



## Revisiting the phylogeny of Ocellularieae, the second largest tribe within Graphidaceae (lichenized Ascomycota: Ostropales)

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### Abstract

We present an updated 3-locus molecular phylogeny of tribe Ocellularieae, the second largest tribe within subfamily Graphidoideae in the Graphidaceae. Adding 165 newly generated sequences from the mitochondrial small subunit rDNA (mtSSU), the nuclear large subunit rDNA (nuLSU), and the second largest subunit of the DNA-directed RNA polymerase II (*RPB2*), we currently distinguish 218 species among the sequenced material, including the outgroup. This corresponds to almost half the species at this point recognized within this tribe. The newly generated sequences include 23 newly described species and one newly described genus published elsewhere in this volume. For the first time, *Sarcographina cyclospora* Müll. Arg., in spite of its distinctly lirellate ascomata, is shown to belong in tribe Ocellularieae, as strongly supported sister to *Ocellularia inturgescens* (Müll. Arg.) Mangold. The following six new combinations are proposed: *Melanotrema lynceodes* (Nyl.) Rivas Plata, Lücking & Lumbsch, *Ocellularia curranii* (Vain.) Kraichak, Lücking & Lumbsch, *O. khasiana* (Patw. & Nagarkar) Kraichak, Lücking & Lumbsch, *O. cinerea* (Müll. Arg.) Kraichak, Lücking & Lumbsch, *O. erodens* (R. C. Harris) Kraichak, Lücking & Lumbsch, and *O. laeviuscula* (Nyl) Kraichak, Lücking & Lumbsch. Further, the new name *Ocellularia hernandeziana* Kraichak, Lücking & Lumbsch is introduced for *Myriotrema ecorticatum*. The nomenclatural status of the name *Ocellularia microstoma* is clarified.

**Key words:** *Ampliotrema*, *Glaucotrema*, phylogenetic resolution, *Redingeria*, *Reimnitzia*, *Rhabdodiscus*, *Sarcographina*, *Stegobolus*, supermatrix

### Introduction

The two largest families of lichenized ascomycetes are the crustose Graphidaceae and the predominantly foliose and fruticose Parmeliaceae. With a recent increase in species discovery, mainly in tropical regions, Graphidaceae

characterize these clades and eventually give them formal generic status. In addition, it becomes apparent that, at least in this clade, nuLSU and also *RPB2* provide a better resolution at species and species group level than mtSSU; on the other hand, the proportion of sequences routinely obtained for taxa within this clade indicates that nuLSU and particularly *RPB2* sequencing often fails. The highlighted cases suggest that especially within *Ocellularia* s.lat., additional data from these two loci may help to better resolve this clade and then either define subgenera or even additional genera.

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