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General Discussion

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General discussion

After discussion from the floor on the mechanism for determining the length of the tail of the T-even bacteriophage, the Chairman E. KELLENBERGER (*Basel*) gave the following summing up:

The following three mechanisms have been proposed. For none of them does any solid, experimental evidence yet exist. For the sake of simplicity I discuss here only length determination of tubular structures. It is obvious that all three mechanisms are also applicable to size determinations in supramolecular structures of other forms (see discussion in Kellenberger 1969).

(1) *The 'template'-model*

The length would be determined by a gene product which is folded into a fibrous protein molecule, comparable, for example, to the triple helix of collagen. The gene length determines therefore the fibre length; the requirements for phage tails are compatible with what is known about the size of genes. I could not track the origin of this proposal, which probably arose simultaneously in several places; it was put forward particularly by J. King for the determination of the length of phage tails. I proposed it as part of prehead cores for determining the position of vertices of larger viruses, particularly of those of which the 'pentamer' is chemically distinct from the 'hexamers', for example, in Adeno virus.

(2) *The 'vernier'-model*

This was published by Anderson & Stephens (1964). It assumes a double-layered, concentric hollow cylinder. The layers would have a different subunit-repeat distance, and the two layers would interact to some degree with each other. Linear growth of this double cylinder would stop as soon as both layers are level, that is, when the two repeats happen to be in register.

(3) *The 'cumulated strain'-model*

This was proposed in a primitive (Kellenberger 1969) and in a more sophisticated form (Kellenberger 1972). It assumes only one type of protomer (repeat unit). At present, after taking into account many other, new observations and discussions with colleagues it has evolved to become rather a 'length determination by *cumulated conformational changes*'; its main feature is, that – once the correct length has been reached – cooperative conformational adjustments of each protomer lead to a stable, minimum energy state. Basically we consider the entire quarternary structure as a sort of single protein in the sense that hydrophobic residues have to be preferentially inside and hydrophilic ones outside. The contact areas between subunits are assumed to involve the same weak interactions as those inside a protein. We assume the individual protomer in solution to have a relatively high amount of hydrophobic residues on the surface; after polymerization the polypeptide chains of all subunits would slightly rearrange so as to minimize the number of hydrophobic residues facing the aqueous outside medium. The hydrophobic residues would form a continuous hydrophobic core throughout the polymer. The nature of interactions in the contact areas would be indistinguishable from

that of the interactions within the subunit. There is no reason to assume that two interacting polypeptide segments do know whether they belong to two different proteins or only to one! Once the minimum energy state is reached, addition of further subunits would stop because of a lack of interaction sites. This model is not entirely unrealistic: indeed it is now generally accepted that tertiary structure is the result of both primary structure and environment. When surrounded by organic solvants or lipids, the tertiary structure of a protein is different from that in an aqueous medium. Hence, in a polymer the contact area has to be considered as a part of the environment. Not only the suspension medium (aqueous salt solutions, lipids, organic solvants) but also the contact areas with neighbours must be taken into account as environmental determinants of the tertiary structure of each protomer within a polymer.

The model is not readily amenable to theoretical calculations, particularly because the assembly process itself cannot be considered in the way of a chemical equilibrium. Only the final product could possibly be amenable to some thermodynamic considerations, by the same methods as one could use to treat the dependence of the tertiary structure of a soluble protein on the surrounding liquid medium.

References

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