Genetic Variation in Marine Bivalvia (Mollusca)

Levinton (*1*) has reported that the absolute and effective number of alleles at the phosphohexose isomerase (PHI) (E.C. 5.3.1.9) and leucine aminopeptidase (LAP) (E.C. 3.4.1.1) loci in six species of bivalve mollusks from the Long Island Sound region decreased with depth of burial within the sediment intertidally and with depth of water subtidally. It was concluded that environmental variability regulates genetic variability at these loci.

However reasonable the postulate that environmental variability may alter significantly levels of genetic variability within populations or species, the data presented by Levinton can not be regarded as strong evidence in its favor. The specific hypothesis tested was "that species which burrow more deeply have less genetic variability at these two loci" (*1*). Of the six species analyzed for PHI variability, five can be said to be burrowing forms. *Mytilus edulis*, as rightly stated, is not a burrowing species, and may not be typical of epifaunal mollusks in PHI variability. [In the nonburrowing species *Ostrea edulis*, for example, only two PHI alleles have been detected in a study of more than 300 individuals (*2*)]. The data on one other species (*Mya arenaria*) are, as stated by Levinton, subject to question. Of the remaining species, the least variable—*Nucula annulata*—is a shallow, not a deep, burrower. Indeed this latter species is included more as an example of a subtidal mollusk than as a burrowing species. What significance, within the terms of the hypothesis, is to be placed on the observed differences between the three remaining species is not clear. At the LAP locus, for instance, there is no difference whatever in the actual number of alleles observed in these three species.

As to the other hypothesis tested, at least implicitly—that genetic variability decreases with depth of water subtidally—it appears unwarranted to generalize from a comparison of one subtidal species with five intertidal.

The real value of Levinton's report lies in its exposition of multiple alleles at the PHI locus in a number of bivalve mollusks. We have observed (*3*) similarly high numbers of alleles at this locus in other burrowing and epifaunal species of mollusks on the west coast of Ireland. The significance of these observations certainly warrants thorough investigation at both molecular and ecological levels.

N. P. WILKINS
Department of Zoology, University College, Galway, Ireland

References

1. J. Levinton, *Science* **180**, 75 (1973).
2. N. P. Wilkins and N. F. Mathers, *Anim. Blood Groups Biochem. Genet.* **4**, 41 (1973).
3. ———, in preparation.

7 September 1973

If Wilkins limited his point to lack of strong diminution of the absolute number of alleles (*A*) with burrowing depth at the LAP locus, then I would agree. However, the data for *A* at the PHI locus and the data for the effective number of alleles at both loci clearly show the trend that I describe. Further, I disagree with the proposition that *Mytilus edulis* cannot be considered comparatively with burrowing species. After all, *Modiolus demissus* is only semi-infaunal, while *Mercenaria mercenaria* is a very shallow burrower. My selection of species was for the purpose of having a gradational series of epifaunal (zero burrowing depth) to deep infaunal species. I mention the difficulty of producing objective field measures of environmental variability. It is all too easy to look at your data and invoke an ad hoc combination of variables to explain them. This was my reason for choosing burrowing depth, a parameter that can be measured. I do not imply that there are no other factors, stochastic included, that contribute to the variation within my data. This must certainly be true. Although some other authors have come to conclusions similar to my own concerning genetic variability and environmental variability within restricted geographic regions (*1*), Wilkins' and other data (*2*) show that it is not possible to make easily interpretable comparisons of different realms of geography or geologic history at present. Some popular models of genetic evolution are certainly too simplistic. I look forward to further research and spirited discussion of this problem in the future.

JEFFREY LEVINTON
Department of Earth and Space Sciences, State University of New York, Stony Brook 11790

References

1. J. L. Hamrick and R. W. Allard, *Proc. Natl. Acad. Sci. U.S.A.* **69**, 2100 (1972); M. S. Johnson, *Heredity* **27**, 205 (1971); R. K. Koehn, F. J. Turano, J. B. Mitton, *Evolution* **27**, 100 (1973); J. R. Powell, *Science* **174**, 1035 (1971); G. Wium-Anderson, *Ophelia* **8**, 267 (1970).
2. J. L. Gooch and T. J. M. Schopf, *Evolution* **26**, 545 (1973); F. J. Ayala, D. Hedgecock, G. Zumwalt, J. W. Valentine, *ibid.* **27**, 177 (1973).

15 October 1973

Vasectomy: Long-Term Effects

Despite the lapse of more than 50 years since vasectomy was first performed for surgical reasons, the long-term effects of this procedure have not yet been completely determined. Nevertheless, Sackler *et al.*'s indictment of vasectomy contained in their opening statement, "Valid social ends do not justify invalid, unscientific means" (*1*), seems premature and unscientific.

The report has several important flaws. Although findings in one species cannot be directly correlated with those in others, these authors extrapolate from their findings in rats to draw conclusions about human vasectomy. The laboratory rat is unique in many ways; certainly with regard to vasectomy, it responds differently from the guinea pig, rabbit, rhesus monkey, and man. After vasectomy, the epithelial cells of the rat epididymis assimilate the dammed spermatozoa (*2*) whereas in the rhesus monkey and apparently in man the blocked spermatozoa are ingested and digested by macrophages (*3*).

Sackler *et al.*'s study was done on immature rats. To base one's conclusions about how vasectomy affects sexually mature human beings on studies performed on immature rats is surely to stretch the limits of valid extrapolation. Moreover, the 17-ketosteroid assay that was used to check the androgen secretion of the testes does not give an unequivocal indication of androgen activity. Dehydroepiandrosterone and some of the corticosteroids contribute more to the urinary excretion of 17-ketosteroids than testosterone and androstenedione (*4*). Perhaps even more importantly, no other studies have shown that vasectomy has effected a change in androgen secretion in man (*5*) or the