

C-4 5.8S rDNA and 28S rDNA D1, D3-5 and D7 Expansion
Segments of *Stylops melittae* (Strepsiptera, Insecta):
Primary Sequence, Secondary Structure Analysis and
Phylogenetic Implications

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Major parts of the 28S rDNA 5' region and the complete 5.8S rDNA sequence were determined for the strepsipteran species, *Stylops melittae*. Together with previously published insect sequences a multiple alignment was produced and the putative secondary structure of the encoded rRNA was reconstructed based on comparative evidence in order to search for phylogenetically informative character states in the secondary structure. We find (I) several unusual but autapomorphic insertions in the 28S rDNA strepsipteran sequence, (II) that the strepsipteran 5.8S rDNA sequence shares a small insertion with the dipteran 5.8S rRNA where the latter is split up in most dipteran species, and (III) that the lack of a stem domain in the 28S rDNA D3 expansion segment is a shared derived character state of the Diptera. Molecular phylogenetic reconstruction with a subset of 737 slowly evolving sites confirms that strepsipterans belong within the Holometabola. While most methods strongly support the sistergroup relationship between the Diptera and the Strepsiptera previously proposed the maximum likelihood method does not. Sequence evolution analysis reveals that both, strepsipteran and dipteran taxa, evolve under significantly elevated AT-pressure. But whereas this is mainly apparent in stem sites of dipteran rDNA, in the strepsipteran sequence the AT-content is also significantly elevated in the single stranded sites. The branch lengths estimated in the phylogenetic trees indicate that Strepsiptera and Diptera diverged before dipteran rDNA went through a period of episodic substitution rate acceleration.