

Phylogenetic investigation on five genera of tintinnid ciliates (Ciliophora, Choreotrichia), based on the small subunit ribosomal RNA gene sequences

Zicong Li^a, Zhenzhen Yi^a, Jinpeng Yang^a, Jun Gong^b, John C. Clamp^c,
Khaled A.S. Al-Rasheid^d, Saud Al-Arifi^d, Abdulaziz A. Al-Khedhairi^d, Weibo Song^{a,*}

^a Laboratory of Protozoology, KLM, Ocean University of China, Qingdao 266003, China

^b Department of Zoology, Natural History Museum, London SW7 5BD, UK

^c Department of Biology, North Carolina Central University, NC 27707, USA

^d Zoology Department, King Saud University, P.O. Box 2455, Riyadh 11451, Saudi Arabia

Received 7 October 2008; received in revised form 6 November 2008; accepted 7 November 2008

Abstract

The phylogenetic relationship among tintinnid ciliates are relatively poorly studied based on molecular data. In the present work, seven species belonging to five genera of the order Tintinnida (*Amphorellopsis acuta*, *Codonellopsis nipponica*, *Favella taraikaensis*, *Stenosemella nivalis*, *Tintinnopsis beroidea*, *Tintinnopsis cylindrica* and *Tintinnopsis lohmanni*) were analyzed using the information on their small subunit ribosomal RNA gene sequences. Phylogenetic trees were constructed using Bayesian inference (BI), maximum parsimony (MP), neighbor-joining (NJ), and least-squares (LS) methods. Generally, similar topologies were revealed with high or moderate supports, in which the main results show that (1) all tintinnids analyzed belong to a single assemblage; (2) congeners in *Tintinnopsis* do not cluster together, which indicates that the lorica-based definition for this genus is not consistent with the SSU rRNA phylogeny; (3) *A. acuta* groups with *Tintinnidium mucicola* but not with *Eutintinnus*, indicating that the traditional family Tintinnidae might be a paraphyletic group; (4) *Stenosemella* and *Codonellopsis* are clearly most related and possibly even merged into one genus regarding their similar morphology and molecular analyses, and possession of a hyaline collar is the only characteristic of the genus.

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Keywords: Phylogeny; Tintinnida; Molecular systematics; SSU rRNA

1. Introduction

Lorica-bearing oligotrich ciliates, also known as tintinnids, are important elements in the planktonic food web [1,2]. The taxa-rich order Tintinnida comprises about 15 families, 74 genera and over 1200 morphospecies [3,4]. Historically, identification and systematic schemes of tintinnid ciliates have emphasized lorica features (e.g. the presence/absence of bowl, aboral horn, collar and oral rim, their rel-

ative size, shape and ornamentation, the capability of agglutination, the structure and texture of the wall). The presence of an agglutinated (hyaline) lorica was considered to be an ancestral (derived) feature by Kofoed and Campbell [3,5], which disagreed with the cladograms based on infraciliature characters [6–9]. This lorica-based classification of tintinnids, which virtually ignored zooid morphology, has recently been demonstrated to be different from their molecular phylogeny, though the monophyly of tintinnids is generally well recognized [8,9].

Resolving the phylogenetic relationships, understanding their evolutionary pathway and thereafter systematic

* Corresponding author. Tel.: +86 532 82032283.
E-mail address: wsong@ouc.edu.cn (W. Song).

revision of tintinnids are just beginning, as the infracilia- ture of numerous species is yet to be characterized, and many families and genera remain non-sampled, under-sampled or unresolved in molecular trees [8–10]. As a contribu- tion, we herein focus on the phylogenetic matter of five tintinnids genera, *Amphorellopsis*, *Codonellopsis*, *Favella*, *Stenosemella* and *Tintinnopsis*, of which the identities were determined based on traditional lorica morphology, and SSU rRNA were sequenced as well.

The present study seeks to further explore the lorica morphology of SSU rRNA phylogenetic relationships by incorporating newly obtained data from seven tintinnids of these five genera. Specific questions are asked: (1) Are *Tintinnidium* and *Amphorellopsis* closely related? (2) Could *Stenosemella* and *Codonellopsis* be congeneric? (3) What is the relationship between the families Codonellopsidae and Codonellidae? (4) Is there more evidence for the paraphy- letic genus *Tintinnopsis*?

2. Materials and methods

2.1. Ciliate collection

Amphorellopsis acuta (Schmidt, 1901) [3], *Codonellopsis nipponica* (Hada, 1964), *Favella taraikaensis* (Hada, 1932), *Stenosemella nivalis* (Meunier, 1910) [3], *Tintinnopsis beroidea* (Stein, 1867), *T. cylindrica* (Daday, 1887), and *T. lohmanni* (Laackmann, 1906) were collected from the coast of Qingdao (Tsingtao, 36° P 08' N; 120° P 43' E), China. Subsequent isolation and identification were carried out according to Xu et al. [11].

2.2. DNA extraction, PCR amplification and phylogenetic analyses

Total DNA extraction, PCR and phylogenetic analyses were performed according to references [12–14]. The SSU rRNA gene sequences of other ciliates were obtained from the GenBank/EMBL databases.

3. Results

3.1. Deposition of sequences

The obtained SSU rRNA sequences of seven tintinnids have been deposited in GenBank, and their accession num- bers are listed in Table 1.

Table 1

GenBank accession numbers of the seven ciliate species' small subunit rRNA gene sequences and information about the gene sequence.

Species	GenBank Accession Nos.	Length (nucleotides)	GC content (%)
<i>Amphorellopsis acuta</i>	FJ196071	1687	47.54
<i>Codonellopsis nipponica</i>	FJ196072	1760	46.93
<i>Favella taraikaensis</i>	FJ196073	1761	47.19
<i>Stenosemella nivalis</i>	FJ196074	1761	46.91
<i>Tintinnopsis beroidea</i>	EF233709	1676	46.90
<i>Tintinnopsis cylindrica</i>	FJ196075	1761	46.73
<i>Tintinnopsis lohmanni</i>	FJ196076	1682	46.55

3.2. Comparison of SSU rRNA gene sequences

The genetic distances (d) among tintinnid ciliates are rather high compared with other spirotrichs. The maxi- mum genetic distance between tintinnid species is 0.131 (*T. beroidea*–*A. acuta*), whereas when compared with all choreotrich species, it is 0.137 (*T. beroidea*–*Pelagostrobili- dium neptuni*). The minimum genetic distance between tin- tinnids is 0 (*T. cylindrica*–*Tintinnopsis tubulosoides*), which shows that the sequences are identical.

3.3. Phylogenetic analyses

Four different methods (BI, MP, LS, and NJ) resulted in basically congruent topologies (Figs. 1 and 2). All the six subclasses of Spirotrichea, viz. Choreotrichia, Hypotrichia, Oligotrichia, Phacodiniidia, Protocruziidia, and Stichotri- chia, appear monophyletic. Within the Choreotrichia, the monophyletic Tintinnida is highly or moderately supported (0.99 BI, 81% MP, 71% LS, and 64% NJ). However, species with agglomerated (e.g. in *Tintinnopsis*) and hyaline (e.g. in *Favella*, *Metacylis*, and *Rhabdonella*) loricae do not form separate groups.

The *Tintinnopsis* species seem highly dispersed. *Tintinn- oopsis tocatinensis*, *T. cylindrica*, and *T. tubulosoides* form a solid group, whereas *T. beroidea* and *Tintinnopsis dadayi* form another, though their relationship is unclear. *T. loh- manni* groups with some hyaline species and is always basal in the group. *Tintinnopsis fimbriata* clusters with the family Codonellopsidae. For some moderate or low poster- ior probabilities and bootstrap supports, the relationship of the seven *Tintinnopsis* species is uncertain. The position of *Stenosemella* is uncertain within the family. In Bayesian, MP and NJ analyses, *S. nivalis* groups with *Codonellopsis americana*, while in LS, it groups outside the two *Codonell- oopsis* species.

Amphorellopsis acuta and *Tintinnidium mucicola* branch basal to all other tintinnids (1.00 BI, 82% MP, 48% LS, and 76% NJ), followed by *Eutintinnus* species (1.00 BI, 76% MP, 64% LS, 82% NJ). In this way, the family Tintinnidae is paraphyletic.

4. Discussion

As demonstrated in the present work, there are strong supports for the monophyly of the order Tintinnida (0.99

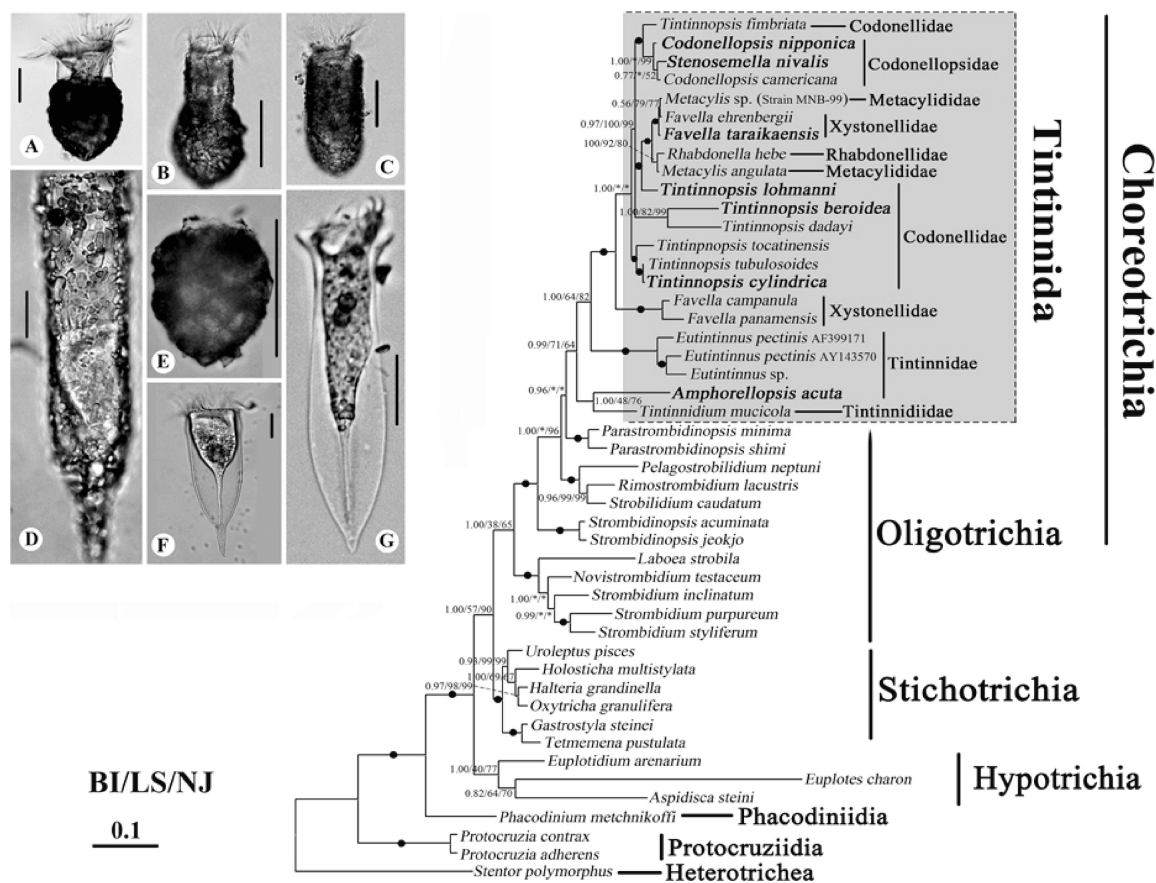


Fig. 1. A Bayesian tree inferred from the nucleotide sequences of the small subunit rRNA (SSU rRNA) gene sequences of Class Spirotrichea. The numbers at nodes represent Bayesian posterior probabilities (PP) using the MrBayes followed by the least-squares (LS) and neighbor-joining (NJ) bootstrap values using PHYLIP package version 3.67. Fully supported (PP 1.00) branches are marked with solid circles. * indicates minor differences in topology that could not be represented on the Bayesian tree. *Stentor polymorphus* (Order Heterotrichida) was selected as the outgroup taxa. Evolutionary distance is represented by the branch length to separate the species in the figure. The scale bar corresponds to ten substitutions per 100 nucleotide positions. The new sequences are highlighted in boldface. Inset: Seven tininnid species analyzed in the present work: (A) *C. nipponica*; (B) *Tintinnopsis lohmanni*; (C) *T. beroidea*; (D) *T. cylindrica*; (E) *Stenosemella nivalis*; (F) *Favella taraiakaensis*; (G) *Amphorellopsis acuta*. Scale bars, 30 μ m.

BI, 81% MP, 71% LS, and 64% NJ), and hyaline and agglutinated loricae do not characterize distinct lineages.

4.1. Genus *Amphorellopsis*

Our result that *A. acuta* groups together with *T. mucicola* with full PP support and moderate/low BP (82% MP, 48% LS, and 76% NJ) contradicts Laval-Peuto and Brownlee's [7] phylogeny. One explanation for the molecular and morphological contradiction is that kinetal density index is a species-specific feature and that the somatic kineties become numerous rather than reduced in Tintinnina [10], so the standard of Laval-Peuto and Brownlee [7] is improper. Besides, the somatic kineties of these two species show little specialization [7], just like the infraciliature of *Strombidinopsis* [15]. This may indicate their transitional position between Tintinnida and Choreotrichida as shown by our phylogenetic analyses.

Our finding also demonstrates that the family Tintinnidae (Claparède and Lachmann, 1858) is paraphyletic, as *A. acuta* and *Eutintinnus* form two separate clades (0.99

BI, 76% MP, 71% LS, and 64% NJ), which supports the conclusion of Laval-Peuto and Brownlee [7] against the assignment of the two species to the same family by Kofoid and Campbell [5].

4.2. Genus *Tintinnopsis*

Genus *Tintinnopsis* has traditionally been defined on the basis of lorica morphology, which includes all species with an agglomerated lorica but lacking collar or other features [3]. Lorica shape is highly variable between species, making species boundaries obscure. Our finding that *T. cylindrica* and *T. tubulosoides* have identical SSU rRNA further supports the idea that lorica may not be so consistent within species and extreme morphotypes can be one species [9]. The infraciliature of *Tintinnopsis* is also highly variable, as *T. cylindrata* has two ventral organelles, while other species have monokinetid ventral kinety; *T. brasiliensis* lacks a posterior kinety, while other species present posterior kinety [6,10,16]. The morphological analyses combined with molecular researches all demonstrate the need to rede-

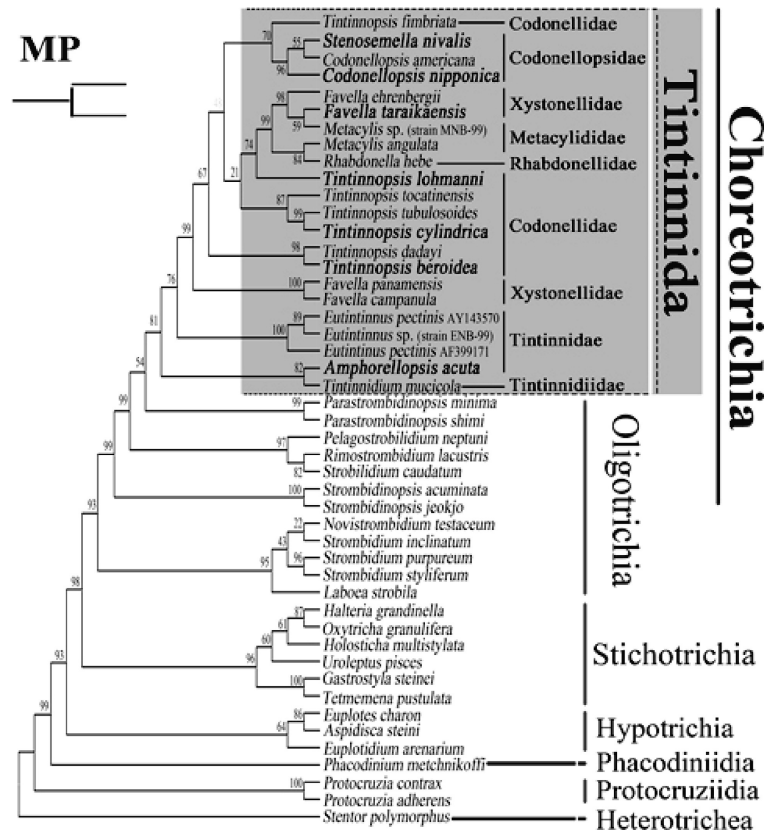


Fig. 2. A maximum parsimony (MP) tree constructed from small subunit ribosomal RNA sequences of the Class Spirotrichea. The numbers at the forks indicate the percentage of times that a specific branch pattern occurred in 1000 trees. No significance is placed on branch lengths connecting the species. The new sequences are highlighted in boldface.

fine the genus and the genus may need to be subdivided into different genera. However, the molecular and cell morphological information of *Tintinnopsis* presented so far is still at a comparatively early stage; thorough investigation will be required to create a more natural and better classification of *Tintinnopsis*.

4.3. Family Codonellopsidae

Codonellopsidae separates from other species quite well and forms a solid group except for *T. fimbriata*. The two genera *Codonellopsis* and *Stenosemella*, which possess hyaline collars, are not well resolved either by morphological analyses or by our result [10]. As indicated by Agatha and Strüder-Kypke [10], *Codonellopsis* species have more than two macronuclear nodules, and *Stenosemella* has two macronuclear nodules. This may be the only one character to separate the two genera; however, this character is not applied much in tintinnid ciliates and can be varied between species. Besides, the genetic distance within the three species is much smaller than with other species (data not shown). So judging by morphological and molecular analyses, the two genera should be merged into one genus. As the *Tintinnopsis* do not form a solid group, the relationship of the two families Codonellopsidae and Codonellidae cannot be deduced. The infraciliature of

Codonellopsidae is almost identical with the family Codonellidae, while the latter family lacks a hyaline collar [16–18]. Thus, the possession of a hyaline collar can be a taxonomic characteristic to separate genus, while the spiral turns may only be used to distinguish species instead of genera.

Acknowledgements

This work was supported by the National Natural Science Foundation of China (30870280 and 30870264), and a joint grant from the Center of Excellence in Biodiversity and the DNA Research Chair, King Saud University. Thanks are also due to Dapeng Xu, Ms. Qianqian Zhang and Jie Huang, postgraduates of the Laboratory of Protozoology, OUC, for their kind help in sampling, species identification etc.

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