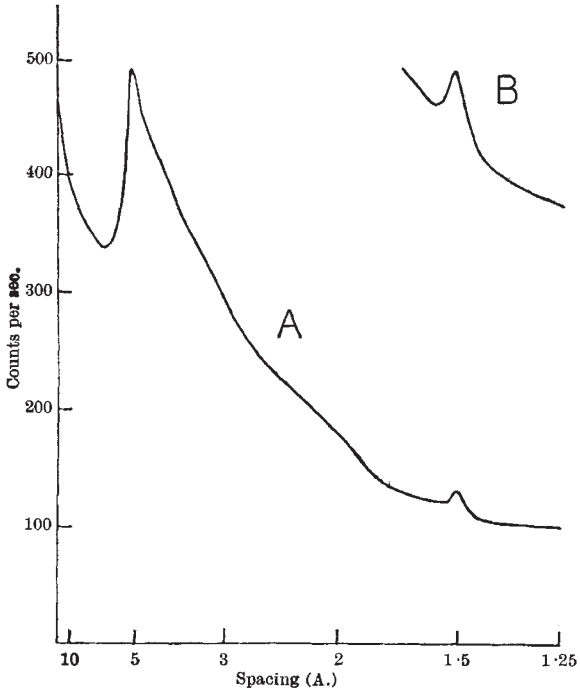

Fig. 2. Geiger counter spectrometer record of horse hair rotated about a normal to the fibre axis. (*A*) Bragg angle for 0*k*0 planes $2\theta = 7°–75°$, taken with reduced aperture of beam. (*B*) Repeat of $2\theta = 55°–75°$ with full aperture of beam

priate Bragg angle revealed no trace of such a reflexion, which shows that the structure proposed by Pauling and Corey must be wrong.

The three-dimensional Patterson synthesis of horse methæmoglobin shows rod-like concentrations of high vector density parallel to the crystallographic *X*-axis[11]. My interpretation of that synthesis led me to the conclusion that the hæmoglobin molecule consists of a compact bundle of close-packed chains running parallel to the *X*-axis and having the α-keratin configuration. The X-ray diffraction pattern of hæmoglobin fades out at a spacing of about 2 A., and no diffraction pattern at smaller spacings had hitherto been observed. Taking the *X*-axis as a possible chain axis, a search was made for reflexions in the 1·5-A. region by taking a 5° oscillation photograph in the appropriate orientation of the crystal. A picture was obtained in which the bulk of the reflexions fade out at a spacing of 2 A. as usual, but protruding from this is a faint bulge with a distinct maximum of intensity at 1·50 A. A preliminary search has not revealed any such effect in other crystallographic directions.

The three-dimensional Patterson synthesis of hæmoglobin shows neighbouring chains to be 10·5 A. apart and arranged in cylindrical close-packing. Taking the density of the protein as 1·30 and the mean residue weight as 112·5 [11], the number of residues in a 'sub-cell', $10·5 \times 10·5 \times 1·5 \times \sin 60° = 143$ A.^{3}, can be calculated:

$$\frac{143 \times 1·3 \times N}{112·5} = 1·00 \text{ residue},$$

which is the number to be expected for the 3·7 residue helix. These results add to the evidence in favour of the hæmoglobin structure proposed by me[11] and indicate that the chains are coiled to form 3·7 residue helices in poly-γ-benzyl-L-glutamate, in α-keratin and in hæmoglobin.

The discovery of the 1·5-A. reflexion shows that even relatively disordered substances like hair may contain an atomic pattern of such high intrinsic regularity that it gives rise to X-ray diffraction effects at spacings where they had never before been suspected.

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Polypeptide Chains in Frog Sartorius Muscle

Oscillation photographs of dried frog sartorius muscle were taken about a direction normal to the fibre axis using a 3-cm. cylindrical camera and copper radiation. The specimens included muscle dried in the stretched, relaxed and contracted state (contraction by electrical stimulus). All photographs show the 1·5-A. reflexion from planes normal to the fibre axis, as described in the preceding communication. The reflexion is most intense on photographs of stretched muscle, slightly weaker on pictures of relaxed muscle, and very faint on photographs of contracted muscle. Thus both stretched and relaxed muscle seem to contain polypeptide chains coiled in the 3·7 residue helix and running parallel to the fibre axis. It is too early to say whether the weakening of the 1·5-A. reflexion on contraction is due to a change in chain configuration or to the disorientation of larger units. In any event, clear evidence on the mechanism of contraction cannot be expected unless X-ray photographs are taken during an actual twitch. In addition to the 1·5-A. reflexion, which can be recognized as an 0*k*0 reflexion by its small angular spread, the photographs also show a wide arc at 2·9–3·0 A. which is about as intense as the 5·1-A. reflexion. This arc is strongest in stretched and weakest in contracted muscle, and was also observed in oscillation photographs of hair.

Our results are incompatible with the mechanism of muscle contraction proposed by Pauling and Corey[1], who suggest that the chains in extended muscle are almost fully stretched, and that they coil up to form 3·7 residue helixes on contraction. On the other hand, our findings are in accord with those of Astbury and Dickinson[2], who showed both extended and relaxed muscle to have the α-keratin structure which becomes disorientated on contraction.

We are grateful to the Medical Research Council for financing the work described above.

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