



Jefferies's restoration of *Lagynocystis*, an ancestor of *Amphioxus*? (from *Phil. Trans. R. Soc.*, 265; 1973).

The urochordate tadpole and vertebrates share specializations — for example, motor endplates — which *Amphioxus* does not. Jefferies reports that he has found fossil evidence for his view in a hitherto obscure group, previously held to be primitive echinoderms. These, which he has renamed the calcichordates, he has resurrected (in a series of papers) with spectacular success. He considers one group of calcichordates, the mitrates, to be the common ancestors of *Amphioxus* on the one hand, and of the urochordates and vertebrates on the other. The common specializations which Jefferies believes are shared by a group of swimming mitrates and vertebrates are: "a brain, a complex nervous system and a body clearly separate from the tail". *Amphioxus* on the other hand he considers to be descended from *Lagynocystis*, a burrowing mitrate, which he describes in this new paper.

It must be said, however, that many of Jefferies's colleagues find it difficult to accept such a radical reassessment of the phylogeny of *Amphioxus*. In trying to convince them Jefferies is up against the perennial problem faced by palaeontologists when describing groups, such as the calcichordates, which are very different from any living today. There is no way of knowing whether the soft parts have been accurately identified; this being the case it is difficult to see how hypotheses concerning the evolutionary relationships of such animals can be tested.

ECOLOGICAL GENETICS

Genic Heterozygosity

from a Correspondent

Selander and Kaufman in a recent paper (*Proc. natn. Acad. Sci., U.S.A.*, 70, 1875; 1973) use data from their own and other electrophoretic studies to show that populations of invertebrates have higher levels of heterozygosity than do those of vertebrates. In the invertebrates studied, polymorphisms occur at a higher proportion of loci and, on average, more alleles are segregating at each polymorphic locus than in the vertebrates. By suggesting that these differences reflect different ways in

which populations of small and large organisms experience their environments, the authors "take sides" in two independent controversies.

First, to account for allozymic variation in adaptive terms implies non-acceptance of the view expressed by several mathematical geneticists that observed levels of heterozygosity are too high to be maintained by natural selection, and that most of the electrophoretic variants must be of neutral survival value relative to each other.

Second, in order to predict differences in the mode of action of selection on vertebrates and invertebrates, Selander and Kaufman use Levins's conclusion (*Evolution in Changing Environments*, Princeton University Press, 1968) that polymorphism is the response of a population to a spatially or temporally unpredictable environment. For example, where a population exists in a spatially variable environment, each individual may either spend most of its life in one type of "patch" or may cover most of the different types in the proportion in which they occur. In the first case, which Selander and Kaufman argue is general for invertebrates, including larvae of flying insects, because of their small size, low mobility and limited potential for homeostatic control, different individuals in the population are exposed to different environments. In the second, supposedly more characteristic of vertebrates, each individual must

survive in all environments. Levins's conclusion that the first type of selection leads to polymorphism whereas the second tends to give a single all-purpose genotype sounds logical, but has been criticized by Hamilton (*Science, N.Y.*, 167, 1478; 1970) who found that it was based on unrealistic population dynamic assumptions.

Although Levins has shown that polymorphism is the optimum population strategy in an unpredictable environment, the classical view has been that disruptive selection, that is, selection acting in more than one direction simultaneously does not give rise to polymorphism unless the selective advantage of an allele is dependent on its frequency, such that individuals with rare alleles are favoured. Thus, it seems that the degree to which Levins's conclusions apply must depend in part on the balance between selection pressures acting at the population and individual levels. This question itself is complex and controversial, the outcome being much dependent on the population structure of the species concerned.

For these reasons it seems that, if the term "neo-Darwinist" is to lose its aura of condensation, the "neutralists" must be attacked in other ways. This can be done by basing predictions of the action of natural selection on specific metabolic functions of the enzymes concerned, or by detailed ecological and

Isolation of H Chain mRNA Precursor

Stevens and Williamson have previously reported that myeloma cell heavy (H) chain mRNA binds to the total protein H_2L_2 and that, after precipitating with antiserum to H_2L_2 , the RNA can be recovered. Using this method three different RNAs have been isolated; two were found in both nucleus and cytoplasm, but the largest only in the nucleus. The two smaller RNAs were shown to direct the synthesis of H chain when injected into *Xenopus laevis* oocytes and in *Nature New Biology* next Wednesday (September 26) Stevens and Williamson describe a technique which allows the largest RNA to be isolated in sufficient quantity for injection into oocytes. Increasing the concentration at which the cells are grown from 5.7×10^6 to 10^7 cells ml^{-1} results in an accumulation of nuclear RNA until 80% of the RNA isolated by binding it to H_2L_2 is nuclear in origin. After separating the three RNAs on polyacrylamide gels the largest can be eluted for injection into oocytes. This results in the production of myeloma H chains.

Because the largest RNA contains the sequence of nucleotides which codes for H chain and is confined to the nucleus, it seems likely to be the precursor of

cytoplasmic H chain mRNA. To prove this the authors performed pulse-chase experiments and were able to show that the largest RNA is synthesized before, and gives rise to, the smaller RNAs. The cleavage takes place in the nucleus — the whole procedure being analogous to the production of ribosomal RNA. The two RNAs (which appear in both the nucleus and cytoplasm), although apparently very different in molecular weight (6×10^5 and 3.1×10^5), are not thought to represent different stages in the processing of mRNA. Their true molecular weights are probably much closer — the large difference arising from different electrophoretic mobilities depending on whether or not they contain poly(A)-rich sequences.

Previous attempts to demonstrate a precursor-product relationship between high-molecular-weight nuclear RNA and cytoplasmic mRNA have not been completely successful because of the difficulty of working with both easily labelled and uniquely identifiable RNA molecules. Stevens and Williamson have met this difficulty by using differentiated cells which grow in culture with the result that the precursor-product relationship is most successfully demonstrated.