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Secondary structure of the small subunit ribosomal RNA sequence of the microsporidium Encephalitozoon cuniculi

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Microsporidia are a group of unusual, eukaryotic, obligate intracellular, protozoan parasites with a wide host range among vertebrates and invertebrates. Their ribosomes and ribosomal RNAs are reported to be of prokaryotic size (1, 2). The uniqueness of microsporidia may be reflected by the sequence of the small subunit ribosomal RNA (srRNA) of the microsporidium Vairimorpha necatrix (3). The srRNA consists of 1244 nucleotides (nt) which is much shorter than a typical prokaryotic srRNA. This small size is due to the absence of several universal and eukaryote-specific helices (4).

We amplified and cloned the srRNA gene of another microsporidium, Encephalitozoon cuniculi. Sequence analysis of the cloned DNA fragment revealed an srRNA of 1299 nt which is also appreciably shorter than its prokaryotic counterpart. The sequence shared a 72% homology with the corresponding sequence of V. necatrix.

The secondary structure model derived for the E. cuniculi srRNA sequence is depicted in Figure 1. With respect to the models presented previously (4, 5), hairpin 19 has been redrawn as a 3-helix structure in order to account for the existence of a tertiary interaction (6). As a consequence, helix numbers 22 to 50 correspond to the old helix numbers 20 to 48.

Like the V. necatrix srRNA, the E. cuniculi sequence lacks the universal helices 11 and 46. Differences with the V. necatrix structure consist in the presence of helix 10 and the absence of helices 18 and 43. In addition, the variable area V4 is not entirely missing, but is formed by a GU-rich sequence of about 50 nucleotides, which can be folded into two possible models (Figure 1). The most plausible alignment with other eukaryotic srRNAs suggests the presence of a pseudoknot consisting of helices E23-8 and E23-9, present in all eukaryotes that possess area V4. In the alternative model (Figure 1, inset), the sequence is folded into a single hairpin, labeled E23-X because no obvious homology is detectable with any of the hairpins in the area V4 of eukaryotic srRNAs, nor with the single hairpin present in bacterial srRNAs. Although the pseudoknot is the most plausible model, it needs to be confirmed by comparison with additional microsporidial srRNAs.

The establishment of microsporidial srRNA sequences and their secondary structures might contribute to their somewhat limited taxonomic classification based on morphology. So far, the E. cuniculi srRNA sequence and its simple secondary structure support the ancient nature of microsporidia, as suggested on the basis of V. necatrix srRNA sequence data (3).

REFERENCES