

UNIVARIATE AND BIVARIATE REML ANALYSIS WITH AN ANIMAL MODEL FOR LITTER SIZE IN MICE

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SUMMARY

The univariate analysis of litter size indicated higher additive (V_a) and environmental (V_e) variances in high lines as compared to the low lines. There was evidence of heterogeneity of V_a and V_e in high and low lines. The estimates from univariate analysis were lower than the estimates from bivariate analysis.

INTRODUCTION

The objectives of study were to estimate the genetic parameters of litter size by univariate and bivariate Restricted Maximum Likelihood Method (REML) (Patterson and Thompson, 1971) using an animal model. The advantage of REML analysis is that by incorporating complete relationships back to the base population, it takes into account the changes in variance due to inbreeding and selection under infinitesimal model. As the selection of mice was based on lean mass, the bivariate analysis of litter size and lean mass was carried out to take into account the correlation between two traits for the unbiased parameter estimation.

MATERIALS AND METHODS

1. Data Structure: The P-lines, selected for lean mass had three replicates and in each replicate three selection treatments, high, low and control giving 9 lines in all. Sixteen full sib families were established by within family selection of males upto generation 7 and 8 pair matings from 8 to 20 generations. Further details are given by Sharp *et al.*, 1984. At generation 20, three replicates within each selected line were crossed to form new replicate, named P6-lines. The P6-lines were not replicated, control lines discontinued and selection criterion was changed to 19 week body weight.

2. Statistical Analysis: The univariate estimates were obtained with the help of derivative-free REML package developed by Meyer (1989) using individual animal model. The model of analysis included additive genetic effects of all animals as a random effect and genetic relationships between all animals back to the base population were incorporated including those without

records. Generations and replicates were included as fixed effects. The pair of lines were also analysed by considering heterogeneous additive and environmental variances of lines (for details, see Beniwal, 1991). The bivariate analysis was carried out for lean mass and litter size fitting different models for each trait i.e. unequal design matrix.

RESULTS

The results of analyses are given in tables 1,2 and 3.

Table 1. Univariate estimates of genetic parameters for litter size in P-Lines (0 - 20 generations).

Line (Replicate 1+2+3)	heritability ± Standard Error	Variance Components		
		Vp	Va	Ve
Control	0.181 ± 0.093	5.533	1.004	4.530
Control + High	0.156 ± 0.053	5.789	0.903	4.895
Control + Low	0.093 ± 0.061	5.009	0.472	4.627

Table 2. Univariate estimates of genetic parameters for litter size in P+P6-Lines (0 - 37 generations).

Analysis	Group	Heritability	Variance Components		
			Vp	Va	Ve
High	--	0.028 ± 0.065	7.532	0.207	7.325
Low	--	0.000 ± 0.084	4.201	0.001	4.200
High + Low	--	0.210 ± 0.027	6.470	1.359	5.111
	High	0.436	8.293	3.615	4.679
High + Low (with heterogeneous Va option)					
	Low	0.000	4.679	<0.001	
	High	0.267	8.547	2.278	6.629
High + Low (with heterogeneous Va & Ve options)					
	Low	0.055	4.201	0.232	3.969

Table 3. Genetic parameters from bivariate and univariate (in parentheses) analyses of lean mass and litter size for Control + High + Low P-lines data (0-20 generations).

Variance Components and parameters	Lean Mass	Litter Size	Genetic Covariance/correlation
Additive Genetic Var.	4.052 (4.309)	0.561 (0.922)	0.412
Common Litter Variance	2.325 (1.914)	--	--
Error Variance	2.479 (2.277)	4.874 (4.623)	--
Phenotypic Variance	8.856 (8.500)	5.435 (5.545)	--
Heritability/Correlation	0.458 (0.507)	0.103 (0.166)	0.273 ± 0.100
C - Square	0.263 (0.225)		

DISCUSSION

Table 1 revealed that the analysis of Control+High lines resulted in heritability estimates for high lines quite close to the estimates from the control lines. This is expected because control and high lines originated from the same base population. However, the estimates from low lines were very low even when analysed with the control line data (0.09 ± 0.06) and with large standard errors.

The analysis of High+Low of P+P6 lines data (Table 2), assuming heterogeneity of additive genetic (V_a) and residual environmental (V_e) variances, revealed that V_e was very high in high lines as compared to low lines. This suggests that high lines are becoming more susceptible to environmental fluctuations.

The heritability estimates for lean mass and litter size from bivariate analysis (Table 3) were observed to be lower than the estimates from univariate analysis. However, differences were significant at the 5 percent not at the 1 percent level. The lower heritability estimated from bivariate analysis of litter size suggest that the univariate estimates were slightly biased due to genetic correlation with lean mass. The genetic correlation between these two traits was positive and moderate.

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