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## Phylogenetic positions of four hypotrichous ciliates (Protista, Ciliophora) based on SSU rRNA gene, with notes on their morphological characters

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### Abstract

The morphology and infraciliature of the four hypotrichous ciliates; *Rigidohymena inquieta* (Stokes, 1887) Berger, 2011, *Pattersoniella vitiphila* Foissner, 1987, *Notohymena australis* Foissner & O' Donoghue, 1990, and *Cyrtohymena* (*Cyrtohymenides*) *australis* (Foissner, 1995) Foissner, 2004, collected from east China, were investigated by using live observation and protargol impregnation method. An improved diagnosis for *R. inquieta* was supplied based on descriptions of present and previous populations. New morphology and morphogenesis information based on Chinese populations of another three hypotrichids were also supplemented. The Small-subunit rRNA (SSU rRNA) gene sequences of the four species were characterized and their phylogenetic positions were revealed by means of Bayesian inference and Maximum-likelihood analysis. The analyses shows that *R. inquieta* clusters with other members of the subfamily Styloynchinae, which confirms the monophyly of the subfamily and verified *R. inquieta* as a separated species from *R. candens* though it differs from others mainly by body size. *C. (C.) australis* occupying the basal position of the clade which contains cyrtohymenids and some other groups, declines the idea of separating *Cyrtohymena* into two subgenus. *Notohymena australis* and China population of *Pattersoniella vitiphila* respectively clustering with their congeners correspond well with the systematics revealed by morphological similarities.

**Key words:** Infraciliature; Morphology; Morphogenesis; Oxytrichids; *Rigidohymena*; Styloynchinae

### Introduction

Hypotrichous ciliates, which are characterized by the dorso-ventral differentiation of cilia, include over 200 genera and more than 700 species that are well-distributed over the world (Berger 1999, 2006, 2008, 2011; Foissner 1997, 2006). Though they have been studied for hundreds of years, the diverse range of morphology of this group causes great taxonomic challenges and unsolved systematic problems. Although the detailed morphological characteristics and morphogenesis events have improved the situation to a great extent, problems still exist, concerning population variations and different systematic classification ideas (Berger 1999, 2006, 2008, 2011; Foissner 1996, Shao *et al.* 2014a). Since early 1990s, molecular analysis of marker genes has given rise to new evolutionary clues and hypotheses regarding this group, which has gradually proved to have a positive effect on improving on the taxonomy by traditional approaches (Foissner and Stoeck 2008, 2011; Chen *et al.* 2013a; Modeo *et al.* 2013; Foissner *et al.* 2014; Heber *et al.* 2014; Kumar *et al.* 2014). Modern systematic research of ciliates requires both accurate identification with marker gene sequences and detailed taxonomy (Chen *et al.* 2013a, b; Fan *et al.* 2014; Jung *et al.* 2014a; Shao *et al.* 2014).