leagues (*2*) have recently provided direct evidence that strains of *A. aegypti* from different regions do vary in the efficiency with which they transmit yellow fever virus. The genetic peculiarity of Asian populations, which do not fall easily into either the African *formosus* group or the African and New World *aegypti* group, may somehow be related to their relatively poor ability to transmit yellow fever. We think that some of the isozyme loci we used for the present studies may mark segments of the genome that are related to disease transmission. Thus further studies into the genetics of transmission efficiency in this species are warranted, and the analysis described here suggests a means of characterizing the genetic basis of variation in transmission efficiency.

Note added in proof: Since this report was written we have analyzed a large field sample of *A. aegypti* from Laredo, Texas. The first and second canonical variables are −10.23 and −1.06, respectively. This population is clearly genetically similar to the Caribbean/Mexican populations and is distinct from Southeast U.S. populations.

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References and Notes

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4. We used the *BMDP Biomedical Computer Programs, P-Series* [Univ. of California Press, Berkeley (1977)], for a stepwise linear discriminant analysis. The measurements $X_1, \ldots, X_p$ on each natural population are allele frequencies [from (*3*)]. The analysis aims to use these measurements to classify populations into different regions. If populations were only from East Africa or West Africa, for example, then a linear discriminant analysis seeks a canonical variable

$$c = a + b_1X_1 + \ldots + b_pX_p$$

to classify populations on the basis of their c values. The procedure used to select $a, b_1, \ldots, b_p$ is to maximize the ratio of the total to within region sums of squares of canonical variable values. If one assumes that the measurements are normally distributed and have common within-region variances and covariances, the canonical variable value of a population can be used to calculate the probability that a population comes from a given region. The classification criterion is to assign a population to the region of most probable origin. Since there are so many measurements ($p = 65$), it is desirable to have a procedure, which searches for measurements providing good classification to enter the canonical variable. A stepwise linear discriminant analysis is a sequence of distinct linear discriminant analyses, in which the analysis at step K is obtained by adding or deleting a measurement to the analysis at step $K - 1$. For the rules for adding or deleting a measurement at each step, see R. I. Jennrich, in *Statistical Methods for Digital Computers*, K. Enstein, A. Ralston, H. S. Wilf, Eds. (Wiley, New York, 1977), pp. 76–95). If a population can be classified into one of several regions, then additional canonical variables are added to the analysis; they are mutually independent within regions. The procedure for constructing the first canonical variable can be used to construct the second canonical variable subject to the independence constraint and so on. The classification criterion is the same, but now depends on additional canonical variables. In our analysis the normality assumption of measurements is reasonable on the basis of the sample sizes used in computing allele frequencies [see (*3*)]. The assumption of common within-group variances and covariances is warranted in that the most important measurements in the canonical variables [see (*5*)] are of moderate frequencies. A variance stabilizing transformation could be used on the measurements, but in previous work we have found that the conclusions reached are not sensitive to the transformations.
5. In the first canonical variable the b coefficients of the allele frequencies for HK-4^{100}, Idh2^{116}, Mdh^{120}, 6Pgd^{100}, and Pgm^{100} were 1.49, −12.51, −13.26, 3.63, and −7.12, respectively. The b coefficients for the second canonical variable were −5.34, 7.57, −1.21, −2.07, and −12.88, respectively. The constant a coefficients for the first and second canonical variables were 6.03 and 15.27.
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11. East African *A. a. aegypti* represent collections from inside houses from three villages in Rabai District Kenya. This represents one of two areas in East Africa where the domestic form is found inside village houses [see M. Trpis and W. Hausermann, *Bull. Entomol. Res.* **68**, 521 (1979)].
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13. We thank the large number of fellow mosquito biologists who generously contributed to this study by providing mosquito collections, and I. R. Savage for pedagogical comments to J. Arnold. Supported by NIH grants AI 05118 and AI 12016.

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