

LETTERS TO THE EDITORS

LEWONTIN-KRAKAUER *test for neutral genes*

LEWONTIN and KRAKAUER (*Genetics* **74**: 175–195, 1973) have proposed a statistical method for testing the neutrality of polymorphic genes. Their method involves testing the observed value of the inter-locus variance (s_p^2) of the estimate (\hat{F}_{ST}) of WRIGHT's F_{ST} against the theoretical variance (σ^2) based on the assumptions that (1) the gene frequency of each subpopulation used is a random sample from a given frequency distribution and (2) F_{ST} is the same for all loci. Their method is supposed to be applicable under any types of migration and mutation. As indicated by J. FELSENSTEIN to us, however, if a high rate of migration occurs among a certain group of subpopulations, there will be a strong correlation of gene frequencies among them, and this will inflate the s_p^2/σ^2 ratio, leading to an erroneous conclusion. (L & K noticed this property but regarded it as unimportant.) The second assumption is also not justified when mutation and special patterns of migration occur. We note that at the molecular level most mutations are unique and the F_{ST} for a particular (mutant) allele among subpopulations of a species changes from time to time, depending on the migration pattern and population size. This will again inflate the variance ratio s_p^2/σ^2 . L & K argue that the effect of new mutations could be detected by examining the pattern of gene frequency distributions within and between *related* populations. Since the *relatedness* of populations is usually judged by the similarity of gene frequencies, this procedure is circular.

To confirm the above arguments, one of us (T.M.) conducted two types of Monte Carlo simulations. The first was to test L & K's assertion that their parameter k is equal to or less than 2 for neutral genes. For this purpose, circular steppingstone models of 20 and 100 colonies were used without mutation. The number of individuals in each colony was 10, and the migration rate (m) was 0.5 per generation. The initial gene frequency (p) was 0.2 in all colonies, and after 50 generations the \hat{F}_{ST} value was computed. This process was repeated 500 times, and k was computed. The k value thus obtained was 4.42 for 20 colonies and 6.14 for 100 colonies. Therefore, σ^2 can be larger than the value given by L & K even for neutral genes. The second simulation was to see the effect of mutation, and the island model of 10 colonies of size 10 was used with $m = 0.368$ and $p = 0.2$. The mutation rate varied with locus from 0.001 to 0.1. After 20 generations, the L & K test was conducted by using 20 loci (independent runs). In three out of the four replicate tests the s_p^2/σ^2 ratio was statistically significant for neutral genes.

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