

Complete Sequence and Secondary Structure of Ribosomal RNA Gene of the *Nosema* sp. C 01

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We present here for the first time the complete DNA sequence data (3779 bp, GenBank Accession No. AY383655) of the ribosomal RNA (rRNA) gene of the Lepidoptera-infecting microsporidia species, *Nosema* sp. C01. The SSU rRNA consists of 1236 bp which is much shorter than a typical prokaryotic SSU rRNA. The predicted secondary structure of SSU rRNA consists of a core (formed by 1, 2, and 31 helices) and 4 branches (formed by 1-21, 22-30, 32-48, and 49-50 helices) from the 5' end clockwise to the 3' end. The helices 10, 11, 18, 37, 43, 45 and 46 were missing. The LSU rRNA is greatly reduced in length (2506 bp). In LSU rRNA secondary structure of LSU rRNA, eleven hypervariable areas are shown and nine helices (B6, B7, B8, B14, B21, D5, E9, E15, and G5) are missing. B7-B9 and D4 helices can be used for taxonomic studies. The ITS region (37 bp), positioned between the SSU and LSU rRNA genes. The establishment of microsporidial rRNA sequences and their secondary structure might contribute to their somewhat limited taxonomic classification based on morphology.