lated according to a developmental program. The proteins can be divided into a few groups A to E. The proteins within each group share homologous amino acid sequences, but differ from each other by amino acid replacements, deletions or insertions. The difficulty of purifying individual mRNAs was overcome by constructing DNA sequences complementary to the mRNA mixture and cloning a pool of hybrid plasmids containing cDNA plasmids for individual messages. Sequencing of some of the cDNA clones revealed previously unsuspected homologies between limited regions of proteins from group A and B. The sequence data suggest that blocks of DNA sequences may be rearranged between genes in the course of evolution. The arrangement of these genes in the chromosomes is not known, but genetic data in the silkmoth *Bombyx mori* indicate that the genes for all four classes are located on the second chromosome and probably are clustered (M. R. Goldsmith, University of California, Irvine). The transcription of these genes is being analysed by hybridisation of *in vivo* synthesised RNA to cloned cDNAs using a newly developed spotting procedure.

Transposable genes

Among the most intriguing genes are the dispersed repetitive gene families such as *copia* and *412* in *Drosophila* (D. Hogness, M. Young, Stanford). The *412* and *copia* elements are approximately 7.2 and 5.2 kb in length, respectively, and are found at 20 to 40 different chromosomal sites. The adjacent sequences are different at the different chromosomal locations. These sequence elements are homologous to abundant poly (A)-containing cytoplasmic RNAs. A curious feature of both families is that the elements are flanked by direct repeats of 0.5 and 0.3 kb respectively. The function of these flanking repeats is not known but by analogy with bacterial systems, one can speculate that these elements are translocated to different positions in the chromosomes by reciprocal recombination events which involve the repeated termini. This hypothesis can be tested in a case in which a *copia* element occurs within one unit of a tandemly repeated sequence, by comparing the sequence of the unit with and without the copia element. Preliminary evidence obtained by restriction mapping is consistent with the model. Evidence for transpositions of these elements at least on an evolutionary time scale comes from the observation that two wild-type strains differ with respect to the chromosomal location of these elements.

From genetic experiments, 'jumping genes' have been known for some time in *Drosophila*. For example, several transposable elements carrying the *white* locus have been described. *White* was the first mutant to be found in *Drosophila* and 'traditionally' it maps on the X chromosome. However, fly stocks have been found in which the *white* locus is transposed to different chromosomal sites and transpositions are observed in these laboratory stocks. At the meetings, the isolation of a hybrid plasmid containing complementary sequences to such a transposable element was reported (W. Gehring, Biozentrum, Basel). The element carries both the *white-apricot* allele and the neighbouring *roughest*$^+$ gene. This plasmid is obviously of great interest for the study of transposable elements in *Drosophila*. It may also provide a general tool for the isolation of genes with no known biochemical function.

RNA processing

from Andrew Travers

THE excision of intervening nucleotide sequences during the production of eukaryotic mRNA and tRNA molecules has recently highlighted the biological importance of post-transcriptional processing. This excision together with postulated subsequent ligation often involves the removal of an RNA sequence at least several hundred nucleotides long.

How do the processing enzymes achieve the exquisite accuracy that is a prerequisite for the maintenance of the continued function of the mature RNA molecules? One possible prokaryotic solution to this problem has recently emerged from the studies of Young and Steitz on the production of the 16S rRNA (*Proc. natn. Acad. Sci. U.S.A.* **75,** 3593; 1978). This rRNA is cotranscribed with the sequences for the 23S and 5S rRNA and is generated by RNase III cleavage of the precursor followed by secondary trimming. The RNase III cleavage sites are contained in the sequences flanking the 16S rRNA gene. By determining the DNA sequences of these regions Young and Steitz have discovered that the proximal and distal sequences are potentially capable of hybridising with each other to form a stem consisting of 26 base pairs. The individual strands of this stem are of course separated by a loop of about 1,700 nucleotides containing the entire 16S rRNA gene. The biological importance of such a structure is given credence by the observation that both proximal, and distal RNase III cuts are contained within the base-paired region. Further, RNase III may require a double helical region of at least 9 base pairs both 5′ and 3′ to the point of scission, a structure which is lacking in the immediate neighbourhoods of the scission sites. Thus the most probable interpretation is that a site for RNA processing can be generated by the interaction of distantly spaced complementary RNA sequences. The authors suggest that an analogous process may operate during the production of eukaryotic messenger RNAs.

Cleavage by RNase III does not by itself generate the normal 16S rRNA sequence, yielding only a 17S precursor. For production of the mature 16S RNA two or more additional processing enzymes are required. One recent addition to the family is the endonuclease RNase M16 which cleaves the 16S precursor immediately proximal to the normal 5′ end of the 16S RNA molecule (Dahlberg *et al. Proc. natn. Acad. Sci. U.S.A.* **75,** 3598; 1978), while yet another enzyme is apparently required for the production of the mature 3′ end (Hayes & Vasseur, *Eur. J. Biochem.* **61,** 443; 1976).

A further quirk in the enzymology of RNA processing is provided by the discovery that RNase P, first detected as the activity required for the production of su^+_{III}tRNA (Altman & Smith *Nature new Biol.* **233,** 35, 1971) contains a specific RNA moiety 350 nucleotides long in addition to the expected protein (Stark *et al. Proc. natn. Acad. Sci. U.S.A.* **75,** 3717; 1978). As normally purified this highly unusual enzyme contains about 80% RNA by mass. Furthermore the RNA component seems to be essential for nuclease activity. This requirement for the RNA molecule could be trivial. For example, it might be needed to stabilise an active conformation of the protein component. Alternatively the authors suggest the biologically more interesting possibility that the RNA molecule may itself participate in the recognition of the RNase P cleavage site by a mechanism involving direct RNA–RNA interaction. Implicit in such a model is of course the potential for varying the substrate specificity of the enzyme by simply changing the sequence of the RNA moiety. Again, if this enzyme is of universal occurrence such a capability might have important implications in the production of eukaryotic RNA species.

Andrew Travers is at the MRC Laboratory of Molecular Biology, Cambridge.