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## THE DIVERGENCE OF NEUTRAL QUANTITATIVE CHARACTERS AMONG PARTIALLY ISOLATED POPULATIONS

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*Abstract.*—The neutral model of phenotypic evolution has yielded several simple predictions about the long-term rates of between-population divergence of polygenic traits and about the equilibrium level of within-population variance when mutation and random genetic drift are the sole evolutionary forces. These conclusions must be modified if populations are only partially isolated. A quantitative model is presented for the development of within- and between-population variance for neutral quantitative characters in pairs of populations with arbitrary effective sizes and migration rates. Both the variance in the base population and subsequent variance generated by mutation are considered, and several dynamical and equilibrium properties are shown to be adequately described by simple approximations. The resultant formulations provide some insight into the sensitivity of measures of morphological distance to gene flow, the necessity of isolation for the accumulation of variation between incipient species, and the consequences of gene flow into captive populations of endangered species.

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Recent work in theoretical quantitative genetics has helped clarify the expected long-term rate of divergence of polygenic traits when the only evolutionary forces are mutation and random genetic drift (Dempster in Bailey, 1959 appendix; Lande, 1976, 1979; Chakraborty and Nei, 1982; Lynch and Hill, 1986). The results of these studies complement the mathematical predictions of the neutral theory of molecular evolution (Kimura, 1983). An extension of the neutral theory to quantitative traits is of practical value, since most of the characters studied by evolutionary ecologists and ethologists have a polygenic basis. This is not to say that very many quantitative characters are neutral. However, neutral models do serve as useful null hypotheses in testing for selection (Lande, 1976, 1977). It is therefore important to evaluate the sensitivity of the predictions of the theory to violations of its assumptions.

The existing formulations for neutral quantitative characters have been derived under the assumption of complete reproductive isolation among population subunits. Under these circumstances, the expected rate of divergence of population mean phenotypes is predicted to be independent of the time since separation. Most statistical tests for natural selection are predicated on this result. There are, however, many situations in which gene flow between popula-

tions may be unobserved but nevertheless existent. For example, barriers between incipient species due to geography, climate, and/or behavior are frequently semipermeable (Endler, 1977). The purpose of this paper is to outline some of the consequences of migration for the within- and between-population components of genetic variance for neutral quantitative traits.

Efforts to incorporate migration into genetic models for quantitative traits have been few. Slatkin and Wade (1978) introduced a model of group selection on a quantitative character that incorporated population subdivision and gene flow. Their focus was on a trait under stabilizing selection in a population containing an effectively infinite number of demes with constant levels of genetic variation and with identical sizes and migration properties. For this special type of population structure, their results yielded some insight into the effects of migration on the steady-state between-population variance when selection is relaxed, although they did not pursue the matter. Slatkin (1978) has also studied the consequences of stabilizing selection over a cline of optimal values with restricted dispersal. As the model population was assumed to be infinite in size, genetic drift was not a factor. Slatkin (1981) and Rogers and Harpending (1983) have produced neutral models that are less constrained by as-

assumptions concerning the internal structure of a population but more restrictive in other ways. In both studies, nonmutable alleles were assumed to be present at each locus, and, in the second study, fixation was prevented by continuous immigration from an external source population with constant gene frequency.

There are several ways to model the migration process. These depend upon whether gene flow is assumed to occur at the zygote and/or gamete stage, whether gene flow occurs before or after population regulation, and whether the magnitude of migration is assumed to be deterministic or stochastic. Sved and Latter (1977) and Nagylaki (1983) have evaluated the consequences of these various alternatives for allelic variation at a single locus under several population structures. The quantitative differences between the models were found to be minor.

In this paper, migration is assumed to occur at the zygote stage and to be followed by population regulation and then by random drift, resulting from sampling of the gamete pool. Variation in the amount of migration and in the gene frequency of immigrants is incorporated in the model. The focus will be on a pair of partially connected populations, since that is the easiest case to analyze. Special attention will be devoted to mutations arising subsequent to the partial isolation, since they eventually determine the steady-state levels of genetic variance. Throughout, it will be assumed that the characters under consideration have an additive genetic basis, caused by  $n$  freely segregating loci, and that each allele can mutate to a potentially infinite number of new allelic states (Kimura and Crow, 1964). For additive genetic systems, the random development of linkage disequilibrium can cause substantial variation in the within-population variance (Avery and Hill, 1979), but it is unlikely to affect the expected within-population variance greatly and has no influence on the expected divergence of population means (Lynch and Hill, 1986).

*Contribution of New Mutations to the Between-Population Variance*

Provided there is some gene flow between two populations, every neutral allele must

eventually become fixed or lost from both populations. Thus, as a mutant allele ages, its expected contribution to the between-population variance diminishes to zero at a rate that depends on the magnitude of gene flow and on the effective sizes of the two populations. This implies that, under a constant population structure, the between-population variance will eventually reach a steady state. At this point the variance caused by new mutations is balanced by the loss due to migration and random drift. Such a result is quite contrary to the situation for completely isolated populations, in which case the asymptotic divergence rate is  $2V_m$ /generation, where  $V_m$  is the mutational input of new variance/generation (Lynch and Hill, 1986).

Consider two diploid, monoecious populations, 1 and 2, whose mean phenotypes can be written as the sum of mean effects from autochthonous (internally derived) and allochthonous (externally derived) mutations:

$$\begin{aligned}\bar{z}_1 &= \bar{z}_{11} + \bar{z}_{21} \\ \bar{z}_2 &= \bar{z}_{12} + \bar{z}_{22}\end{aligned}$$

where  $\bar{z}_{xy}$  is the contribution to the mean phenotype of population  $y$  from mutations that arose in population  $x$ . Provided there is no genotype  $\times$  environment interaction, as is assumed below,  $\bar{z}$  is equivalent to the mean genotypic value. Let  $a_{x,i}$  be the additive effect of a mutant allele that arose in the  $x$ th population at the  $i$ th locus, and, maintaining the same  $xy$  notation, let  $q_{xy,i}$  be the frequency of this allele in population  $y$ . While no constraints are placed on the effects of new mutations, it is assumed that no more than two alleles are segregating per locus at any time. If  $N_T$  is the total effective population size and  $\mu$  the genic mutation rate, this requires that  $4N_T\mu \ll 1$  (Kimura and Crow, 1964). Scaling the genotypic values of original homozygous genotypes to zero and that of mutant homozygotes to  $2a_{x,i}$ , and summing over all  $n$  loci,

$$\bar{z}_1 = 2 \sum_{i=1}^n (a_{1,i}q_{11,i} + a_{2,i}q_{21,i}) \quad (1a)$$

$$\bar{z}_2 = 2 \sum_{i=1}^n (a_{1,i}q_{12,i} + a_{2,i}q_{22,i}). \quad (1b)$$

When only two populations are being compared, the between-population variance can be simply expressed as

$$\text{Var}(\bar{z}) = \frac{(\bar{z}_1 - \bar{z}_2)^2}{2}. \quad (2)$$

The expected value of this quantity can be partitioned into the contributions from mutations of all ages. Assuming that the genic mutation rate and distribution of mutation effects are the same for both populations and that the gametic mutation rate  $n\mu$  is much smaller than one, the expected between-population variance resulting from the cohort of mutations that have been present for  $t'$  generations since the partial isolation is obtained by the approach of Lynch and Hill (1986) as

$$E\{\text{Var}_M[\bar{z}(t')]\} \approx 2V_m[N_1E\{[q_{11}(t') - q_{12}(t')]^2\} + N_2E\{[q_{21}(t') - q_{22}(t')]^2\}] \quad (3)$$

where  $V_m = 2n\mu E(a^2)$ ,  $N_1$  and  $N_2$  are the effective sizes of populations 1 and 2, and  $E[q_{11}^2(t')]$ , for example, is the expected second moment of the frequency of an autochthonous mutation that arose in population 1  $t'$  generations ago. The total divergence due to new mutations after  $t$  generations of partial isolation,  $E[\text{Var}_M(\bar{z}, t)]$ , is obtained by summing over all cohorts of mutations that arose subsequent to the split.

The evaluation of Equation (3) requires expressions for the gene-frequency moments. It is assumed here that a fraction of the mating pool of each population is derived from immigrants each generation. However, this fraction need not be the same for both populations, and it may vary between generations. Letting  $\bar{m}_x$  and  $\bar{m}_y$  be the expected proportions of mating individuals in populations  $x$  and  $y$  that are derived from immigrants, then

$$E[q_{xx}(t' + 1)] = (1 - \bar{m}_x)E[q_{xx}(t')] + \bar{m}_xE[q_{xy}(t')], \quad (4a)$$

$$E[q_{xy}(t' + 1)] = \bar{m}_yE[q_{xx}(t')] + (1 - \bar{m}_y)E[q_{xy}(t')]. \quad (4b)$$

With initial frequencies of a new mutation of  $E[q_{xx}(0)] = 1/2N_x$  and  $E[q_{xy}(0)] = 0$ , the solution to these equations becomes

$$E[q_{xx}(t')] = \frac{\bar{m}_y + \bar{m}_x(1 - \bar{m}_x - \bar{m}_y)^{t'}}{2N_x(\bar{m}_x + \bar{m}_y)} \quad (5a)$$

$$E[q_{xy}(t')] = \frac{\bar{m}_y - \bar{m}_y(1 - \bar{m}_x - \bar{m}_y)^{t'}}{2N_x(\bar{m}_x + \bar{m}_y)}. \quad (5b)$$

Expressions for the higher-order moments,  $E[q_{xx}^2(t')]$ ,  $E[q_{xx}(t')q_{xy}(t')]$ , and  $E[q_{xy}^2(t')]$  are derived in the Appendix.

The buildup of between-population variance caused by new mutations is obtained by iteration of Equation (3) and cumulative summation over all cohorts of mutations. Particularly simple approximations emerge for the special case in which both populations are equal in size and have identical migrational properties ( $m$  and  $\bar{m}^2$ ). If the expected number of immigrants/generation is on the order of one or more, but the migration intensity is not too strong ( $\bar{m} \leq 0.1$ ), then

$$E[\text{Var}_M(\bar{z}, t)] \approx \frac{V_m}{\bar{m}} \left[ 1 - \exp\left(-\frac{t}{4N}\right) \right]. \quad (6)$$

The equilibrium level of between-population variance is therefore very close to  $V_m/\bar{m}$  (Table 1), which is consistent with Nei and Feldman's (1972) conclusion that the mean genetic distance over many loci is approximately  $\mu/\bar{m}$ . Thus, for the special case of equal population sizes and migration rates, a doubling in the migration rate generally will halve the asymptotic divergence.

Although between-generation variation in the rate of migration has some influence on the divergence process, its effect on the dynamics of the expected between-population variance will often be very small, and it does not influence the equilibrium expected level of divergence. The results of simulations indicated that the difference between values of  $E[\text{Var}_M(\bar{z}, t)]$  when the number of migrants is fixed or binomially distributed is never more than 10%. Thus, Equation (6) has rather general applicability for the case of strong migration ( $\bar{m}N > 1$ ). Approximately  $3N$  and  $12N$  generations are required to attain 50% and 95% of the equilibrium level of between-population variance.

TABLE 1. Equilibrium levels of expected between-population genetic variance ( $E[\text{Var}(\bar{z}, \infty)]$ ), scaled by ( $V_m/\bar{m}$ ), for various combinations of population size ( $N_1 = N_2 = N$ ) and number of immigrants ( $\bar{m}N$ ). The number of immigrants is assumed to be binomially distributed. The actual between-population variance is obtainable by multiplying the tabulated values by  $V_m/\bar{m}$ .

N	$\bar{m}N$				
	0.01	0.1	1	2	10
2	1.01	1.06	2.00	—	—
4	1.00	1.03	1.33	2.00	—
10	1.00	1.01	1.11	1.25	—
50	1.00	1.00	1.02	1.04	1.25
100	1.00	1.00	1.01	1.02	1.11
500	1.00	1.00	1.00	1.00	1.02

The approach to equilibrium can extend for a much greater period of time when the rate of migration is small ( $\bar{m}N \ll 1$ ). In this case, when both populations are identical with respect to  $N$ ,  $\bar{m}$ , and  $m^2$  and when the number of migrants is binomially distributed, the following approximation applies for most practical purposes:

$$E[\text{Var}_M(\bar{z}, t)] \approx \frac{V_m}{\bar{m}} [1 - \exp(-2\bar{m}t)]. \tag{7}$$

With weak migration, the equilibrium level of divergence is always very close to  $V_m/\bar{m}$ , but the dynamics depend on  $2\bar{m}$  rather than  $1/(4N)$ . In this case, approximately  $0.35/\bar{m}$  and  $1.5/\bar{m}$  generations are required for new mutations to generate 50% and 95% of the equilibrium variance. Thus, if migration is very weak, divergence may continue for many hundreds of generations.

The consequences of unidirectional gene flow between two populations are also of interest. "Wild" genes may be periodically introduced into populations of endangered species housed in zoological parks or botanical gardens and for some domesticated populations, but gene flow in the opposite direction is often entirely absent. A similar situation will sometimes exist for species that consist of a well defined central population that subsidizes smaller marginal populations. Prevailing wind patterns, pollinator behavior, reproductive strategies, and certain geographical barriers may also promote unidirectional gene flow.

Table 2 lists the equilibrium levels of be-

TABLE 2. Equilibrium levels of expected between-population genetic variance ( $E[\text{Var}(\bar{z}, \infty)]$ ), scaled by  $V_m/\bar{m}$  with unidirectional gene flow.  $N_r$  and  $N_s$  are, respectively, the effective sizes of the recipient and source populations, and  $\bar{m}N_r$  is the number of immigrants into population  $r$  per generation. The frequency of migration is assumed to be binomially distributed. The actual between-population variance is obtainable by multiplying the tabulated values by  $V_m/\bar{m}$ .

$\bar{m}$	$N_r$	$N_s$		
		10	100	1,000
0.001	10	1.97	2.14	3.88
0.010	10	1.75	3.09	16.47
0.100	10	1.36	5.88	51.01
0.001	100	1.96	2.14	3.87
0.010	100	0.95	1.21	4.90
0.100	100	0.62	1.14	6.31
0.001	1,000	0.80	0.94	1.20
0.010	1,000	0.55	0.59	1.03
0.100	1,000	0.54	0.59	1.11

tween-population genetic variance ( $E[\text{Var}(\bar{z}, \infty)]$ ) for various combinations of effective sizes for source ( $N_s$ ) and recipient ( $N_r$ ) populations and different rates of immigration ( $\bar{m}$ ). For any  $\bar{m}$ ,  $E[\text{Var}(\bar{z}, \infty)]$  is a positive function of  $N_s$ , but varies inversely with  $N_r$ . This is a simple consequence of the number of migrants ( $\bar{m}N_r$ ) being a subsample of the members of the source population for which the within-population genetic variance is  $2N_s V_m$ . The sampling variance of the mean genotypic value of migrants in each generation is  $2N_s V_m/\bar{m}N_r$ .

Only some rough approximations are possible for  $E[\text{Var}(\bar{z}, \infty)]$  for the case of unidirectional gene flow. If migrants are very infrequent ( $\bar{m}N_r \ll 0.1$ ), the expected between-population variance is close to  $2V_m/\bar{m}$  provided  $N_r$  and  $N_s$  are not very different. This is twice the asymptotic divergence noted above for reciprocal gene flow. On the other hand, with strong migration ( $\bar{m}N_r \geq 1$ ), the asymptotic between-population variance is approximately  $V_m/\bar{m}$ , provided  $N_r \approx N_s$ , and approximately  $V_m/2\bar{m}$  if  $N_s \ll N_r$ .

Table 3 provides some additional estimates of the expected between-population variance when there is deterministic gene flow in both directions but the exchange is unequal ( $N_1 \neq N_2$  and/or  $\bar{m}_1 \neq \bar{m}_2$ ). Again, some simple approximations emerge. For the case in which population sizes are unequal but migration rates are equivalent,

TABLE 3. Equilibrium levels of expected between- and within-population genetic variance for cases of unequal population sizes and/or migration rates. Populations 1 and 2 have effective population sizes  $N_1$  and  $N_2$ , respectively. Frequencies of migrants are assumed to be binomially distributed, with  $m_1$  and  $m_2$  being the migration rates from population 2 into population 1 and from population 1 into population 2, respectively. The actual variances are obtainable by multiplying the tabulated values by  $V_m$ .

$N_1$	$N_2$	$m_1$	$m_2$	$E[\text{Var}(\bar{z}, \infty)]/V_m$	$E[\text{Var}(w, 1, \infty)]/V_m$	$E[\text{Var}(w, 2, \infty)]/V_m$
100	100	0.0001	0.010	122	204	281
100	100	0.0001	0.100	11	200	209
100	100	0.010	0.100	12	236	244
1,000	1,000	0.0001	0.001	1,247	2,388	3,087
1,000	1,000	0.0001	0.010	104	2,040	2,135
1,000	1,000	0.001	0.010	112	2,392	2,477
1,000	1,000	0.001	0.100	11	2,038	2,046
1,000	1,000	0.010	0.100	12	2,369	2,376
10	100	0.010	0.010	101	57	170
10	100	0.100	0.010	57	171	217
10	100	0.100	0.100	11	59	75
10	1,000	0.010	0.010	101	70	257
10	1,000	0.001	0.001	1,001	61	1,373
10	1,000	0.100	0.001	509	1,520	2,019
10	1,000	0.100	0.100	11	65	84
100	1,000	0.001	0.001	1,001	619	1,745
100	1,000	0.010	0.001	495	1,858	2,227
100	1,000	0.010	0.010	101	700	857
100	1,000	0.010	0.100	6	239	253
100	1,000	0.100	0.001	64	1,991	2,035
100	1,000	0.100	0.010	62	2,108	2,160
100	1,000	0.100	0.100	11	648	664

$$E[\text{Var}(\bar{z}, \infty)] \approx \frac{V_m}{\bar{m}}, \tag{8}$$

$$\text{Var}(w) = 2 \sum_{i=1}^n a_i^2 q_i (1 - q_i) + 4 \sum_{i \neq j} a_i a_j D_{ij} \tag{10}$$

just as in the above case with equal population sizes. If, however, the population sizes are equal, but the migration rates are not,

$$E[\text{Var}(\bar{z}, \infty)] \approx \frac{V_m}{\bar{m}_{\max}}. \tag{9}$$

Thus, consistent with the above, the degree of population differentiation is primarily a function of the largest migration rate.

*Contribution of New Mutations to the Within-Population Variance*

For neutral characters in completely isolated populations, it is well known that the equilibrium level of within-population variance is approximately  $2NV_m$ , provided the genic effects are purely additive (Clayton and Robertson, 1955; Lande, 1979; Chakraborty and Nei, 1982; Lynch and Hill, 1986). This result does not strictly apply to partially isolated populations.

The within-population genetic variance consists of quantities due to single-locus effects and to linkage disequilibrium (Avery and Hill, 1979):

where  $D_{ij}$  is a measure of disequilibrium of the joint distribution of genes at loci  $i$  and  $j$ . The expected value of the second term is clearly zero if the average effect of mutations is zero since  $E(a_i a_j) = E(a_i)E(a_j)$ . It is known that population subdivision can cause temporary linkage disequilibrium between unlinked loci (Nei and Li, 1973). However, the expected steady-state variance due to linkage disequilibrium is zero. The positive disequilibrium from pairs of mutations that arise in the same population is balanced by the negative disequilibrium from pairs that arise in different populations (Lynch, unpubl.). In the following, it is assumed that the expected total within-population genetic variance is defined by the first term in Equation (10).

Taking expectations and summing over mutations that arose in populations  $x$  and  $y$ , the expected genetic variance in population  $x$  from mutations that appeared  $t'$  generations in the past is

$$E[\text{Var}_M(w, x)]_t = 2V_m \{N_x(E[q_{xx}(t')] - E[q_{xx}^2(t')]) + N_y(E[q_{yx}(t')] - E[q_{yx}^2(t')])\}. \quad (11)$$

The cumulative within-population variance due to  $t - 1$  generations of mutations,  $E[\text{Var}_M(w, x, t)]$ , is obtained by summing this expression over generations  $t' = 1$  to  $t - 1$ . As  $t$  becomes large, the summation converges on a level of genetic variance at which the input of new variation by mutation and migration is balanced by loss via genetic drift.

Approximate analytical expressions for the equilibrium levels of within-population variance also can be obtained by use of the input-output equation,

$$E[\text{Var}(w, x, t + 1)] = \lambda_x(1 - \bar{m}_x)E[\text{Var}(w, x, t)] + \lambda_y\bar{m}_xE[\text{Var}(w, y, t)] + \bar{m}_x(1 - \bar{m}_x)E[\text{Var}(\bar{z}, t)] + V_m. \quad (12)$$

The first term accounts for the loss of genetic variance among the residents due to random drift, while the second term is the input of variance from immigrants, also discounted by drift in the previous generation. The third term is the increment in within-population variance due to variation between residents and immigrants, while the fourth term is the input of new variance due to mutation. The joint solution of Equation (12) and its companion equation for population  $y$  yields Equation (13) below, where  $\phi_x = 1 - \lambda_x(1 - \bar{m}_x)$ . [The actual equilibrium solution of Equation (12) has been multiplied by  $\lambda_x$  to account for the slight positive bias of the input-output approach (Lynch and Hill, 1986).]

For the special case of equal population sizes and balanced reciprocal migration ( $\bar{m}_1 = \bar{m}_2 = \bar{m}$ ), it is known (from above) that  $E[\text{Var}(\bar{z}, \infty)] \approx V_m/\bar{m}$ . Equation (13) then reduces to

$$E[\text{Var}(w, \infty)] \approx (2N - 1)(2 - \bar{m})V_m. \quad (14)$$

For most  $N$  and  $\bar{m}$ , this rather simple der-

TABLE 4. Equilibrium levels of expected within-population genetic variance ( $E[\text{Var}(w, \infty)]$ ), divided by  $(2N - 1)(2 - \bar{m})V_m$ , for various combinations of population size ( $N_1 = N_2 = N$ ) and number of migrants ( $\bar{m}N$ ). The numerical values are the cumulative asymptotic solutions to Equation (9). The frequency of immigrants is assumed to be binomially distributed.

N	$\bar{m}N$					
	0.01	0.1	1	2	5	10
2	0.9	0.8	0.7	—	—	—
4	0.9	0.9	0.8	0.7	—	—
10	1.0	1.0	0.9	0.9	0.7	—
100	1.0	1.0	1.0	1.0	1.0	0.9
500	1.0	1.0	1.0	1.0	1.0	1.0

ivation yields solutions that are essentially the same as those obtained by the iteration of gene-frequency moments and the asymptotic solution of Equation (9) (Table 4). Thus, provided  $\bar{m} < 0.1$  and  $N > 4$ , the within-population variance is very close to  $4NV_m$  the level expected if there were no subdivision. For a given  $N$ , the within-population variance declines as  $\bar{m}$  increases. This is because migration reduces the degree of differentiation between populations, which is responsible for the inflation of  $E[\text{Var}(w, \infty)]$ .

Similar simplifications of Equation (13) are possible for cases of unequal population sizes or asymmetrical rates of migration by use of the approximations for  $E[\text{Var}(\bar{z}, \infty)]$  given above, keeping in mind that the degree of accuracy of the latter is in some cases rather poor. Some direct computations from Equation (9) are provided in Tables 3 and 5.

Contrary to the situation for equal population sizes and migration rates, an increase in the migration rate can sometimes cause an inflation of the within-population variance if  $N_1 \neq N_2$  and/or  $\bar{m}_1 \neq \bar{m}_2$ . However, in some asymmetrical cases, an increase in one of the migration rates has little influence on the within-population variance. These subtleties arise with unequal  $N$  and  $\bar{m}$  because the equilibrium levels of within-population variance differ between the two subpopulations. Thus, although a

$$E[\text{Var}(w, x, \infty)] \approx \lambda_x \frac{\lambda_y\bar{m}_x\{\bar{m}_y(1 - \bar{m}_y)E[\text{Var}(\bar{z}, \infty)] + V_m\} + \phi_y\{\bar{m}_x(1 - \bar{m}_x)E[\text{Var}(\bar{z}, \infty)] + V_m\}}{\phi_x\phi_y - \lambda_x\lambda_y\bar{m}_x\bar{m}_y} \quad (13)$$

TABLE 5. Equilibrium levels of genetic variance expected within a recipient population ( $E[\text{Var}(w, r, \infty)]$ ), divided by  $V_m$ , under unidirectional gene flow.  $N_r$  and  $N_s$  are the sizes of the recipient and source populations, respectively, and  $\bar{m}N_r$  is the expected number of immigrants into population  $r$  per generation.

$\bar{m}$	$N_r$	$N_s$		
		10	100	1,000
0.001	10	56	63	120
0.010	10	45	91	553
0.100	10	26	161	1,509
0.001	100	431	482	990
0.010	100	135	279	1,710
0.100	100	34	209	1,957
0.001	1,000	1,215	1,359	2,799
0.010	1,000	164	341	2,097
0.100	1,000	35	214	2,008

high migration rate will reduce the variance between mean phenotypes of residents and migrants (as noted above), if the size of the source population is relatively large, the high variance among immigrants can overwhelm the low variance among residents and vice versa.

For unidirectional gene flow (Table 5), it can be seen that the expected equilibrium within-population variance of the recipient population,  $E[\text{Var}(w, r, \infty)]$ , always increases with the size of the source population, and with a high rate of migration ( $\bar{m} \geq 0.1$ ) approaches the expected variance for the source population,  $2N_s V_m$ . On the other hand, if the source population is much smaller than the recipient population, the variance within the latter may be substantially depressed below the level expected without migration ( $2N_r V_m$ ). This is a simple consequence of the heterozygosity in the recipient population being displaced by the relatively homozygous source pool.

#### *Variance Existing in the Base Population*

In the early stages of population fragmentation, the genetic variation in the base population,  $\text{Var}_B(w, 0)$ , will contribute to subpopulation differentiation as allele frequencies drift apart. As in the case for new mutationally derived variance, the magnitude of the between-population variance that is generated by initial variation will be inversely related to the intensity of gene flow. Moreover, provided there is even a trickle

of gene flow, this source of the between-population variance must eventually decline to zero as all original alleles become globally fixed or lost.

Recalling Equation (3), the between-population variance due to initial variance,  $\text{Var}_B(\bar{z}, t)$ , can be seen to be proportional to  $E\{[q_1(t) - q_2(t)]^2\}$  where  $q_1$  and  $q_2$  refer to gene frequencies in populations 1 and 2. Thus, the expected between-population variance can be projected to any future generation by iteration of the equations for the gene-frequency moments given in the Appendix. Initially,  $E[q_1^2(0)] = E[q_2^2(0)] = E[q_1(0)q_2(0)]$ .

Figure 1 illustrates the dynamics of between-population variance (relative to the variance in the base population) for the case of equal population sizes and migration rates, under the assumption of strong migration ( $\bar{m}N > 1$ ). When the time scale is weighted by  $1/N$  and the variance by  $1/\bar{m}N$ , the dynamics are very similar over a wide range of population sizes and migration rates. For this special case, the between-population variance due to initial variation reaches a maximum of approximately  $\text{Var}_B(w, 0)/(4.5\bar{m}N)$  within  $0.1N$  to  $0.6N$  generations. Thereafter, it declines at a rate of approximately  $\exp(-1/[4N])$ , so that about 95% of the peak variance is eliminated in an additional  $12N$  generations.

On the other hand, with weak migration ( $\bar{m}N < 0.1$ ), random genetic drift initially prevails, with little counteracting force from gene flow. With equal population sizes and migration probabilities, the between-population variance reaches a maximum of about  $2\text{Var}_B(w, 0)$  within approximately  $6N$  generations (Fig. 2). This is the expected maximum divergence due to variance in the base population in the absence of migration (Wright, 1951). The subsequent decay of the between-population variance due to the homogenizing forces of migration can be very slow, proceeding at the approximate rate of  $\exp(-2\bar{m})$ . For example, with  $\bar{m} = 10^{-3}$  (one migrant every 10 generations for population sizes of 100), it would take 1,500 generations for a 95% loss of the peak between-population variance due to initial variation.

The rate of decline of the initial variance within populations has limits that depend

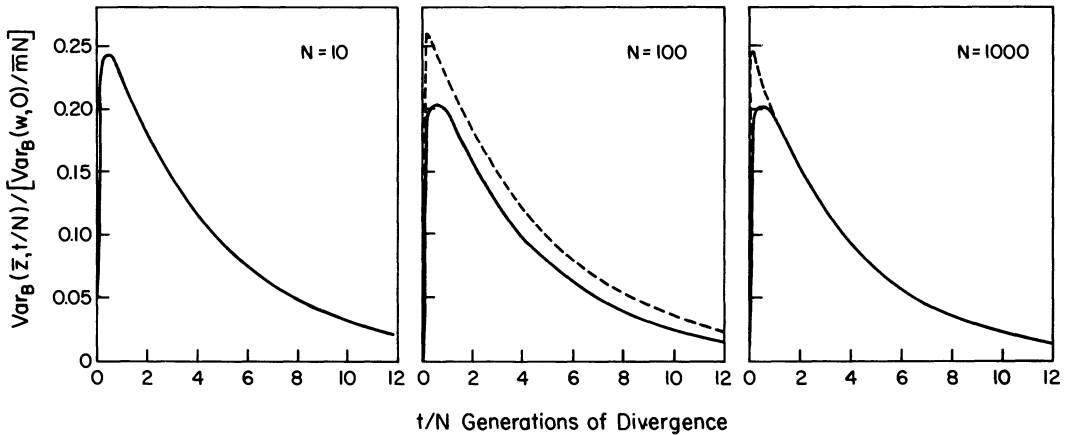


FIG. 1. The expected amount of between-population variance, scaled by the initial within-population variance,  $\text{Var}_B(w, 0)$  divided by the number of migrants per generation ( $\bar{m}N$ ), resulting from variation in the base population. Plots are for populations of equal size exchanging 2 (solid lines) and 25 (broken lines) individuals per generation on average. The actual frequency of migrants is assumed to be binomially distributed.

upon the intensity of migration. With strong migration ( $\bar{m}_x N_x > 1$ , and  $\bar{m}_y N_y > 1$ ), random drift proceeds in each subpopulation as though its effective size were equal to  $(N_x + N_y)$ . However, with weak migration, the loss of alleles is largely independent in each population. Thus, for the case of equal population sizes, the fraction of initial within-population variance remaining after  $t$  generations of partial isolation is between  $[1 - 1/(4N)]^t$  and  $[1 - 1/(2N)]^t$ . With exponential approximations, these become  $\exp(-t/[4N])$  and  $\exp(-t/[2N])$ . Thus, half of the initial within-population variance is expected to be lost within  $1.4N$  to  $2.8N$  generations, and an expected loss of 95% of the initial variance will occur within  $6N$  to  $12N$  generations.

DISCUSSION

The results of single-locus migration models are frequently cited to support the notion that subpopulations are effectively fused if the number of migrants between them exceeds one individual per generation (Crow and Kimura, 1970; Kimura and Ohta, 1971; Roughgarden, 1979; Hartl, 1980). However, this criterion for subpopulation homogeneity can be somewhat misleading. The between-population variance is inversely proportional to the expected migration rate. From this standpoint, the degree of migration above which two populations can be considered to be fused is subjective,

since a doubling of the migration rate always results in a 50% reduction in the expected between-population variance.

It is clear from Figure 3 that the between-population variance is small ( $< 10V_m$ ) and relatively insensitive to increasing levels of gene flow when the frequency of migration is greater than 0.1. However, this pivotal point is equivalent to one immigrant/generation only if  $N = 10$ . With larger population sizes, more immigrants are required to maintain the between-population vari-

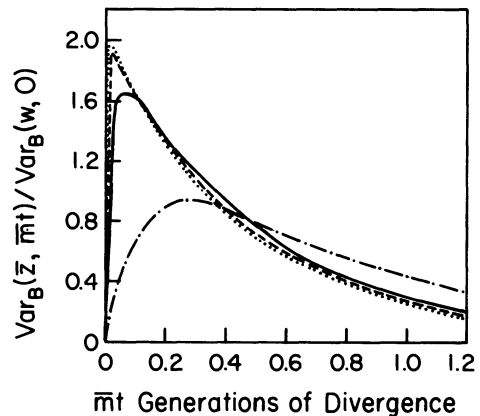


FIG. 2. The expected amount of between-population variance, scaled by the initial within-population variance, resulting from variation in the base population when migration between the derived populations is weak. The two populations are of equal size, each having binomially distributed migration rates with expectation  $\bar{m} = 0.1$  (alternate dashes and dots), 0.01 (solid line), 0.001 (dashes), and 0.0001 (dots).

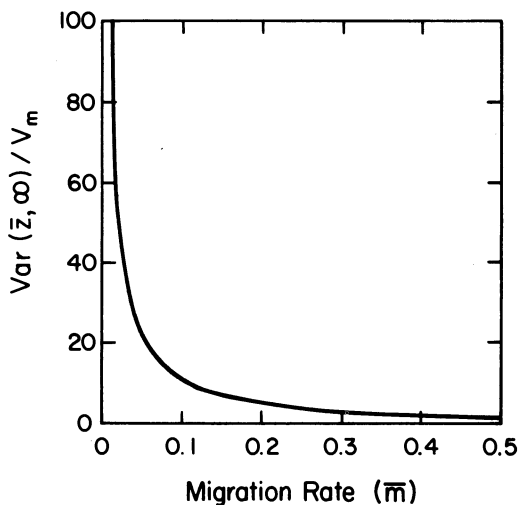


FIG. 3. The expected equilibrium level of between-population variance, scaled by  $V_m$ , for two populations of equal size ( $N$ ) and expected proportions of immigrants ( $\bar{m}$ ).

ance below  $10V_m$ . On the other hand, when the within-population genetic variance is the standard of comparison (as in an analysis of variance), it can be stated that a single migrant per generation is generally sufficient to render the equilibrium between-population variance negligible. Assuming equal population sizes, symmetrical migration, and  $\bar{m} = 1/N$ , then  $E[\text{Var}(\bar{z}, \infty)] \approx NV_m$ , which is 25% of the within-population genetic variance from Equation (14). With greater rates of migration, the expected variance between populations would always be less than 10% of that within populations.

Simple algebraic expressions have been given for the dynamics and equilibrium levels of within- and between-population genetic variance where possible. However, while the accuracy of these approximations is excellent under many conditions, they are not completely satisfactory. In any practical applications of the theory, it is advisable to compute the variances directly by iteration of the recursion equations given in the text. This is not a serious task for a microcomputer.

Two situations in which the approximations hold very well are when reciprocal migration is either strong ( $\bar{m}N > 1$ ) or very weak ( $\bar{m}N < 0.1$ ) and when population sizes are equal. It is instructive to compare the results for these special cases with the ex-

pectations for completely isolated populations. In the following, it is assumed that a panmictic base population of effective size  $N$  is suddenly split into two subpopulations, each of size  $N$ . Assuming the base population to be in drift-mutation equilibrium, its expected within-population variance will be  $2NV_m$ .

Under complete isolation, the between-population variance arising from the genetic variance in the base population is

$$E[\text{Var}_B(\bar{z}, t)] \approx 4NV_m \left[ 1 - \exp\left(-\frac{t}{2N}\right) \right]$$

(Crow and Kimura, 1970), while that arising from new mutations is

$$E[\text{Var}_M(\bar{z}, t)] \approx 4NV_m \left\{ \frac{t}{2N} - \left[ 1 - \exp\left(-\frac{t}{2N}\right) \right] \right\}$$

(Lynch and Hill, 1986). Thus, the total divergence due to both sources of variation is simply

$$E[\text{Var}(\bar{z}, t)] \approx 2V_m t.$$

The expected degree of divergence is linear with time.

With strong migration ( $1 < \bar{m}N < 10$ ),

$$E[\text{Var}_B(\bar{z}, t)] \approx \left(\frac{V_m}{2\bar{m}}\right) \left[ 1 - \exp\left(-\frac{8t}{N}\right) \right] \cdot \left[ \exp\left(-\frac{t}{4N}\right) \right],$$

and

$$E[\text{Var}_M(\bar{z}, t)] \approx \left(\frac{V_m}{\bar{m}}\right) \left[ 1 - \exp\left(-\frac{t}{4N}\right) \right].$$

Thus, for an initial period of  $N/4$  generations, there is an approximately linear buildup of between-population variance due primarily to variation in the base population (Fig. 4). However, the rate of divergence during this period ( $\approx 2V_m/\bar{m}N$ ) may be reduced substantially relative to the situation for completely isolated populations. The expected between-population variance at  $N/4$  generations is approximately half the asymptotic level. Thereafter, the divergence

due to preexisting variation begins to decline, and the subsequent increase to  $V_m/\bar{m}$  is due entirely to new mutations.

With very weak migration ( $\bar{m}N < 0.01$ ),

$$E[\text{Var}_B(\bar{z}, t)] \approx 4NV_m \left[ 1 - \exp\left(-\frac{t}{2N}\right) \right] \cdot \left[ \exp(-2\bar{m}t) \right],$$

$$E[\text{Var}_M(\bar{z}, t)] \approx \left( \frac{V_m}{\bar{m}} \right) [1 - \exp(-2\bar{m}t)].$$

Under these circumstances, the total divergence rate is very close to  $2V_m$  for the first  $0.1/\bar{m}$  generations and averages  $V_m$  for the first  $0.8/\bar{m}$  generations (Fig. 4). Thus, for very weakly connected populations, the rate of divergence of neutral quantitative traits may be linear and undetectably different from that for completely isolated populations for hundreds or thousands of generations. However, even with extremely infrequent migration, the expected between-population variance eventually stabilizes at the steady-state,  $V_m/\bar{m}$ .

As in all models, several assumptions have been made in the development of the theory in this paper. The focus has been on the simple case of a single base population fragmented into two partially connected subpopulations. Such a model seems particularly relevant to speciation events that are facilitated by random drift following the fission of an ancestral population. It also applies to captive populations of endangered species that periodically receive genetic supplements from the wild. Nevertheless, there are many common forms of population structure that involve more than two subpopulations. Given the diversity of factors that must be considered for only two subpopulations (the relative sizes of the two populations, the relative and absolute magnitudes of the migration rates and their temporal variance, and the amount of genetic variance in the base population), it is clear that any model involving more complicated substructure should be carefully tailored to the particular situation. The analytical tech-

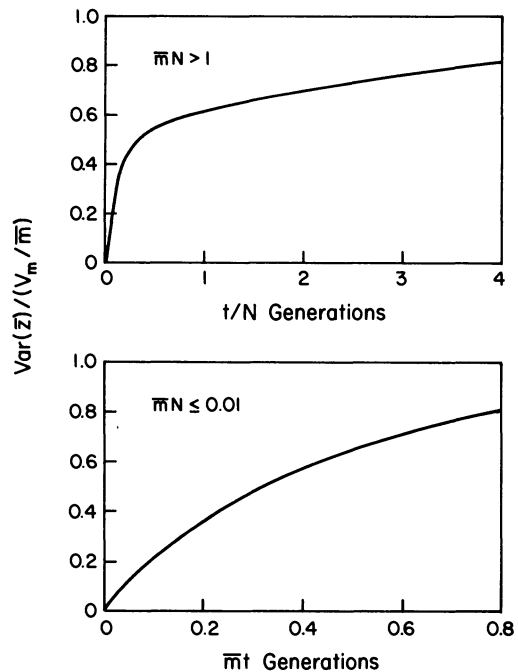


FIG. 4. The expected dynamics of between-population variance for neutral quantitative characters resulting from both variation present in the base population and variation resulting from new mutations. Limiting results are given for strong and weak migration between two populations of equal size.

niques used in this paper are readily extended to multiple subpopulations by expanding the set of gene-frequency moments to all pairs of source and resident populations. The use of a migration matrix, as introduced by Bodmer and Cavalli-Sforza (1968), would facilitate such endeavors.

The assumption of purely additive gene action may further limit the generality of the conclusions in this paper, but perhaps not greatly. The genetic basis of many quantitative traits appears to be primarily additive (Falconer, 1981). Moreover, it has been shown elsewhere for completely isolated populations (Lynch and Hill, 1986) that the conclusions of the neutral model are either unaffected by dominance (equilibrium between-population variance) or relatively insensitive to it (equilibrium within-population variance). In principle, dominance could be incorporated into the migration model using the techniques outlined above and in Lynch and Hill (1986). In reality, however, this would be an enormous task, involving third and fourth mo-

ments of gene frequencies as well as several gene-frequency cross-products.

Finally, it should be noted that the formulations provided in this paper give only the expected within- and between-population variances. A knowledge of the variance around these expectations would be of use in any statistical application of the theory. It is known for completely isolated populations that the coefficients of variation for the within- and between-population variance can often exceed one and depend on the linkage structure (Lynch and Hill, 1986). With the addition of stochastic migration, the variation will be even greater. Some insight into the variance of  $\text{Var}(\bar{z})$  for connected populations is provided by Rogers and Harpending (1983).

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#### APPENDIX

##### *Gene-Frequency Moments with Migration Between Two Populations*

The first-order gene-frequency moments have been given in the text as Equations (5a, b). The second-order moments are obtainable by making use of the expansion

$$q_{xy}(t') = q_{xy}(t' - 1) + \Delta q_{xy}(t' - 1),$$

which leads to the general expectation

$$E[q_{xy}(t')q_{uv}(t')] = E_k E_{t'-1} \{ q_{xy}(t' - 1)q_{uv}(t' - 1) + q_{xy}(t' - 1)E_\Delta[\Delta q_{uv}(t' - 1)] + q_{uv}(t' - 1)E_\Delta[\Delta q_{xy}(t' - 1)] + E_\Delta[\Delta q_{xy}(t' - 1)\Delta q_{uv}(t' - 1)] \} \quad (A1)$$

where  $E_\Delta$  denotes the expected change in gene frequency moments and where  $E_{t'-1}$  and  $E_k$  respectively denote the expectations conditional on gene frequencies and number of immigrant genes in generation  $t' - 1$ . The subscripts  $x$  and  $u$  refer to the original source

TABLE A1. Coefficients for the second-order gene-frequency moments with  $\lambda_{nx} = 1 - n/(2N_x)$ .

Coefficient	$E[q_{xx}^2(t')]$	$E[q_{xx}(t')q_{xy}(t')]$	$E[q_{xy}^2(t')]$
$\alpha_1$	$(1 - \bar{m}_x + \overline{m_x^2})/(2N_x)$	0	$\bar{m}_y/N_y$
$\alpha_2$	$\bar{m}_x'/N_x$	0	$(1 - \bar{m}_y + \overline{m_y^2})/(2N_y)$
$\alpha_3$	$\lambda_{1x}(1 - 2\bar{m}_x) + \lambda_{2x}\overline{m_x^2}$	$\bar{m}_y(1 - \bar{m}_x)$	$\lambda_{1y}\overline{m_y^2} - [\bar{m}_y/(2N_y)]$
$\alpha_4$	$2\lambda_{1x}(\bar{m}_x - \overline{m_x^2})$	$(1 - \bar{m}_x - \bar{m}_y + 2\bar{m}_x\bar{m}_y)$	$2\lambda_{1y}(\bar{m}_y - \overline{m_y^2})$
$\alpha_5$	$\lambda_{1x}\overline{m_x^2} - [\bar{m}_x'/(2N_x)]$	$\bar{m}_x(1 - \bar{m}_y)$	$\lambda_{1y}(1 - 2\bar{m}_y) + \lambda_{2y}\overline{m_y^2}$

population of an allele, while  $y$  and  $v$  denote the resident population; each subscript has potential values 1 or 2.

The changes in gene frequencies are functions of both random drift and migration,

$$\begin{aligned} \Delta q_{xx}(t' - 1) &= \Delta_D q_{xx}(t' - 1) + \Delta_M q_{xx}(t' - 1), \\ \Delta q_{xy}(t' - 1) &= \Delta_D q_{xy}(t' - 1) + \Delta_M q_{xy}(t' - 1). \end{aligned}$$

Letting  $\bar{m}_x$  and  $\bar{m}_y$  be the expected proportions of genes in populations  $x$  and  $y$  that are derived from immigrants each generation,

$$\begin{aligned} \Delta_M q_{xx}(t' - 1) &= \bar{m}_x[q_{xy}(t' - 1) - q_{xx}(t' - 1)], \\ \Delta_M q_{xy}(t' - 1) &= \bar{m}_y[q_{xx}(t' - 1) - q_{xy}(t' - 1)]. \end{aligned}$$

These expressions are also equivalent to  $E_\Delta[\Delta q_{xx}(t' - 1)]$  and  $E_\Delta[\Delta q_{xy}(t' - 1)]$ , since the expected change in gene frequency due to drift is zero.

On the other hand, the expected squared changes are influenced by both drift and migration. For example,

$$\begin{aligned} E_\Delta\{\Delta q_{xx}(t' - 1)\}^2 &= E_\Delta\{\Delta_M q_{xx}(t' - 1)\}^2 \\ &\quad + 2[\Delta_D q_{xx}(t' - 1)][\Delta_M q_{xx}(t' - 1)] \\ &\quad + [\Delta_D q_{xx}(t' - 1)]^2 \\ &= E_\Delta\{\Delta_M q_{xx}(t' - 1)\}^2 + [\Delta_D q_{xx}(t' - 1)]^2. \end{aligned}$$

The first term is the squared gene-frequency change resulting from migration

$$\begin{aligned} E_\Delta\{\Delta_M q_{xx}(t' - 1)\}^2 &= \left(\frac{k_x}{2N_x}\right)^2 [E_\Delta\{[q_{xy}(t' - 1) - q_{xx}(t' - 1)]^2\}] \\ &= \left(\frac{k_x}{2N_x}\right)^2 [\text{Var}[q_{xx}(t' - 1)] + \text{Var}[q_{xy}(t' - 1)] \\ &\quad + [q_{xx}(t' - 1) - q_{xy}(t' - 1)]^2] \end{aligned}$$

where Var refers to the variance in gene frequency among the members of the population sampled during the migration phase. Provided the migration rate is low ( $k_x \ll 2N_x$ ), the two variance terms are  $q_{xx}(t' - 1)[1 - q_{xx}(t' - 1)]/2N_x$  and  $q_{xy}(t' - 1)[1 - q_{xy}(t' - 1)]/k_x$ . The variance in gene frequency resulting from the sampling of gametes after migration is

$$\begin{aligned} E_\Delta\{[\Delta_D q_{xx}(t' - 1)]^2\} &= E_\Delta\left\{\left[q_{xx}(t' - 1) + \frac{k_x}{2N_x}[q_{xy}(t' - 1) - q_{xx}(t' - 1)]\right]_D^2\right\} \\ &= -\frac{k_x^2}{8N_x^3}[q_{xy}(t' - 1) - q_{xx}(t' - 1)]^2 \\ &\quad + \frac{k_x}{4N_x^2}[1 - 2q_{xx}(t' - 1)][q_{xy}(t' - 1) - q_{xx}(t' - 1)] \\ &\quad + \frac{q_{xx}(t' - 1)[1 - q_{xx}(t' - 1)]}{2N_x}. \end{aligned}$$

Expressions for  $E_\Delta\{[\Delta q_{xy}(t' - 1)]^2\}$  and  $E_\Delta\{\Delta q_{xx}(t' - 1)\Delta q_{xy}(t' - 1)\}$  are obtained in a similar manner.

The recursion equations for the higher-order gene-frequency moments are obtained by substituting the  $E_\Delta$  terms back into Equation (A1) and taking expectations, noting that  $E(k_x/2N_x) = \bar{m}_x$  and  $E(k_x^2/4N_x^2) = \overline{m_x^2}$ . The final solutions are of the form

$$\begin{aligned} E[q_{xu}(t')q_{yv}(t')] &= \alpha_1 E[q_{xx}(t' - 1)] \\ &\quad + \alpha_2 E[q_{xy}(t' - 1)] \\ &\quad + \alpha_3 E[q_{xx}^2(t' - 1)] \\ &\quad + \alpha_4 E[q_{xx}(t' - 1)q_{xy}(t' - 1)] \\ &\quad + \alpha_5 E[q_{xy}^2(t' - 1)] \end{aligned}$$

where  $u$  and  $v$  refer to  $x$  and/or  $y$ . The coefficients are given in Table A1, where  $\lambda_{ux} = 1 - n/(2N_x)$ .