

PLMitRNA, a database for mitochondrial tRNA genes and tRNAs in photosynthetic eukaryotes

Fabrizio Damiano, Raffaele Gallerani, Sabino Liuni¹, Flavio Licciulli² and Luigi R. Ceci^{1,*}

Dipartimento di Biochimica e Biologia Molecolare, Università di Bari, Via Amendola 165/A, 70126 Bari, Italy,

¹Centro di Studio sui Mitocondri e Metabolismo Energetico, CNR, Via Amendola 165/A, 70126 Bari, Italy and

²Area di Ricerca, CNR, 70126 Bari, Italy

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ABSTRACT

The PLMitRNA database for mitochondrial tRNA molecules and genes in *Viridiplantae* (green plants) [Volpetti, V., Gallerani, R., DeBenedetto, C., Liuni, S., Licciulli, F. and Ceci, L.R. (2000) *Nucleic Acids Res.*, **28**, 159–162] has been enlarged to include algae. The database now contains 436 genes and 16 tRNA entries relative to 25 higher plants, eight green algae, four red algae (*Rhodophytae*) and two *Stramenopiles*. The PLMitRNA database is accessible via the WWW at <http://bio-www.ba.cnr.it:8000/PLMitRNA>.

DATABASE DESCRIPTION

Algae are photosynthetic eukaryotic organisms that can be found in very different habitats (sea and freshwater, ice and snow and desert soils) showing an enormous variety of cell morphologies and life cycles. Nowadays algae constitute an artificial group of organisms with polyphyletic origins within the crown-eukaryotes radiation. Phylogenetic relationships among algae are still a matter of controversy and several attempts are in progress to also elucidate relationships by using molecular data from chloroplasts, mitochondria and nuclei (1–6). We therefore thought it useful to enlarge the PLMitRNA database established for green plants (higher plants and green algae) mitochondrial tRNA molecules and genes (7) also to include algae mitochondria.

A list of algae mitochondrial tRNA genes has been obtained essentially as already described for green plants in the previous version of PLMitRNA (7). A set of master sequences, containing a single gene sequence for each tRNA species has been produced for both *Rhodophytae* and *Stramenopiles* thanks to the SRS (Sequence Retrieval System) service at the European Bioinformatics Institute (EBI), <http://srs.ebi.ac.uk/>. No other algae lineages were found for which mitochondrial tRNA genes have been described. Master sequences were then used to re-analyse the EMBL database with the FastA program for retrieval of similar sequences (<http://www2.ebi.ac.uk/fasta3/>). The database was updated in July 2000 using each set of master sequences in *Viridiplantae*, *Rhodophytae* and *Stramenopiles*. Sugar beet sequences have been downloaded from the EMBLNEW database (accession no. AP000396 and AP000397).

The organisation of PLMitRNA is similar to that described for the previous version (7). Multialignments for *Viridiplantae*, *Rhodophytae* and *Stramenopiles* genes are reported separately.

Table 1 shows all complete genes present in PLMitRNA, highlighted according to their genetic origin. For more details on the different origin of genes coding for plant mitochondrial tRNAs see <http://bio-www.ba.cnr.it:8000/PLMitRNA>. A hypertext link from any coloured square in Table 1 to the related PLMitRNA entry is also available at the database web site. Other links in the site are:

- <http://bio-WWW.ba.cnr.it:8000/srs6/> for retrieval of entries sharing common features;
- <http://bigarea.area.ba.cnr.it:8000/BioWWW/fasta.htm> where sequences in PLMitRNA are available for database searching.

Users of the database should cite the present publication as a reference. Comments, corrections and new entries are welcome.

SUPPLEMENTARY MATERIAL

Supplementary tables on the database are available at NAR Online.

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*To whom correspondence should be addressed. Tel: +39 080 544 3311; Fax: +39 080 544 3317; Email: luigi.ceci@area.ba.cnr.it

