



## A case of taxonomic inflation in coccoid algae: *Ellipsoidion parvum* and *Neocystis vischeri* are conspecific with *Neocystis* (= *Nephrodiella*) *brevis* (Chlorophyta, Trebouxiophyceae)

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### Abstract

Determining the actual phylogenetic diversity of unicellular coccoid algae, and developing a biologically appropriate classification system for them, pose challenges. We studied the phylogenetic and morphological diversity of a series of algal strains identified as *Nephrodiella* spp., *Ellipsoidion parvum*, and *Neocystis* spp. By determining sequences of the 18S-ITS1-5.8S-ITS2 rDNA region we showed that the strains studied represent just two genotypes; differences in the ITS2 region of the two genotypes, including one compensatory base change (CBC) in the helix II, suggested that they may be considered as two separate species. We then employed geometric morphometrics to evaluate the extent of morphological differences among the strains. This analysis revealed that the degree of morphological variability is higher among strains of the same genotype than between the genotypes. Our results thus suggest that all the strains represent only two closely related cryptic species of trebouxiophycean algae, which may be identified as *Neocystis brevis* and *Neocystis mucosa*. Two previously described species, *Ellipsoidion parvum*, originally described as a heterokont alga, and *Neocystis vischeri*, are revealed as junior synonyms of *N. brevis*. We discuss our findings as a case of taxonomic inflation that may be a general, yet somewhat neglected, aspect of the current taxonomy of unicellular algae.

**Key words:** Heterokonten, morphological plasticity, phylogenetic diversity, Xanthophyceae

### Introduction

The advent of molecular taxonomy has revealed that the classification of eukaryotic microbes as developed during the era of traditional (morphology-centred) systematics grossly underestimated the real diversity existing in nature (Adl *et al.* 2007, 2012, Medlin *et al.* 2007, Epstein & López-García 2008). The poor reflection of actual microbial diversity is mainly caused by the paucity of discriminating morphological characters, which may result in polyphyletic taxa lumping together distantly related organisms. Consequently, traditional species concepts often include multiple cryptic or semicryptic species. These problems can now be reassessed with the aid of appropriately variable genetic markers, such as the internal transcribed spacer 2 (ITS2) in the rRNA operon, the plastid *rbcL* gene, or the mitochondrial *cox1* gene, although the question of actual species delimitation often persists due to the ambiguous nature of species concepts (Fenchel & Finlay 2006, Medlin *et al.* 2007, Coleman 2009, Edwards 2009, Boenigk *et al.* 2012). The traditional genus *Chlorella* is a prototypical case of a failure to distinguish the actual extent of phylogenetic diversity behind a single morphotype, as the use of molecular markers, primarily 18S rDNA and the ITS2 region, has led to its separation into several genera, often very distantly related and collectively comprising many more species than distinguished before (Huss *et al.* 1999, Luo *et al.* 2010, Bock *et al.* 2011, Fučíková & Lewis 2012).