news and views

Homology and structure of transfer RNA

MUCH interest at present centres on initiator transfer RNA which in its aminoacylated form donates a methionine residue to the N-terminal position of nascent proteins in the initiation of protein synthesis. These tRNA,^{Mot} species are distinguished from other methionine specific tRNAs in that they can only participate in initiation and not in elongation; this second role is reserved for $tRNA_m^{Met}$. All the initiator species have several common biochemical properties in that they can all act as substrates for Escherichia coli methionyl-tRNA synthetase and for E. coli methionyl-tRNA transformylase. On the other hand initiators from prokaryotes and cell organelles are distinguished from those from eukaryotic cytoplasm in that the latter are not formylated in vivo. There is also some evidence that the course of initiation in mammalian cytoplasm proceeds in a different manner than in prokaryotes; thus the binding of tRNA,^{Met} to the 40S ribosomal subunit in mammals is independent of template suggesting perhaps that the tRNA bound to the ribosome selects the initiation region of the mRNA rather than the reverse.

It is to be expected that these differences and similarities in the behaviour of initiator tRNA species is reflected in their three-dimensional structures and hence in their sequences. Research by two groups of workers reported on pages 516 and 518 of this issue of *Nature* suggest that this is the case.

Piper and Clark describe the complete sequence of cytoplasmic tRNA_t^{Met} from mouse P3 myeloma cells and Simsek, RajBhandary, Boisnard and Petrissant give that for rabbit liver cytoplasmic initiator tRNA. It turns out that these two sequences are identical. Moreover, Simsek *et al.* provide strong evidence based on the identity of olignucleotide fingerprints that the initiator from sheep mammary gland cell cytoplasm is also the same. It would thus seem that all mammalian initiators are identical. Although this identity does not extend to all initiator molecules, comparison with other published sequences shows extensive homologies between the mammalian sequence and that from yeast; indeed, notable homologies even exist with *E. coli* tRNA_t^{Met}. No doubt these homologies are related to the biochemical similarities between the initiators already noted, as well as their special role in protein synthesis.

On the other hand, the prokaryotic and eukaryotic initiators are sharply distinguished in that the latter—in mammals and yeast—both possess in loop IV of the clover leaf structure the unique sequence A-U-C-G-m¹A-A-A whereas *E. coli* has the sequence T- Ψ -C-A-A-U with the conventional T- Ψ -C triplet and a pyrimidine in the last position. Unpublished work quoted by Simsek *et al.* shows that plant cytoplasm initiator also has A-U*-C-G-m¹-A-A sequence with a modified U so that the odd sequence seems to be universal in eukaryotic cytoplasmic initiators.

Another feature of interest in the mammalian sequence is the presence of a C residue immediately preceeding the anticodon instead of U which is otherwise universal. This feature is absent in yeast and its significance remains unclear.

Piper and Clark quote unpublished work to the effect that the two isoaccepting $tRNA_m^{Met}$ species from mouse myeloma cytoplasm contain conventional sequences in loop IV. These molecules are not formylated but they do act as substrates for $E.\ coli$ methionyl-tRNA synthetase. These observations strengthen the notion that the unconventional sequence in the eukaryotic initiators is related to their peculiar role in protein synthesis. It is to be presumed that this relation is mediated through alterations in the three-dimensional structure of loop IV but at present there is no evidence on this point.

The question of the secondary structure of tRNA has been taken up by Kearns, Wong, Hawkins and Chang in a communication in the same issue of *Nature* (page 541). These authors are concerned with the difference between the secondary structures of native and denatured tRNA as manifested particularly by yeast tRNA_a^{Leu} and they have compared the high resolution nuclear magnetic resonance (NMR) signals obtained from these two stable conformers. Previous work had established that each Watson-Crick base pair produces a single resonance in the low field (11 - 15 p.p.m.) region and analysis of the low field spectrum of the denatured and native forms of tRNA₃^{Leu} revealed that the first has 18 ± 2 base pairs and the second about 4 more. The detailed analysis

Oil and Earthquakes

A REMARKABLE and exciting set of observations is reported by Arieh and Merzer on page 534 of this issue of *Nature*. Oil-field technology and earthquake prediction are brought to each other's aid by means of an astute comparison.

For several years the oilflow from wells in the Gulf of Suez has been subject to periods of large fluctuations interspersed between times of relative uniformity. These periods have correlated across a set of several wells. Oil is forced out of the wells by the hydrostatic pressure of the overlying rocks and so fluctuations in flow are presumably caused by variations in the pressure at depth. The weight of the rocks clearly does not change so what are observed must be variations in the way that this pressure is transmitted to the interstitial fluid. That is, effects of varying pore pressure are being seen. Arieh and Merzer observe that the times of maximum fluctuation precede the occasions of large earthquakes a hundred kilometres away at the north end of the Red Sea. The quakes seem to restore calm to the oil flow. Their first figure tells the whole story.

The observations cannot but strengthen the seismologist's belief that some earthquakes are predictable by precursory dilatancy changes in the rocks in the vicinity of the focal region. The time duration of the effect is in good agreement with previous approximate relationships between precursor time and magnitude. Moreover, the observations demonstrate that the dilated region is large, also in agreement with other work that has been published during the past year.

Oil companies and earthquake geophysicists have a lot to tell each other in the months ahead.

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