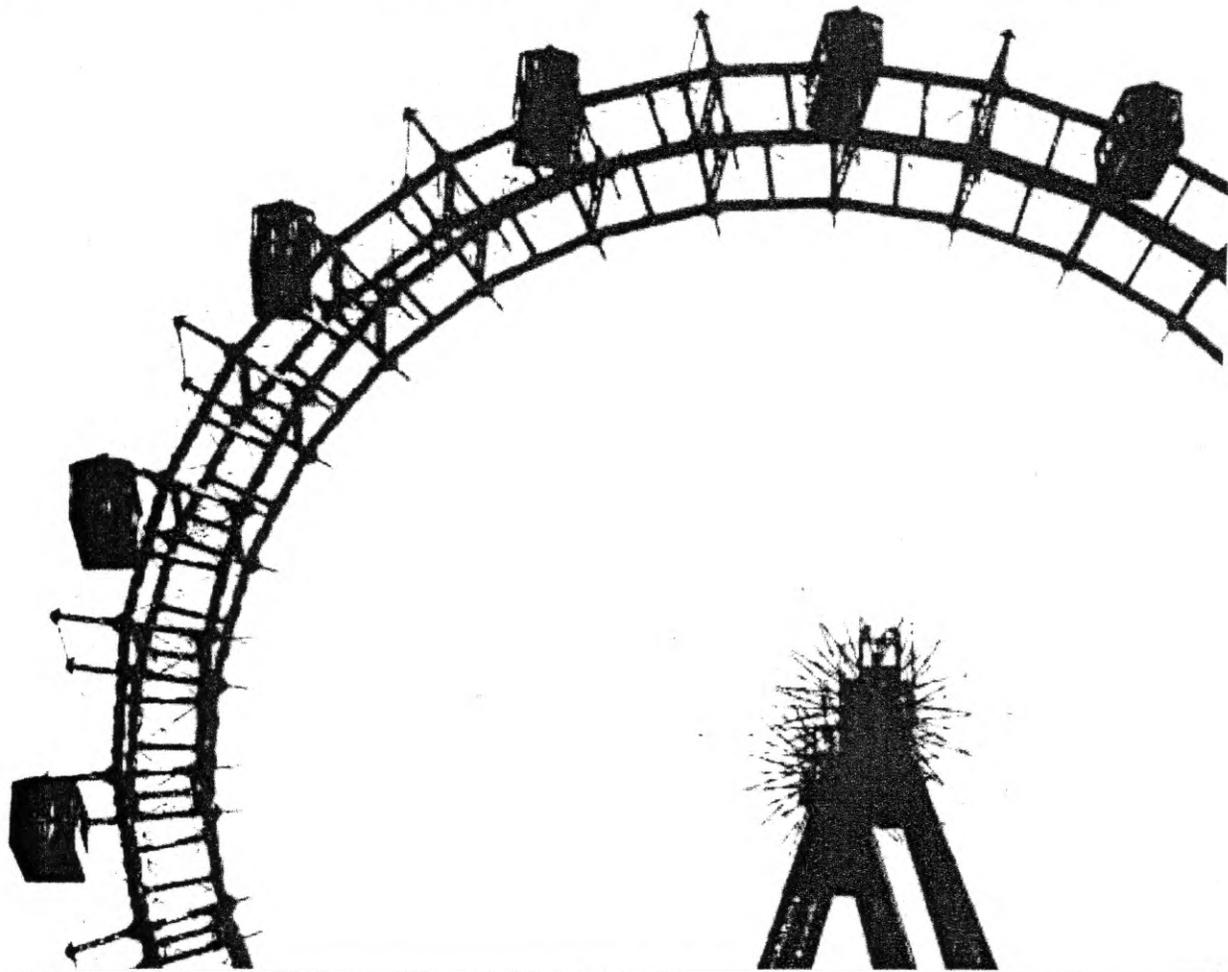




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## Abstract booklet

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## Re-analysis of the 18 rDNA gene phylogeny of the class Colpodea (Ciliophora)

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The ciliate class Colpodea is characterized by a specific somatic fibrillar system. As yet, 80 colpodid genera with 218 species have been described. The senior author has about 30 new taxa in his laboratory notebook. The small subunit ribosomal DNA is available for 35 genera and 58 species.

We critically review gene phylogeny, using several molecular methods. As in previous studies, four main lineages are recognizable: (1) Bursariomorpha including bryometopids, (2) Platyophryida including sorogenids, (3) Cyrtolophosidida, and (4) Colpodida including bryophryids and grossglockneriids. The Platyophryida branch off first and the Cyrtolophosidida and Colpodida are classified as sister groups. On basis of multiple statistical tests, we unravel three problematic issues in colpodean phylogenies: the positions of the Bursariomorpha and Platyophryida are unstable and depend on alignment masking; a sister relationship of the Platyophryida and Cyrtolophosidida cannot be excluded by any statistical tree topology test; and clustering of bryophryids and grossglockneriids outside the Colpodida are also statistically valid possibilities. Natural classification of the highly diverse order Colpodida remains puzzling, possibly due to the lack of a phylogenetic signal and morphostasis of the oral ciliature in several *Colpoda*-like lineages. According to the "Ur-*Colpoda*" hypothesis, *Colpoda* represents the stem lineage from which both *Colpoda*-like and morphologically more derived taxa might have branched off. This evolutionary concept preserves not only information on morphology, ecology, and evolutionary processes of colpodid ciliates, but also aids practicability because the connection to the traditional literature is optimally maintained. There is a main difference in the gene phylogeny 2011 and 2018: the core colpodids form a "good" (dichotomous) tree in the former while a massive paraphyly in the latter in spite of the advanced methods used.

When Foissner started with colpodids in 1985, he was convinced to clarify their phylogeny if he could get good data from further 10 genera and 30 new species. But the trouble increased, and now the same happens with the molecular phylogenies. For instance, our most recent and painstakingly tested molecular tree shows: (1) a massive polyphyly in the core colpodids, (2) taxa whose classification is difficult morphologically are also difficult to classify with molecular technics, for instance the genera *Bardeliella*, *Ilsiella*, and *Kalometopia*, (3) the family Sandmanniellidae is not "basal" to the class though it has a long cytopharynx highly resembling the outgroup viz., the order Nassulida, and (4) the largest species of the class, i.e., the Bursariomorpha give rise to all other colpodids contrasting the "rule" that large groups begin with small species.

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