

Genomic DNA sequences of mitochondrial tRNA genes in fungi *Penicillium chrysogenum* KCTC1262: tRNA^{arg}, tRNA^{asn} and tRNA^{tyr} genes

Joonho Sheen, Seungmoak Kim, Yung Hee Kho and Kyung Sook Bae

Korean Collection for Type Cultures, Genetic Engineering Research Institute, Korea Institute of Science and Technology, PO Box 17, Taedok Science Town, Taejeon 305-606, Korea

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The nucleotide sequences of three mitochondrial tRNA genes and their flanking regions from filamentous fungi *Penicillium chrysogenum* KCTC1262 were determined. *P. chrysogenum* NRRL1951 contains the circular 26 kb mitochondrial genome (1) and KCTC1262 (NRRL 1951.B25) contains the same size mitochondrial genome (2). We have cloned and determined the sequence of one of the *Hind*III fragments of mitochondrial genome, so called H2, containing the region of mitochondrial small ribosomal subunit RNA (further abbreviated as SSU rRNA) gene and three mitochondrial transfer RNA genes. The mitochondrial tRNA genes were identified by their highly conserved DNA sequences and the canonical tRNA cloverleaf structure of their putative transcripts. They were assigned to the amino acid arginine, asparagine and tyrosine by their anticodon sequences UCU, GUU and GUA, respectively.

The basic local alignment search tool for nucleic acid, BLASTN (3) on IRIS 4D/340 was used to search and find the sequence similarity for three putative mitochondrial tRNA gene sequences with DNA database (GenBank Rel.72.0). The mitochondrial tRNA genes are strikingly homologous to their counterparts of genomic DNA sequences in *Aspergillus nidulans* and *Neurospora crassa* (87% homologous to tRNA^{arg}, 94% homologous to tRNA^{asn} and 88% homologous to tRNA^{tyr} in *A. nidulans* and 76% homologous to tRNA^{arg}, 71% homologous to tRNA^{tyr} in *N. crassa*). Also, the locations on the mitochondrial genome of the three tRNA genes are highly conserved (4). The gene cluster composed of mitochondrial tRNA^{arg} gene and mitochondrial tRNA^{asn} gene is located at the upstream of the SSU rRNA gene and mitochondrial tRNA^{tyr} gene is at the down stream of the SSU rRNA gene (2).

The three mitochondrial tRNAs contain the highly conserved GG sequence in D loop, and are expected to contain the constant TΨC sequence in TΨC loop. Especially, the mitochondrial tRNA^{tyr} in *P. chrysogenum* is 85 nucleotides long and has a large variable loop similar to those from *A. nidulans*, *N. crassa* and *E. coli* (5). In Figure 1, the deduced cloverleaf structures of mitochondrial tRNAs in *P. chrysogenum* and mitochondrial tRNA^{tyr} in *N. crassa* are described and compared. In sequence alignment of mitochondrial tRNA^{tyr}s from three fungi (Figure 2), it is conspicuous that the sequences for modified nucleotide residues are highly conserved.

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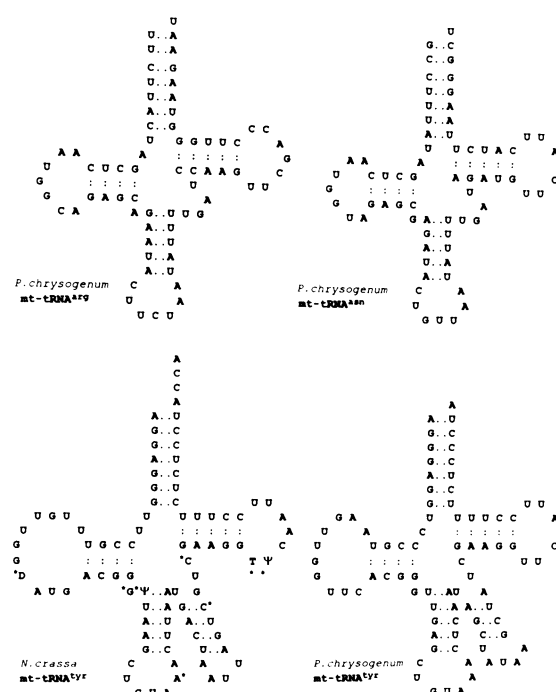


Figure 1. Cloverleaf structures of mitochondrial tRNAs deduced from gene sequences. Mitochondrial tRNA^{tyr} from *P. chrysogenum* contains a large variable loop similar to that from *N. crassa*. Modified nucleotides of mitochondrial tRNA^{tyr} from *N. crassa* (5) are indicated by asterisks.

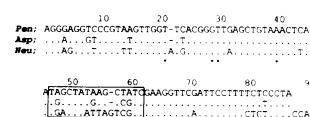


Figure 2. Alignment of mitochondrial tRNA^{tyr} gene sequences from *P. chrysogenum*, *A. nidulans* (4) and *N. crassa* (5). Nucleotide sequences of variable loops are boxed. Identical nucleotides are indicated by dots and modified nucleotides of mitochondrial tRNA^{tyr} from *N. crassa* (5) are indicated by asterisks.