(PMR) spectrum, not evident in the intact membrane, and corresponding to the spectrum of extracted lipids in solution. By contrast, when membranes are heated, the breakdown of the protein structure can be followed by the change in CD, and this is associated with the appearance of the PMR spectrum of unfolded protein chains, but not of the methylene resonances of the fatty acid lipid chains, which evidently remain essentially immobile. It thus seems that the disordering of the proteins and of the lipids are independent and unrelated processes. Glaser *et al.* infer that the proteins are directly associated with only the minor fraction of phospholipids that are not destroyed by phospholipase, and are distributed in self-contained packets in a lipid bilayer matrix.

POLIO VIRUS

All or Nothing

from our Cell Biology Correspondent

At first sight the RNA coliphages have much in common with polio virus and its relatives. Both the RNA phages and the RNA viruses have a single stranded RNA molecule for a genome which also doubles as a messenger RNA. Moreover, the phage RNA certainly, and the viral RNA most probably, specifies a replicase enzyme for its own replication. But there the similarities end; the way in which the phage and viral proteins are made could hardly be more different.

The phages specify three proteins, their coat, their replicase and a maturation protein. Polio virus, on the other hand, has enough genetic information to specify about ten proteins, four of which are in the capsid and a fifth is the replicase. On the face of things polio virus is far more sophisticated than the coliphages, but compared with them it makes its proteins in a curiously unregulated fashion.

Both *in vivo* and *in vitro* the coat protein gene of the RNA phages is translated more efficiently than the other two genes. Apparently the coat protein molecules act as repressors for translation of the replicase gene while the maturation protein gene is initiated with a base sequence for which *E. coli* ribosomes have a comparatively low affinity. The net result is the preferential synthesis of coat, which one imagines confers a selective advantage on the phage, which needs 180 coat molecules but only one maturation protein to encapsidate one RNA molecule.

By contrast the translation of polio virus RNA, as the work of Baltimore and his associates has shown, is a profligate affair. The results of experiments carried out during the past several years suggest that the whole genome is translated into a single polypeptide chain which is then cut up to yield the specific viral proteins. By using three amino-acid analogues, Jacobson, Asso and Baltimore (*J. Mol. Biol.*, **49**, 657; 1970) now claim to have isolated for the first time this mammoth polypeptide. It has a molecular weight in excess of 200,000 daltons and, in the uniquely cumbersome terminology polio workers have saddled themselves with, is labelled non-capsid viral protein –00 (NCVP–00). Apparently the amino-acid analogues prevent NCVP–00 from being cleaved as it usually is before its synthesis is complete; the largest nascent polypeptides recoverable from cells infected with polio virus in the absence of analogues have molecular weights of less than 130,000.

Drawing on their own earlier work and that of others, and by isolating the various cleavage products of NCVP–00 and making tryptic peptide maps to sort out their relationships, Jacobson *et al.* have proposed the following scheme for the origin of polio virus proteins. NCVP–00 is envisaged as the common precursor which, when cleaved, yields NCVP–1, NCVP–2 and NCVP–X. Only NCVP–1 provides the proteins found in the virus. It is split to yield viral proteins VP1 and 3 of the procapsid as well as VP–0. VP–0 is envisaged as the precursor of the two other viral proteins VP2 and VP–4 which are generated as the procapsid matures. NCVP–2 and NCVP–X are presumably the precursors of the viral proteins involved in RNA replication and the switching off of host metabolism.

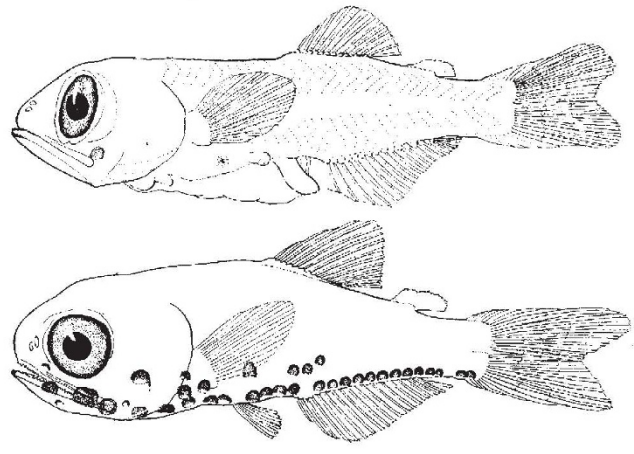
Apart from the problems of controlling the specificity of these cleavages the most surprising aspect of this process is that to make a coat protein polypeptide, polio virus apparently has to make all its other proteins. By comparison the RNA phages are models of cellular economy.

DEVELOPMENT

New Light on Lantern Fishes

from our Marine Vertebrates Correspondent

Lantern fishes, recently the subject of a valuable developmental study, are both abundant and widespread in the upper layers of the oceans, and therefore one of the primary forage foods for larger and commercially important oceanic fishes. In some cases densely shoaling species are fed on directly by tunas in the Pacific, and numerous lantern fish have been found in the food of the germon (*Thunnus alalunga*) in the Golfe du Gascogne.



Developmental stages of the lantern fish *Electrona rissoi*: upper, 9·2 mm larva; lower, 9·9 mm juvenile.

But the principal place of these myctophid fish in the feeding relationships of the ocean is at one remove, for they are preyed on by the smaller predators which are then eaten by the larger fish. They thus form a vital link in the food web of the seas. Lantern fishes are perhaps the most widely distributed family of fish in the world's oceans, represented by many species, which, in spite of some revisionary studies, are not fully understood. A recent important contribution to the better undertanding of the eastern Pacific species has