5S ribosomal RNA database Y2K

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ABSTRACT

This paper presents the updated version (Y2K) of the database of ribosomal 5S ribonucleic acids (5S rRNA) and their genes (5S rDNA), http://rose.man/poznan.pl/5SData/index.html. This edition of the database contains 1985 primary structures of 5S rRNA and 5S rDNA. They include 60 archaebacterial, 470 eubacterial, 63 plastid, nine mitochondrial and 1383 eukaryotic sequences. The nucleotide sequences of the 5S rRNAs or 5S rDNAs are divided according to the taxonomic position of the source organisms.

CURRENT STUDIES ON 5S rRNA

Bacterial ribosomes (70S) consist of two unequal subunits, 30S (small) and 50S (large) (1–3). The 30S subunit contains 34 different proteins (L1–L34), a 23S rRNA of 2904 nt and a 5S rRNA which includes the loops D and E has been determined by internal loop E have been determined at 3.0 and 1.5 Å, respectively. The ribosomal structure requires proteins L18, L25 and L5 but not L5, which proteins L5, L18 and L25. The 5S rRNA assembly to 23S rRNA requires proteins L18, L5 and L25, whereas in bacteria it interacts with three ribosomal proteins before it is incorporated into the ribosomes both in prokaryotes and eukaryotes.

In eukaryotes, the 5S rRNA molecule binds only ribosomal protein L5, whereas in bacteria it interacts with three ribosomal proteins L5, L18 and L25. The 5S rRNA assembly to 23S rRNA requires proteins L18, and L5 but not L25, which already binds to 5S rRNA (28). The tertiary structure of L25 showed high similarity to rRNA anticodon-binding domain of glutaminyl-tRNA synthetase (29). A limited trypsinisation of euakryotic ribosomes releases two peptides of 32 and 14 kDa suggesting that the N- and C-terminal ends of the L5 protein were the first to be hydrolysed and exposed on the surface of the ribosome (30). Protein L5 being a central component of the 5S rRNA export system interacts also with euakryotic initiation factor 5A which also binds HIV-1 Rev (31). 5S rRNA binds the viral protein (32) and enhances the methionyl- and isoleucyl-tRNA synthetase activities by direct interactions with...
MetRS and tRNA\textsuperscript{Met} in the macromolecular aminoacyl-tRNA synthetase complex (33). Recently 5S rRNA has been identified in the degradosome complex (34). It was demonstrated that it is complementary with 12 and 15 nt strings to the intron 1 sequences of cobrotoxin b and cobrotoxin genes (35).

It seems that in addition to 5S rRNA–protein interactions an important role is played by the contacts of 5S rRNA with 23S rRNA. Multiple cross-links from 5S rRNA to two distinct regions of the 23S rRNA were observed. The first and second regions were located at sites between nt 885 and 992 and 2272 and 2345 of 23S rRNA, respectively (36). Base-paired interaction between 5S rRNA (residues 91–110) in the large subunit and 18S rRNA in small subunit could contribute to the reversible association of the ribosomal subunits (37).

Thus 5S rRNA is an attractive model system for exploring fundamental issues of RNA conformation and RNA protein interaction due to its relatively small size, ease of preparation and its rich array of non-canonical base pairs (16).

To get a consistent picture of structure–function relationships of 5S rRNA, detailed knowledge concerning the primary structure of this RNA species from different sources is required.

THE DATA BANK

This edition of the database contains 1985 nt sequences of 5S rRNAs and 5S cDNAs published through September 1999. In comparison with the 1999 edition of the database (11), 96 entries are new. Most of them are partial sequences of plant 5S rRNA genes. The database entries use the format of the EMBL Nucleotide Sequence Data Bank. The 5S rRNA nucleotide entries contains the 5S rRNA coding sequence as well as information on the length of the original clone and location of the structural gene.

Files with the primary structure data and the nucleotide sequence alignments are available via the WWW at http://rose.man.poznan.pl/5SData/index.html. Any nucleotide sequence can be retrieved using the taxonomy browser or from an alphabetical list of organisms.

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