"macrophage inhibition factor" secreted by T cells, which binds to local macrophages and there presents antigen to the B cells.

The general validity of the model of cell cooperation that emerged from the two meetings seems to be established and marks an advance in knowledge of the immune response which should influence the planning and the interpretation of experiments throughout immunology. There are some topics—the function of the thymus hormone and antibody formation in humans with immune deficiency states and in chickens after bursectomy or thymectomy—where the implications are so vital that it is a pity that there was no opportunity to discuss them.

ALGAE

Remarkable Membranes

from our Microbiology Correspondent

THE gas vacuoles of the blue-green alga *Microcystis aeruginosa* have been found to have limiting membranes composed entirely of protein, without the lipids usually expected in biological membranes. Gas vacuoles, which are found in the cells of many blue-green algae and some bacteria, seem to regulate the vertical distribution of these organisms in water. Their most remarkable feature now seems to be their limiting membrane, as Jones and Jost have found recently (*Arch. Mikrobiol.*, **70**, 43; 1970).

They lysed algal cells by treatment with penicillin and prepared and purified vacuoles by a combination of liquid polymer partitioning and molecular sieving on 'Sephacrose'. In this way the principal soluble and insoluble lysate components such as proteins, pigments, thylakoids and the polysaccharide α -granules were removed. Radioactive cross-contamination tests indicated that the final membrane was only 4 per cent contaminated by extraneous material. The membrane comprised a protein which had 52 per cent non-polar, 18 per cent basic and 10 per cent acidic amino-acids, from which imino and sulphur amino-acids were absent. Isoelectric focusing gave a value of 7 for the isoelectric point of the membrane protein, and its molecular weight was found to be about 14,000.

Membranes from gas vacuoles of *Halobacterium* are composed largely of protein, but allegedly contain nucleic acid and carbohydrate (Stoeckinius and Kunau, *J. Cell Biol.*, **38**, 337; 1968). Jones and Jost's findings, however, suggest that the non-protein components in the bacterial system are contaminants. Nevertheless amino-acid and density characteristics clearly distinguish the membrane protein of *Halobacterium* from that of *Microcystis*.

To complement the chemical data, Jost and Jones have made a structural analysis of the membrane of the gas vacuole of *Microcystis* (*Canad. J. Microbiol.*, **16**, 159; 1970). They found that the vacuole was $70 \times 350 \times 2.8$ nm in size, and composed of a single layer of subunits $2.8 \times 4.2 \times 3$ nm. Frozen-etched preparations show that the inner face of the vacuole has a ribbed appearance and that the ribs are made up from the protein subunits. Each turn of a rib is composed of about seventy subunits and the vacuole as a whole contains about 6,000 subunits. Measurements of folding angles in flattened vacuoles made it possible to determine a value of 25 nm for the distance between

subunits in the ribs.

Clearly the membranes of gas vacuoles are very different from other biological membranes in which interactions between lipids and proteins are thought to define the structural and physico-chemical properties. The "unit membrane" concept is not appropriate to the gas vacuole membrane in which interactions are between proteins and proteins. The molecular organization of the membranes of gas vacuole remains to be deciphered, but such protein membranes may be derived from covalent linking analogous to the bacterial peptidoglycan, or non-covalent interaction of the type proposed for virus particle construction. Further investigations of these prokaryotic organelles will certainly be watched with interest.

SYNTHETIC POLYPEPTIDES

Models for Models

from our Molecular Biology Correspondent

ALTHOUGH it is true that the analogy between synthetic polypeptides and proteins, hard pressed in its day, is now barely discernible, these versatile molecules retain a certain fascination, and have become a study in their own right. At the same time the experimental and theoretical treatment of conformational transitions has been based to a great extent on synthetic homopolymers: they have provided the whetstone on which the tools fashioned for the assault on the structure of real proteins are still being sharpened.

The calculation of stable conformations of polypeptide chains is an activity that has so far been judged almost wholly on the basis of its success in predicting the known characteristics of synthetic polypeptides in solution. An interesting example here is the series of esters of poly-L-aspartic acid. Most of these form right-handed α -helices, but others turn out left-handed. Scheraga and his colleagues (Yan *et al.*, *J. Amer. Chem. Soc.*, **92**, 1109; 1970) have performed calculations of the conformations of the three isomeric chlorobenzyl esters (*ortho*, *meta* and *para*) of poly-L-aspartic acid. Their report rouses the confident expectation of a dramatic result—that these polymers, chemically so similar, will differ conformationally—and of the ineluctable convergence of theory and experiment. And so indeed it turns out. In order to improve the physical basis of the calculations, Scheraga and his colleagues have recently introduced molecular orbital methods for determining energy functions. Minimization of energy involves varying all dihedral angles in the residue and calculating a series of energy contributions for each combination. Two large contributions in the aspartates come from the interaction of the amide with the side chain ester dipole, and with the carbon-chlorine bond dipole. In all cases the dipole-dipole interaction energy is lower in the left-handed than in the right-handed conformation, but whereas in the *ortho* and *meta* polychlorobenzylaspartates it dominates the total energy difference between the two states, in the *para* isomer it is insufficient to overcome a torsional energy favouring the right-handed helix. The calculation, it must be said, is delicately poised, the result being a small resultant of large positive and negative terms. Nevertheless, examination of the three isomers (Erenrich, Andreatta and Scheraga, *ibid.*, 1116) bears out the prediction: in four helix-forming solvents the *para*