

Nucleotide sequence of spinach cytoplasmic serine (IGA) tRNA

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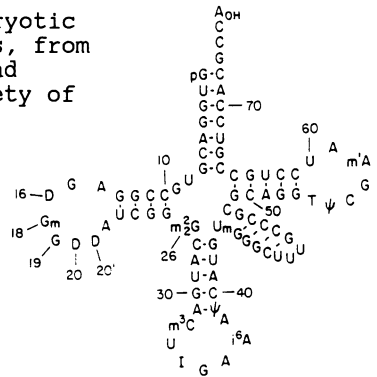
EMBL accession no. X15421

The nucleotide sequence of spinach cytoplasmic tRNA^{ser}(IGA) is:pGUGGACGUGCCGGAGDm²GDAUCGm²GCAUGAm³CUIGAI⁶AA^ψCAUGUmGGGCUUUGC

CCGCGCAGGT^ψCGm¹AAUCCUGCCGUCCACGCCA. This tRNA was unexpectedly present as a specific contaminant of total spinach chloroplast tRNA preparations prepared as described (1), and was sequenced by post-labelling procedures (2). This tRNA was shown not to be a chloroplast tRNA by the absence of hybridization to spinach chloroplast DNA under conditions in which other spinach chloroplast tRNAs hybridized. Spinach tRNA^{ser} has characteristic eukaryotic cytoplasmic base modifications (3) and shows relatively extensive sequence homology (71-79%) to other eukaryotic cytoplasmic tRNA^{ser}(IGA) (or the unmodified anticodon AGA) isoacceptors.

Comparison of the sequences of eukaryotic serine tRNA(IGA) or (AGA) isoacceptors, from yeast, drosophila, rat liver, human and spinach, shows the presence of a variety of conserved features. These include:

- all are the same size, 85 bases
- a conserved diHU loop consisting of A-G-T/C-G-G-T-T-A
- a conserved anticodon region G-A-C/T-T-A-G-A-A-T-C
- a large minor loop of exactly 14 residues with 3-4 G-C base pairs
- a conserved T^ψC region consisting of A-G-G-T-T-C-G/A-A-A/G-T-C-C



tRNA^{ser}
spinach cytoplasm

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References

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