The tmRNA website

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ABSTRACT

tmRNA (10Sa RNA) has a central role in trans-translation, in which a peptide tag encoded in tmRNA is added to the abnormally short protein product of a broken mRNA, as a signal for proteolysis of the entire tagged protein. The tmRNA website was established in 1997 as a resource for phylogenetic considerations of tmRNA structure and function. Since then, three partial tmRNA sequences have been completed, and sequences from 13 more species have been identified. Forty-six species from 10 bacterial phyla and chloroplasts are now represented in the database. Provisional sequence alignments and predicted proteolysis tag sequences are provided, as well as a literature review and a guide to searching for new tmRNA sequences. The tmRNA website is accessible via WWW at a new URL: http://sunflower.bio.indiana.edu/~kwilliam/tmRNA/home.html

Table 1. Phyla represented in the tmRNA website

| Phylum                          | No. species represented |
|---------------------------------|-------------------------|
| Thermophilic oxygen reducers    | 1                       |
| Thermotogales                   | 1                       |
| Green non-sulfur bacteria and relatives | 2                       |
| Flexibacter-cytophaga-bacteroides phylum | 1                       |
| Green sulfur bacteria           | 1                       |
| Planctomycyes and relatives     | 1                       |
| Cyanobacteria and chloroplasts  | 6                       |
| Spirochetes and relatives       | 2                       |
| Purple bacteria                 | 19                      |
| Gram positive bacteria          | 12                      |

*Phylum names are from the Ribosomal Database Project (13).

tmRNA directs a process in Escherichia coli termed trans-translation, in which the ribosomes switches from a ‘broken’ mRNA (lacking a stop codon) to a short reading frame in tmRNA during the synthesis of a single polypeptide (1). Trans-translation solves two problems that would arise from translation of broken mRNA. The first problem, the production of proteins that are abnormally short and possibly deleterious, is solved by trans-translationally tagging the truncated protein with a tmRNA-encoded peptide tag, signalling proteases to degrade the entire tagged protein (1,2). The second problem, the long stall expected at the end of a broken mRNA, is solved by providing a stop codon, from tmRNA, to the stalled ribosome.

The tmRNA website was established in 1997 as a resource for phylogenetic considerations of tmRNA structure and function (3). Phylogenetis sequence comparison has met great success in revealing tmRNA secondary structure, first in establishing a tRNA-like structure involving the termini of tmRNA (4,5), and eventually providing evidence for a total of 12 paired regions (6), all of which are confirmed by chemical probing (7,8). A long stem exits the tRNA-like domain, capped by a large loop that contains the tag reading frame located between the first and second pseudoknots. The phylogenetic distribution of tmRNA also provides clues about its biological roles.

I have continued the search for new tmRNA sequences primarily by careful monitoring of the many ongoing microbial genome sequencing projects, using the computer programs Blast (9) and PatScan (R.Overbeek), identifying tmRNA sequences in 13 more species since last year, bringing representation to three more phyla. Sequences in the website can be viewed or downloaded individually or altogether in a provisional alignment. Predicted proteolysis tags are presented, but note that only the E.coli tag has been ascertained by protein sequencing work (1,10). A review of the literature is provided. A new feature is a guide to searching for new tmRNA sequences; this page lists ongoing genome projects from which tmRNA sequence has not yet been identified, and suggests tmRNA sequences from the closest available relatives as probes for Blast searches; also presented is the PatScan algorithm that succeeded in the identification of chloroplast and Chlamydia tmRNA sequences, where Blast had failed. The tmRNA website is accessible via WWW at a new URL: http://sunflower.bio.indiana.edu/~kwilliam/tmRNA/home.html; pages at the old URL will no longer be updated. Research benefiting from the tmRNA website should cite this article.

As of the submission date of this article, tmRNA genes have been found in broadly diverse bacteria (from 10 phyla) and in all 12 bacterial species whose genome sequences are both complete and publicly available (Table 1). The induction that tmRNA is universal among bacteria is however being challenged. Preliminary Blast and PatScan searches of the completed genome sequence of Rickettsia prowazekii have not revealed a tmRNA gene (S.Andersson, personal communication). Nor have tmRNA genes been found in mitochondria, thought to be descendents of
the Rickettsiaceae (11,12). The anticipated public release of the Rickettsia sequence and of the nearly complete sequences of larger genomes from two other α-proteobacteria, Caulobacter crescentus and Rhodobacter capsulatus, will help resolve this issue.

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