Stability of estimated breeding values for average daily gain in Pannon White rabbits

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ABSTRACT: Stability of estimated breeding values for average daily gain (ADG) between 5 and 10 weeks of age was analysed for 47 242 Pannon White rabbits, reared in 7470 litters and born between 2000 and 2008. The dataset was divided into 5 successive 5-year periods: (1) 2000–2004, (2) 2001–2005, (3) 2002–2006, (4) 2003–2007, and (5) 2004–2008. Then, after selecting the appropriate part of the pedigree for these sub-datasets, genetic parameters and breeding values were estimated for ADG using REML and BLUP methods. In the applied models sex, year-month, animal and random litter effects were considered. Estimated heritabilities for all 5 periods from 1 to 5 were moderate and stable (0.28 ± 0.01, 0.28 ± 0.02, 0.29 ± 0.02, 0.27 ± 0.02, and 0.28 ± 0.02). Magnitudes of random litter effects were low and stable (0.14 ± 0.01, 0.15 ± 0.01, 0.15 ± 0.01, 0.16 ± 0.01, and 0.16 ± 0.01). After breeding value estimation the dataset of period 5 was merged pair-wise with the other periods 4, 3, 2 and 1 using an inner join. Thus only the common records of the datasets representing the periods 5-4, 5-3, 5-2, and 5-1 were included in the merged datasets. In these merged datasets each rabbit had two breeding values for ADG based on two different periods. Spearman's rank correlation coefficients were calculated between the breeding values based on the dataset of period 5 and the other periods. With the successive years the rank correlation coefficients decreased (0.989, 0.979, 0.965 and 0.924). The correlation coefficients between ranks remained moderately high, even when the proportion of the common rabbits in the merged datasets was low. However, a reasonable re-ranking occurred among the top animals. Rank correlations for the top 100 and 1000 animals varied from 0.41 to 0.55 and from 0.37 to 0.54, respectively, which could influence selection efficiency if the rolling base were used for genetic evaluation.

Keywords: sub-datasets; inner join; rank correlation

The BLUP procedure is the most widely accepted and used method for breeding value estimation, which probably can be explained by its favourable mathematical properties (Kennedy et al., 1988). Its first application in cattle was published three decades ago and nowadays it is also applied in most rabbit breeding programmes (Baselga, 2004). One of the favourable characteristics of BLUP is that it accounts for the effect of selection when the pedigree of each animal is traceable to an unselected base population (Sorensen and Kennedy, 1988). This requirement can hardly be fulfilled in real breeding programmes as the selection of several breeds was initiated more than a century ago, therefore the resulting datasets would become unmanageably large. One solution to this problem can be to cut the dataset and the pedigree according to a predefined time interval. Using this practice with the progressing time the dataset is modified both by incoming and outgoing records. One may

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be interested what the stability of the estimated breeding value for a given animal and trait is like with the progressing time. The objective of this study was the investigation of the stability criterion (rank correlation).

MATERIAL AND METHODS

In the present study records of 47 242 Pannon White rabbits were analysed. These animals descended from 590 bucks and 1849 does. The rabbits were born between 2000 and 2008 and reared in 7470 litters. Growing rabbits were housed in a closed rabbit house, in fattening cages (2–3 rabbits per cage). After weaning (day 35) they were fed a commercial pellet (16.3% crude protein, 15.2% crude fibre, and 10.6 MJ DE/kg). In winter the rabbit house was heated to a minimum temperature of 15–16°C, while in the absence of air conditioning, in summer the temperature occasionally reached levels as high as 28°C. The animals were weighed at 5 and 10 weeks of age to calculate their average daily weight gain (ADG). The dataset was divided into 5 successive 5-year periods: (1) 2000–2004, (2) 2001–2005, (3) 2002–2006, (4) 2003–2007, and (5) 2004–2008 and they were analysed separately. Descriptive statistics of the dataset and of the sub-datasets are presented in Table 1.

ADG was evaluated by the REML and BLUP procedures in order to estimate its genetic parameters and breeding values. The PEST (Groeneveld et al., 1990) and VCE 5 (Kovac and Groeneveld, 2003) software was used.

The applied linear model was as follows:

$$\mathbf{y} = \mathrm{X}\mathbf{b} + \mathrm{Z}\mathbf{a} + \mathrm{W}\mathbf{c} + \mathbf{e}$$

where:

$\mathbf{y}$ = vector of observations
$\mathbf{b}$ = vector of fixed effects
$\mathbf{a}$ = vector of random animal effects
$\mathbf{c}$ = vector of random litter effects
$\mathbf{e}$ = vector of random residual effects

X, Z and W incidence matrices relating records to fixed and random animal and random litter effects, respectively.

Expected values of **a**, **c** and **e** were
$E(\mathbf{a}) = E(\mathbf{c}) = E(\mathbf{e}) = 0$

The variance-covariance structure was assumed to be:

$$\mathrm{V(a)} = \mathrm{A}\sigma^2 a,\ \mathrm{V}(c) = I\sigma^2 c,\ \mathrm{V}(e) = I\sigma^2 e, \text{ and } \mathrm{cov}(a, e) = \mathrm{cov}(e, a) = 0$$

where:

A = numerator relationship matrix
Also $\mathrm{cov}(y,a) = \mathrm{ZA}I\sigma^2 a$

Using univariate animal models for the various sub-datasets the authors considered sex, year-month, animal and random litter effects (Table 2). After breeding value estimation the dataset of pe-

Table 1. Descriptive statistics for the measured traits in different time periods

Trait	Analyzed period	No. of records	Mean	S.D.
BD05	2000–2008	47 242	0.88	0.17
BD10	2000–2008	47 242	2.37	0.29
ADG	2000–2008	47 242	42.50	6.35
	2000–2004	28 305	41.70	6.22
	2001–2005	30 585	42.20	6.13
	2002–2006	29 021	42.30	6.26
	2003–2007	27 873	42.80	6.34
	2004–2008	25 132	43.20	6.47

BD05 = body weight at 5 weeks of age (kg)
BD10 = body weight at 10 weeks of age (kg)
ADG = average gaily gain (g/day)

Table 2. The number of levels of fixed and random effects in the different time periods

Effect	Type	2004–2008	2003–2007	2002–2006	2001–2005	2000–2004	2000–2008
Sex	fixed	2	2	2	2	2	2
Year-month	fixed	55	58	58	59	60	102
Animal	additive genetic	27 081	29 609	30 816	32 345	30 063	49 130
Litter	random	3 775	4 235	4 558	4 870	4 676	7 470

riod 5 was merged pair-wise with that of period 4, 3, 2 and 1 using the inner join. Thus only the common records of the datasets representing periods 5–4, 5–3, 5–2 and 5–1 were included in the merged datasets. In these merged datasets each rabbit had two breeding values for ADG based on two different 5-year datasets. Spearman's rank correlation coefficients were calculated between the breeding values based on the dataset of period 5 and that of the other periods using SAS statistical software (SAS, 2002–2003).

RESULTS AND DISCUSSION

The estimated heritabilities and random litter effects for ADG based on the various datasets can be seen in Table 3. Estimated heritabilities for periods 1-5 were moderate and stable. Magnitudes of random litter effects were low and stable. The estimated genetic parameters were in accordance with previous estimates (Garreau et al., 2000; Szendrő et al., 2004; Nagy et al., 2006;) for Pannon white rabbits. Farkas (2008) analysed the stability of breeding values based on Hungarian pig breeds. Using the Hungarian National Pig Dataset Farkas (2008) also observed stable heritabilities for ADG (0.17–0.22) using successive 5-year datasets. Similar values were found for Czech and Slovakian pig populations (Groeneveld and Pescovicova, 1999; Wolf et al., 2005). In the study of Farkas (2008) slight irregular modifications of the ADG heritability estimates might have been caused by the changing environmental effects and/or by the ca. 20% change of individuals in the successive sub-datasets. Wolf et al. (2001) analysed the effect of adding new data to the National Czech Pig Dataset from a slightly different aspect. Using several traits (lean meat content, average daily gain, valuable cuts) and different tests (field, station), changes of the genetic variance estimates were lower than 5% for Czech Landrace when the data of the last 9 or 18 months were added. Slightly larger changes of the genetic parameters were observed for the White Meaty pig breed (up to 12%) when the data for the last 48 months were added. According to Wolf et al. (2001) the accuracy of the estimated variance components depends on the data structure. If all traits are measured on all animals, then accurate estimates might be obtained from a relatively small dataset especially when no genetic correlations are estimated. Another problem in farm animal production can be missing pedigree information that can reduce the accuracy of genetic parameter estimates (Wolf et al., 2001). Because the Pannon white rabbit population has been closed since 1992, all animals obtained records for ADG and the pedigree information could be traced back to the establishment of the breed. Thus it can be suggested that the estimated genetic parameters of this study were accurate.

Table 3. Heritability estimates (h^2) and magnitudes of random litter effects (c^2) for ADG. Standard errors of estimates are given in brackets

Analyzed period	h^2	c^2
2004–2008	0.28 (0.02)	0.14 (0.01)
2003–2007	0.28 (0.02)	0.15 (0.01)
2002–2006	0.29 (0.02)	0.15 (0.01)
2001–2005	0.27 (0.02)	0.16 (0.01)
2000–2004	0.28 (0.02)	0.16 (0.01)
2000–2008	0.28 (0.01)	0.15 (0.01)

Number and percentage of common records between the various sub-datasets and the correlation coefficients based on different sub-datasets (stability of breeding values) are shown in Table 4. With the successive years the rank correlation coefficients between the breeding values based on different datasets decreased. However, the rank coefficients were moderately high, even when the

Table 4. The number and percentage of common animals and correlations of breeding values between the period 2004–2008 and the other 5-year periods

Merged datasets (periods)	No. of common records	Common records (%)	r^1
2004–2008 to 2003–2007	20 777	64.5	0.989***
2004–2008 to 2002–2006	16 003	41.9	0.979***
2004–2008 to 2001–2005	12 562	29.1	0.965***
2004–2008 to 2000–2004	6 195	13.1	0.924***

[1] Spearman rank correlation coefficient between breeding values based on the most recent sub-dataset and breeding values based on other 5 year long sub-datasets

***$P < 0.001$

proportion of the common rabbits in the merged datasets was low (Table 4). Applying the same stability criterion as in this study but using much larger datasets Farkas (2008) observed much lower stability of breeding values, the *R*-square estimates ranged between 0.56 and 0.87. The proportions of the incoming and outgoing records for the successive 5-year sub-datasets analysed by Farkas (2008) were similar, like in this study. The lower stability for ADG in pigs compared to Pannon white rabbits can probably be explained by the large number of pig herds included in the analysis, while in this study we only evaluated the population of the experimental rabbit farm of the Kaposvár University. In the study of Wolf at al. (2001) the change in the variance component estimates caused by the addition of new records had a very small effect on estimated breeding values for the Czech Landrace pigs. The rank correlations for all traits were higher than 0.99. Somewhat lower rank correlations were calculated for the White Meaty breed (0.94–0.99). Still an overwhelming majority of animals ranked well. Besides the overall stability, the breeding value stability of the top 100 and 1000 rabbits was also examined (Tables 5 and 6). It can be seen in Table 5 that contrary to the good overall stability of genetic parameters (Table 3) and breeding values (Table 4) the common proportion of the highest ranked rabbits based on the different datasets was relatively low. Moreover, for periods 5-4, 5-3, 5-2 and 5-1 rank correlations between the top 100 and 1000 animals were 0.43, 0.55, 0.45 and 0.41; 0.53, 0.51, 0.37 and 0.54, respectively. Consequently, the highest ranked rabbits according to the different datasets also represented substantially different average genetic merit (Table 6). However, from a totally different perspective, examining the stability of dairy cattle models using rank reduction Leclerc et al. (2005) found out that contrary to the very high overall correlations among breeding values (0.995–0.999), the number of common French bulls in the top 100 lists of the full rank and reduced rank models varied only between 81 and 89 (depending on the magnitude of reduction). This result was in accordance with our findings and suggests that substantial re-ranking could occur among the top animals despite of the very high overall rank correlations between breeding value equivalents.

Table 5. Stability of the breeding values expressed as the common representatives of the top 100 and 1000 rabbits according to the different 5-year periods

Period	Top ranked rabbits	
	100	1000
2004–2008; 2003–2007	63	846
2004–2008; 2002–2006	67	863
2004–2008; 2001–2005	75	824
2004–2008; 2000–2004	55	761

Table 6. Differences between the average breeding values of the top 100 and 1000 rabbits according to the different 5-year periods (on the scale of the most recent period)

Trait	Top ranked rabbits	
	100	1000
2004–2008; 2003–2007	0.47	0.14
2004–2008; 2002–2006	0.35	0.10
2004–2008; 2001–2005	0.17	0.12
2004–2008; 2000–2004	0.46	0.24

CONCLUSIONS

The estimated genetic parameters of ADG were very stable for the different 5-year periods. By merging these datasets by twos, the proportion of common rabbits in the datasets decreased together with the stability of breeding values. However, the overall stability of breeding values remained relatively high even though the evaluation was based on merged datasets with a very low proportion of common records. At the same time, the common proportions of the highest ranked animals based on the different datasets were relatively low and they also represented substantially different average genetic merit. Therefore when successive datasets of predefined long periods (e.g. 5 years) have to be used due to the lack of computing capacity, it must not be done routinely but the stability of the estimated breeding values has to be tested.

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