These features render it unlikely that the water–phosphate exchange is a result of reversal of the ATPase reaction. On the other hand, the exchange reaction, when inhibited by sodium, can be set going again by addition of ATP. This points to a phosphorylation step in the mechanism, and there is also evidence that ouabain operates by stabilizing an acyl phosphate intermediate of the enzyme.

The inferences are supported by the second study (Kanazawa and Boyer, *ibid.*, 3163), which concerns the calcium–magnesium ATPase of sarcoplasmic reticulum. This enzyme stimulates the same exchange of oxygen between water and phosphate in the absence of calcium, which is a strong inhibitor. Neither ouabain nor oxidative phosphorylation uncouplers affect the reaction. The turnover efficiency is greater than that of the calcium ATPase reaction by more than an order of magnitude. The calcium-dependence is strongly cooperative, and the inhibition can be reversed by chasing off the calcium with high magnesium concentrations. Exchange is inhibited by ATP and by ADP. Again, the exchange reaction can be linked to phosphorylation of the enzyme, for under the same conditions phosphorus from orthophosphate is incorporated into the protein. Calcium exerts a strongly cooperative control over this, as over the exchange reaction. These observations, it should be noted, pertain to sarcoplasmic reticulum vesicles. A monionic detergent, which leaves the ATPase activity unimpaired, stops both ion transport in the vesicles, and the oxygen exchange reaction, to which the process is evidently related.

On the basis of these results, Kanazawa and Boyer have constructed an active transport scheme, involving a conformational "pre-equilibrium" of the enzyme, with an allosteric response to calcium, for which the existence of two sites per molecule is surmised. In the state of high calcium affinity the enzyme is responsible for translocation of calcium ions. The other conformational isomer has a single magnesium site (because there is no cooperative response to magnesium), and does not bind calcium, and is responsible for moving magnesium ions across the membrane. The transport cycle contains phosphorylation and dephosphorylation steps, and the exchange of the oxygen can be accommodated in the scheme as a consequence of reversal of the reactions involving the uptake of phosphate in the presence of magnesium, and the covalent coupling of the phosphate group to a side chain, with elimination of water. The exchange reaction may thus prove to be the key to the model for active transport and related energy transduction processes, and the implications that Kanazawa and Boyer have found in it will now need to be digested by biochemists at large.

An at least superficially simpler system is the glucose transport machinery of red cells. This has served therefore as something of an archetype for pencil-and-paper models of active and passive transport. The directness of some observations and their interpretation by Edwards (*Biochim. biophys. Acta,* **307**, 415; 1973) on this system comes as an agreeable anodyne after the alarums and excursions of ion pumps. It is known that glucose transport is inactivated by exposure of the red cells to the amino group-specific reagent, fluorodinitrobenzene. What Edwards now finds is that the rate of inactivation, which must be a reflexion of the conformation or accessibility of the target protein, is modified by the presence of glucose, and differs by more than two-fold according to whether the glucose is inside or outside the cell. The regulation of the reaction is specific for glucose, and is not simply an osmotic phenomenon. The results are most easily explained in terms of two alternative states for the glucose receptors, which, Edwards suggests, may be the outward and inward-facing orientations of a carrier protein.

MARINE BIOLOGY

Fish Eggs and Larvae

from a Correspondent

A SYMPOSIUM on the early life history of fish, sponsored by a number of international organizations including FAO, ICES (the International Council for the Exploration of the Sea), SCOR (the Scientific Committee for Oceanic Research) and IABO (the International Association of Biological Oceanography) was held at the Dunstaffnage Marine Research Laboratory of the Scottish Marine Biological Association, Oban, Argyll, Scotland, from May 17 to 23.

The meeting generally accepted that high mortalities in the early stages are an important factor in determining the future brood strength and success of a year-class on recruitment to the subsequent fishery. From the results of plankton surveys on fish eggs an extensive mortality seems to occur in some species, like sole (J. D. Riley, Fisheries Laboratories, Lowestoft) and pilchard (A. J. Southward and N. Demir, Marine Laboratory, Plymouth), which cannot be explained by current systems carrying them out of the area, nor by predation. Indeed, in the case of buoyant eggs dead specimens are commonly found in the plankton hauls. It seems that in the developmental process there may be imperfections which could vary from year to year, which could be caused by maternal effects, and which could be enhanced by unfavourable environmental conditions. The extent to which eggs in delicate stages of development, for example before gastrulation, could be killed during capture has obviously been inadequately investigated and needs further study. After hatching, losses due to starvation and predation are heavy. Many larvae are extremely small and need food organisms of less than 10μ in size (B. R. de Mendiola, Institut del Mar, Lima). Attempts to quantify the nutritional status of larvae, and therefore their viability, have been attempted in the laboratory by using chemical and morphological techniques. There is some evidence that starving larvae, which are inactive and near neutral buoyancy, may be selectively sampled by plankton nets (J. H. S. Blaxter and K. F. Ehrlich, Dunstaffnage Laboratory). Predation has been studied experimentally and it is likely that unsuccessful strikes by predators may cause additional mortality because of the

φX174 Promoter Regions Isolated

By using bacterial restriction endonucleases to cleave viral DNA molecules into sets of fragments that can be ordered molecular virologists can now obtain physical maps of viral genomes. At the same time, by using ribosomes or DNA dependent RNA polymerase to protect respectively ribosome binding sites or polymerase binding sites from nuclease attack, it has proved possible to isolate these interesting regions of various nucleic acids and a few such fragments have been sequenced. In *Nature New Biology* next Wednesday (June 20) Chen, Hutchison and Edgell report how they have combined these two techniques to isolate and localize the promoter regions, or to be more precise the RNA polymerase binding sites, of coliphage ϕX174 DNA.

Having previously analysed and ordered the fragments produced by the digestion of double stranded replicative form ϕX174 DNA with three endonucleases, Chen and his colleagues assayed the extent to which these various fragments bind RNA polymerase. They also bound RNA polymerase to intact ϕX174 DNA, digested the DNA with pancreatic DNase and isolated the pieces of DNA protected by the polymerase. These fragments were then identified by hybridizing them to fragments of ϕX174 DNA obtained with restriction enzymes.

The results of these and other experiments indicate that the ϕX174 genome has three ribosome binding sites which may not be identical. No doubt Chen *et al.* will now begin to sequence these fragments which presumably code for the initiation of transcription.

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