both decrease the affinity of λ DNA for repressor and allow expression of only one of the two adjacent operons. The conclusion, of course, is that v_2 and v_3 are mutations in two separate operators each controlling independently one of the two operons adjacent to the immunity region by independently binding repressor. What the products of these two operons are and why they are essential for the functioning of the rest of the λ genome is still a mystery.

Apart from controlling the expression of the λ phage genome, the λ repressor directly prevents λ DNA replication. By superinfecting bacteria lysogenic for λ with one of the three λ virulent strains, λv_2 , λv_3 or $\lambda v_1 v_3$ and another λ strain, Ptashne and Hopkins have found that only the $\lambda v_1 v_3$ strain replicates in these conditions. Why do the v_1 and v_3 mutations in combination release the inhibition of DNA replication by the repressor? There seem to be two possible alternatives; either the v_1 mutation is not in the operators containing the v_2 or v_3 mutations but in a third site where DNA replication is initiated, or v_1 might be a second mutation in the operator already mutated at v_3 and this might still further decrease the affinity of this operator for the repressor and so allow even more of the right hand operon to be made. This operon might contain some as yet undetected gene the product of which is required in replication; at the moment the second alternative seems the most favoured.

MOLECULAR BIOLOGY

More Polynucleotide Interactions

from our Molecular Biology Correspondent

SOME weeks ago the new results of Bangerter and Chan on the binding of purine to polyuridylic acid (poly U) were published (see *Nature*, **219**, 679; 1968). The mechanism of interaction was shown by nuclear magnetic resonance to involve planar association of the heterocycles. The same authors have now made a further study (Bangerter and Chan, *Proc. US Nat. Acad. Sci.*, **60**, 1144; 1968), in which purine is replaced by adenosine, so that there is the additional possibility of base-pairing with the uridylic acid residues. When adenosine is introduced into a solution of poly U at high concentration, the uracil proton resonances shift upfield, indicating that the adenosine stacks onto the bases of the polymer. There is little change of the spectrum with temperature above about 20° C. Below this temperature, however, a striking broadening occurs, until at 4° C no lines are resolved. This may be taken to reflect the cooperative appearance of an ordered structure, and the inference is that this is a base-paired, rather than merely a stacked, complex. The downfield shift of the adenine (A) resonances, moreover, indicates that stacking of A upon A prevails in this complex, whereas, because the uracil (U) resonances are undisturbed, there is no appreciable stacking of A on U. (Stacking of U on U is not detectable by this method, because the ring-current anisotropy is too small.) The effect is strong in 1 : 2 complexes of A and poly U, whereas in 1 : 1 mixtures, only half the adenosine appears to be involved in the complex. It thus appears that at low temperatures a triple stranded complex is formed between poly U and monomeric adenosine.

These results are complemented by the work of Ts'o and his group, also just published. Ts'o and Huang (*Biochemistry*, **7**, 2954; 1968) have prepared complexes of poly U with adenine nucleotides—AMP, ATP and their deoxy-analogues. The presence of magnesium is a necessary condition for association, for charge repulsion between the phosphates would otherwise evidently be too great for stability of the complexes. In these circumstances, and at low temperatures, a precipitate is formed. The stoichiometry is again 1A : 2U. On warming, the complex breaks down in strongly cooperative fashion, at a temperature which depends on the concentration of magnesium, and a sharp pH-induced transition can also be observed. In the corresponding system of polycytidylic acid (poly C) and guanosine phosphates, 1 : 1 complexes usually seem to be formed (though one 2 : 1 complex is reported). At appreciable concentrations of magnesium ions, poly U and poly A have long been known to form three-stranded complexes, whereas the poly G + poly C system is always two-stranded.

In their second article, Ts'o and Schweizer (*Biochemistry*, **7**, 2963; 1968) have examined the nuclear magnetic resonance spectra of the same mixtures in solution to confirm that soluble complexes with nucleotides do not form. With adenosine, in the absence of magnesium ions, at 28° C the nuclear magnetic resonance spectra of mixtures are the sum of their constituent parts, indicating the absence of complex formation. (Although Bangerter and Chan did observe association of these components, their concentrations were usually higher.) When magnesium is added, there is broadening of both adenine and uracil resonances. It is interesting that when the magnesium (0.033 M) is replaced by a high concentration (0.82 M) of sodium ions, the broadening of the uracil resonance is diminished but that of the adenosine is increased. Thus although the extent of the association is reduced, relatively more adenosine is bound. This is consistent with a change in stoichiometry towards a 1 : 1 complex. (Thus between these results and those of Bangerter and Chan, a pseudo-phase diagram could be compiled, to relate the stability of 1 : 1 and 2 : 1 complexes to concentrations of sodium and magnesium ions and temperature.) With adenine nucleotides (as in the mixtures of poly C and guanine nucleotide) the spectrum is throughout the sum of its parts, down to the temperature at which precipitation occurs. This confirms, as expected, that the formation of hydrogen-bonded complexes is cooperative and perforce involves a phase separation.

PROTEIN CHEMISTRY

Homologous Protein Molecules

from a Correspondent

THE Biochemical Society has included two colloquia on protein chemistry at recent meetings. In Aberdeen two weeks ago the term "homologous proteins" took on a special significance. As Professor A. Neuberger, the chairman, pointed out, "homologous proteins" should be reserved for proteins with a common ancestral gene. In practice, a common ancestry is usually inferred only for proteins the functions of which are sufficiently alike to warrant their comparison