semi-permeable membrane. The reconstructed fibres contract on addition of ATP, but their fragility makes tension measurements very difficult.

We have now found that a similar reconstruction can be achieved for frog skeletal muscle. This system has certain distinct advantages, in that though the membrane is swollen and presumably perforated during incubation in potassium phosphate solution (many soluble proteins escape), the solubilized myosin is almost entirely retained within the tissue. Further, if the muscle is incubated in Ringer solution for an extended period (at least 10× that required for reconstruction), the excitability of the membrane is restored. Tension measurement can thus be made.

We feel that the reconstruction of the A-band is particularly accurate in frog muscle, with very exact definition of the filament length, 'missing cross-bridge' near the tip, and of the M-line region. Tension measurements show that least 90% of the tension generated by a matched control can be regained. We believe that these findings confirm that the A-band region and filaments are capable of self-assembly, and also confirm the importance of high local myosin concentration in achieving this phenomenon. A remarkable self re-annealing property of the sarcolemma is also apparent.

The conformation of C-protein in solution: use of new hydrodynamic shape functions

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We have re-examined solution data for C-protein [Offer *et al.*, *J. molec. Biol.* **74**, 653–76 (1973)] using relatively new hydrodynamic formulations in terms of the widely used ellipsoid of revolution models. Offer *et al.* had proposed a prolate ellipsoidal model of axial ratio (a/b) ~ 10:1 based on intrinsic viscosity $[\eta]$ data. Uncertainty in this model has remained because this data had been interpreted only after *assuming* a value for the hydration. In addition, an oblate model was apparently not considered, although we can now justify this latter assumption. Using their values for $[\eta]$ and the sedimentation regression coefficient, k_s (13.6 ml g^{-1} and 11 ml g^{-1} respectively) the sensitive and volume-independent R function [Rowe, *Biopolymers* **16**, 2575–611 (1977)] $\equiv k_s/[\eta] = 0.81$. However, re-examination of their Fig. 4 suggests that $k_s = 10.2$ ml g^{-1} and after correction for solution density (Rowe, 1977) and radial dilution $k_s = 10.7$ ml g^{-1}. R is therefore = 0.79, corresponding to an a/b of 8.0:1 for a prolate model. A (prolate) *model-dependent* estimate for the swollen specific volume v_s of 1.3 ml g^{-1} can then be obtained from the relation $v_s = [\eta]/\nu$ where ν is the viscosity increment, and since $\bar{v} = 0.739$ ml g^{-1} the 'swelling' $v_s/\bar{v} \sim 1.8$. A *model-independent* estimate is available from the ratio k_η/k_s, (Rowe, 1977) where k_η is the viscosity regression coefficient: from Fig. 6 of Offer *et al.*, $k_\eta = 17.7$ ml g^{-1} and hence $v_s/\bar{v} \sim 1.7$. The prolate model originally proposed by Offer *et al.* therefore appears reasonable: an oblate model would only be compatible with the R value if a/b > 50:1, but this corresponds to a model-dependent estimate for $v_s/\bar{v}$ of ≤ 0.5. We are employing the recently described function Π [Harding, *Int. J. Biol. Macromol.* **3**, 340 (1981)] to test this conclusion further.

CELL MOTILITY

Platelet-derived growth factor induces reorganization of actin in glia-like cells

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Platelet-derived growth factor is a mitogen for several cell types in culture. It binds to specific cell surface receptors [Heldin *et al.*, *Proc. natn. Acad. Sci., U.S.A.* **78**, 3664–8 (1981); Glenn *et al.*, *J. biol. Chem* **257**, 5172–6 (1982); Huang *et al.*, *J. biol. Chem.* **257**, 8130–6 (1982)] and induces phosphorylation of several membrane associated proteins [Ek *et al.*, *Nature, Lond.* **295**, 419–20 (1982); Nishimura *et al.*, *Proc. natn. Acad. Sci., U.S.A.*, in press]. We have documented by phase contrast microscopy that PDGF also induces an intensive motile activity in serum-starved cells. Within minutes after addition of PDGF large numbers of small ruffles form on the surface of the cells. Thin lamellae grow out almost all around the cell circumference. Later, small ruffles in circular arrangements appear in different regions of the cells. These rings of ruffles vary in size. Some encircle almost the whole cell. We studied the organization of actin by indirect immunofluorescence using DNAse I and by transmission electron microscopy of detergent-treated negatively stained cells. The ultrastructure of the thin lamellae is similar to that of the lamellae in the advancing edge of normally growing cells [Höglund *et al.*, *J. Musc. Res. Cell Motility* **1**, 127–46 (1980)]. In the regions surrounded by circu-