

against—say—the United States, it will find itself preoccupied with more immediate and more local problems. In particular, the Chinese government is likely to find itself increasingly made militarily impotent in the immediate neighbourhood of mainland China by the lack of advanced conventional weapons. For one thing, this deficiency is likely to limit the extent to which the Chinese are able to think of using their new nuclear explosives even in the affairs of south-east Asia.

In other words, one of the immediate and somewhat paradoxical consequences of the speed with which nuclear explosives have been developed in China may well turn out to be a recognition that single-mindedness has created a lopsided military apparatus. Obviously it would be folly to hope that the Chinese will noticeably slacken their efforts on nuclear weapons for the sake of a more balanced programme, but the next few years are likely to bring some sharp reminders that the mere possession of nuclear weapons does not make up for a lack of conventional strength. China, like the other nations which have developed nuclear weapons for themselves, will soon begin to learn that nuclear explosives do not bring instant prowess.

What will happen after that? If it is reasonable to assume that Chinese nuclear weapons will be substantial by the middle seventies, it is natural to expect that the existing nuclear powers will be forced in some way to respond. The development and deployment of anti-ballistic missiles in the United States is one obvious possibility, although it is not immediately obvious why the kind of strategic balance which has developed between the Soviet Union and the United States should not also help to nullify the Chinese threat. Is it so entirely outrageous to look for some kind of dialogue between China and the other members of the nuclear club? In practice it is hard to think that the isolation of China from the rest of the world can persist unchanged for yet another decade. In the long run, and possibly in the immediate future as well, it may be more profitable for the rest of the world to respond to what is happening in China by talk rather than by the development of nullifying hardware.

MOLECULAR MODELS

A REALIZATION of the importance of molecular model building was a major factor in Pauling's determination of the α -helix of proteins and Watson and Crick's discovery of the structure of DNA. But model building—apart from providing a way of refining molecular structures which are being determined by X-ray crystallography and giving tangible representations of the final molecular structure—can by itself, in the right hands, provide a method for predicting the probable atomic structures of macromolecules which, for one reason or another, cannot be directly determined by X-ray diffraction. Such predictive model building is, however, fraught with pitfalls and only when it is

treated as a strict discipline can any reliance be placed on the results it yields. Of necessity, assumptions must replace data, and the validity of a model structure entirely depends on the validity of the principal assumptions; but a model must in addition bring together every scrap of relevant chemical and stereochemical data that is available, no matter how obtained, and synthesize it into a coherent whole.

The elucidation of a unique structure of a small but very interesting part of the transfer-RNA molecule, the anticodon loop, by Fuller and Hodgkin, which is reported on page 817, is a case in point. Crystallographic analyses of *t*RNA are impossible simply because, despite numerous efforts and some red herrings, it has so far proved impossible to crystallize the material. However, since Holley and his collaborators determined the nucleotide sequence of alanyl *t*RNA, the sequences of three other species of *t*RNA have revealed certain features common to the four molecules. Moreover, the structure of double helical RNA, that of reovirus, has been determined by X-ray diffraction, and the importance of the phenomena of base stacking in non-helical regions of nucleic acid molecules has been recognized. Fuller and Hodgkin have used these data and the accumulated information on bond lengths and angles in ribonucleotides and nucleotides to construct their model of the anticodon loop. By restricting their effort to this small region of the *t*RNA molecule, Fuller and Hodgkin have provided themselves with fixed points—the two free ends of the loop and a region of base-pairing. When the seven unpaired nucleotides that form the anticodon loop are arranged to maximize base stacking, taking into account all the known stereochemical constraints, there appears to be a unique structural solution for the four species of *t*RNA: five bases are stacked and two are in a less ordered configuration.

The model engenders confidence because of its stereochemical neatness and because it is based on two eminently reasonable assumptions—that there should be maximum base pairing and maximum base stacking. Moreover, any model must of course be reconcilable with the known biological functions of a molecule and the proposed structure of the anticodon loop is. It accommodates the genetic data on which Crick based his wobble hypothesis and it allows two *t*RNA molecules simultaneously to recognize adjacent codons of a messenger RNA molecule.

Obviously the structure of a molecule can never be proved by model building alone. Sometimes it may only show what structures are impossible, but may leave several alternative probabilities. When, however, a model accounts uniquely for all the known structural and functional properties of a molecule, it is probably substantially correct. It remains to be seen whether or not the model now proposed will stand when the nucleotide sequences of more species of *t*RNA have been determined. Meanwhile, model building may well be used to find the probable structure of another vital part of the *t*RNA molecule—the amino-acid recognition site.