

# Sequence and structure of *Tetrahymena* SRP RNA

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Signal recognition particle (SRP) is a ribonucleoprotein required for targeting of presecretory proteins to the endoplasmic reticulum (reviewed in 1). The well-studied canine particle is composed of six polypeptides and one RNA molecule often referred to as 7SL. We report here the sequence and proposed structure of an SRP RNA homolog from *Tetrahymena*, initially identified on the basis of size and subcellular location (J.A.W., unpubl.). Nitrocellulose filter-binding experiments indicate that this RNA specifically interacts with canine pancreas SRP proteins (V.S., P.W. and J.A.W., unpubl.). Enzymatic RNA sequencing of 3' end-labeled *T. rostrata* RNA allowed the design of an oligonucleotide complementary to the terminal 17 residues, which was used to prime cDNA synthesis. The cloned cDNA was sequenced and also used to screen a *T. thermophila* genomic library; a single plaque was chosen for further characterization. The main sequence in the figure is that of the RNA encoded by this gene. The 5' end of *T. thermophila* 7SL RNA was determined by primer extension RNA sequencing and the 3' end by partial enzymatic digestion of end-labeled RNA. Genomic Southern analysis revealed at least two additional hybridizing bands in *T. thermophila* DNA (P.J.B. and J.A.W., unpubl.). The sequences of cloned partial cDNAs corresponding to nucleotides 13–39 (probably derived from RNA self-priming) and nucleotides 50–282 of *T. rostrata* 7SL are identical to the corresponding segments of the *T. thermophila* RNA except at the positions indicated in bold on the figure. The secondary structure shown

conforms to the accepted model derived by phylogenetic comparison (2), and is partially supported by compensatory changes between the two *Tetrahymena* species. *Tetrahymena* 7SL is intermediate in size between fission yeast and metazoan SRP RNAs. Its 5' end lacks pairing in one of the arms of the tRNA-like structure found in homologs from higher eukaryotes (and related RNAs from some prokaryotes), yet is more similar to the corresponding region of mammalian SRP RNA than to 7SL from other lower eukaryotes (see, e.g., 3). The sequence and structure of nucleotides 159–208 fit the consensus previously derived for this region (3, 4) which is the only highly conserved domain in this family of RNAs.

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