

THE EFFECT OF AGE SLICING INTERVAL ON THE VARIANCE COMPONENTS AND DATA EFFECTIVENESS FOR BIRTH AND 200 DAY WEIGHTS IN ANGUS CATTLE

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SUMMARY

In BREEDPLAN analyses, contemporary groups for birth weight and 200d weight are sliced at 45 day intervals to avoid possible inaccuracies in age adjustment, rapid changes in environmental conditions and confounding of sires and seasons biasing the estimated breeding values. However age slicing can have a significant impact on data structure and effectiveness of records. The aim of this study was to re-estimate the variance components and examine the effectiveness of the data for birth and 200day weights from Angus cattle with different contemporary group slicing intervals. The result showed that altering the slicing interval from 15 to 60 days did not have a significant impact on the variance components for birth or 200day weight. However increasing slice interval significantly improved the average effectiveness of the data for both traits. On average the animal record effectiveness increased by 10% and the average total effective progeny records per sire more than doubled. The results suggest that the age slicing interval could be altered from 45 to 60 days to increase the effectiveness of the data available without impacting on the genetic parameters. However altering the contemporary group structure will cause changes to the existing estimated breeding values.

INTRODUCTION

BREEDPLAN genetic evaluation limits the spread of age within any contemporary group through the use of age slicing. Slicing reduces errors from age adjustments, accounts for the effects of rapid environment change within management groups and reduces confounding of sires within seasons when natural mating is used (Graser *et al.* 2005). Currently in BREEDPLAN, birth and 200day weight contemporary groups are sliced at 45 day intervals. This is achieved by ordering the group by ascending date of birth and then incrementing new groups at each 45 day interval.

With expansion in the use of modern reproductive technologies like artificial insemination and embryo transfer, data collected from many bull breeding enterprises may have changed the variation in age (within contemporary groups) than was historically observed. This may result in different requirements for age slicing.

The effectiveness of data is dependant on the number of records, number of sires used in each contemporary group and the distribution of animals across sires. As slicing effects the size of contemporary groups it is likely that changing the slicing interval will also influence the effectiveness of data for evaluation at the animal and sire levels.

The aim of this study was to estimate the variance components for birth and 200day weights and examine the effectiveness of the data for Angus cattle with different contemporary group age slicing intervals.

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MATERIALS AND METHODS

Angus data extracted from the National Beef Recording System (NBRS) database were used in this study. For computational ease a subset of the database was used based on a random sample of approximately half of the performance recording herds from the state of Victoria. Raw data included pedigree information for 98,828 animals, 62,966 birth weight records and 75,567 200day weight records. Basic edits eliminated a small proportion of the records for missing birth date or date of measurement, unknown sex and observations or ages out of ranges. Only 1 record of 200day weight was used per animal. There were up to 3,441 sires and 31,182 dams across 33 years and 187 herds. A summary of the data is shown in Table 1. Average age for the 200day weight was 234.7 days with a standard deviation of 40.1 days.

Table 1. Summary of the data analysed for birth weight and 200 day weight

	Animals with data	Total pedigree	Dams	Sires	Herds	Years	Mean	SD
Birth weight (kg)	62,966	84,075	21,057	2,382	163	31	35.3	5.6
200d weight (kg)	75,567	98,828	26,811	2,959	114	33	234.7	40.1

Using these data, four standard BREEDPLAN analyses were conducted as described by Graser *et al.* (2005) each with varying age slicing intervals. The four slicing intervals examined were; 15, 30, 45 and 60 days. These preliminary analyses were used to adjust the data for the standard BREEDPLAN adjustments and to form the contemporary groups (including slicing) for further analysis.

Variance components were obtained for each data set using an animal model in ASREML (Gilmour *et al.* 2006). The model included a single fixed effect of contemporary group (CG) which was defined as herd, sex, day of measurement (for 200d weight only) and breeder-defined management group. The additive genetic effects of animal, maternal genetic, maternal permanent environmental and sire x herd effects were fitted as random effects. The genetic covariance between direct and maternal genetic effects was only fitted for birth weight.

Data structure and record effectiveness for both traits was examined for each of the four slicing intervals by summarising the total number of CG, average CG size, individual record effectiveness and total number of effective progeny for each sire.

The effectiveness of an individual animal record was calculated as:

$NEF_i = 1 - (1 / N_{ij})$, where NEF_i = record effectiveness for the i th animal and N_{ij} = the total number of animals in CG_j .

The total effective number of progeny for each sire was calculated as:

$NEFsire_k = \sum_j (n_{kj} (N_j - n_{kj}) / N_j)$, where $NEFsire_k$ = total number of effective progeny for the k th sire, n_{kj} = the number of progeny of sire $_k$ in CG_j , and N_j = the total number of progeny in CG_j .

RESULTS AND DISCUSSION

Phenotypic variance (Table 2) increased as slice interval increased which was most likely a direct result of increased age variation due to inaccuracies in age adjustment and therefore weight variation within each contemporary group. The heritabilities did not change significantly as the slicing interval

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was increased, this implies that there was a proportional increase in genetic variance. This result was plausible given that the average number of sires with progeny in each contemporary group increased thus creating more head to head comparisons of different sires. The remaining ratios did not change significantly as slice interval changed. There was however some indication of a reduction in the direct maternal genetic correlation which could have been a result of the improved data structure and data effectiveness for both the direct and maternal effects.

Table 2. Phenotypic variance (σ_p^2), direct heritability (h^2), maternal heritability (m^2), permanent environment due to dam (pe^2), sire x herd interaction (s^2), direct maternal genetic correlation (r_{dm}) and approximate standard errors (in brackets)

Trait	Slice Days	σ_p^2	h^2	m^2	pe^2	s^2	r_{dm}
Birth Wt	15	14.20 (0.13)	0.32 (0.03)	0.06 (0.01)	0.05 (0.01)	0.02 (0.005)	-0.15 (0.08)
	30	14.52 (0.13)	0.32 (0.03)	0.06 (0.01)	0.05 (0.01)	0.02 (0.005)	-0.12 (0.08)
	45	14.58 (0.13)	0.32 (0.03)	0.06 (0.01)	0.04 (0.01)	0.03 (0.005)	-0.10 (0.09)
	60	14.79 (0.13)	0.31 (0.03)	0.05 (0.01)	0.04 (0.01)	0.03 (0.005)	-0.07 (0.09)
200d Wt	15	492.50 (3.91)	0.16 (0.01)	0.08 (0.01)	0.15 (0.01)	0.05 (0.004)	
	30	501.10 (3.84)	0.16 (0.01)	0.08 (0.01)	0.15 (0.01)	0.05 (0.004)	
	45	507.30 (3.85)	0.17 (0.01)	0.08 (0.01)	0.15 (0.01)	0.05 (0.004)	
	60	513.80 (3.85)	0.16 (0.01)	0.08 (0.01)	0.15 (0.01)	0.05 (0.004)	

The slicing interval had a large impact on the number of contemporary groups in the analysis and the effectiveness of the records (Table 3). Using an interval of 60 days results in approximately half the number of contemporary groups and nearly double (7.1 vs. 4.2 for birth weight) the average contemporary group size compared to slicing at 15 days. This also resulted in fewer single animal and single sire contemporary groups. There was also a large reduction in the number of sires with no effective data for both traits. The net result was that average effective records and progeny records for sires across all contemporary groups increased when age slicing interval was increased from 15 days to 60 days.

Table 3. Contemporary group (CG) structure for each of the 4 slicing intervals

Slice (days)	Birth weight				200day weight			
	15	30	45	60	15	30	45	60
No. of CG	15,042	11,496	9,848	8,835	17,931	13,345	11,339	10,185
Av. CG Size	4.2	5.5	6.4	7.1	4.2	5.7	6.7	7.4
No. single animal CG	6,281	4,572	3,781	3,338	7,057	5,146	4,396	3,992
No. single sire (SS) CG	9,261	6,798	5,576	4,863	9,644	6,909	5,774	5,153
No. SS CG > 1 animal	2,980	2,226	1,795	1,525	2,587	1,763	1,378	1,161
No. Sires NEFsire ¹ = 0	433	331	266	240	248	176	138	125
Av. CG NEF ²	3.2	4.5	5.4	6.1	3.2	4.7	5.7	6.4
Av. total CG NEFsire	2.1	3.0	3.7	4.3	2.2	3.3	4.1	4.7
Av. NEF	0.76	0.82	0.84	0.86	0.76	0.82	0.85	0.86

¹ Number of effective progeny for a sire

² Effectiveness of each animal's record

CONCLUSIONS

Changing age slicing from 15 to 60 days did not have a significant impact on the variance components for birth or 200day weight. However, this change significantly improved the average effectiveness of the data such that on average there were twice as many effective records for sire evaluation and 10% more effective records at the animal level. Increasing the age slicing interval from the current 45 days up to 60 would increase the effectiveness of the data available. For traits measured later in life, where differences in age become less important, the age slice interval may also be able to be extended.

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REFERENCES

- Gilmour, A.R., Gogel, B.J., Cullis, B.R., and Thompson, R. (2006) "ASReml User Guide Release 2.0" VSN International Ltd, Hemel Hempstead, HP1 1ES, UK.
- Graser, H-U., Tier, B., Johnston, D.J. and Barwick, S.A. (2005) *Aust. J. Exp. Agric.* **45**:913.