ESTIMATION OF GENETIC PARAMETERS IN MICE

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INTRODUCTION

Results of selection experiments have usually been analysed using regression of response on selection differentials, Falconer 1989. Analyses of variance have also been used to partition variation into within and between litter variation. Analysis of variance assumes independence of observations (or at least error terms) and most analyses are carried out using statistical packages, such as SAS (PROC GLM) and Harvey's programme, which assume, in addition, that all effects are fixed, whereas animals and litters should be considered as random effects as well as incorporating relationships between animals. Recently the animal model has been suggested to be the preferred method of analysis (Meyer,1989; Sorenson and Kennedy, 1984).

Urrutia and Hayes (1988a,b) reported the results from selection in mice at two different ages, analysed using the regression of response on cumulative selection differential. The object of this study was to re-analyse the direct responses to selection using an animal model and to examine and compare the parameter estimates obtained, both between replicates, across selection criteria and with the results obtained by Urrutia and Hayes (1988a).

EXPERIMENT

Selection was for 28 to 38 day weight gain or 48 to 58 day weight gain under ad libitum or restricted feeding. There were 2 replicates for each selection criteria and a replicated control fed ad libitum was maintained. Thus there were 10 line-replicates with between 2100 and 2300 animals in each line-replicate distributed over 15 generations. The experiment and further details of the direct and correlated responses are described by Urrutia and Hayes (1988a,b). Selection was within families with 20 pair matings per generation. Litters were standardised to 6 young, 3 males and 3 females and weaning was at 21 days.

ANALYSES

Traits analysed were 28 to 38 day weight gain and 48 to 58 day weight gain. Lines 2, 3 and 4 were fed ad libitum whilst lines 1 and 5 were fed 80% of the ad libitum intake. Lines 1 and 2, selected on 48 to 58 day weight gain, were analysed for this trait; lines 4 and 5, selected on 28 to 38 day weight gain, were analysed for this trait and line 3, the control, which was measured at both ages, was analysed for both traits. Univariate Restricted Maximum Likelihood (REML) (Meyer, 1989) analyses were carried out using an animal model fitting direct effects and maternal effects and including a direct-maternal covariance with litters as an additional random effect. Fixed effect of generation was fitted and each line-replicate-sex was analysed separately since Urrutia

and Hayes (1988a,b) had reported differences between sexes when analysing results from generations 1 to 9.

RESULTS

Table 1 gives characteristics of the data for the various line-replicates and sexes; and Table 2 gives the parameter estimates. There were considerable differences between replicates within the same line for the estimates of the variance components. The phenotypic variance in males was consistently greater (130 to 250%) than in females. There were large differences between the sexes in the estimates of the parameters, thus one is not simply faced with a scale/variability effect.

The data in these lines trace back to the same randomly allocated base population. Since all relationships have been included in the relationship matrix and the trait being analysed is that for which selection was practised then it is expected that, regardless of the selection, unbiased estimates of the base population parameters should be obtained Meyer, 1989; Sorenson and Kennedy, 1984. For 28 to 38 day weight gain under ad libitum feeding there are essentially 4 line-replicates, in both males and females, and the estimates of the heritability of the direct effect range from 5 to 32% in males and 5 to 41% in females with somewhat similar variability in the other parameters, e.g. the common environmental effect (c^2). Neither was the intra-class correlation between full-sibs any more consistent, ranging from 14 to 34%. Lines 1 and 5, selected under restricted feeding, cannot be directly compared to the controls since no control restricted feeding was maintained. However, the replicates differed in the estimates of the parameters. Thus one is seeing what is essentially a sampling effect, assuming that the infitesimal model holds (Bulmer, 1980), i.e. that there are very many unlinked additive genes such that their frequencies do not change as a result of selection. In a majority of the cases the correlation between direct and maternal effects was negative, which may partially explain why Urrutia and Hayes (1988a) reported little change over the 9 generations in most of the selection lines. The lines were not consistent in the significance of the maternal and common environment (c^2 or litter effects), some of the lines had both maternal and litter effects significant whilst in others either maternal or litter effect was significant; it was not the case that the effect was either ascribed to litter or maternal effect. These results are at considerable variance with the realised heritabilities reported by Urrutia and Hayes (1988a). It should be noted that the model used in this analysis includes direct and maternal variances and a direct-maternal covariance as additive genetic effects as well as a random common environmental (litter) variance. Thus it is expected that this model should be a more realistic description of the data and the differences between these results and those obtained by Urrutia and Hayes (1988a) may be expected. It is clear that analyses of selection experiments using animal models that include relationship matrices should be carried out so as to provide a more detailed and informative description of the selection results.

References

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Table 1 Number of records, total number of animals in the model, number of litters and mean gain for base animals during the test period for each line-replicate-sex.

Line-rep -sex	No. of records	No. of animals	No. of litters	Gain
11 males	1100	2533	420	-5.40
11 females	1069	2533	420	-2.53
12 males	985	2325	387	-5.40
12 females	1002	2325	387	-2.53
21 males	993	2179	364	2.91
21 females	985	2179	364	1.98
22 males	1012	2232	368	2.91
22 females	1028	2232	368	1.97
31 males	993	2131	356	4.96
31 females	986	2131	356	3.64
32 males	967	2124	362	4.97
32 females	977	2124	362	3.64
41 males	1060	2350	392	4.19
41 females	1064	2350	392	3.41
42 males	1032	2202	372	4.19
42 females	975	2202	372	3.41
51 males	1061	2394	412	-0.27
51 females	1019	2394	412	0.76
52 males	1030	2358	399	-0.27
52 females	975	2358	399	0.76

Table 2 Estimates of additive genetic variance, maternal genetic variance, direct-maternal covariance, common environmental variance, residual variance and penotypic variance for each line-replicate-sex.

line-rep -sex	σ_a^2	σ_m^2	σ_{am}	σ_c^2	σ_e^2	σ_p^2
11 males	1.719	1.862	-1.456	0.636	2.088	4.849
11 females	2.207	0.493	-0.904	0.143	0.780	2.719
12 males	2.740	0.503	-0.961	0.950	1.987	5.218
12 females	1.960	0.545	-0.853	0.279	1.108	3.039
21 males	0.693	0.324	-0.278	0.000	1.549	2.288
21 females	0.035	0.045	0.040	0.057	1.564	1.742
22 males	0.335	0.411	-0.303	0.000	2.435	2.879
22 females	0.075	0.026	0.044	0.159	1.619	1.923
31 males	0.816	0.249	-0.242	0.228	1.436	2.487
31 females	0.063	0.017	0.033	0.132	0.824	1.069
32 males	0.750	0.272	-0.023	0.171	1.157	2.327
32 females	0.383	0.110	-0.195	0.135	0.503	0.936
41 males	0.511	0.038	0.139	0.445	1.636	2.766
41 females	0.157	0.007	-0.034	0.135	0.797	1.063
42 males	0.159	0.003	0.004	0.793	1.647	2.605
42 females	0.229	0.039	-0.039	0.103	0.576	0.908
51 males	1.116	0.149	-0.041	1.497	2.513	5.234
51 females	0.392	0.024	0.097	1.144	1.757	3.415
52 males	1.236	0.365	0.005	1.102	2.390	5.097
52 females	0.839	0.316	0.005	0.689	1.642	3.491