

Erratum

Sequences of initiator and elongator methionine tRNAs in bean mitochondria

Localization of the corresponding genes on maize and wheat mitochondrial genomes

Laurence Marechal, Pierre Guillemaut, Jean-Michel Grienenberger, Geneviève Jeannin & Jacques-Henry Weil

Institut de Biologie Moléculaire et Cellulaire, Université Louis Pasteur, 15 Rue Descartes, 67084 Strasbourg Cedex, France

The above paper was published in *Plant Molecular Biology* Volume 7, No. 4 (1986) pp. 245–253. Below can be found the correct version of the Summary, the legend to Table 2, and a line on page 252, respectively.

Summary

Two bean mitochondria methionine transfer RNAs, purified by RPC-5 chromatography and two-dimensional gel electrophoresis, have been sequenced using *in vitro* post-labeling techniques.

One of these tRNAs^{Met} has been identified by formylation using an *E. coli* enzyme as the mitochondrial tRNA_F^{Met}. It displays strong structural homologies with prokaryotic and chloroplast tRNA_F^{Met} sequences (70.1–83.1%) and with putative initiator tRNA_F^{Met} genes described for wheat, maize and *Oenothera* mitochondrial genomes (88.3–89.6%).

The other tRNA^{Met}, which is the mitochondrial elongator tRNA_m^{Met}, shows a high degree of sequence homology (93.3–96%) with chloroplast tRNA_m^{Met}, but a weak homology (40.7%) with a sequenced maize mitochondrial putative elongator tRNA_m^{Met} gene.

Bean mitochondrial tRNA_F^{Met} and tRNA_m^{Met} were hybridized to Southern blots of the mitochondrial genomes of wheat and maize, whose maps have been recently published (15, 22), in order to locate the position of their genes.

Table 2. Percentage of sequence homology between bean mt tRNA_m^{Met} and various tRNAs_m^{Met} genes. All these tRNA and tRNA gene sequences can be found in ref. 26 and 27 except that of *Zea mays* mt tRNA_m^{Met} gene (19).

Page 252, second column, line 11:

with aminoacyl-tRNA synthetases extracted from