present in the earliest, Cretaceous, marsupials.

The only marsupial known from Europe, early Eocene *Peratherium*, is also known from North America, but the migration route of this genus is still unknown. The complete absence of fossil marsupials from continental Asia makes it difficult to estimate the migration route of the Australian marsupials, but these may have been already established and differentiated there by the Oligocene. Clemens believes that comparison of the dentitions of the oldest known Australian marsupials with those of the North American late Cretaceous forms shows that the Australian types could have been derived from a didelphid type similar to *Alphadon*.

PROTEIN STRUCTURE

Similarities between Distinct Species

from our Molecular Biology Correspondent

LAST year proinsulin, the precursor of porcine insulin, was isolated and shown to consist of a single polypeptide chain. Insulin is formed when a section of this chain is excised, the two residual chains being linked by disulphide bonds. The sequence of porcine proinsulin was reported recently by Chance, Ellis and Bromer.

One of the many interesting questions arising out of this work is the extent to which the structure and characteristic properties of insulin are reflected in the precursor molecule, and a study of the physical properties of the proinsulin by Frank and Veros (*Biochem. Biophys. Res. Commun.*, **32**, 155; 1968) is the first evidence of work along these lines. In the first place, sedimentation equilibrium studies at pH 2 are reported to give evidence of strong association, just as in insulin. Few details are given, but the lower limit of molecular weight seems to be about 9,000, which corresponds to the monomer, whereas the high value is 18,600. The authors state that their data can be explained by an equilibrium involving monomer, dimer and tetramer, as can be the association of insulin, and that the apparent equilibrium constants for the self-association of the two proteins are comparable. This leads to the reasonable postulate that the mode of association is the same in the two cases, and that

the conformation is therefore most probably conserved. Optical rotatory dispersion and circular dichroism indicate that the fraction of α -helical structure is less in proinsulin, but that the total number of helical residues in the two proteins (molecular weights 9,100 and 6,000) is essentially the same. The suggestion, then, is that the extra length of 33 residues in the porcine proinsulin is non-helical, and this is supported by the presence in this segment of three proline and seven glycine residues. Frank and Veros also quote unpublished data by Chance on the sequence of bovine proinsulin. The corresponding part of the chain—that lost on conversion to insulin—consists of 30 residues, four of them proline and eight glycine. The likelihood that this segment is non-helical thus also applies to this species.

The work of Harris and Perham (*Nature*, **219**, 1025; 1968) on the enzyme glyceraldehyde 3-phosphate dehydrogenase affords an interesting example of similarities of sequence and structure between corresponding proteins from different species. Following their work on the lobster muscle enzyme, they have now sequenced the porcine protein and find a degree of homology which is remarkable for two such distantly related species: 72 per cent of the 332 residues (or 333 in the lobster protein) are identical, and the great majority of the substitutions are conservative (polar for polar and non-polar for non-polar residues). The substitution of valine for isoleucine occurs twelve times. There is one insertion in the porcine protein, and two extra residues at the C-terminus in the other. The degree of homology is very much greater than in the haemoglobins and in the cytochrome *cs*. Another striking aspect of this enzyme is that although it is tetrameric in its native state, with each chain binding one molecule of the cofactor NAD, all four chains are identical. This is the first time that such an identity has been unequivocally demonstrated. Co-operative function in glyceraldehyde 3-phosphate dehydrogenase has been reported (though not so far in the porcine and lobster enzymes), and the principle that a protein made up of identical subunits can show such effects is of considerable interest. Harris and Perham refer to incomplete sequence data on three further species (rabbit, ox and yeast), which also give evidence of extensive conservation of sequence and therefore presumably of conformation as well.

Memorandum to the Select Committee on Science and Technology

by
P. M. S. BLACKETT

When the Select Committee on Science and Technology was discussing the organization of defence research, Professor Blackett, President of the Royal Society, suggested that industry could profitably take a greater part in research and development.

I WANT to make it clear that the views I express are my own personal views and commit no one else.

At the outset, I want to remind you of some things which you certainly know already. Britain has the highest

research and development (R and D) expenditure of any country in Europe; in fact, nearly £1,000 million per annum, or nearly 3 per cent of the gross national product (GNP). But she also has, and has had for at least a decade or more,