sup> Wld. Cong. Gen. Appl. Livs. Prod. 23: 483  
 Westell, R.A. and Van Vleck, L.D. (1987) *J. Dairy Sci.* 69: 3106