The rate of polygenic mutation

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Summary

By application of the neutral model of phenotypic evolution, quantitative estimates of the rate of input of genetic variance by polygenic mutation can be extracted from divergence experiments as well as from the response of an inbred base population to selection. The analytical methods are illustrated through a survey of data on a diversity of organisms including Drosophila, Tribolium, mice, and several crop species. The mutational rate of introduction of genetic variance \( (V_m) \) scaled by the environmental variance \( (V_e) \) is shown to vary between populations, species, and characters with a range of approximately \( 10^{-4} \) to \( 5 \times 10^{-2} \). \( V_m/V_e \) for Drosophila viability is somewhat below this range, while hybrid dysgenesis may temporarily inflate \( V_m/V_e \) beyond \( 10^{-1} \). Potential sources of bias and error in the estimation of \( V_m \) are discussed, as are the practical implications of the observed limits to \( V_m/V_e \) for projecting the long-term response to selection and for testing adaptational hypotheses.

1. Introduction

The rate of phenotypic evolution ultimately depends on the frequency at which new adaptive mutations arise. Little information exists on this phenomenon. The vast majority of studies on the mutation rate have involved major mutations with individually discernible and primarily deleterious effects. Mutations with small effects (often called micromutations, minor mutations, or polygenic mutations) are obviously less amenable to quantitative investigation and consequently have attracted little attention from empiricists. Yet there are a number of reasons to suspect that polygenic mutation plays an important role in the evolution of complex characters in natural populations.

Even when the fixation of a macromutation does result in a major evolutionary advance, fine-tuning of the polygenic background is likely to be essential for the persistence of a population in a variable environment. As an aggregate, polygenic mutations often appear at a much higher frequency than macromutations (Mukai, 1979), and some evidence suggests that the mutation rate varies inversely with mutational effect (Gregory, 1965). Unlike macromutations, mutations with small effects often arise in a non-directional manner, having little or no average effect on the mean of a character in an unselected base population (Oka et al., 1958; Gregory, 1965; Hollingdale & Barker, 1971; Mukai et al., 1984). If the pleiotropic effects of mutant polygenes are also highly variable (and little information on this exists), then polygenic mutation would provide a potential mechanism for the evolution of adaptive suites of characters that is unlikely to be matched by macromutation.

Recent work based on fundamental principles of quantitative genetics has helped clarify the relationship between polygenic mutation and the evolutionary response to selection. In an early model, Kimura (1965) considered a character exposed to mutation and a selection function with fixed optimum and fitness declining with the squared deviation from the optimum. More recently, the case for characters exposed to Gaussian selection has been evaluated for sexual (Latter, 1970; Bulmer, 1972, 1980; Lande, 1975; Barton, 1986; Barton & Turelli, 1987; Turelli, 1987) and for asexual and heterogonic life cycles (Lynch & Gabriel, 1983). Lande (1980) and Turelli (1985) have extended the analysis to multivariate evolution, while Hill (1982a, b), Keightley & Hill (1983), and Zeng & Hill (1986) have investigated the special case of truncation selection. Turelli (1984, 1986) provides a broad overview of the stabilizing selection theory and analyses its sensitivity to violation of the underlying assumptions; Felsenstein (1977, 1981) and Fleming (1979) also address the latter issue. Although variation exists between the quantitative
predictions of these studies, all are in agreement that 
mutation plays a significant role in determining the 
amount of genetic variance circulating in a population. 

It is a major challenge to obtain quantitative 
estimates of the parameters underlying these models 
and to establish the degree to which they vary between 
species and characters. With respect to polygenic 
mutation there are three phenomena to consider at 
each locus: \( \mu \), the mutation rate, \( \sigma_n^2 \), the variance 
of mutational effects (effect being measured as one-half 
the mutation rate, \( \frac{\mu}{2} \)), and \( k \), the degree of 
dominance of mutations. Except in the study of Hill 
(1982a), only the case of pure additivity of mutations 
(\( k = 0.0 \)) has received much attention and epistasis has 
been ignored uniformly. Consequently, the composite 
parameter

\[
V_m = 2 \sum_{i=1}^{n} \mu_i \sigma_i^2 
\]

where \( n \) is the number of loci underlying the trait, 
plays a prominent role in much of the stabilizing 
(Latter, 1970; Lande, 1975; Fleming, 1979) and 
truncation (Hill, 1982a, b) selection theory. Turelli 
(1984), however, has made a clear case that depending 
upon the magnitude of selection, mutation rate per 
locus, and variance of mutational effects, the total 
mutation rate,

\[
\lambda = 2 \sum_{i=1}^{n} \mu_i, 
\]

may be a more significant quantity from the standpoint 
of stabilizing selection than \( V_m \) (see also Latter, 1970; 
Bulmer, 1972, 1980).

Since the accurate domains of the Kimura– 
Lande–Fleming models and Latter–Bulmer–Turelli 
models are largely non-overlapping (Turelli, 1984), 
and since both sets of models are likely to be useful 
under some circumstances, it is premature to dismiss 
\( V_m \) as a relevant parameter in issues of stabilizing 
selection. Moreover, as pointed out by Hill (1982a, b), 
\( V_m \) is of significance in forecasting the outcome 
of long-term truncation selection programs; and it is \( V_m \), 
not simply \( \lambda \), which determines the rate of divergence 
of unselected characters (Chakraborty & Nei, 1982; 
Lynch & Hill, 1986).

My intentions here are to summarize existing data 
on the rate of polygenic mutation. I will begin by 
considering in some detail the manner in which 
estimates of \( V_m \) may be extracted from various 
laboratory and field experiments. Before proceeding, 
however, some clarification of the definition of the 
polygenic mutation rate is required.

2. Definition of \( V_m \)

Throughout the theoretical literature (Kimura, 1965; 
Latter, 1970; Lande, 1975; Chakraborty & Nei, 1982; 
Hill, 1982a, b) the rate of \textit{input} of new genetic 
variance by polygenic mutation is defined as in 
equation (1) or as

\[
V_m = 2n\mu\sigma_0^2 
\]

for the special case in which all loci are considered to 
have equivalent properties. An attractive feature of 
equations (1) and (2) is that \( V_m \) is independent of 
the total population size, \( N \).

There are, however, problems in strictly defining 
\( V_m \) as the rate of input of new genetic variance via 
mutation. It may seem that such a definition ought 
only to involve first-generation mutations whose gene 
frequencies (and hence influences on the variance) 
have not been altered by random sampling drift. 
However, first-generation mutants have not yet 
segregated into the homozygous state; in the case of 
separate sexes, this requires two generations. The 
problem with a ‘first generation’ focused definition 
for the production of new genetic variance is most 
apparent for purely recessive mutations which have 
zero influence on the observed variance until they 
have segregated out. Only in the case of purely 
additive mutations is the first generation variance 
produced by new mutations equal to \( V_m \) [Lynch 
& Hill, 1986, equation (2)].

Thus, an accurate description of the rate of 
production of genetic variance by mutation needs to 
involve the effects of mutant alleles on the variance in 
their first generation of segregation. Once this point is 
accepted, however, then it is clear that the rate of 
production of genetic variance via mutation is not 
density-independent since, prior to segregation, the 
gene frequency moments will be altered by random 
drift.

For these reasons, it seems best simply to regard 
\( V_m \) as a fundamental quantitative genetic parameter 
which, in the special case of additive effects, becomes 
equivalent to the amount of new genetic variance 
introduced/generation via mutation. In the absence of 
drift and selection, \( V_m \) is the steady-state rate of 
increase in within-population variance regardless of 
the degree of dominance. In the absence of selection, 
\( 2V_m \) is the expected steady-state rate of increase 
between-population variance regardless of population 
size and degree of dominance (Lynch & Hill, 1986).

The following analyses are performed under the 
assumption of additivity, and the traditional definition 
of \( V_m \) is relied upon. As will be discussed below, the 
assumption of additivity has empirical support for 
most of the studies cited, and extreme and unlikely 
deviations from this assumption would be necessary 
to alter significantly the major conclusions of this 
paper (Lynch & Hill, 1986).

For comparative purposes, it is useful to record the 
rate of polygenic mutation in dimensionless form. 
Generally, this is accomplished by dividing \( V_m \) by 
the environmental component of variance for the trait, 
\( V_e \), a procedure that will be adhered to below. A 
conceptual advantage of such a scaling is that \( V_m/V_e \)
is approximately the expected heritability of an initially homozygous population following one generation of mutation. We may refer to this quantity as the mutational heritability. The usual precautions should be exercised in extrapolating scaled estimates of $V_m$ since $V_E$ may vary with experimental circumstances and with the degree of inbreeding.

3. Estimation of $V_m$

(i) *Drosophila bristle numbers*

Two types of experiments, both utilizing long-inbred stocks of *D. melanogaster*, provide an ample basis for estimating $V_m$ for bristle number, a character known for its primarily additive genetic basis (Falconer, 1981). The first approach entails the analysis of selection responses in highly inbred lines and is best exemplified by an experiment of Mather & Wigan (1942). After maintaining a line by full-sib mating for 78 generations, Mather & Wigan (1942) relaxed the inbreeding and attempted to select for higher and lower bristle numbers. A response to truncation selection was observed in all of their experiments, the magnitude of response increasing with the experimental duration. Data on the progressive response of mean bristle number to upward and downward selection (Tables 1 and 2; Mather & Wigan, 1942) can be utilized to estimate $V_m$ as follows.

Assuming no selection for bristle number in the initial inbred line, the expected genetic variance, $\text{var}(w, 0)$, will represent a balance between the opposing forces of drift and mutation. Under full-sib mating the expected equilibrium is reached within ~15 generations (Lynch & Hill, 1986), and by use of Robertson's (1952) transition matrix is found to be $4V_m$ for additive mutations [Lynch & Hill, 1966, equation (21)]. During their selection experiments, Mather & Wigan allowed three single-pair matings each generation, each selected individual being the extreme of 20 measured sibs of its sex. Brother–sister matings were avoided intentionally, but there were a few unavoidable instances. Therefore, I have assumed the effective number of breeding adults to be 5 for the experimental period.

With such a small effective population size, random drift is the dominant force in the erosion of genetic variance, and as the population adjusts to the new $N$, the expected dynamics of $\text{var}(w, t)$ will be closely approximated by a drift-mutation model. One simple model, first suggested by Clayton & Robertson (1955) for additive genes, is

$$E[\text{var}(w, t) | \text{var}(w, t-1)] = \left(1 - \frac{1}{2N}\right)\text{var}(w, t-1) + V_m. \tag{3}$$

Although the random generation of linkage disequilibrium can temporarily cause the rate of erosion of genetic variance to deviate substantially from $[1-(1/2N)]$, computer simulations of Bulmer (1976) support the use of this expression for calculating the expected loss of genetic variance via random drift (see also Lynch & Hill, 1986). Lynch & Hill (1986) have shown that the Clayton-Robertson model consistently overestimates the expected genetic variance by a factor of $\sim (1/2N)$, an amount that is of negligible importance for large $N$ but that can be an important consideration for $N$ in the range of those for Mather & Wigan's (1942) experiment. Thus, in all of the following analyses, the more precise formulation of Lynch & Hill [1986; equation (29)] has been used. With the assistance of a computer, the latter model generates the expected dynamics of $\text{var}(w, t)$ in terms of $V_m$ given the effective population sizes before and after the transition. By equating observed and expected estimates of $\text{var}(w, t)$, multiple estimates of $V_m$ are obtained. Although the model of Lynch & Hill (1986) was not formally derived for the extreme case of full-sib mating, it provides an excellent fit to those conditions if $N$ is set equal to 2-33.

Under truncation selection, the additive genetic variance can be estimated by the rearrangement of the standard selection equation, $\text{var}(w, t) = [\Delta^2\bar{z}(t) \cdot V_m^2]/i$, where $\Delta^2\bar{z}(t)$ is the change in mean phenotype, $V_m$ is the phenotypic variance, and $i$, the standardized selection differential, is a function of the proportion of selected individuals (Falconer, 1981). For Mather & Wigan's experiment, $i = 1.867$. I used the mean of the upward and downward responses to selection in each generation as an estimate of $\Delta^2\bar{z}(t)$ and Mather & Wigan's measures of phenotypic variance in the inbred base population as estimates of $V_m$. In order to calculate $V_m/V_E$, $V_E$ was estimated by subtracting the mean estimate of $\text{var}(w, t)$ for Mather & Wigan's (1942) first experiment from their pooled estimate of $V_E$ (their table 3) for the same experiment.

Mather & Wigan performed four selection experiments, one for sternopleural bristle number and three for abdominal bristle number. The upward-selected lines in the last two abdominal selection experiments were branched off from the initial downward-selected line at generations 17 and 34 and were treated as starting with levels of genetic variance predicted by equation (29) of Lynch & Hill (1986). The three estimates of $V_m/V_E$ obtained for abdominal bristle number (0-0006, 0-0050, 0-0028) do not appear to be related to this change in genetic background, and their mean (0-0028) is similar to the single estimate for sternopleural bristles (0-0023). Several other bristle selection experiments with inbred *Drosophila* lines provide the information necessary to calculate $V_m/V_E$ in the above manner (Table 1).

A second approach to estimating $V_m$ in *Drosophila* takes advantage of the Curly/Plum marker technique and the lack of recombination in males to isolate second chromosomes on an isogenic background. The amount of genetic variance attributable to second chromosomes can be determined by performing a diallel cross and dividing the difference between
Table 1. Survey of estimates of $V_m/V_E$ for four characters in *Drosophila melanogaster*. $S$ refers to selection on an inbred base population, $C$ to chromosomal divergence.

<table>
<thead>
<tr>
<th>Trait</th>
<th>Method</th>
<th>$V_m/V_E$</th>
<th>Range</th>
<th>s.d.</th>
<th>$n$</th>
<th>Reference</th>
</tr>
</thead>
<tbody>
<tr>
<td>Abdominal bristle number</td>
<td>S</td>
<td>0.0028</td>
<td>0.0006–0.0050</td>
<td>0.0022</td>
<td>3</td>
<td>Mather &amp; Wigan (1942)</td>
</tr>
<tr>
<td></td>
<td>S</td>
<td>0.0006</td>
<td>—</td>
<td>—</td>
<td>1</td>
<td>Clayton &amp; Robertson (1955)</td>
</tr>
<tr>
<td></td>
<td>S</td>
<td>0.0003</td>
<td>0.0001–0.0009</td>
<td>0.0003</td>
<td>6</td>
<td>Clayton &amp; Robertson (1964)</td>
</tr>
<tr>
<td></td>
<td>S</td>
<td>0.0034</td>
<td>0.0000–0.0012</td>
<td>0.0050</td>
<td>7</td>
<td>Kitagawa (1967)</td>
</tr>
<tr>
<td></td>
<td>S</td>
<td>0.0006</td>
<td>—</td>
<td>—</td>
<td>1</td>
<td>Hollingdale &amp; Barker (1971)</td>
</tr>
<tr>
<td></td>
<td>C</td>
<td>0.0016</td>
<td>0.0024–0.0041</td>
<td>0.0012</td>
<td>2</td>
<td>Durrant &amp; Mather (1954)</td>
</tr>
<tr>
<td></td>
<td>C</td>
<td>0.0017</td>
<td>—</td>
<td>—</td>
<td>1</td>
<td>Paxman (1957)</td>
</tr>
<tr>
<td>Sternopleural bristle</td>
<td>S</td>
<td>0.0023</td>
<td>—</td>
<td>—</td>
<td>1</td>
<td>Mather &amp; Wigan (1942)</td>
</tr>
<tr>
<td>number</td>
<td>C</td>
<td>0.0034</td>
<td>0.0058–0.0077</td>
<td>0.0013</td>
<td>2</td>
<td>Durrant &amp; Mather (1954)</td>
</tr>
<tr>
<td></td>
<td>C</td>
<td>0.0008</td>
<td>—</td>
<td>—</td>
<td>1</td>
<td>Paxman (1957)</td>
</tr>
<tr>
<td>Viability</td>
<td>C</td>
<td>0.00004</td>
<td>—</td>
<td>—</td>
<td>1</td>
<td>Mukai (1964)</td>
</tr>
<tr>
<td></td>
<td>C</td>
<td>0.00003</td>
<td>0.00001–0.0006</td>
<td>0.0003</td>
<td>3</td>
<td>Mukai et al. (1972)</td>
</tr>
<tr>
<td></td>
<td>C</td>
<td>0.00001</td>
<td>—</td>
<td>—</td>
<td>1</td>
<td>Cardellino &amp; Mukai (1975)</td>
</tr>
<tr>
<td></td>
<td>C</td>
<td>0.00002</td>
<td>—</td>
<td>—</td>
<td>1</td>
<td>Ohnishi (1977a)</td>
</tr>
<tr>
<td>ADH activity</td>
<td>C</td>
<td>0.0006</td>
<td>0.00059–0.00065</td>
<td>0.0004</td>
<td>2</td>
<td>Mukai et al. (1984)</td>
</tr>
</tbody>
</table>

*chromosome and error mean square by twice the number of times that the chromosome appeared in the assay. By these means, Durrant & Mather (1954) and Paxman (1957) were able to establish the amount of genetic variance for bristle number in the Oregon line of *D. melanogaster* after 300 and 400 generations of continuous full-sib mating. Prior to the two experiments reported by Durrant & Mather (1954), full-sib mating was relaxed for an average of 2-5 and 8 generations and var ($w$) was assumed to be equal to $6.5V_m$ and $12V_m$ respectively. Paxman (1957) reports a pooled analysis of variance for second chromosomes that were allowed to diverge via spontaneous mutation for an average of 34 generations, and I assumed var ($w$) = $38V_m$ at the time of the dihedral cross. In order to scale var ($w$) estimates for second chromosomes to the entire genome, I multiplied by 2.5 based on observations that the second chromosome constitutes approximately 40% of the *Drosophila* genome. Estimates of $V_E$ for these experiments were obtained by summing chromosomal and error sums of squares and dividing by the total degrees of freedom to obtain an estimate of $V_E$ free of sex and block effects, subtracting the estimate of var ($w$), and multiplying by 10 to account for the usage of means of 10 measures. This procedure yielded estimates of $V_E$ that averaged twice as high as the estimates derived from the previously cited selection experiments. This was possibly because of the confounding of background genetic variation in the experiment of Durrant & Mather (1954) but not in Paxman (1957) for which the genetic background was randomized. Since both chromosomal studies yielded similar estimates of $V_E$, these estimates were used. The resultant estimates of $V_m/V_E$ are quite comparable to those derived from selection experiments (Table 1).

Some small differences exist among the $V_m/V_E$ estimates obtained for *Drosophila* bristle numbers by myself, Lande (1975), and Hill (1982a), most likely because of slightly different approaches and rounding errors, but in general we are in good agreement. The 11 independent estimates have a mean and standard deviation equal to 0.0017 and 0.0012.

(ii) *Drosophila* viability

Another series of mutation-accumulation experiments involves polygenes encoding for viability in *Drosophila melanogaster*. By use of the Curly/Plum marker technique, several investigators have isolated initially identical second chromosomes into different sublines, allowed them to diverge by spontaneous mutation with a minimum of selection, and then periodically determined their viability properties using a standard assay developed by Wallace (1956). As expected in the absence of selection, the temporal increase in genetic variance for viability of quasi-normal lines (those with viabilities $>\sim 60\%$ of that expected for second chromosomes without mutations) is generally linear.

A parameter recorded in all of the viability mutation
studies is $\Delta V$, the average increase in genetic variance for homozygous second chromosomes per generation. (The scale on which $V$ is measured varies between studies.) Since mutant viability alleles act in an additive fashion (Mukai & Yamazaki, 1964, 1968; Ohnishi, 1977b; Mukai & Nagano, 1983) and the second chromosome constitutes approximately 40% of the Drosophila genome, $5\Delta V / 2$ is an approximate measure of $\Delta \mu$ for the entire genome. Dividing by 2, we then have an estimate of $V_m$ as in equation (2). All estimates of $V_m$ were obtained by multiplying the variance of replicate means (within chromosomal lines) by the number of flies assayed/replicate. As an estimate of $V_m$ in Mukai et al. (1972) and Cardellino & Mukai (1975), I used the mean of the individual estimates provided in Mukai (1964), Mukai et al. (1982), and Mukai & Nagano (1983), after conversion to the appropriate scale by Taylor expansion. The average within-line mean square from Ohnishi (1977b) was used to compute $V_m$ for Ohnishi (1977a).

All of the resultant estimates of $V_m / V_E$ for viability are certainly too low since they do not include mutations of major effects and since the environmental variance estimates, based on within-line variance, are potentially inflated by the existence of any genetic variance for viability in the marker strain. Nevertheless, the average of the four independent estimates of $V_m / V_E$ for viability in Table 1, 0.0000013 (s.d. = 0.0000013) is nearly two orders of magnitude less than that for bristle numbers. Given that mutational properties are subject to modification by natural selection, it is perhaps not surprising that $V_m / V_E$ for viability, a major fitness component, should be relatively low. A fifth estimate for viability obtained from Mukai & Yamazaki (1968) but not included in Table 1 is anomalously high ($V_m / V_E$ = 0.00061). While this estimate was obtained with the same set of lines employed by Mukai (1964) that yielded an estimate of $V_m / V_E$ = 0.00004, it was measured after a much greater period of chromosomal divergence. All of the estimates of $V_m$ are expected to be quite accurate since most of the cited studies involved assays of approximately $10^6$ flies.

Yoshimaru & Mukai (1985) have shown that the pleiotropic effects of viability mutations on development time are very great, the genetic correlation being nearly 1.0. The reported data, however, do not allow a computation of $V_m / V_E$ for the latter character.

(iii) Drosophila ADH activity

A final result of interest for D. melanogaster concerns the activity of alcohol dehydrogenase (ADH). Using essentially the same procedures as described above for the experiments with viability polygenes, Mukai et al. (1984) performed an analysis of variance of second chromosomes in an isogenic background after 300 generations of divergence. Two experiments were run, each initiated with a different wild and marker chromosome. Significant between-line variance was detected in both experiments. The authors convincingly demonstrated that the variation was unlikely to be a product of structural gene mutations and argued for the modification of ADH activity by multiple factors in non-coding regions.

The ADH assays were performed on Cy/+ heterozygotes on an isogenic genetic background. Therefore, I took the between-line variance of the experimental populations to be an estimate of $0.0000013 V_m$. The error mean square, multiplied by 10 to account for pooling in individual assays, was taken to be the estimate of $V_E$. The two estimates of $V_m / V_E$ for ADH activity are in excellent agreement with each other and are intermediate to those for viability and bristle numbers (Table 1).

(iv) Tribolium pupal weight

Goodwill & Enfield (1971) successfully selected for 21-day pupal weight in two highly inbred lines of Tribolium castaneum (CSI-5 and CSI-10). Prior to selection both lines had passed through 46 generations of single full-sib matings. The fact that 13 additional generations of full-sib mating in CSI-10 did not result in a depression of genetic variance is consistent with these populations being in approximate drift-mutation equilibrium with $\text{var}(w) = 4 V_m$. Two-way selection was imposed on both sexes in each population for 17 generations. During this period, each selected male was randomly mated with 3-5 selected females. The number of selected individuals varied somewhat each generation, but the population size was maintained at 40-50 full-sib families. Assuming a mean male: female ratio of 1/4 and an average of 45 females, the effective population size estimated by $4 N_m N_f / (N_m + N_f)$ is 36. This is similar to the estimate ($N_e$ = 30) that the authors provide without explanation (p. 11; Goodwill & Enfield, 1971). Accepting the latter estimate, the expected dynamics of genetic variance generated by equation (29) of Lynch & Hill (1986) yield an expected mean genetic variance over the 17 generations of selection of $10^{-5} V_m$.

In their tables 4 and 5 the authors provide two heritability estimates pooled over sexes and selection directions for three experiments. The first estimate is based on the regression of cumulative selection response on cumulative selection differential, the second on parent–offspring and sib analyses. For the six data sets, I estimated $\text{var}(w)$ by $h^2 V_T$ and $V_E$ by $(1 - h^2) V_T$. The average phenotypic standard deviations ($\sqrt{V_T}$) for lines CSI-5 and CSI-10 over 17 generations are approximately 225 and 250 respectively (Figures 1 and 2; Goodwill & Enfield, 1971). The four estimates of $V_m / V_E$ obtained for line CSI-10 (0.0100, 0.0100, 0.0134, 0.0183) are substantially higher than those for line CSI-5 (0.0028, 0.0000) for unknown reasons. These yield a pooled estimate of $V_m / V_E$ for Tribolium pupal weight of $0.0091 \pm 0.0034$. 

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More recent work on the CSI-5 line (Enfield, 1987) yields estimates of $V_m/V_E = 0.001$, consistent with my derivations from the earlier work on this line.

(v) Mouse skeletal traits

In order to maintain as uniform a genetic background as possible for biomedical research, many laboratory strains of mice have been maintained by brother–sister mating for decades. Several such strains have been subdivided periodically and the sublines extended by further brother–sister mating. Two studies involving continuously distributed skeletal characteristics have been performed to quantify the rate of divergence of such sublines.

Baily (1959) performed a nested analysis of variance on four skull measures and lengths of the ulna and ilium of two sublines from the C57BL/6 and BALB/cAn strains. Prior to subdivision, the two strains had been maintained by full-sib mating for 30 and 78 generations respectively. The sublines were also maintained by single full-sib matings (D. Bailey, pers. comm.) and were allowed to diverge for an average of 46.5 and 9 generations respectively. Bailey (1959) detected significant subline divergence (within strains) in 8 of 12 comparisons. Since the effective population size of the original lines and the derived sublines was stable for a long period, the expected genetic variance between sublines after $t$ generations of divergence is simply $2V_m$ (Lande, 1976; Chakraborty & Nei, 1982; Lynch & Hill, 1986). The sum of the variances between individuals within litters and between litters within mothers provides an estimate of $(V_m + 4V_m)$. The data suggest that $V_m/V_E$ for skull metrics ($0.0046 ± 0.0015$) is lower than that for lengths of limb bones (ilium: $0.0158 ± 0.0105$; ulna: $0.0311 ± 0.0192$), there being almost no overlap between the two types of characters (Table 2).

Festing (1973) performed a multivariate analysis of variance on 13 linear measures of the mandibles of nine British sublines of strain C57BL/Gr. Ten of the characters were found to vary significantly between sublines. The ancestral strain had been full-sib mated for at least 40 generations prior to its subdivision and the subsequent pedigree is well-known (Deol et al. 1957; Yong, 1972). Table 1 in Festing (1973) contains the phenotypic means ($\bar{z}$) of the 13 characters for each of the nine strains as well as the pooled within-subline standard deviations ($MS_w$). The square of the latter provides an estimate of $(V_m + 4V_m)$. For any two sublines, the between-subline variance, $\text{var}(\bar{z})$ can be estimated by analysis of variance as $[(\bar{z}_1 - \bar{z}_2)^2/2] - [2MS_w/(n_1 + n_2)]$, where $n_1$ and $n_2$ are the sample sizes for the two populations. From the nine sublines, 36 estimates of $\text{var}(\bar{z})$ were made for each character, and then regressed on the respective divergence times. The expected value of the slope of such a regression is $2V_m$. Following these procedures, the mean value of $V_m/V_E$ ($±$ s.e.) obtained for the thirteen mandible traits ($0.0231 ± 0.0065$) appears to be significantly greater than the previous estimates for the skull but is of the same order as that for limb bones.

A second set of studies with inbred mice has involved discontinuous skeletal characteristics. Such traits are believed to be dependent upon an underlying continuous variable that is influenced by multiple loci and that, upon reaching a critical threshold, produces the variant (Gruneberg, 1955; Falconer, 1981). Using the same sublines that were studied by Festing (1973) plus three American sublines, Carpenter et al. (1957), Deol et al. (1957), and Yong (1972) have recorded the incidences of 25 skull variants. Sample size were on the order of 100–200 for most sublines. Assuming the underlying distribution to be standard normal, then the variance within populations can be equated to $1 = V_m + 4V_m$. The incidence of the trait can be transformed into the deviation from the threshold, $x_p$, by use of approximation (26.2.23) in Abramowitz & Stegun (1972). An unbiased estimate of the variance between any two sublines is then $[(x_{p1} - x_{p2})^2/2 - 2/(n_1 + n_2)]$.

Table 2. Survey of estimates of $V_m/V_E$ for skeletal traits of inbred lines of mice

<table>
<thead>
<tr>
<th>Trait</th>
<th>$V_m/V_E$</th>
<th>s.d.</th>
<th>$n$</th>
<th>Reference</th>
</tr>
</thead>
<tbody>
<tr>
<td>Skull measures (metric)</td>
<td>0.0046</td>
<td>0.0000–0.0018</td>
<td>0.0039</td>
<td>8</td>
</tr>
<tr>
<td>Skull measures (threshold)</td>
<td>0.0057</td>
<td>0.0000–0.00426</td>
<td>0.0088</td>
<td>25</td>
</tr>
<tr>
<td>Mandible measures</td>
<td>0.0231</td>
<td>0.00004–0.0716</td>
<td>0.0235</td>
<td>13</td>
</tr>
<tr>
<td>Ilium length</td>
<td>0.0158</td>
<td>0.0084–0.0233</td>
<td>0.0105</td>
<td>2</td>
</tr>
<tr>
<td>Ulna length</td>
<td>0.0311</td>
<td>0.0175–0.0447</td>
<td>0.0192</td>
<td>2</td>
</tr>
</tbody>
</table>
the expectation of which is \(2tV_m\). This quantity was estimated for all 66 possible pairs of sublines, the divergence times for which varied widely, and then regressed on \(t\) to obtain an estimate of \(2V_m\). \(V_m/V_e\) was then equated to \(V_e/(1 - 4V_m)\). The mean estimates of \(V_m/V_e\) for metric and threshold skull characters are not significantly different (Table 2).

(vi) \textit{Daphnia life history traits}

Obligately asexual organisms provide a useful opportunity for measuring the rate of polygenic mutation since the random drift that normally accompanies the sampling of gametes is not a factor and since divergence between lines cannot possibly be caused by segregation of residual heterozygosity. For such organisms, however, the mutational variance cannot be dissected into its additive and dominance components. Experimental and statistical procedures for measuring \(V_m\) with divergent clones are outlined in Lynch (1985) where 11 estimates of \(V_m/V_e\) for a lineage of \textit{Daphnia pulex} are presented for life-history characters (several of which are pleiotropically constrained). The mean value of \(V_m/V_e\) for that study, 0.0017 (s.d. = 0.0010), is on the order of that observed for spontaneous mutations for bristle number in \textit{Drosophila}.

(vii) \textit{Corn vegetative and reproductive traits}

Utilizing several long-time (> 10 generation) inbred lines of corn, Russell et al. (1963) performed a lengthy mutation-accumulation experiment that provides information on \(V_m/V_e\) for nine polygenic traits. During the experiment each line was maintained by selfing \((N = 1)\) with a minimum of selection (only ears with > 150 seeds were utilized) and subdivided each generation, thereby resulting in 16 sublines/line in the fifth generation. In order to eliminate year-to-year variation in environmental effects, seed stored from each generation was simultaneously grown for the final analysis of variance. Pooled estimates of the total genetic variance between sublines for each character (Table 4; Russell et al. 1963) exhibit pronounced and approximately linear increases for generations 2–5.

The interpretation of the dynamics of the variance between sublines is somewhat complicated under the dichotomous branching scheme because many pairs of sublines are not independent and the degree of independence varies depending on the position in the hierarchy. Taking this covariance structure into consideration, it can be shown that the variance between sublines after \(t\) generations of branching has expectation

\[
E[\text{var}(\xi, t)] = 2V_m \left[ t - 2^{t-1} \sum_{s=1}^{t-1} 2^{s-1} \right].
\]

so at the 2, 4, 8, and 16 subline stages, \(E[\text{var}(\xi, t)] = 200V_m\), 3-33 \(V_m\), 4-86 \(V_m\), and 6-53 \(V_m\). For the experiment of Russell et al. (1963), a pooled estimate of \(V_m\) was obtained by equating the four observed var \(\xi, t\) with their expectations and averaging the individual estimates of \(V_m\). The error variances of plot means given by Russell et al. (1963) have expectations of \((V_m + 2V_m)/10\). The nine resultant estimates of \(V_m/V_e\) for vegetative and reproductive characters have an average of 0-008 (Table 3).

An additional set of conservative estimates of \(V_m/V_e\) for these same characters can be derived from a divergence experiment performed on doubled haploid strains of corn (initially homozygous at all loci) (Sprague et al. 1960). The experimental design was basically the same as that of Russell et al. (1963), but instead of performing an analysis of variance, the authors detected mutants by \(t\) test comparisons (0.05% significance level) of the mean phenotypes of individuals and their ancestors. Differences that were detected at one point in a pedigree but later disappeared (possibly due to segregation and drift) were not included in these mutation rate estimates. Thus, the reported estimates of the mutation rate are too low since they primarily include mutations of relatively large effects that became fixed. With this in mind, an average of 0.060 (range 0.032–0.088) mutations/attribute/gamete (\(n_i\) in the notation of equation (2)) was detected. This compares favourably

### Table 3. Survey of \(V_m/V_e\) for vegetative and reproductive characters in plants

<table>
<thead>
<tr>
<th></th>
<th>Mean</th>
<th>Range</th>
<th>s.d.</th>
<th>(n)</th>
<th>Reference</th>
</tr>
</thead>
<tbody>
<tr>
<td>Barley</td>
<td>0.0001</td>
<td>0.0000–0.0004</td>
<td>0.0002</td>
<td>8</td>
<td>Cox et al. (1987)</td>
</tr>
<tr>
<td>Corn</td>
<td>0.0078</td>
<td>0.0031–0.0192</td>
<td>0.0054</td>
<td>9</td>
<td>Russell et al. (1963)</td>
</tr>
<tr>
<td></td>
<td>&gt; 0.0024</td>
<td>0.0012–0.0034</td>
<td>0.0009</td>
<td>9</td>
<td>Sprague et al. (1960)</td>
</tr>
<tr>
<td>Rice</td>
<td>0.0028</td>
<td>0.0015–0.0038</td>
<td>0.0017</td>
<td>2</td>
<td>Oka et al. (1958)</td>
</tr>
<tr>
<td></td>
<td>0.0034</td>
<td>0.0018–0.0056</td>
<td>0.0014</td>
<td>6</td>
<td>Sakai &amp; Suzuki (1964)</td>
</tr>
</tbody>
</table>
with an estimate of 0.064 obtained in the study of Russell et al. (1963).

Lande (1975) suggested how such incidence measures might be used to compute a minimum estimate of \( V_m/V_e \). Let \( V_e \) be the within-line variance. Then, in units of \( \sqrt{V_e} \), the minimum detectable difference between two samples of equal size \( n \) is \( z_1 - z_2 = t_{0.05} \left[ 2V_e/n \right] \). In the experiment of Sprague et al. (1960), 100 seeds were sown for each plant, so \( t_{0.05} = 1.982 \), and the minimum value of \( z_1 - z_2 \) that would be recorded as a mutation was \( 0.280 \sqrt{V_e} \). If it is assumed that mutants were only detected in the homozygous state, then \( (0.280 \sqrt{V_e}/2)^2 = 0.0196V_e \) provides a lower bound for the variance of mutational effects, \( \sigma^2 \). Substituting into equation (2) and dividing by \( V_e \), which will be approximately \( V_e \) for a selfed line, we obtain \( V_m/V_e > 0.0392 \) (np). Based on these computations, it appears that the mean \( V_m/V_e \) can be no less than 0.0024. The two types of studies are therefore in rough accord.

(viii) Barley biomass and grain yield

Cox et al. (1987) recently completed an experiment with three inbred lines of barley grown at two nutrient levels following the design of Russell et al. (1963) In their table 3, the authors record successive variance components for new sublines within lines. The expectation of each of these is \( 2V_m \). The sampling variance of mean phenotypes is reported in Table 2 (Cox et al. 1987) as \( \text{Error (b)} \); multiplication of these by the sample size (30) generates estimates of \( V_e \). The resultant estimates of \( V_m/V_e \) for biomass (0.0001 and 0.0004) and grain (< 0.0001 and 0.0004) yield are quite low, the higher estimates arising under low nutrient conditions. Grain yield behaved erratically, its total genetic variance remaining stable for the first five generations and then increasing dramatically in generation 6 under both nutrient conditions. Two additional characters, plant height and 100-kernel weight, exhibited no genetic variation, at least not enough to prompt the authors to publish the results.

(ix) Rice vegetative and reproductive traits

Data on the control of an irradiation experiment provide two estimates of \( V_{ml}/V_e \) for the self-fertilizing Oryza sativa (rice) (Oka et al. 1958). A 'pure line' obtained by repeated self-fertilization of a single plant formed the base population. Prior to analysis the plants were propagated in bulk for four generations. Assuming the genetic variance of the base population to be in drift-mutation equilibrium, then from equation (11) of Lynch & Hill (1986) \( \text{var} (w, 0) = 1.5V_m \), and the expected genetic variance for the unselected population in the fifth generation is \( 1.5 + (5 \times 2) V_m = 11.5V_m \). At that time the authors grew 75 families in 3 subplots with 10 plants/family in each subplot and performed an analysis of variance on family means for two traits (heading data and plant height). For each character I estimated \( (V_e + 1.5V_m) \) by multiplying the error mean square (Table 2; Oka et al. 1958) by 10. The between-family variance was obtained by equating the mean squares to the expectations and provided an estimate of 10\( V_m \). The resultant estimates of \( V_m/V_e \) for heading data and plant height are 0.0038 and 0.0015. There are reasons to suspect that these are underestimates, since prior to analysis, an unknown number of recognizable mutants (dwarfs, etc.) were intentionally discarded.

The control of another irradiation experiment performed by Sakai & Suzuki (1964) provides the basis for several estimates of \( V_{ml}/V_e \) of a less reliable nature. The commercial breed of rice, described as 'almost completely self-fertilizing', was separated into 160 lines each of which was subsequently maintained as a single plant for four generations. In their table 3, the authors provide estimates of genetic and environmental variance for six vegetative and reproductive traits in the fourth-generation plants. A more appropriate description of the reported environmental variance is \( (V_e + 1.5V_m)/12 \), since the analysis was performed on means of 12 family members. The expected genetic (between-family) variance in generation 4 is 8\( V_m \). The mean estimate of \( V_m/V_e \) over six characters is not significantly different from that of Oka et al. (1958) (Table 3).

4. Discussion

It is important to be cognizant of factors that could result in biased estimates of \( V_m \) in the preceding computations. I have operated under the assumption of perfect additivity of new mutations. Based on the properties of complex biochemical pathways, Kacser & Burns (1981) present an argument for why this might be so for genes of small effect; and as noted above, the assumption does not appear to be unreasonable for bristle number and viability mutations in Drosophila. It is not possible to draw any inferences about dominance effects in the Daphnia study since the clone was an obligate parthenogen (Lynch, 1985), and I am aware of no pertinent data for the mouse skeletal traits, the rice or barley attributes, or several of the maize characters. However, Enfield et al. (1966) suggest partial dominance in the direction of higher pupal weight in Tribolium; letting \( k = 0 \) denote perfect additivity, \( k = 1 \) complete dominance, and \( k = -1 \) complete recessivity, their results indicate \( k \) is between 0.1 and 0.5. Data from Moll et al. (1964) provide estimates of \( k \) for four of the maize characters analysed above: grain yield (1.4), ear diameter (−0.1), ear length (0.5), and plant height (−0.2). These estimates may in part be an artifact of linkage disequilibrium. Thus, with the possible exception of grain yield in corn, the existing evidence suggests that the alleles underlying the traits focused
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upon in this paper exhibit partial dominance approaching additivity.

This is not an entirely satisfactory answer to the question of dominance since the properties of new mutations may differ from those of alleles that are well-established in a population. Nevertheless, even if mutant polygenes do tend to be non-additive, most of the computations presented above would not be influenced greatly. For divergence experiments in which the base population is in drift-mutation equilibrium and the lines are maintained at the same effective population size, the expected rate of increase in between-line variance is $2V_m$ regardless of the level of dominance (Lynch & Hill, 1986). This result arises because only the homozygous effects of alleles contribute to the development of between-lines variance as new mutations ultimately become fixed or lost. Thus, an experiment of the form utilized by Russell et al. (1963) is a useful design when one is interested in measuring $V_m$, i.e. the variance due to homozygous effects of mutant alleles.

When selection experiments are used to estimate $V_m$, dominance becomes a more serious problem. The dominance properties of mutant alleles have a direct influence on the additive component of genetic variance which in turn determines the response to selection (Falconer, 1981). Relative to the case for additive mutations, the additive genetic variance is inflated two-fold when new mutations are completely dominant, and variance in the level of dominance results in a further inflation by a factor of approximately $2\sigma^2/3$ (Lynch & Hill, 1986). On the other hand, recessivity of new mutations ($k < 0$) results in a reduction of the additive component of variance (by approximately 40% for complete recessives). Thus, depending upon whether new mutations are dominant or recessive in the direction of selection, $V_m$ may be over- or underestimated when it is calculated from the realized heritabilities of selection experiments. Since the genes underlying Drosophila bristle numbers tend to be additive, the estimation of $V_m$ for this trait from the selection response does not seem inappropriate and indeed does not give greatly different results than divergence experiments (Table 1). However, given the results of Enfield et al. (1966), it is possible that my estimate of $V_m$ for 21-day pupal weight in Tribolium using the selection results of Goodwill & Enfield (1971) may be inflated.

Another reason for concern with the data analysed above is the potential existence of residual heterozygosity (in excess of that expected for drift-mutation equilibrium) in some of the inbred lines. It is well-known that heterozygote superiority can result in a balanced polymorphism in infinitely large populations. However, in small populations, selection for heterozygotes can at best reduce the rate of fixation and under a range of circumstances may even enhance the fixation process relative to completely neutral alleles (Robertson, 1962). While I have provided arguments against the presence of excess heterozygosity in the inbred lines that I have analysed above, to avoid any possibility of such a problem in the future, attempts to measure $V_m$ might start with lines that are known with certainty to contain no heterotypically-maintained genetic variance. Doubled haploid plants are logical candidates (Sprague et al. 1960; Lange, 1971; Deaton et al. 1982).

On the other hand, in the estimation of $V_m$ it is not necessarily desirable to start with a completely homozygous base population since, for example, the simple rule that the variance of population mean phenotypes increases at the rate $2V_m$ applies only to populations in drift-mutation equilibrium. The initial divergence rate of lines derived from a homozygous base will be less than $2V_m$ by an amount that depends on the effective population size (Lynch & Hill, 1986). Failure to correct for the departure from this equilibrium assumption will result in underestimates of $V_m$ whenever the effective size of the initial population is smaller than that of the divergent lines.

Selection is always a potential source of bias in estimates of $V_m$. It is difficult to quantify the magnitude of such bias but it will usually be in the downward direction. A conflict between stabilizing natural selection and directional artificial selection will result in underestimates of $V_m/V_e$ derived from long-term selection experiments. Stabilizing selection will also reduce the rate of divergence of 'unselected' lines. The problem will be minimized if the effective sizes of lines are kept as small as possible so that the force of random genetic drift is large relative to that of selection, but such a procedure has the negative aspect of increasing the probability of loss of extreme lines.

Consideration also needs to be given to the inherent difficulties in measuring $V_m$ due to the random production of mutations. For replicate populations in drift-mutation equilibrium, the coefficient of variation of var ($w$) is approximately $[4(n\mu)^{-1} + (2/3N)]^{-1}$ for mutations with normally distributed effects (Lynch & Hill, 1986). If a large number of loci contribute to the character so $(4n\mu) \approx 1$ and $n \gg N$, this is very roughly $(2/N)^{1/2}$. Thus, for small laboratory populations ($N < 10$), the standard error of $V_m$ based on $L$ replicate analyses of the within-population variance is on the order of $V_m\sqrt{(2/NL)}$ or larger. This ignores the additional variation that can arise from measurement error, maternal effects, etc. For mutations with normally distributed effects, the standard error of $V_m$ based on between-lines variance is essentially independent of the effective population size of the lines and of the divergence time, and equal to $V_m\sqrt{(2/L)}$ (Lynch & Hill, 1986). Thus, when the divergence is assayed for only two lines, the standard error will be on the order of $V_m$. Since these computations involve only the variance in the realization of the drift-mutation process and do not
include sampling variance on the part of the investigator, it is clear that the inaccuracies in estimates of $V_m$ are not trivial.

Since Lande (1975) first suggested that $V_m/V_e \approx 10^{-3}$ for a variety of species and characters, reference to this figure has frequently been made in the literature (Franklin, 1980; Hill, 1982a, b; Lynch & Gabriel, 1983; Turelli, 1984). However, in light of the preceding analyses, the general application of this estimate may be questioned. Considerable variation for $V_m/V_e$ appears to exist between species, populations, and characters. The only generalization possible is that, with the exception of viability mutations, $V_m/V_e$ is almost always within the range of $10^{-4}$ to $5 \times 10^{-2}$.

Occasionally, rates of polygenic mutation may even exceed $V_m/V_e \approx 5 \times 10^{-2}$. Mackay (1985, 1986, 1987, 1988) and Yukuihiro et al. (1985) have documented that the enhancement of transposon activity in dysgenic cultures of Drosophila melanogaster is associated with greatly elevated rates of mutation for genes affecting many quantitative traits. For abdominal and sternopleural bristle number, the results of selection and mutation accumulation experiments consistently indicate that $V_m/V_e \approx 0.1$–0.2 during periods of hybrid dysgenesis (Mackay, 1985, 1987, 1988). This is an approximately 100-fold inflation above the spontaneous rate and even greatly exceeds rates computed from X-ray induced lines (Mackay, 1987). In a study of a P-element-bearing but non-dysgenic strain, Mackay (1988) found a threefold inflation of $V_m/V_e$ over the normal rate, further supporting the idea that $V_m$ is a function of the genetic background.

Despite a potential range to $V_m/V_e$ of three orders of magnitude, a knowledge of these limits may be of some practical use. For example, Hill (1982a) has argued that the response to truncation selection will ultimately approach $\Delta z = (2N V_m) / \sqrt{V_e}$ as the utilizable genetic variance from the base population becomes exhausted. This may be rewritten as $\Delta z = 2N(1 + 2N V_m/V_e) / \sqrt{V_e}$. Taking $10^{-4}$ as the lower limit to $V_m/V_e$ and $i \approx 2$ for 5% truncation selection, then the lower limit to the asymptotic selection response is $0.0004 N / \sqrt{(1 + 0.0002 N)} / \sqrt{V_e}$. The data for $V_m/V_e$ in Table 3 suggest that substantially higher expectations may be reasonable for many crop species. Thus, if conventional selection programs can be applied to large outbred populations, considerable advance due to new mutations can be anticipated. A doubling in $N$, the number of selected individuals, will magnify the asymptotic response by a factor of $\sqrt{2}$ (for large $N$) to 2 (for small $N$).

As discussed in the introduction, $V_m$ is also a central element in the neutral model of phenotypic evolution. Such models are needed for the resolution of a number of problems in palaeontology and evolutionary ecology (Lande, 1976; Gould, 1980; Charlesworth et al. 1982; Reyment, 1983). In comparing the mean phenotypes of isolated populations or species, it is often assumed that the observed differences are adaptive. If the divergence time ($t$ generations) of the lineage is known, the validity of such an assumption can be explicitly tested by reference to the expectation that the between-line variance is $2V_m t$ for neutral characters. Taking $5V_e \times 10^{-2}$ to be the upper limit to $V_m$ and noting that $V_e < V_m$, then observed levels of var ($z$) that are significantly greater than $0.1 V_m t$ can be taken as evidence of significant diversifying selection on the lineages. Provided the phenotypic expression of the isolated lineages has not been differentially affected by the environment, this test requires only phenotypic data. By similar reasoning, measures of var ($z$) that are significantly less than $0.0002 V_e t$ can be taken as support of stabilizing or convergent selection on the isolates. This leaves a range in var ($z$) of approximately three orders of magnitude that is consistent with neutral expectations.

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References


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