Optical-rotatory-dispersion studies on polygalacturonic acid in the visible and near-ultraviolet region of the spectrum indicated a simple plain positive dispersion, which could be fitted to a single-term Drude equation. The Drude constant λ_c obtained from this treatment was found to be dependent on the pH of the polymer solution, and yielded a titration curve similar to that obtained for the metachromic effect. Stone (1965) observed the first peaks of the Cotton effects of heparin and chondroitin sulphate in the far ultraviolet region of the spectrum, and studies with polygalacturonic acid in this region showed the first peak of a positive Cotton effect at about $208m\mu$ at pH 6.5. The position of this Cotton effect appears to be sensitive to pH.

Viscosity measurements on solutions of polygalacturonic acid at neutral pH values and under Newtonian flow indicated that the apparent axial ratio of the molecule varies with dilution. At concentrations greater than 6 g./l. the axial ratio (assuming 30% hydration) was approx. 20 and this value increased with dilution, reaching a value of over 50 at concentrations lower than 1 g./l. This behaviour is inconsistent with a stiff rod-like shape for the molecule at this pH. The specific viscosity showed a marked dependence on pH in the vicinity of the pK indicated by the above studies; similar results have been reported by Schultz, Lotzkar, Owens & Maclay (1945).

These results are interpreted as indicating that there is a pH-dependent transition in the conformation of polygalacturonic acid, associated with the ionization of the carboxyl groups.

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The Use of Hinged Movements in Biological Masking/Unmasking Processes

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The masking and unmasking of genetic control sites and of transmembrane transport control sites have generally been discussed in terms of association/dissociation reactions, which involve respectively the attachment and complete removal of the partnering molecule. Such formulations can involve difficulty in allowance for specificity of attachment and sequence of removal required in various repetitive biological processes. We therefore reconsidered the above processes in terms of hinged movements which allow for the relevant difficulties and also enable faster rates of reaction. The

proposed hinge can be formed from an electrostatic bond to which the respective partnering molecules donate oppositely charged groups.

Using correctly proportioned molecular models, we found such systems to be stereochemically and energetically permissible. The systems are feasible in histone-DNA interaction (Lewin, 1968), which involve masking and unmasking of genetically potential sites on DNA (for references see Busch, 1965, and de Reuck & Knight, 1966), and in phospholipid-protein interaction concerned in transmembrane transport. In the former, the electrostatic hinge can be formed from the positively charged groups of lysine or arginine (situated at an edge of a histone molecule) and the negatively charged phosphate groups lining the wide groove of the double helix of DNA; in the latter, the hinge can be formed from the negatively charged phospho groups of the lipid and the positively charged nitrogenous groups of the protein.

The masking is effected by association of the areas of the respective macromolecules by forces much weaker than those of the electrostatic hinge. In the histone-DNA association, this is achieved by $H\cdots$ donation from the overall positively charged histone $H\cdots$ donor groups to the $H\cdots$ acceptor electron lone pairs of the groups of DNA (e.g. the amino groups of cytosine and adenine in the wide groove of the double helix; Lewin, 1967a,b,c). In the phospholipid-protein association the masking is effected by interaction between the hydrophobic groups of the respective macromolecules.

In the histone-DNA association, unmasking can be achieved by the attachment of the highly negatively charged groups of nucleotide diphosphates or triphosphates to the masking histone whose overall positive charge, and respective $H\cdots$ donation, are thereby minimized.

In the case of the phospholipid-protein association, the unmasking can follow the attachment of a third molecule with a higher hydrophobic potential as a result of which original hydrophobic associations are disrupted.

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