by g.l.c. to contain glucosamine, galactosamine, galactose, glucose and sialic acid. Glycoproteins and enzymes were released from brush-border preparations by treatment with an equal volume of ice-cold butanol. In the soluble fraction invertase was obtained in 80% yield with a fourfold increase in the specific activity. Hydrolysis and g.l.c. showed the presence of bound galactosamine and glucose in these macromolecular components. The biosynthesis of the above brush-border components was examined after pre-injection of rabbits with D-[1-¹⁴C]glucosamine (20 μ Ci/1½ kg animal) 3 h before isolation of the brush borders. The glycoprotein components of isolated brush border appear to become labelled considerably faster than the glycolipids.

The very marked difference in the rates of labelling of the glycoprotein and glycolipid components of the brush border suggests that separate biosynthetic pathways may operate. The results are consistent with the view of a rapid continuous biosynthesis of the glycoproteins and a relatively low rate of turnover of the glycolipids that is possibly more closely related to the rate of cellular renewal.

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The Cyanogen Bromide Fragments of Rabbit Skeletal-Muscle Tropomyosin

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A repeating pattern of hydrophobic residues in tropomyosin has been predicted to account for its 'coiled-coil' structure (Crick, 1953; Cohen & Holmes, 1963). The presence of at least two non-identical chains in tropomyosin has been indicated by the results of polyacrylamide-gel electrophoresis in concentrated urea and in sodium dodecyl sulphate (Weber & Osborn, 1969; Sender, 1971; Cummins & Perry, 1972). Similarly, a larger number of unique cysteine-containing sequences than would be predicted from the cysteine content of the protein has been demonstrated (Hodges & Smillie, 1970, 1972a). However, the numbers of unique methionine-containing and histidine-containing sequences are

consistent with a high degree of similarity in the amino acid sequences of these chains (Hodges & Smillie, 1970, 1972b). Fragments derived from CNBr treatment of the S-carboxymethylated protein were separated into small and large components by gel filtration on Sephadex G-50. Sequence analysis of the smaller fragments, combined with previous information (Hodges & Smillie, 1972b), has increased the number of unique methionine-containing sequences to a minimum of seven, a result still consistent with very similar polypeptide chains. From the mixture of the larger CNBr fragments a component was isolated by ion-exchange chromatography on QAE-(quaternary amino ethyl) Sephadex in 8M-urea at pH 7.5. In aqueous buffers it had a molecular weight of 35000 and circular dichroism indicated an α -helical content of about 60%. In 8M-urea the molecular weight was decreased to 17000. Since it contained both histidine residues of the intact protein, one of which is known to be near the C-terminus (Hodges & Smillie, 1972b), it was derived from the C-terminal half of the molecule. Chymotryptic digestion of this fragment and sequence analysis of the resulting peptides have produced an extended sequence (33 residues) about the two homologous cysteine residues previously described (Hodges & Smillie, 1972a). In this sequence nine positions with single amino acid substitutions and one position with three substitutions were observed, indicating a minimum of four different polypeptide chains in our tropomyosin preparation. No simple pattern of repeating hydrophobic residues was evident. The complete primary structure of this CNBr fragment will hopefully provide information on the relationship between the unique structural features of this protein and its amino acid sequence.

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