

Predicted editing of additional transfer RNAs in *Acanthamoeba castellanii* mitochondria

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Recently we demonstrated a novel form of RNA editing that alters the transcripts of four out of a cluster of five tRNA genes in the mitochondrion of *Acanthamoeba castellanii*, an amoeboid protozoan (1). Editing is localized to the 5′-half of the acceptor stem and is confined to the first three base pairs, where it effectively corrects mis-pairing at these sites. Editing occurs in a highly predictable pattern whereby the 5′-mis-matched nucleotide is altered to one that is complementary to its 3′-partner (which is always a pyrimidine), resulting in a standard G-C or A-U.

We describe here a second tightly linked cluster of five tRNA genes, immediately upstream of the large subunit rRNA gene (*rnl*) (see ref. 1), having the arrangement 5′-*trnQ*-[-1]-*trnK*-[4]-*trnE*-[5]-*trnI*-[5]-*trnL*-[36]-*rnl*-3′ (numbers in square brackets indicate the lengths of spacers separating the tRNA genes, with *trnQ* and *trnK* exhibiting a 1-bp overlap). The 3′-CCA terminus is not encoded by any of these genes, all of which are transcribed in the same direction as *rnl* (from left to right). Secondary structure modeling (see Figure 1) indicates that the transcripts of four of these five genes display the same pattern of mis-matching in the acceptor stem as four previously characterized *A.castellanii* mitochondrial tRNAs that were shown to be edited (1). The predicted sites and nature of editing are indicated by arrows in Figure 1; only *trnQ* would encode a tRNA with a completely base-paired acceptor stem that would not need editing (secondary structure not shown). Thus, eight out of ten *A.castellanii* mitochondrial tRNAs characterized to date have been shown or are predicted to undergo RNA editing. In the case described here, the predicted editing comprises one C-to-A, four A-to-G and three U-to-G changes.

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REFERENCE

1. Lonergan,K.M. and Gray,M.W. (1993) *Science* **259**, 812–816.

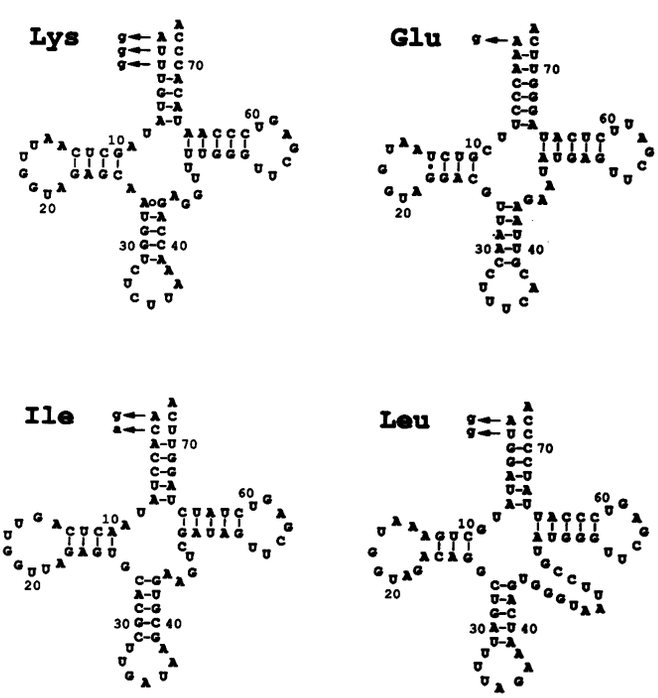

Figure 1.

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