

Alveolata (Ciliophora), Opisthokonta (Fungi, Animalia) and Amoebozoa. In contrast, the majority of SGA is confined to several lineage of just a single class of Chlorophyta, the Trebouxiophyceae. Phylogenetic diversity of the exhibitants generally exceeds that of the SGA, e.g. a single *Coccomyxa* species may be associated with various lineages of Ascomycota and Basidiomycota. With respect to species numbers, Asco- or Basidiomycota (lichens) are by far the most frequent exhibitants, followed by Ciliophora. Both types of symbioses are each dominated by just a single trebouxiophycean lineage, the Trebouxiiales and *Chlorella*-clade. Cryptic diversity is significant in SGA. In lichen algae molecular phylogenies reveal a variety of lineages of which only a small number can be recognized by morphology as well. Also, though most SGA from Ciliophora/Animalia are *Chlorella*-like, they are distributed on various lineages of the Trebouxiophyceae. Symbioses with Ciliophora/Animalia and Fungi seem to exclude each other, i.e. trebouxiophycean lineages from Ciliophora may also occur in Animalia, but cannot be found in lichens and vice versa. While next closest non-symbiotic relatives of SGA may be found among subaerial or freshwater species, some SGA may also be restricted to the symbiotic life style.

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## CHANGES IN THE BIODIVERSITY OF ALGAE IN SOILS ALONG GRADIENTS OF LAND USE INTENSITIES

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Algae communities in soils are highly influenced by environmental factors because they are integrating environmental and seasonal changes over several weeks. To study whether changes in the algal/cyanobacterial community structures are more affected by land use than by physico-chemical parameters of the soil we use both a microscopic culture and a molecular culture-independent (rDNA cloning/sequencing) approach in this ongoing project. Both approaches agreed in the detection of six green algal genera as being most common in the studied soils with the molecular approach showing a larger genetic diversity below the genus level. Each approach revealed a number of additional taxa which were retrieved either by microscopy or rDNA phylogenetic analyses. As a first trend, *Stichococcus* spp. exhibited a preference towards soils of intensively treated research plots in forests and grasslands, while *Chlorella vulgaris* was dominant in the extensively treated plots. Algal diversity in the intensively treated plots was decreased compared to that of the extensively treated-ones. Forest and grassland soil algal communities were clearly different and differed also among the three studied large-scale research sites (www.biodiversity-exploratories.de). The composition of algae communi-

ties in soils was clearly different from that of tree barks. To test for their functional roles, isolates of tree bark algae will be used in feeding experiments with microarthropods as their possible consumers.

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## CONFUSION CAUSED BY LIMITED MORPHOLOGY: TWO CASE STUDIES IN GREEN COCCOIDS.

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The depauperate morphology of coccoid green algae has frequently led to a sharp contrast between morphology-based and molecular classification. Traditionally, potential variation or plasticity of morphological traits used for taxonomic decisions was seldom taken into account. DNA sequences provide a high number of characters that are not subject to phenotypic plasticity and therefore offer a more direct measure of phylogenetic relationships. As part of a monographic study of the chlorophycean genus *Bracteacoccus*, several strains deposited in culture collections under this generic name were found to belong to other green algal genera, both in Chlorophyceae and in Trebouxiophyceae. Although morphologically similar to young cells of *Bracteacoccus*, these algae were demonstrated to belong to the genera *Myrmecia* and *Pseudomuriella* based on 18S and *rbcL* sequence data. A formal transfer of *Bracteacoccus engadinensis* into the genus *Pseudomuriella* is hereby proposed. A contrasting case was found in the genus *Dictyococcus*, which was examined as putative sister taxon to *Bracteacoccus*. Only two type cultures of *Dictyococcus* are available worldwide: *D. schumacherensis* and *D. varians*. Analysis of the DNA sequences showed *D. schumacherensis* to be nested in *Bracteacoccus* and therefore a new combination, *Bracteacoccus schumacherensis*, is proposed here. Determination of the phylogenetic position of *D. varians* requires further analysis, but this taxon is clearly distinct from *B. schumacherensis* and falls outside the genus *Bracteacoccus*. These cases likely represent two of many discrepancies of morphological and sequence data across coccoid green algae.

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## MORPHOLOGY AND MOLECULAR PHYLOGENY OF THE GENUS OSMUNDEA (CERAMIALES, RHODOPHYTA) FROM CANARY ARCHIPELAGO, EASTERN ATLANTIC

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