water *et al.* are unaffected by any such controversies concerning the precise nature of the carcinogenic binding site, and so may well be found to be roughly correct. □

The sequence of *E. coli* 16S ribosomal RNA

from Richard Brimacombe

THE development of rapid gel techniques for sequencing nucleic acids has provoked a scramble to finalise the sequences of the *E. coli* ribosomal RNA molecules. Several research groups have taken part in this race, and two complete sequences of the 16S RNA have just been published. Pride of place goes to the Californian group (Brosius, Palmer, Kennedy & Noller, *Proc. natn. Acad. Sci. U.S.A.* **75,** 4801; 1978) whose sequence was determined from a plasmid DNA containing one of the 16S ribosomal RNA genes, using the DNA techniques of Sanger and Coulson (*J. molec. Biol.* **94,** 441; 1975) and of Maxam and Gilbert (*Proc. natn. Acad. Sci. U.S.A.* **74,** 560; 1977). This sequence was first reported at the EMBO ribosome workshop in Salamanca in June (see *News and Views* **247,** 743; 1978), and it has been closely followed into print by a complete sequence from the Strasbourg group who presented a partial sequence based on gel data in Salamanca, which has since been finalised (Carbon, Ehresmann, Ehresmann & Ebel, *FEBS Lett.* **94,** 152; 1978).

This latter sequence, obtained entirely independently and without so much as a mention of the Californian group, is derived from a direct analysis of RNA-fragments, using the technique first applied to a polyribonucleotide by Donis-Keller *et al.* (*Nucleic Acids Res.* **4,** 2527 (1977)).

Publication of these two sequences closes a subject which has been a matter of controversy for some years. Work on the 16S sequence using classical techniques was initiated by the Strasbourg group about 10 years ago, and led, after some preliminary papers, to the publication of a detailed oligonucleotide catalogue (Fellner *et al. Biochimie* **54,** 853; 1972) and to a first tentative sequence of the molecule (Ehresmann *et al. Biochimie* **54,** 901; 1972). However, two years later a paper appeared from Woese's group in Illinois (Uchida *et al. J. molec. Evol.* **3,** 63; 1974) which claimed that over 50% of the ribonuclease T_1 sequences published by the Strasbourg group for oligonucleotides of eight or more bases in length were incorrect, and this was shortly followed by a second confirmatory paper by the same group (Magrum *et al. Nature* **257,** 423; 1975). At about this time the Strasbourgers went to press with a new version of the 16S sequence (Ehresmann *et al. Biochimie* **57,** 711; 1975). This sequence, which claimed to be 90–95% complete, was very considerably modified with respect to the 1972 version, and some but by no means all of the T_1-oligonucleotide sequences were altered to agree with those of Woese's group. At this stage about 25% of the T_1-oligonucleotides remained to be finally ordered within the sequence, but there were also queries being raised concerning some of the existing orderings (see for example Noller *Biochemistry* **13,** 4694; 1974).

The next version of the Strasbourg sequence appeared in 1977 (Ehresmann *et al. FEBS Lett.* **84,** 1977), and contained a number of substantial improvements. Additional information was given for nucleotides in regions totalling over 300 bases, the number of T_1-oligonucleotides remaining not finally ordered was reduced to a total of just over 200 bases, and almost all of the T_1-oligonucleotide sequences were in agreement with Woese's data At this stage, recognising that application of the classical methodology was becoming subject to a law of rapidly diminishing returns, the Strasbourg group turned their attention to gel sequencing technology, and have now completed the sequence as quoted above. In this final version, all the T_1-oligonucleotides are ordered and in addition there are alterations to sequences involving a total of almost 200 bases with respect of the 1977 data, which of course brings us to the crucial question—how well does this latest RNA sequence agree with the DNA sequence obtained by Noller's group? And the answer is, the agreement is excellent. The Californian sequence is 1,541 bases long, the Strasbourg sequence 1,542 bases, and within this whole length there are (by my count) only eight single-base discrepancies. The data agree also with sequences at the 3′ and 5′ ends of the molecule obtained by Young and Steitz (*Proc. natn. Acad. Sci. U.S.A.* **75,** 3593; 1978), and all of the Woese T_1-oligonucleotide sequences (with one possible exception, containing one of the eight above-mentioned disputed bases) are correct. So everybody should be happy, and the way is now clear for serious attempts to be made to determine the secondary and tertiary structure of the molecule.

It is perhaps worthwhile to consider very briefly here the relative merits of the DNA compared with the RNA gel methodology for the sequencing of long RNA molecules. Aside from the purely technical viewpoint (where any comparison of the two sets of sequencing data is difficult, since the Strasbourg publication contains no experimental documentation), there are several points to consider. First, the DNA method gives the sequence of a single cistron, whereas the RNA method gives the 'average' of all the cistrons for the RNA molecule concerned; this undoubtedly accounts for the small but significant number of heterogeneities observed in the 16S RNA by the Strasbourg group. Second, the DNA method has an obvious advantage in allowing the use of restriction enzymes to generate the fragments for sequencing; in the RNA method, the production of suitable fragments is a rather hit-and-miss affair, although here it is noteworthy that the Strasbourg group have for this purpose made good use of the double-strand-specific cobra venom nucelase of Vassilenko and Ryte (*Biokhimia* **40,** 578; 1975). Third, while the DNA method is for this last reason certainly the cleanest and quickest for sequencing the whole molecule (once the appropriate cistron has ben isolated), the RNA method is likely to prove most useful for people working with ribosomes or similar particles and wanting a rapid analysis of a particular region of the structure. Finally, it should not be forgotten that the classical methods of oligonucleotide analysis are still needed, both to establish the nature and location of any post-transcriptional modifications such as methylation, and —particularly in the case of the RNA gel method, as has been clearly shown in a similar sequencing study by Gross *et al.* (*Nature* **273,** 203; 1978)—to confirm the sequence. □

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Meteorology over the tropical oceans

from D. B. Shaw

A CONFERENCE on meteorology over the tropical oceans was held in London during August this year.* By its very nature, meteorology is a science requiring international cooperation and it was fitting that the conference was jointly arranged by the Royal

*The proceedings of the conference, in which the current state of the science is reviewed by ten leading authorities in their fields, are to be published early in 1979 by the Royal Meteorological Society, James Glaisher House, Grenville Place, Bracknell, Berkshire.

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