The guide RNA database

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Received October 2, 1996; Accepted October 8, 1996

ABSTRACT

The RNA editing process in protozoan parasites is controlled by small RNA molecules known as guide RNAs (gRNAs). The gRNA database is a comprehensive compilation of published gRNA sequences from eight different kinetoplastid organisms. In addition to the RNA primary sequences, information on the gene localization, the experimental verification of the transcripts, and literature citations are provided. Accessory information includes the secondary structures of four Trypanosoma brucei gRNAs as well as a computer modelled three dimensional gRNA structure. The database is made available as a hypertext document accessible via the World Wide Web (WWW) or from the authors in a printed form.

INTRODUCTION

Guide RNAs (gRNAs) are small, metabolically stable mitochondrial transcripts identified only in kinetoplastid organisms such as Trypanosoma, Leishmania or Crithidia. The molecules carry out a central function during the unusual mitochondrial RNA processing reaction known as kinetoplastid (k) RNA editing (for recent reviews see 1,2). During editing uridylate residues get inserted into and deleted from mitochondrial transcripts thus completing the sequence information of these mRNAs. Guide RNAs provide the information for the U insertion/deletion process by base pairing to pre-edited mRNAs. They are encoded on the mitochondrial mini- or maxicircle DNA elements in kinetoplastid organisms and the RNAs are presumably primary transcripts. Guide RNAs have an average length of 50–70 nucleotides (nt) with a strong A/U nucleotide bias. The primary sequence of gRNAs can be divided into three functional domains: first, a region of complementarity located at the 5'-end, termed anchor sequence, which is thought to create the initial contact with the pre-edited mRNA; second, an informational sequence domain which presumably directs the editing reaction; and third, a posttranscriptionally added 3' oligo(U) extension, sometimes of >20 nt in length. More than 200 different gRNAs have been estimated to be required for the editing of all encrypted genes in Trypanosoma brucei (3) and there is an ~3-fold higher coding capacity for gRNA genes in that organism. Thus, in addition to the large number of different gRNAs the potential for gRNA redundancy exists (4). Guide RNAs have been suggested to fold into simple secondary structures, comprising two consecutive stem loop elements with both terminal ends in a single-stranded conformation (5).

DESCRIPTION OF THE DATABASE

Release 1.0 of the database contains 235 gRNA sequence entries including published sequences through September 30, 1996. The sequences stem from eight different kinetoplastid species: Trypanosoma brucei, Trypanosoma cruzi, Trypanosoma congolense, Trypanosoma equiperdum, Leishmania tarentolae, Leishmania infantum, Leishmania gyrodactyli and Crithidia fasciculata. The compilation is arranged in tabular form, listing for each entry: organism and name of the gRNAs, their primary sequence of gRNAs, the experimental verification of the transcripts, and literature citations are provided. Accessory information includes the secondary structures of four gRNAs from Trypanosoma brucei gRNAs as well as a computer modelled three dimensional gRNA structure. The database is made available as a hypertext document accessible via the World Wide Web (WWW) or from the authors in a printed form.

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The guide RNA database

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- **Release 1.0 of the database** contains most published gRNA sequences along with an explanatory note.
  The sequences are presented in tabular form and catalogue the following information:
  - kinetoplastid species
  - name of the mRNA to be edited
  - gRNA name (and individual clone names, if present)
  - gRNA sequence
  - mitochondrial genome localization
  - expression
  - references to the literature

- The references cited in the database are listed here. Some of the MEDLINE unique identifiers are useful only if you search the full MEDLINE database and not the free-access, WWW-available, genetics subsection.

- Secondary structures for four gRNAs derived in our laboratory are available as .gif files. Additionally, a working model for the 3D-structure of a gRNA is available. If you derive, or know of, any higher order structural information on gRNAs we would be happy to fit it in here:
  - gA6-14 (4k)
  - gA6-48 (4k)
  - gCyh-SSS (4k)
  - gND7-506 (4k)
  - 3D model of a gRNA (58k).

- Links to related WWW sites:
  - Determination of nucleic acid extinction coefficients (USA)
  - The Zuker Home Page (USA)
  - RNA (the journal and the society; UK)
  - RNA2Draw (Sweden)

Please note that while we have attempted to ensure the accuracy of the given material, sequences extracted from this database should be cross-checked with those in the original references. Corrections, new information, and other material for inclusion in this page are welcome.

### Table

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**Figure 1.** Homepage of the gRNA database (URL: http://www.biochem.mpg.de/~goeringe/) including an example of the data presentation.
Figure 2. (A) Secondary structure model of gRNA gND7-506 from T. brucei based on surface probing data (5). Sensitivities of the RNA molecules to the various reagents and enzymes are indicated by the following symbols: kethoxal, open square; DMS, filled circle; DEPC, filled square; CMCT, open circle; CV, filled arrow plus bracket; S1, T1, T2: open arrow. X annotates frequent termination sites in untreated control samples. The oligo(U) tail and the achor region are boxed. (B) Three dimensional model of gND7-506 (Göringer and Hermann, unpublished). Helical regions are annotated in green, loop regions in orange, and the oligo(U) tail is in blue.

AVAILABILITY

The gRNA database is accessible via the URL: http://www.biochem.mpg.de/~goeringe/. A printed version can be obtained upon request from any of the authors who can be contacted by electronic mail (goeringe@alf.biochem.mpg.de/souza@alf.biochem.mpg.de) or by mail at the address given above. Users of the database should cite this publication. Corrections, new entries, errors or omissions or other materials for inclusion in the database are welcome. Submission of new information will be accepted in any form. Unpublished data will be held confidential if required.

ACKNOWLEDGEMENTS

This work was supported by grants from the German ministry for education and research (BMBF) and the German research foundation (DFG) to H.U.G.

REFERENCES