New insights on the genetic diversity of the honeybee parasite *Nosema ceranae* based on multilocus sequence analysis.

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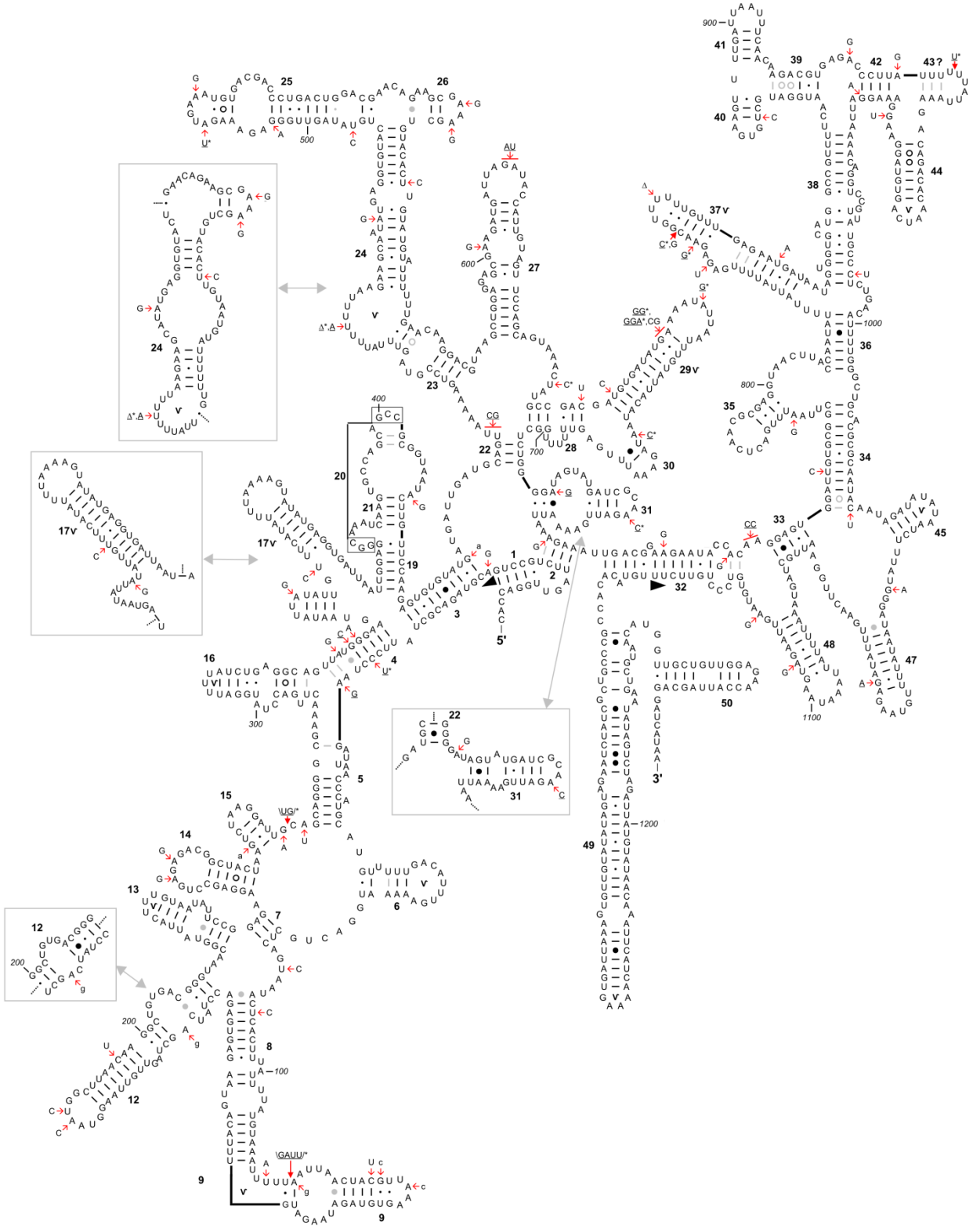
Supplementary Fig. S1. Secondary structure model for *N. ceranae* ribosomal RNA small subunit.



The secondary structure model for *N. ceranae* ribosomal RNA small subunit has been modified from the computed microsporidian model of the Comparative RNA Web Site (Cannone *et al.* 2002) according to other published structures (Hartskeerl *et al.* 1993; Tsai *et al.* 2002; Wang *et al*. 2002; Dong *et al.* 2011). Helices common to prokaryotic models are indicated by a single number. "∇" signs indicate highly variable domains in microsporidian sequences. Bonds in grey are not present in all models proposed in the literature. Insets show alternative secondary structures.

Polymorphic sites emanating from all the 39 sequences obtained in this work and from 88 other deposited sequences (Accession Number DQ673615, FJ481912, DQ078785, DQ329034, U26533, DQ374655-6, DQ486027-8, GU131043-GU131121), including the set from Sagastume *et al.* (2011), were positioned on the secondary structure. Since no experimental quality control had been performed in the later 88-sequences set, polymorphic sites found only once within this set but not in our data have been neglected. The two filled black triangles show the limits of the sequence data obtained in this work. Variable sites with nucleotide substitution are indicated by letters, deletions by "Δ" and insertions by letters bracketted with slashes (\ /). Capital, lower-case and underlined letters indicate polymorphic sites present in our data (N), at least twice in the 88-sequences set from the databank (n), or in both our data and at least once in the databank (N) respectively. Stars indicate a polymorphic site occurring in at least 5% of the compared sequences.

Helices were less submitted to variability than non-helix domains, with 4.6% and 9% of their nucleotides showing polymorphism respectively. About 63% of the mutations in helices did not strongly alter the base pairing of the structure, *i.e*. changing a canonical (or non-canonical) bond to another one. Among the nucleotide modifications inducing mispairing, some were located in hypervariable regions of the microporidian SSU-rRNA (*e.g.* in the helices 29 and 37), other generated non-canonical pairing commonly found in eukaryotic (*e.g.* at positions 324 and 649) or other SSU models (*e.g.* in archeal and mitochondrial SSU at positions 504 and 969 respectively), and some appeared to be rare non-canonical pairings that however join the most common nucleotides found at those positions in the microporidian SSU (*e.g.* at positions 36 and 325).

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