the yield in every coupling step 100 per cent? A negative reply to the first question shows the reliability of the method, but on the second count the technique falls short of perfection (Bayer *et al.*, *J. Amer. Chem. Soc.*, **92**, 1735, 1738; 1970).

The first question was answered using precision gas chromatography. Derivatives of enantiomeric amino-acids can be resolved on columns with an optically active stationary phase. The amino-acids produced by acid hydrolyses of both synthetic L-peptides and natural bovine albumin were found to contain about 1 per cent of D-enantiomer and so it seems that solid phase synthesis of peptides proceeds without racemization, though hydrolysis does not.

Incomplete coupling can have two consequences. When the reacting end of the growing peptide chain becomes inert during synthesis, truncated sequences are produced; these are readily separated from the desired product by virtue of their different size. When, however, a truncated sequence recovers normal activity and is further elongated after missing a few synthetic steps, the protein produced is similar to the required product in size and homology but has a small deletion. Such failure sequences may be inseparable from the true product. If the efficiency of coupling is 99 per cent then calculation shows that a ribonuclease synthesis would give 29 per cent of pure enzyme together with 36 per cent of proteins containing one amino-acid less.

A delicate probe for such failure sequences is the analysis of synthetic peptides which consist of alternating copolymers of composition $(A–B)_n$. Failure sequences will give dipeptides containing *A–A* and *B–B* on partial hydrolysis while truncated and normal sequences will provide *A–B* and *B–A* only, easily resolved by gas chromatography and mass spectrometry.

Less than 10 per cent of failure sequences were detected in synthetic dodecapeptides containing Phe, Leu and Ala, which indicates that the coupling efficiency exceeds 99 per cent. But results for Arg, Hys and Lys are less satisfactory and call for an improved solid phase technology.

TUMOUR VIRUS

Much in Common

from our Cell Biology Correspondent

SIMILARITIES between the lysogenic bacteriophages and the small DNA tumour viruses, SV40 and polyoma, are becoming more obvious with the improvement of techniques for manipulating tumour viruses and their host cells. The stable transformation of mammalian cells by SV40 and polyoma, for example, seems to involve the permanent association of the viral genome with one or more host chromosomes, just as the lysogenization of *E. coli* by phage results from integration of the viral genome into the bacterial chromosome. Double lysogens, bacteria lysogenized by two different phages or two mutants of the same phage, have long been recognized and exploited. They were used, for example, by Thomas and his colleagues to show the existence of the Ter enzyme system which chops concatamers off λDNA during the vegetative replication of λ phage. As a result, the isolation of double viral lysogens, mouse cells transformed with two plaque morphology mutants of SV40, reported by Dubbs and Kit (*Proc. US Nat. Acad. Sci.*, **65**, 536; 1970), comes as no great surprise.

Inevitably, proving that SV40 can give rise to double lysogens is a far more tedious and less clear cut business than showing the double lysogenization of *E. coli*. For one thing, only SV40 plaque morphology mutants, which are less satisfactory than defined biochemical mutants, are available; and for another, SV40 cannot be rescued from cells which it has transformed simply by exposing the cells to ultraviolet light. Instead, the transformants have to be fused with cells permissive for the SV40 lytic cycle. Furthermore, there are problems stemming from the low plating efficiencies of mammalian cells.

Dubbs and Kit, however, seem to have overcome these obstacles. They found that mouse cells transformed by simultaneous exposure to two SV40 mutants—one producing large, turbid and fuzzy plaques and the other small clear plaques—contain the genomes of both mutants. Viruses of both plaque morphologies are present in the progeny produced when clones of such transformants, claimed to be grown from single cells, are fused with permissive cells. The experiment establishes that two distinct viral genomes can be integrated into one cell, but it throws no light on the key questions of how and where integration occurs. Indeed, it remains to be seen whether such double viral lysogens will prove to be more than a curiosity.

There are, of course, parallels between phage and DNA tumour viruses during lytic infection as well as during lysogenization and transformation. During lytic infection with many phage, but most notably some of the *B. subtilis* phages, pieces of bacterial host DNA are encapsulated in phage coat protein. The same process also occurs during the lytic growth of polyoma virus and now it has been observed during SV40 infections of Vero cells, a continuous green monkey cell line, by Trilling and Axelrod (*Science*, **168**, 268; 1970). When centrifuged in caesium chloride gradients, the SV40 virus from these cells formed two distinct bands, one containing virus with SV40 closed circular DNA, the other containing linear DNA which hybridizes with host DNA. Estimates of the size of this encapsulated host DNA, made by centrifugation in alkaline sucrose gradients, indicate that it is some 15 per cent smaller than viral DNA. Nevertheless, the amount of host DNA in the pseudovirions is sufficient to code for four or five host proteins and, as Trilling and Axelrod point out, pseudovirions may be an efficient vehicle for the transfer of host genes from one cell to another.

DEEP SEA

Five Miles of Fish

by our Marine Vertebrates Correspondent

THE recent capture of a fish of the genus *Bassogigas* at a depth of 7,965 metres (nearly five miles below the surface) by the American research vessel John Elliott Pillsbury represents a new world depth record for a marine vertebrate. The ship was trawling in the Puerto Rico Trench, an ocean chasm some 200 miles long, up to 40 miles wide and in places 8,700 metres deep, which lies in the Atlantic rather north of the

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