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The European Small Subunit Ribosomal RNA database

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ABSTRACT

The European database of the Small Subunit (SSU) Ribosomal RNA is a curated database that strives to collect all information about the primary and secondary structure of completely or nearly-completely sequenced rRNAs. Furthermore, the database compiles additional information such as literature references and taxonomic status of the organism the sequence was derived from. The database can be consulted via the WWW at URL http://rrna.uia.ac.be/ssu/ . Through the WWW, sequences can be easily selected either one by one, by taxonomic group, or by a combination of both, and can be retrieved in different sequence and alignment formats.

INTRODUCTION

Due to specific characteristics such as its ubiquity, size and low evolutionary rate, the small subunit ribosomal RNA (SSU rRNA) has proven to be an invaluable tool in molecular phylogenetic studies. The molecule has accounted for numerous new insights in evolutionary biology and its impact on our understanding of the origin and diversity of both prokaryotes and eukaryotes has been tremendous (1–3). Because of its popularity as a molecular marker, many thousands of complete or nearly complete SSU rRNA sequences are available now, from thousands of different species. Hence, a coherent and curated database is an incomparable tool for many areas of comparative biology, a role for which the SSU rRNA is still uniquely suited. The extent of the rRNA sequence collection is still far and away unrivaled among other molecular markers and constitutes by far the single most comprehensive database available for large-scale phylogenetic studies, and will undoubtedly remain so for a long time.

Although the SSU rRNA has been used primarily as a molecular marker in phylogenetic studies, it has also been the subject of many structural and functional studies. As a result, the secondary structure of both prokaryotic and eukaryotic rRNAs is now well resolved (4,5) and several functional domains have been identified and described (6,7).

THE SSU rRNA DATABASE

The SSU rRNA database, housed in Antwerp, Belgium, is continuously updated by scanning the international nucleotide sequence libraries such as GenBank (8) and EMBL (9) for corrected or newly determined ribosomal RNA sequences. In general, only complete or nearly complete sequences are compiled. Partial SSU rRNA sequences are included in the database only if the combined length of the sequenced segments amounts to at least 70% of the estimated chain length of the molecule. The chain length of a partially determined sequence is estimated by comparing it to a complete sequence of a presumed close relative. All SSU rRNA sequences are stored in the form of an alignment and contain the postulated secondary structure pattern in encoded form. The SSU rRNA sequence alignment is based on two different secondary structure models. The first is the prokaryotic model (4,5), which is applicable to bacteria, Archaea, plastids and mitochondria, while the second is the eukaryotic model, applicable to all Eukaryotes (5). The two models are slightly different, each containing a number of structural elements specific for the group.

The SSU rRNA database is made available via the WWW at URL http://rrna.uia.ac.be/ssu/ . In order to simplify access to the Web data, each SSU rRNA sequence is stored in a separate file. Each of these files contains primary and secondary structure information, as well as annotations such as accession number, literature reference, and detailed taxonomic specifications. From January 2000 onwards, taxonomic specifications will be the same as those used by EMBL and GenBank, contrary to taxonomic descriptions used in previous releases of the SSU rRNA database (10).

Supplementary information available on line includes:

- detailed secondary structure models of prokaryotic, eukaryotic, plastidial and mitochondrial rRNAs
- nucleotide variability maps of the prokaryotic and eukaryotic SSU rRNA

Additional information directly available online on our server in Antwerp includes:

- information about the current status of the database
- taxonomic and alphabetic lists of prokaryotic and eukaryotic taxa represented in the database
- information about primers for sequencing SSU rRNA sequences
- phylogenetic trees of prokaryotes and eukaryotes
- software available for sequence alignment, tree construction and sequence alignment format conversion
- links to other relevant databases and resources

If problems occur in connecting to the server or in retrieving data, the authors can be contacted by Email to yves.vandepeer@uni-konstanz.de or dwachter@uia.ua.ac.be

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Users publishing results based on data retrieved from our database are requested to cite this paper.

SUPPLEMENTARY MATERIAL

See Supplementary material available at NAR Online.

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