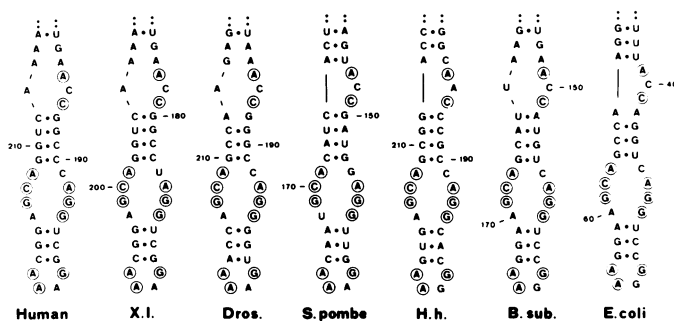


Common structural features between eukaryotic 7SL RNAs, eubacterial 4.5S RNA and scRNA and archaeobacterial 7S RNA

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In mammals, protein translocation across the endoplasmic reticulum is mediated by the signal recognition particle (SRP), which consists of six polypeptide chains and one RNA, the 7SL RNA (300 nucleotides) (1). We have analysed the known eukaryotic 7SL RNAs with regard to structural similarities to prokaryotic RNAs. While all 7SL RNAs share a similar secondary structure, conservation of sequence elements is essentially restricted to a hairpin located around position 200 (2). This secondary structural element - including the conserved nucleotides at the same relative positions - is found to exist also in the 4.5S RNA (114 nucleotides) from *Escherichia coli* (3), the scRNA (271 nucleotides) from *Bacillus subtilis* (4) and the 7S RNA (304 nucleotides) from *Halobacterium halobium* (3). The function of these prokaryotic RNAs is not known. The *E. coli* 4.5S RNA is essential for viability and possibly involved in protein biosynthesis (5,6). The scRNA contains the secondary structure motif of the 4.5S RNA and shares the sequence of the tip of the 4.5S RNA (4). A global similarity with the secondary structure of 7SL RNAs has been noted for the halobacterial 7S RNA (7). Parts of the three prokaryotic RNAs and the 7SL RNAs from *Homo sapiens* (3), *Xenopus laevis* (3), *Drosophila melanogaster* (3) and *Schizosaccharomyces pombe* (8), can adopt a common secondary structure, wherein eleven nucleotides are perfectly conserved (encircled), none of which is involved in intramolecular base pairing. Four additional nucleotides are identical in six out of seven species. Due to the significant structural homology of the RNAs in this part, we suppose this element to be implicated in a homologous function in all species. Therefore, either the function of the bacterial RNAs could be related to protein secretion, or they share a functional feature of the 7SL RNA not discovered so far.



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