Genet. Res. Camb. (1985), **45**, *pp.* 287–297
With 2 text-figures
Printed in Great Britain

Covariance between direct and maternal genetic effects in mice, with a model of persistent environmental influences

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(*Received 21 August 1984 and in revised form 23 January 1985*)

SUMMARY

Covariance between direct and maternal genetic effects on body weight in random-bred ICR mice at 2 through 10 weeks of age was estimated from cross-fostering experiments. The covariance contributes only a few percent of phenotypic variance at 2 weeks, but increases to 10–15% at later ages. Nearly all estimates are positive. We suggest that genes active during later parts of growth affect maternal performance more than those active during early growth, causing increased covariance at later ages. A model of combined genetic and persistent environmental effects on maternal performance is presented. Persistent effects of genetic or environmental variation in recent ancestors can influence covariance between relatives and response to selection.

1. INTRODUCTION

Adaptive evolution and progress under artificial selection are both possible because the phenotypic value of a trait is correlated with its genetic value. Response to selection can be predicted by the regression of breeding value on phenotypic value of the selected trait (Falconer, 1981):

$$R = bP \tag{1}$$

where R is response, b is the regression slope of breeding values on phenotypes, and P is the phenotypic value of selected individuals, all measured as deviations from the mean after standardization to unit variance. An individual's breeding value for a given trait and population is twice the expected phenotypic value of offspring produced by mating with a randomly chosen individual from the population. Multiplication by two is required because the expected breeding value of a randomly chosen mate is simply the population mean (zero), and the expected value of the offspring is halfway between the individual's breeding value and that population mean. Phenotypic values differ from breeding values because of non-additive and non-genetic variation. Usually, b is the heritability of the trait, but if related individuals affect a trait indirectly by modifying the environment, and if the propensity to affect the environment is heritable in the related individuals, the similarity between relatives and the covariance between breeding value and phenotypic value might be altered.

A common example is provided by maternal effects in mammals (Falconer, 1965; Willham, 1972). The mother makes both a 'direct' genetic contribution to the offspring through the action of genes inherited by the offspring from the mother, and an 'indirect' genetic contribution through the environment she provides for the offspring (milk quality and quantity, nest structure, care of young, etc). This indirect contribution is genetic to the extent that these maternal qualities are

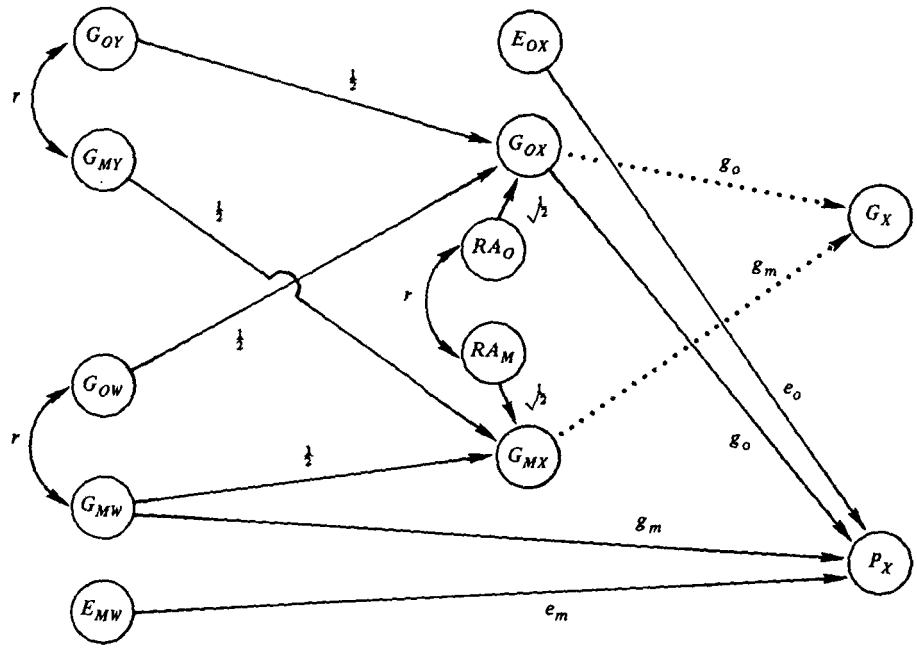

Fig. 1. Path diagram representing model of heritable maternal effects and covariance between direct and maternal genetic effects. G_{OX}, additive genetic value of direct effects in individual X; G_{MX}, additive genetic value of maternal effects in individual X; RA_O, RA_M, correlated residuals corresponding to random assortment, accounting for deviation of offspring additive genetic value from average of parents; G_X, breeding value of individual X; P_X, phenotypic value of individual X; E_{OX}, residual corresponding to environmental and non-additive, non-maternal deviation; E_{MW}, residual corresponding to environmental and non-additive deviations of maternal effects of individual W from additive value G_{MW}; r, correlation between direct and maternal additive genetic effects. Subscript W refers to mother, Y to father, X to daughter.

heritable in the mother, even though experienced by her offspring as an environmental effect. Because genes that determine the mother's 'indirect' effect on the offspring's phenotype can be inherited by the offspring, they may cause additional covariance between the offspring's breeding value and its phenotype. Depending upon the sign of this covariance, heritable maternal effects may either retard or accelerate response to selection (Dickerson, 1947; Willham, 1963, 1972; Falconer, 1965; Hanrahan, 1976).

This model of heritable maternal effects is depicted by the path diagram in Fig. 1. In Fig. 1, P_X is a phenotype, such as body weight, determined by both genetic and environmental effects. The paths e_o and g_o represent the direct (i.e.

non-maternal) environmental and direct genetic effects. In the absence of maternal effects, P_X would be completely determined by these two paths, and g_o^2 would be the heritability of the trait. In the maternal effects model, however, the additional path g_m represents the effect of the mother's genotype, through her maternal performance, on her offspring's phenotype. The mother's maternal performance will probably not be completely determined by her genotype, however, and the path e_m represents the remaining, environmentally determined, portion of the maternal effect, as it affects offspring phenotype.

G_X in Fig. 1 is the breeding value of individual X.The definition of breeding value is slightly modified here to accommodate the maternal effects model. For direct effects, the breeding value is twice the expected deviation of offspring produced when a female is mated to a randomly chosen male. This doubling of the deviation is required because the mother contributes only half the offspring's genes. For the indirect genetic contribution, however, represented by a path such as $G_{MW}\ P_X$, the mother contributes the entire effect, with no counterpart contributed by the father, and no doubling is necessary. G_X thus represents twice the direct-effect deviation of the offspring from the population mean, plus the entire indirect effect. The direct contribution of a mother to her offspring's phenotype is $\frac{1}{2}g_o$, as shown, for example, by the path $G_{OW}\ G_{OX}\ P_X$. Since the expected contribution of a randomly chosen father is the population mean, the direct-effects deviation of individual X's offspring is $\frac{1}{2}g_o$. The direct-effects portion of X's breeding value is twice this, or simply g_o. This is represented by the dotted path $G_{OX}\ G_X = g_o$ in Fig. 1. In addition, individual X will make an indirect genetic contribution to her offspring's phenotype. This is represented by the dotted path $G_{MX}\ G_X = g_m$. The breeding value of individual X is thus $G_X = g_o\ G_{OX} + g_m\ G_{MX}$, plus other sources of variation in offspring phenotype. These other sources, e.g. random assortment and environmental variation, could be included for completeness in Fig. 1 as paths leading to the phenotype of an offspring of X, but are not directly relevant for our purposes.

Using the rules of path analysis (Wright, 1968; Li, 1975; Sokal & Rohlf, 1981), it can be seen that the correlation between G_X and P_X, the breeding value and phenotypic value, is the sum of the paths

$$G_X\ G_{OX}\ P_X = g_o^2,$$

$$G_X\ G_{OX}\ G_{OW}\ G_{MW}\ P_X = \tfrac{1}{2}g_o\ r\ g_m,$$

$$G_X\ G_{MX}\ RA_M\ RA_O\ G_{OX}\ P_X = \tfrac{1}{2}g_o\ r\ g_m,$$

$$G_X\ G_{MX}\ G_{MY}\ G_{OY}\ G_{OX}\ P_X = \tfrac{1}{4}g_o\ r\ g_m,$$

$$G_X\ G_{MX}\ G_{MW}\ G_{OW}\ G_{OX}\ P_X = \tfrac{1}{4}g_o\ r\ g_m,$$

$$G_X\ G_{MX}\ G_{MW}\ P_X = \tfrac{1}{2}g_m^2,$$

which total to

$$g_o^2 + (\tfrac{3}{2})\ g_o\ r\ g_m + (\tfrac{1}{2})\ g_m^2 \qquad (2)$$

where g_o^2 is the direct-effects portion of the heritability, g_m^2 is the indirect-effects portion of the heritability, and r is the correlation between direct and indirect genetic effects (Dickerson, 1947; Willham, 1972). If maternal effects are ignored,

(2) reduces to the direct-effects heritability g_o^2. For standardized traits this is the slope b in (1). Under this model of heritable maternal effects, however, expression (2) replaces g_o^2 as the standardized regression slope b of equation (1) (Dickerson, 1947; Willham, 1972; Hanrahan, 1976). When r is negative, b may also be negative, and the phenotype may be such a poor indicator of breeding value that it is theoretically possible to obtain a negative response to selection; selecting for increased value of a trait may cause it to decrease (Hanrahan, 1976). Negative, slowed, or accelerated response to selection is obviously important in programs designed to improve domestic species. It may also be important in adaptive evolution by natural selection. Cheverud (1984) applied this model to the theory of evolution by kin selection.

Another potential source of covariance between relatives is the residual effect of the dam's maternal performance on her offspring's maternal performance (Falconer, 1965). An environmental effect on a grandmother's maternal performance may influence the maternal performance of the mother, and thus affect phenotypic values in grandchildren (Willham, 1972). This effect, which is a kind of 'environmental inheritance', is possible because the maternal performance phenotype of the mother can directly modify the maternal performance phenotype of the daughter, even in the absence of genetic heritability. The model in Fig. 1, although allowing an effect of maternal performance on phenotype P_X, does not incorporate non-genetic transmission of maternal performance or other phenotypes. P_X, for example, has no effect on later generations.

In this paper we present estimates of covariance between direct and maternal genetic effects on body weight at ages 2 through 10 weeks in a population of random-bred mice, and discuss the possible biological origins of this covariance. Also, we briefly present a model incorporating both genetic and persistent environmental effects on maternal performance, with consequences for other phenotypes affected by maternal performance.

2. MATERIALS AND METHODS

Random-bred ICR mice were obtained from Spague–Dawley and randomly mated. Litters were standardized at birth to eight pups, four of each sex where possible. A random half of each standardized litter was exchanged at birth with half the standardized litter of an unrelated dam, using equal numbers of males and females where possible. Litters thus paired for cross-fostering were born on the same day. Pups were weaned at 3 weeks of age, and kept in single-sex cages of less than five mice each, with food and water *ad libitum*. Four mice from each composite postnatal litter, two fostered and two non-fostered, were weighed every 7 days at ages 2 through 10 weeks. The other four mice from each composite litter were used in another experiment. A total of 345 cross-fostering pairs (pairs of dams between whom halves of litters were exchanged) provided data for 1346 male and 1347 female offspring.

The model used to interpret phenotypic variation in body weight was:

$$\sigma_P^2 = \sigma_{AO}^2 + \sigma_{DO}^2 + \sigma_{AM}^2 + \sigma_{DM}^2 + \sigma_{AOAM} + \sigma_C^2 + \sigma_E^2,$$

https://doi.org/10.1017/S0016672300022278 Published online by Cambridge University Press

where σ^2_P is phenotypic variance of a pup nursed by its own mother; σ^2_{AO}, additive direct genetic variance; σ^2_{DO}, dominance direct genetic variance; σ^2_{AM}, additive maternal ('indirect') genetic variance; σ^2_{DM}, dominance maternal genetic variance; σ_{AOAM}, direct-maternal additive genetic covariance; σ^2_C, common environmental variance (maternal and cage), and σ^2_E, residual environmental variance.

The covariance σ_{AOAM}, corresponding to r in Fig. 1, represents the genetic covariance between direct genetic effects (subscript AO) and indirect genetic effects through the maternal effect (subscript AM). This covariance or correlation can be interpreted as representing the pleiotropic effects of genes that influence growth in two ways: directly, by mediating growth in the individual possessing them, and indirectly, by affecting maternal performance and thus influencing the growth of offspring. As both of these genetic sources contribute to the phenotype, phenotypic variance will be augmented by both kinds of genetic variance. In addition, any covariance between these sources will increase or decrease phenotypic variance, depending upon whether this covariance is positive or negative. Normally, the variance of a sum of two components is the sum of their two variances plus twice their covariance, so one might expect phenotypic variance, which is the sum of all components, to include $2\,\sigma_{AOAM}$. In this case, however, the contribution of the covariance is attenuated by half because the sources of direct and indirect components are one generation apart and the mother has contributed only half of the offspring's genes, and thus only half of the direct component.

In Fig. 1, r is $\sigma_{AOAM}/(\sigma_{AO}\,\sigma_{AM})$. Our experimental design allowed us to estimate σ_{AOAM} as a component of phenotypic variance, but we have no reliable estimate of σ^2_{AM}, so we cannot express σ_{AOAM} in standardized form as the genetic correlation r. In the cross-fostering design, those offspring nursed by an unrelated female experience a maternal effect produced by genes unrelated to their own. Because the direct and indirect genetic contributions in this case come from two different and unrelated genotypes (the offspring's and the foster mother's), there can be no covariance between these effects as experienced by fostered mice. The experimental design thus eliminates the contribution of σ_{AOAM} to the phenotypic variance of fostered mice, but not of unfostered mice. The phenotypic variance of fostered mice is therefore:

$$\sigma^2_P - \sigma_{AOAM}.$$

These data were analysed by Riska, Atchley & Rutledge (1984) using the linear model

$$Y_{hijk} = \mu + p_h + D_{hi} + N_{hj} + (DN)_{hij} + W_{hijk}$$

where Y_{hijk} is the weight of the kth pup of the ith dam, nursed by the jth nurse, in the hth pair of litters used for cross-fostering, μ is the mean weight for the population and sex, and W_{hijk} is the residual deviation of the kth pup from the $h_{ij\text{th}}$ dam-nurse mean.

Genetic expectations of the ANOVA components, estimated following Willham (1963), are:

$$\sigma^2_D = \tfrac{1}{2}\sigma^2_{AO} + \tfrac{1}{4}\sigma^2_{DO}$$

$$\sigma^2_N = \sigma^2_{AM} + \sigma^2_{DM} + \sigma^2_C,$$

$$\sigma^2_{(DN)} = 0,$$

$$\sigma^2_W = \tfrac{1}{2}\sigma^2_{AO} + \tfrac{3}{4}\sigma^2_{DO} + \sigma^2_E.$$

Note that the genetic expectation of the dam-nurse interaction term is zero. This result differs from that of Rutledge *et al.* (1972; see also Nagai *et al.* 1978), who reported that the interaction component had an expectation of σ_{AOAM}. Although σ_{AOAM} does not appear in the ANOVA expectations, it can be estimated from the cross-fostering design because σ_{AOAM} contributes to the covariance of full sibs nursed by their own mother but not to the covariance of full sibs nursed by an

Table 1.

Age (Weeks)	$\sigma_{AOAM}(1)$	$\sigma_{AOAM}(2) \pm$ S.E.	$\sigma_{AOAM}(3)$	$\%V_p(1+2)$	$\%V_p(3)$	P_t	P_S
2	0.050	0.038 ± 0.098	0.000	3.6	0.0	0.698	0.332
3	0.101	0.155 ± 0.255	0.311	4.2	9.8	0.545	0.163
4	0.247	0.391 ± 0.546	0.453	5.0	7.0	0.474	0.171
5	0.584	0.553 ± 0.396	0.420	10.9	8.3	0.163	0.113
6	0.678	0.652 ± 0.349	0.415	14.2	9.3	0.063	0.084
7	0.587	0.601 ± 0.395	0.233	11.4	4.8	0.129	0.275
8	1.071	0.975 ± 0.413	0.479	16.6	8.6	0.019	0.016
9	0.878	0.849 ± 0.562	-0.060	12.0	-1.0	0.132	0.574
10	1.191	0.999 ± 0.606	0.847	13.4	10.7	0.101	0.042

$\sigma_{AOAM}(1)$, Estimate from ANOVAs for fostered and nonfostered mice; $\sigma_{AOAM}(2)$, mean of 283 estimates; $\sigma_{AOAM}(3)$, median of 283 estimates; $\%V_P$ $(1+2)$, percent of total phenotypic variance, based upon mean of (1) and (2); $\%V_P$ (3), percent of total phenotypic variance, based upon (3); P_t, two-tailed probability from t test of null hypothesis $\sigma_{AOAM}(2) = 0$; P_S, two-tailed probability from signed-ranks test of null hypothesis $\sigma_{AOAM} = 0$.

unrelated dam (Ahlschwede & Robison, 1971). We therefore estimated σ_{AOAM} by performing two separate analyses of variance, one to estimate the among-litter variance, within pairs, for pups nursed by their own mothers, and another for pups nursed by unrelated forster mothers. The among-litter component for fostered pups was subtracted from that for unfostered pups to obtain an estimate of σ_{AOAM}.

To determine the reliability of our σ_{AOAM} estimates, we obtained an estimate for each cross-fostering pair that had at least two pups per dam-nurse combination. Each such pair yields a 1 D.F. estimate of among-litter variance for fostered mice, which can be subtracted from the corresponding 1 D.F. estimate for non-fostered mice. An estimate of σ_{AOAM} derived from a single cross-fostering pair is not very reliable, but our data allowed 283 independent estimates of this kind, providing a reliable mean estimate with an empirical standard error. Significance of average estimates was tested by two-tailed t and signed-ranks tests in the SAS UNIVARIATE procedure (SAS Institute, Inc., 1982, p. 581).

The data were first adjusted for sex differences and then pooled. Estimates of phenotypic variances were obtained by averaging the estimates for males and females reported in Riska *et al.* (1984). σ_{AOAM} was added to Riska *et al.*'s estimates, as this covariance was not included in their phenotypic variance estimates. Analyses of logarithmically transformed data gave qualitatively similar results. In this population, log transformation is appropriate for data from later ages, but not from earlier ages (Riska *et al.* 1984).

3. RESULTS

Table 1 shows three kinds of estimates of σ_{AOAM}: (1) the difference between among-litter components for fostered and non-fostered mice, (2) the mean of 283 estimates from individual cross-fostering pairs and (3) the median of these 283 estimates. Estimate (1) is based upon 60 more pairs than the other two estimates, but these had reduced sample sizes. Although there is considerable variation among these estimates, they agree well in sign and general magnitude. The covariance between direct and maternal effects on weight in this population is negligible (a few percent of σ_P^2) at 2 weeks of age, but increases to about 10 or 15% of σ_P^2 at 5 weeks of age and beyond, becoming significantly positive at 8 and 10 weeks of age. The 9-week estimate does not differ significantly from zero, although the mean estimate appears to be inflated by a few extreme values. Except for the median estimate at 9 weeks, all estimates are positive.

4. DISCUSSION

Previous estimates of σ_{AOAM} for body weight and other traits in mammals have generally been negative (Hanrahan & Eisen, 1973, 1974; Hohenboken & Brinks, 1971; Burfening, Kress & Friedrich, 1981; Kuhlers, Chapman & First, 1977; Ahlschwede & Robison, 1971; Vesely & Robison, 1971), although Ahlschwede & Robison (1971) reported a positive covariance for weight in swine before 4 weeks of age, which then became negative. Eisen, Legates & Robison (1970) report positive values for 12-day weight in mice, and Hanrahan (1976) found positive σ_{AOAM} for 6-week and weaning weight in sheep. Cheverud (1984) found positive covariances for body weight, but negative for other traits, of mice. Cheverud's estimates were derived from a small sample of sibs of the mice used in this study.

Negative σ_{AOAM} could result from the effects of litter size on offspring size. Larger female mice generally produce larger litters, but with smaller pups within those litters (Falconer, 1965; Eisen & Durrant, 1980). This might cause an association between direct effects promoting larger size and indirect (maternal) effects that produce smaller offspring. This source of covariance should disappear, however, if litter size is standardized (Eisen, 1970). An important question, then, is whether litter size has varied substantially in populations used to estimate σ_{AOAM}. In the present study, litter size was standardized at birth. Negative σ_{AOAM} estimates in other studies cannot be blamed entirely on effects of litter size either, however, as negative estimates are common in cattle, which typically produce but one offspring per calving (Hohenboken & Brinks, 1971). Also, negative σ_{AOAM} estimates have been obtained from mice even though litter size was standardized at 5 days postpartum (Eisen *et al.* 1970).

Another important question about σ_{AOAM} estimates is whether the maternal effects model includes prenatal, postnatal or both kinds of maternal effects. Our estimates are based upon postnatal maternal effects, with any prenatal maternal effects included in the genetic component. Although prenatal maternal effects are probably very small in these data, especially after a few weeks of age (Riska *et al.* 1984), our σ_{AOAM} estimates could contain covariance between prenatal and

postnatal maternal effects. This seems unlikely, however in view of the pattern of increase in positive covariance as the pups age.

A more plausible explanation for the increase with age is that direct effects at later ages are more closely correlated with maternal performance than are direct effects at earlier ages. If later postnatal growth, especially fat deposition (Eisen, 1975), has a marked effect on nursing performance, then direct effects appearing in the later growth of pups would be more closely associated with maternal effects that their offspring will experience at early ages. Postnatal maternal effects on weight in this population change in magnitude during postnatal growth, but the ranking of nurses by maternal effect is relatively constant, as shown by very high maternal correlations between ages (Riska *et al.* 1984). Direct genetic effects, however, change in both magnitude and pattern during postnatal growth (Riska *et al.* 1984), so that changes in σ_{AOAM} during growth are more likely to be affected by changes in the direct than in the maternal genetic component. If the positive covariance between direct and indirect effects arises from a correlation of later growth, especially fat deposition, with maternal performance, this may explain why estimates of σ_{AOAM} for body weight differ in sign from those for some other traits measured by Cheverud (1984). These traits (head length and tail length) are less likely to be affected by fat deposition, while body weight certainly would be.

Up to now we have considered the case in which heritable maternal performance influences the phenotype of the next generation, but the only inheritance considered has been that caused by transmission of genes from parent to offspring. Another sort of 'inheritance' of maternal performance might also be considered. If, for example, a mother is subjected to an environment that causes her to grow larger and thus produce larger litters, this may decrease her maternal performance measured as postnatal contribution to growth of an average offspring. If this causes her average offspring to produce smaller litters, it may increase this offspring's maternal contribution to postnatal growth of the average grandchild. Grandchildren would thus be larger (and fewer) because of an environmental deviation in the grandmother's growth rate.

Fig. 2 depicts a model in which this sort of persistent environmental influence is combined with the more usual genetic model. The major differences between the path diagram of Fig. 1 and that of Fig. 2 result from the addition of M, a 'maternal performance' phenotype, and the path m_m, which represents the effect of M_{dam} on M_{daughter}. In Fig. 2, g_m of Fig. 1 is represented by the compound path $g_m\ m_p$ (g_m is not the same quantity in the two figures), as the mother's indirect genetic effect on P_X is interpreted as acting only through the phenotype M_W. M_W is determined by the mother's own genes (G_{MW}), the grandmother's maternal performance (M_Q), plus a residual environmental effect (R_{MW}). 'G'$_X$ in Fig. 2, like G_X in Fig. 1, is a breeding value composed of both a direct and an indirect component. The direct component is totally genetic, representing the effect of genes inherited by the offspring, corresponding to the dotted path g_o, as in Fig. 1. In Fig. 2, however, the indirect component of the breeding value is composed of both genetic and persistent environmental effects acting through maternal performance. This model allows prediction of offspring phenotype on the basis of both genetic and persistent environmental effects. 'G'$_X$ is not a breeding value in the traditional

sense of a completely genetic contribution to offspring phenotype, but it is a breeding value in the operational sense, as it predicts offspring phenotype from maternal phenotype, and explains phenotypic covariance among relatives. In addition to persistent environmental effects, this model also accounts for persistent effects of genes not transmitted to offspring. For example, genes that affect a grandmother's maternal performance might thus indirectly affect the mother's (her daughter's) maternal performance, and this may in turn affect the granddaughter's

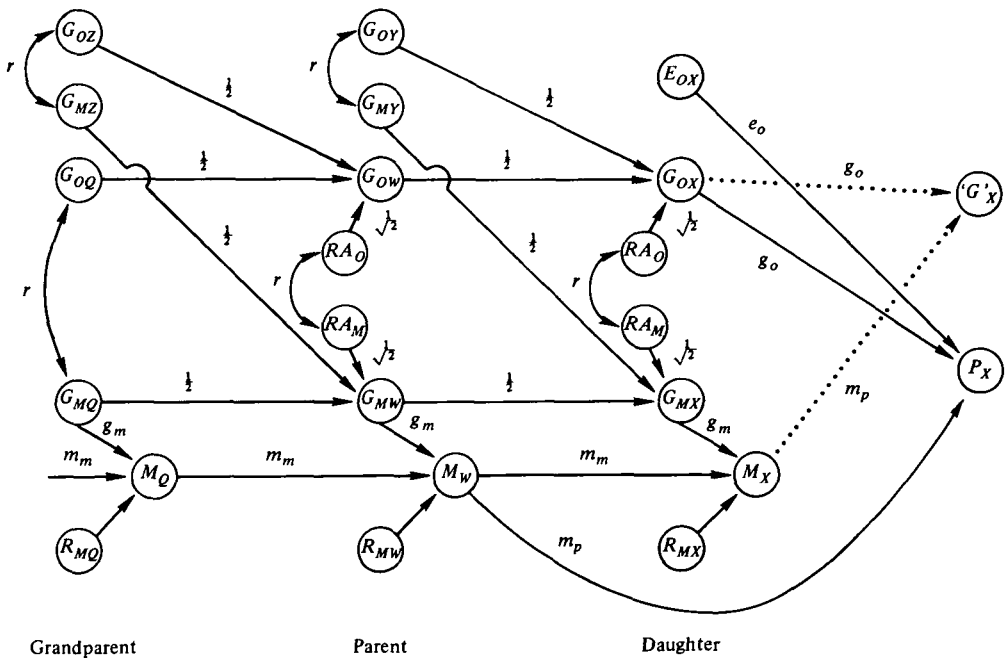

Fig. 2. Same as Fig. 1, but including persistent effects of environmental variation on traits influenced by maternal performance. Explanation as for Fig. 1, plus: M_X, maternal performance phenotype of individual X; R_{MX}, residual corresponding to variance of M_X not explained by additive genetic value (G_{MX}) and maternal performance of mother (M_W), includes environmental and non-additive effects. Subscript Q refers to grandmother, Z to grandfather.

phenotype for maternal performance and other traits, even though these genes were inherited by neither the mother nor the granddaughter. Such persistent genetic effects would be possible because of the path m_m, representing the effect of mother's on daughter's maternal performance, regardless of the original source of variation in the mother's maternal performance.

These 'persistent' effects, although contributing to covariance between mother and offspring, are likely to be vanishingly small after several generations. At any point in time, however, new environmental and genetic deviations are arising and initiating new persistent effects, so there may be patterns of non-genetic covariance between relatives that can affect response to selection. This could be important for short-term success of artificial selection programs, and may either hinder or assist short-term ecological adaptation under natural selection, depending upon

https://doi.org/10.1017/S0016672300022278 Published online by Cambridge University Press

the sign of the path m_m. For example, if only large females survive to reproductive age, and because they are large produce more but smaller young, these young may be less likely to survive to reproductive age in the environment that selected for large mothers. Any system capable of producing negative or slowed response to selection may influence adaptation and probabilities of extinction.

Applying the rules of path analysis to Fig. 2, it can be shown that

$$\sigma^2_{PX} = 1 = g_o^2 + m_p^2 + 2g_o\, r_{(G_{OX},\, M_W)}\, m_p + e_o^2$$
$$= g_o^2 + m_p^2 + g_o\, r\, (1 + (m_m/2) + (m_m/2)^2 + (m_m/2)^3 + \ldots + (m_m/2)^\infty)\, g_m\, m_p + e_o^2,$$

and

$$r_{('G'_X,\, P_X)} = g_o^2 + \tfrac{3}{2} g_o\, r\, g_m\, m_p + \tfrac{1}{2} g_m^2\, m_p^2 + m_m\, m_p^2$$
$$+ g_m\, m_p\, r\, g_o (m_m/2 + (m_m/2)^2 + (m_m/2)^3 + \ldots + (m_m/2)^\infty).$$

In both of these equations, the infinite series involving m_m represents the increasingly diminished influence of increasingly distant female forbears.

If the absolute magnitude of m_m is less than 2, then we have

$$\sigma^2_P = \sigma^2_{AO} + \sigma^2_{DO} + \sigma^2_{AM} + \sigma^2_{DM} + 2\sigma_{AOAM}/(2-m_m) + \sigma^2_C + \sigma^2_E,$$

and

$$\sigma_{'G'_X, P_X} = \sigma^2_{AO} + \tfrac{3}{2}\sigma_{AOAM} + \tfrac{1}{2}\sigma^2_{AM} \text{ (as in the previous model)},$$
$$+ m_m\, (\sigma^2_{AM} + \sigma^2_{DM} + \sigma^2_C) + m_m\, \sigma_{AOAM}/(2 - m_m),$$

where 'G'_X now includes not only genetic, but also other predictable maternal influences on offspring phenotypes, and m_m is the partial regression coefficient of daughter's maternal performance on mother's maternal performance, holding genetic variation in maternal performance constant. This is closely related to the model used by Falconer (1965) to explain the relationship between litter size and maternal effects, but also incorporates the separate 'direct' and 'indirect' genetic effects model of Willham (1972). Estimates of σ_{AOAM} from our cross-fostering design actually estimate $2\sigma_{AOAM}/(2-m_m)$, and, depending upon the sign of m_m, may over- or underestimate σ_{AOAM}.

Under this model b in (1) is:

$$\sigma_{'G'_X, P_X}/\sigma^2_P.$$

This model may be helpful in understanding discrepancies between realized heritabilities and those estimated from covariances between relatives. The difference between b in (1) for the two models may be considerable, as that for the model of Fig. 2 includes a term corresponding to the entire maternal effect multiplied by m_m. According to this model, response to selection may be affected even if maternal effects are not heritable, and perhaps to a larger extent than predicted by the model of Fig. 1.

We thank Scott Newman and an anonymous reviewer for comments on the manuscript. This research was supported by the National Science Foundation (DEB-8109904), and the College of Agricultural and Life Sciences of the University of Wisconsin, Madison,

This is contribution 2791 from the Laboratory of Genetics, University of Wisconsin, Madison.

REFERENCES

AHLSCHWEDE, W. T. & ROBISON, O. W. (1971). Prenatal and postnatal influences on growth and backfat in swine. *Journal of Animal Science* **32**, 10–16.

BURFENING, P. J., KRESS, D. D. & FRIEDRICH, R. L. (1981). Calving ease and growth rate of simmental-sired calves. III. Direct and maternal effects. *Journal of Animal Science* **53**, 1210–1216.

CHEVERUD, J. M. (1984). Evolution by kin selection: a quantitative genetic model illustrated by maternal performance in mice. *Evolution* **38**, 766–777.

DICKERSON, G. E. (1947). Composition of hog carcasses as influenced by heritable differences in rate and economy of gain. *Iowa Agricultural Experiment Station, Research Bulletin 354*, pp. 489–524. Ames, Iowa.

EISEN, E. J. (1970). Maternal effects on litter size in mice. *Canadian Journal of Genetics and Cytology* **12**, 209–216.

EISEN, E. J. (1975). Results of growth curve analysis in rats and mice. *Journal of Animal Science* **42**, 1008–1023.

EISEN, E. J. & DURRANT, B. S. (1980). Genetic and maternal environmental factors influencing litter size and reproductive efficiency in mice. *Journal of Animal Science* **50**, 428–441.

EISEN, E. J., LEGATES, J. E. & ROBISON, O. W. (1970). Selection for 12-day litter weight in mice. *Genetics* **64**, 511–532.

FALCONER, D. S. (1965). Maternal effects and selection response. In *Genetics Today*, vol. 3, *Proceedings of the Eleventh International Congress of Genetics* (ed. S. J. Geerts), pp. 763–774. Oxford: Pergamon Press.

FALCONER, D. S. (1981). *Introduction to Quantitative Genetics*, 2nd ed. New York: Longman.

HANRAHAN, J. P. (1976). Maternal effects and selection response with an application to sheep data. *Animal Production* **22**, 359–369.

HANRAHAN, J. P. & EISEN, E. J. (1973). Sexual dimorphism and direct and maternal genetic effects on body weight in mice. *Theoretical and Applied Genetics* **43**, 39–45.

HANRAHAN, J. P. & EISEN, E. J. (1974). Genetic variation in litter size and 12-day weight in mice and their relationship with post-weaning growth. *Animal Production* **19**, 13–23.

HOHENBOKEN, W. D. & BRINKS, J. S. (1971). Relationships between direct and maternal effects on growth in herefords. II. Partitioning of covariance between relatives. *Journal of Animal Science* **32**, 26–34.

KUHLERS, D. L., CHAPMAN, A. B. & FIRST, N. L. (1977). Estimates of maternal and grandmaternal influences on weights and gains of pigs. *Journal of Animal Science* **44**, 181–188.

LI, C. C. (1975). *Path Analysis – a primer*. Pacific Grove, California: Boxwood Press.

NAGAI, J., EISEN, E. J., EMSLEY, J. A. B. & MCALLISTER, A. J. (1978). Selection for nursing ability and adult weight in mice. *Genetics* **88**, 761–780.

RISKA, B., ATCHLEY, W. R. & RUTLEDGE, J. J. (1984). A genetic analysis of targeted growth in mice. *Genetics* **107**, 79–101.

RUTLEDGE, J. J., ROBISON, O. W., EISEN, E. J. & LEGATES, J. E. (1972). Dynamics of genetic and maternal effects in mice. *Journal of Animal Science* **35**, 911–918.

SAS INSTITUTE, INC. (1982). *SAS User's Guide: Basics, 1982 ed.* Cary, North Carolina: SAS Institute, Inc.

SOKAL, R. R. & ROHLF, F. J. (1981). *Biometry. The Principles and Practice of Statistics in Biological Research*, 2nd ed. San Francisco: Freeman.

VESELY, J. A. & ROBISON, O. W. (1971). Genetic and maternal effects on preweaning growth and type score in beef calves. *Journal of Animal Science* **32**, 825–831.

WILLHAM, R. L. (1963). The covariance between relatives for characters composed of components contributed by related individuals. *Biometrics* **19**, 18–27.

WILLHAM, R. L. (1972). The role of maternal effects in animal breeding: III. Biometrical aspects of maternal effects in animals. *Journal of Animal Science* **35**, 1288–1293.

WRIGHT, S. (1968). *Evolution and the Genetics of Populations*, vol. 1: *Genetic and Biometric Foundations*. Chicago: University of Chicago Press.