electrophoresis in 6M-urea and 15mM-mercapto-ethanol in tris-glycine buffer, pH8.5, tropomyosin from rabbit white skeletal muscle free of the '37000 component' of the troponin complex (Wilkinson *et al.*, 1971) separated into two bands of similar mobility. This pattern was observed on electrophoresis in 6M-urea and in sodium dodecyl sulphate in the presence of thiol compounds and after carboxymethylation. The faster of the two components was estimated to be present in four times the amount of the slower, which, as judged by its radioactivity after carboxymethylation with iodo[¹⁴C]acetate, contained half as much cysteine as the more negatively charged component.

Similar two-band patterns were also persistently observed on the electrophoresis of tropomyosin isolated from white skeletal muscle of the cow, sheep and pig. Tropomyosins isolated from rabbit heart and the adductor muscle of *Pecten maximus* migrated as one band only. These findings suggest that tropomyosin preparations may vary according to the type of muscle from which they are isolated. The observation that all tropomyosin preparations possessed both biological activities described above implies that they are associated with one, if not both, of the components observed. The consistent presence of two subunits of different charge and molecular weight (cf. Weber & Osborn, 1960; Sender, 1971; Bodwell, 1967) may explain the primary sequence data of Smillie *et al.* (1971), which imply that rabbit skeletal-muscle tropomyosin may exhibit polymorphism.

Bodwell, C. E. (1967) *Arch. Biochem. Biophys.* **122**, 246-261

Ebashi, S. E. & Kodama, A. (1966) *J. Biochem. (Tokyo)* **60**, 733-734

Hodges, R. S. & Smillie, L. B. (1970) *Biochem. Biophys. Res. Commun.* **41**, 987-994

Schaub, M. C. & Perry, S. V. (1969) *Biochem. J.* **115**, 993-1004

Schaub, M. C., Perry, S. V. & Hartshorne, D. J. (1967) *Biochem. J.* **104**, 263-269

Sender, P. M. (1971) *FEBS Lett.* **17**, 106-109

Weber, K. & Osborn, M. (1969) *J. Biol. Chem.* **244**, 4406-4412

Wilkinson, J. M., Perry, S. V., Cole, H. & Trayer, I. P. (1971) *Biochem. J.* **124**, 55P-56P

Quaternary Structure of Oligomers with Dihedral Symmetry

By E. J. MILNER-WHITE (*Department of Biochemistry, University of Glasgow, Glasgow G12 8QQ, U.K.*)

Oligomeric proteins with dihedral symmetry are very common in biological systems. This communication presents formulae for describing all the types of 'perfect' geometrical structures that are theoretically possible for such proteins. The formulae

hold for component protomers of any shape. The approach and terminology of Milner-White (1971) is used. First, the angles θ , ϵ and ζ must be defined.

A point is taken as the 'centre' of the protomer. Any fixed point in a known protomer may be used. Two angles are necessary to describe the geometry of a single site-pair: θ and ϕ . θ is the angle between the centres of three adjacent protomers linked by that site-pair. ϕ need not be defined since for oligomers it is 0°, because the angles of θ in adjacent protomers always lie in the same plane.

Two types of angle are necessary to describe the relationships between two different site-pairs (A and B) on one protomer: ϵ and ζ . ϵ is the angle formed between the lines that bisect the angles θ_A and θ_B . ζ_A is the angle formed by the clockwise rotation (as seen from the outside of the protomer) of the plane of the angle θ_A with respect to the plane of the angle ϵ , measured in a plane perpendicular to the line bisecting ϕ_A . ζ_B is defined similarly. When θ is 0° (the isologous case) its plane is taken as that perpendicular to the dyad axis. Finally the ratio of the distance between the centres joined by site-pair A to the between the centres joined by site-pair B is defined as q .

Three types of site-pairs are theoretically possible in oligomers with dihedral symmetry. Two must be isologous and one heterologous (see Hanson, 1966), except for tetramers in which all are isologous. Any two of these site-pairs are, however, sufficient for a stable structure. Since heterologous binding is apparently rare among proteins (see also Monod *et al.*, 1965) it was suggested (Milner-White, 1971) that the structure with two isologous site-pairs may be the preferred mode of binding in dihedral oligomers. For n -mers of this type (which may in some cases be knotted):

$$\sin^2 \left(\frac{360}{n} \right) \cdot (q^2 - 1) = \sin^2 \epsilon \cdot (q^2 \cdot \sin^2 \zeta_A - \sin^2 \zeta_B)$$

$$\sin^2 \left(\frac{360}{n} \right) \cdot (q^2 + 1 - 2q \cdot \cos \epsilon) = \sin^2 \epsilon \cdot$$

$$\left[q^2 \cdot \sin^2 \zeta_A + \sin^2 \zeta_B \pm 2q \cdot \sin \zeta_A \cdot \sin \zeta_B \cdot \cos \left(\frac{360}{n} \right) \right]$$

For the case with one isologous and one heterologous (A) site-pair the relationships are:

$$\sin^2 \zeta_A \cdot \sin^2 \epsilon = 1 - \frac{q \cdot \cos \epsilon}{\sin \left(\frac{360}{n} \right)}$$

$$\sin^2 \zeta_B \cdot \sin^2 \epsilon = 1 - \frac{1}{q} \cdot \cos \epsilon \cdot \sin \left(\frac{360}{n} \right)$$

Hanson, K. R. (1966) *J. Mol. Biol.* **22**, 405-409

Milner-White, E. J. (1971) *Biochem. J.* **124**, 78P-79P

Monod, J., Wyman, J. & Changeux, J.-P. (1965) *J. Mol. Biol.* **12**, 88-118