GENETIC AND ENVIRONMENTAL PARAMETERS FOR POSTWEANING GROWTH TRAITS OF RABBITS USING AN ANIMAL MODEL

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Abstract - Records on 3,939 New Zealand White rabbits for weaning weight (WW), postweaning gain (final-starting weight)/days = ADG, or the regression of the weekly weights on age (REGAIN), made between 1983 and 1992 were analyzed to estimate direct and maternal additive genetic, common dam and litter and residual environmental variances. The MTDFREML package was used for a single trait individual animal model. The fixed effect of year-season-parity was included in the model to represent contemporary environmental groups. Direct and maternal heritabilities were .00 and .08 for WW, .18 and .02 for ADG, and .16 and .03 for REGAIN. Ratios of common dam, litter and residual environmental variances to phenotypic variance were .17, .50 and .25 for WW, .04, .31 and .46 for ADG, and .02, .32 and .47 for REGAIN. For ADG, maternal genetic and permanent environmental influences accounted for only 6% of total variance. Best linear unbiased predictions of mean direct genetic value (plotted across years) showed progress for ADG and REGAIN, but little change for WW. Based on these results, only direct breeding value selection for ADG is recommended.

INTRODUCTION

In rabbits, as opposed to other polytocous species, phenotypic variation for growth traits is commonly reported to be overwhelmed by environmental effects attributable to the dam and (or) litter. One explanation is the short time between weaning and marketing ages. This phenomenon may also account for the low heritabilities and slow rates of genetic response to selection for growth traits that have been reported (MGHENI and CHRISTENSEN, 1985; ROCHAMBEAU et al., 1989; ESTANY et al., 1992; LUKEFAHR et al., 1996).

Better understanding of sources of random environmental variation that influence growth, and that can be controlled by management, is required to effectively enhance the amount of genetic variation that can be exploited through selection in rabbit populations. The application of animal models with REML procedures is useful to partition trait variances due to additive genetic (direct and maternal), and to common maternal and litter, and within-litter (residual) environmental effects. In terms of the latter environmental sources, one practical issue is how much emphasis or control should be placed on management of does (e.g., breeding regimen and culling strategies) versus litters (e.g., litter size standardization and pen stocking density) ?

The main objective of this investigation was to estimate direct and maternal heritabilities and permanent dam and litter and residual effects for growth traits in commercial New Zealand White rabbits. A second objective was to compare genetic and environmental components of variance for two alternative measures of growth rate in fryers.

MATERIALS AND METHODS

Stock Housing and Management

The data used in this analysis were collected from 3,939 New Zealand White rabbits born in the Southern University rabbitry between 1985 and 1992. The herd was an open population of commercial stock used for production research at the Small Farm Family Resource Development Center at Southern University and A&M College, Baton Rouge, LA (latitude 30° 32'N). The rabbits were housed in groups of up to four in suspended all wire cages (76 x 76 x 46 cm) inside a building with opened side panels that provided protection from rain and sun. Fans were used for air circulation when ambient temperatures exceeded about 23°C.
Lights were turned off daily at 22:00 hr. A commercial, alfalfa-based, pelleted rabbit ration with a guarantee analysis of 18% crude protein, 18% crude fibre and 2.5% crude fat was available ad libitum with fresh feed added daily. Water was available continuously from automatic valves.

Animals and Traits studied

The 3,939 fryers were from 738 litters and involved 26 sires and 155 dams. An additional 102 base animals were included to account for genetic relationships. Matings were not planned but full-sib and parent-offspring matings were avoided. A total of 1,439 animals were inbred. Doe parities ranged from 1 to 28 but for analysis were grouped in three classes (1, 2-7, >7).
Replacement stock was selected on the basis of growth rate and subjective assessment of loin width and depth.

All rabbits were weaned at four weeks of age. They were weighed and eartagged at weaning (WW) and then weighed once weekly until they were marketed. Rabbits were marketed on a weekly basis and a shipment included all that weighed at least 1,600 g live weight at the latest weighing. Data were included in this study for all fryers which reached at least 1,600 g or had not been removed from the herd before the sixth weighing after weaning (a maximum of 76 d). Using the weekly weights, a linear regression coefficient of body weight on day of age during the postweaning growth period was computed for each fryer as an estimate of the individual postweaning rate of gain (REGAIN) (LIU et al., 1990). Average daily gain was also computed by subtracting the starting weight from the final weight and dividing by the number of days on the trial (ADG).

Statistical Procedures

A full animal model was employed to estimate genetic and environmental variances by derivative-free REML (DFREML) as described by MEYER (1989).
The multiple trait DFREML (MTDFREML) package developed by BOLDMAN et al. (1993), which utilizes sparse matrix techniques (GEORGE et al., 1980), was used. Performance records on growth traits (WW, REGAIN, ADG) for 3,939 rabbits traced pedigree information back to 102 "base animals". A univariate, mixed model was used as follows:

$$y = X\beta + Z_1 d + Z_2 pd + Z_3 pl + \varepsilon \quad \text{(Model I)}$$

where y is a vector of growth trait records; β is a vector of unknown fixed effects due to year-season-parity; X, Z_1, Z_2 and Z_3 are known incidence matrices relating records to appropriate fixed and random effect classes; and d, pd, pl and ε are vectors of unknown random direct additive genetic (0, $A\sigma^2_d$), permanent maternal environmental (0, $I\sigma^2_{pd}$), permanent litter environmental (0, $I\sigma^2_{pj}$), and residual environmental (0, $I\sigma^2\varepsilon$) effects, respectively. An additive genetic model was assumed.
Permanent litter environmental effects may also include temporary maternal environmental effects of the dam. The A is the numerator relationship matrix and I is an identity matrix. Different classes of random effects were assumed to be uncorrelated. Sex effects were excluded from the model since sexual dimorphism does not exist in rabbits for postweaning growth traits (OZIMBA and LUKEFAHR, 1991a,b; GOMEZ and BLASCO, 1992; McNITT and LUKEFAHR, 1993). A similar model which included the maternal additive genetic effect (0, As^2m) was also evaluated.

$$y = X\beta + Z_1 d + Z_2 m + Z_3 pd + Z_4 pl + \varepsilon \quad \text{(Model 2)}$$

A total of 9,064 mixed-model equations were involved (year-season-parity = 89, breeding value (direct) = 4,041, breeding value (maternal) = 4,041, dams = 155 (permanent maternal environmental), and litters (permanent litter environmental) = 738). From initial runs, the last set of variance components (convergence criterion of 1×10^{-9}) was computed by iteration by the Simplex method (NELDER and MEAD, 1965), and used as priors to perform several restarts of analyses to ensure that convergence was at a global maximum of the likelihood function. Solutions from the univariate animal model were also used to estimate direct and maternal breeding values for growth traits for all animals (including base animals). Breeding values were averaged by year and plotted to illustrate annual genetic trends for each growth trait.
Least square solutions for year were plotted to illustrate environmental trends.

RESULTS AND DISCUSSION

Components of Variance

Variance component estimates expressed as a proportion of the total phenotypic variance are shown in Table 1. The weaning weight at four weeks of age was influenced by the maternal genetic effect but not by the direct genetic effect of the individual fryers. At this age, the permanent litter variance was three times the permanent dam effect. At a later age when REGAIN and ADG were measured, the litter effect was six to ten times that of the dam.

Table 1 : Variance component estimates for WW, ADG and REGAIN asproportions of total phenotypic variance (σ^2_p).

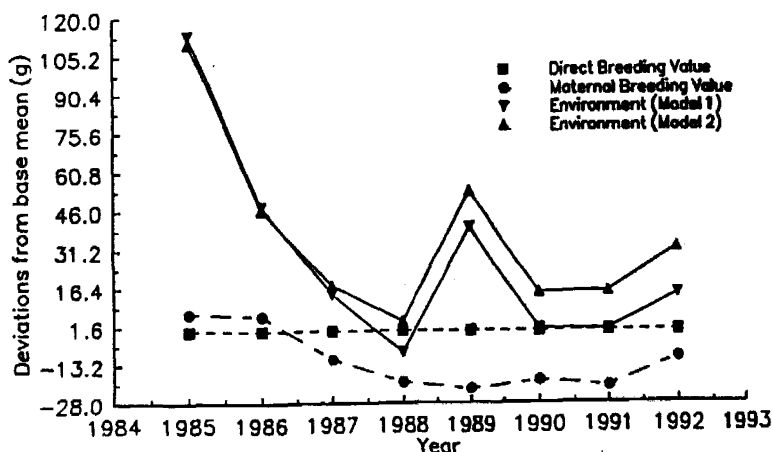| Trait	Parameters *					
	h^2_d	h^2_m	d_i	l_{ij}	Residual	σ^2_p
WW						
Model I	.00		.25	.50	.25	16,168
Model 2	.00	.08	.17	.50	.25	16,276
ADG						
Model 1	.19		.05	.31	.45	33.89
Model 2	.18	.02	.04	.31	.46	33.87
REGAIN						
Model 1	.19		.03	.32	.46	38.01
Model 2	.16	.03	.02	.32	.47	38.02

* h^2_d = direct heritability; h^2_m = maternal heritability; d_i = permanent maternal environmental effects; l_{ij} = permanent litter environmental effects

Furthermore, the direct heritability had increased to 16-19%, while the maternal heritability decreased to a negligible 23%. Comparison of values from models 1 and 2 showed that there was very little change in any of the variance component estimates except the permanent dam effect (pd_i) when maternal effects were not included in the model. These results are in close agreement with several previous studies. ESTANY *et al.* (1992), FERRAZ *et al.*(1992) and LUKEFAHR *et al.* (1996), also using animal models, reported direct heritabilities for WW of, .15, .01 and .04, respectively. FERRAZ *et al.* (1992) also reported a maternal heritability of .09. JOHNSON *et al.* (1988) reported direct heritabilities of .22 for ADG from days 28-56. ROCHAMBEAU *et al.* (1989) and LUKEFAHR *et al.* (1996) reported direct heritabilities of .23 and .17 for ADG for days 28 to 70, respectively. *

In a supplementary analysis, the covariance between direct and maternal genetic effects was estimated for ADG and REGAIN. While the analysis did not appreciably change variance component estimates compared to Model 2 results, genetic correlations between direct and maternal genetic effects were -.12 and .20 for ADG and REGAIN, respectively.
Despite the discrepancy in signs, results do not suggest a strong antagonism.

Figure 1 : Direct and maternal breeding values and environmental trends for weaning weight

Genetic and Environmental Trends

As shown in Figure 1 there was no change in the direct breeding value means for WW over the time period of this study whereas the mean maternal breeding values declined between 1986 and 1989 with a slight increase in 1992. There was a large decrease in the environmental deviations between 1985 and 1988 with smaller rises in 1989 and 1992. Inclusion of the maternal genetic effect resulted in higher mean estimates of the environmental trend in those years when the maternal breeding value was low. The reasons for this are unclear.

Figure 2 : Direct breeding value and environmental trends for ADG and REGAIN (Model 1)

Figure 2 : Direct breeding value and environmental trends for ADG and REGAIN (Model 1)

Figure 3 : Direct and maternal breeding values and environmental trends for ADG and REGAIN (Model 2)
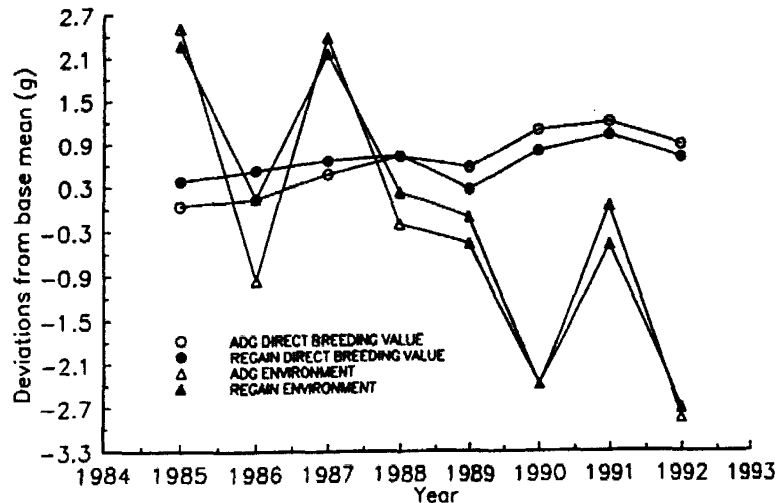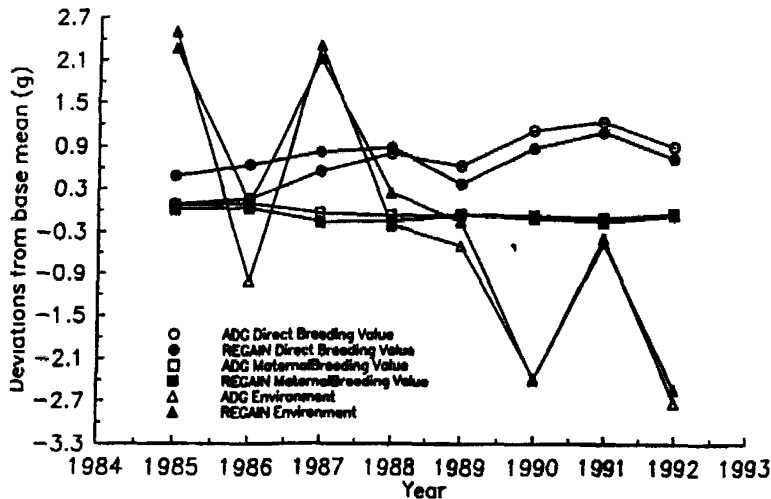

Figure 3 : Direct and maternal breeding values and environmental trends for ADG and REGAIN (Model 2)

Using both Model 1 and 2, there was a slight but important ($P<.01$) increase in mean direct breeding value and, with Model 2, there was a decrease ($P<.05$) in maternal breeding value for ADG over the time period of this study ($.15 \pm .03$ and $-.02 \pm .01$, respectively for Model 2) (Figure 3).

The changes for REGAIN were not significant and, for direct breeding value using either model, were nearly three times less than for ADG (*i.e.*, from Model 1, $.06 \pm .03$ and, $.16 \pm .03$ g/yr, respectively). The shape of the curves was essentially the same although the REGAIN estimates tended to be higher than ADG in the earlier years and lower in the later years.

There is no readily apparent explanation for the differences between these two measures of growth. At the same time, there was a deterioration of the environment - especially from 1987 onward.There is no suitable explanation for this decline. Inclusion of maternal genetic effects in the model had little effect on the shape of the curves. As shown above the maternal genetic effects are declining and are essentially zero at this stage of growth.

Implications

Because of the lack of direct additive genetic variation and the substantial dam contribution for growth characteristics at weaning, management should instead focus on doe culling strategies on the basis of estimated producing ability. conversely, selection for post-weaning growth should concentrate on individual breeding value. Use of ADG for determining growth rate is a suitable method because the extra work of REGAIN is not justified.

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