

Table S1. Primers

Primer	Position	Forward/ Reverse	PCR/ Sequencing	Primer Sequence (5'-3')	Reference
18S rDNA primers for outgroups, <i>Neomicrorbis</i> and <i>Helicosiphon</i>					
TimA		F	P,S	AMCTGGTTGATCCTGCCAG	Norén and Jondelius (1999)
1100R2		R	P,S	CGGTATCTGATCGTCTTCGA	Norén and Jondelius (1999)
18s2F		F	P,S	TAAAGYTGYTGCAGTTAAA	Nygren and Sundberg (2003)
18s2R		R	P,S	ACCTTGTTAGCTGTTTACTTCCTC	Nygren and Sundberg (2003)
18S rDNA primers, this study					
18s1F	1-20	F	P, S	AYCTGGTTGATCCTGCCAGT	Medlin <i>et al.</i> (1988)
18s2F	673-688	F	P, S	TAAAGYTGYTGCAGTTAAA	Nygren and Sundberg (2003)
18s1R	1214-1235	R	P, S	TASGACGGTATCTGATCGTCTT	Nygren and Sundberg (2003)
18s2R	2050-2073	R	P, S	ACCTTGTTACGACTTTTACTTCCTC	Nygren and Sundberg (2003)
18sFA	80-104	F	P, S	GGTCATTAATCATAYGTGATTT	This study
18sFB	333-353	F	S	GCGACRTATCTTTYAAGCGTA	This study
18sFC	1085-1100	F	S	AGGGACTGCCGGGGGC	This study
18sFD	1414-1434	F	S	TTAATTTGACTCAACACGGG	This study
18sFE	1716-1738	F	S	AGGTCTGTGATGCCCTTAGATGT	This study
18sRA	151-174	R	S	GCTCTAGAATTRCCACAGTTATCC	This study
18sRB	473-493	R	S	TTTRCGCGCCTGCGGCCTTCC	This study
18sRC	969-983	R	S	TTCYATTATTCCATG	This study
18sRD	1551-1569	R	S	AGAGTCTCGTTCGTTATCG	This study
18sRE	1933-1960	R	S	CCATCCAATCGGTAGTAGCGACGGGCGG	This study
18sFCR	1085-1100	R	P, S	GCCCCCGGCAGTCCCT	This study
28S rDNA primers, this study					
28sF	8-26	F	P, S	ACCCSCTGAAYTTAAGCAT	Brown <i>et al.</i> (1999)
28s R		R	P, S	AACTCTCTCMTTCARAGTTC	Brown <i>et al.</i> (1999)
Po28R4	1046–1069	R	P, S	GTT CAC CAT CTT TCG GGT CCC AAC	Struck <i>et al.</i> (2006)

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Figure S1. Maximum likelihood tree with branch lengths derived from the molecular-only concatenated datasets (18S rDNA, 28S rDNA). Numbers at nodes are bootstrap (BS) values. BS values below 50 and posterior probabilities below 0.7 are not shown.

