



Morphological and mitochondrial genomic traits of *Spinibdella lignicola* (Trombidiformes, Eupodina, Bdelloidea) and evolution of Trombidiform mites from comparative genomics*

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Numerous trombidiform mites have been elucidated for their morphological features and mitochondrial (mt) genomes. However, the mitochondrial genomes of *Spinibdella lignicola* has never been described yet. In this study, we accounted for the morphological characteristics and complete mitochondrial genome of *S. lignicola* (the first mitogenome of Bdelloidea). Furthermore, combined with other 26 trombidiform mitogenomes, we conducted gene order (GO) comparative analyses of trombidiform mites. *S. lignicola*, pear-shaped, bright red in color, is about 950 µm in length and featured by Coxa I with 4 setae. The mitogenome of *S. lignicola* have a typical set of 37 genes in arthropods, exhibiting a novel gene cluster of “*trnA-trnQ-trnS1-trnR*” among trombidiform mites. Phylogenetic reconstruction revealed that *S. lignicola* is closely related to *Riccardoella reaumuri*, supporting its position within Eupodides. In line with previous studies, the monophyly of Trombidiformes is rejected because the Eriophyoidea lies outside of Trombidiformes. Four derived gene clusters (*cox1-cox3*; *nad6-trnS2*; *nad1-trnL2*; *trnM-trnC*) were suggested as synapomorphies in trombidiform mites. Furthermore, we propose the possible ancestral GO of Trombidiformes and provide GO evidence for eriophyoid mites evolving independently from non-eriophyoid trombidiform mites. Our study confirms that comparative analysis of GO is a valuable information approach in improving our understanding of mitogenome evolution and phylogeny of trombidiform mites.

Keywords: *Spinibdella lignicola*, Trombidiformes, morphological identification, gene order, mitochondrial genome, phylogeny