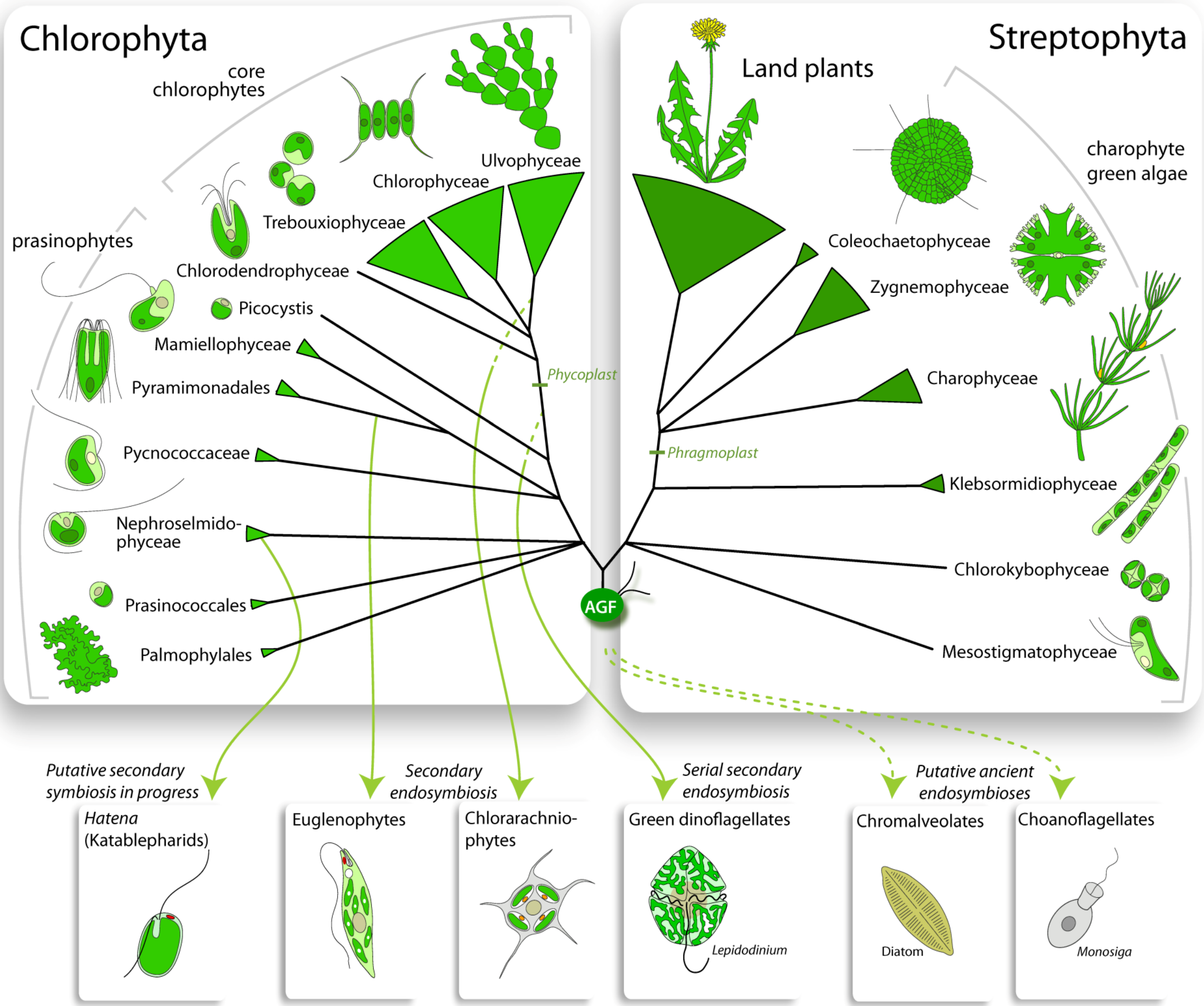
Kingdom: Plantae

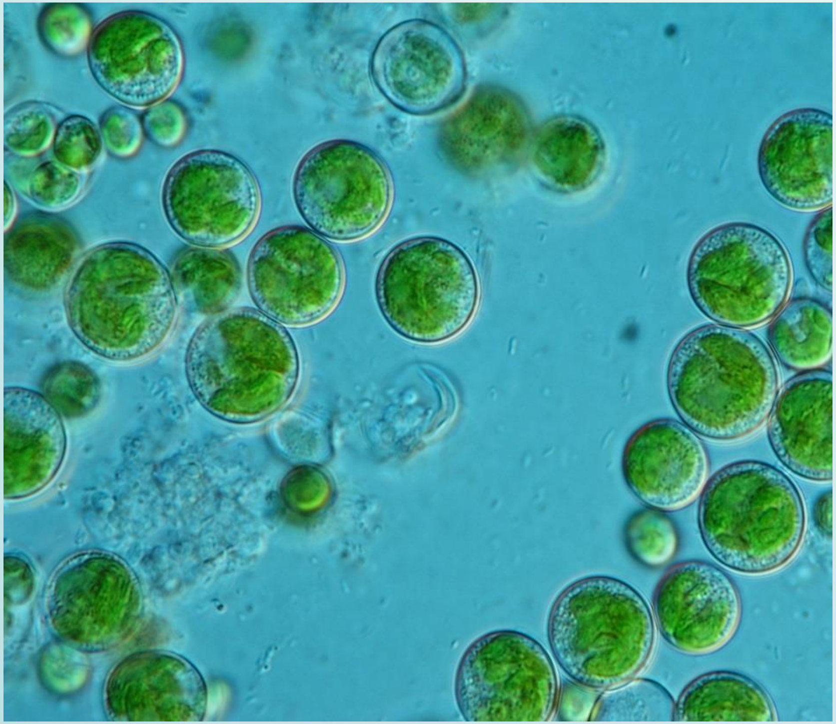
Order: Chlorophyta

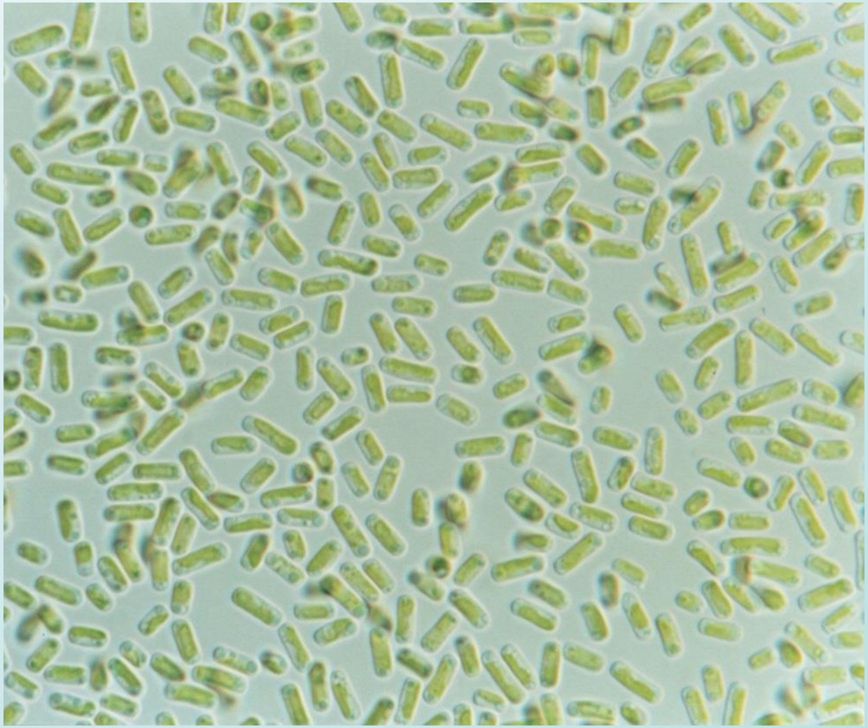
Class: Trebouxiophyceae


Chlorophyta
core chlorophytes
Ulvophyceae
Chlorophyceae
Trebouxiophyceae
prasinophytes
Chlorodendrophyceae
Picocystis
Mamiellophyceae
Pyramimonadales
Pycnococcaceae
Nephroselmido-phyceae
Prasinococcales
Palmophylales
Phycoplast
AGF
Streptophyta
Land plants
charophyte green algae
Coleochaetophyceae
Zygnemophyceae
Charophyceae
Phragmoplast
Klebsormidiophyceae
Chlorokybophyceae
Mesostigmatophyceae
Putative secondary symbiosis in progress
Secondary endosymbiosis
Serial secondary endosymbiosis
Putative ancient endosymbioses
Hatena (Katablepharids)
Euglenophytes
Chlorarachnio-phytes
Green dinoflagellates
Lepidodinium
Chromalveolates
Diatom
Choanoflagellates
Monosiga

General features

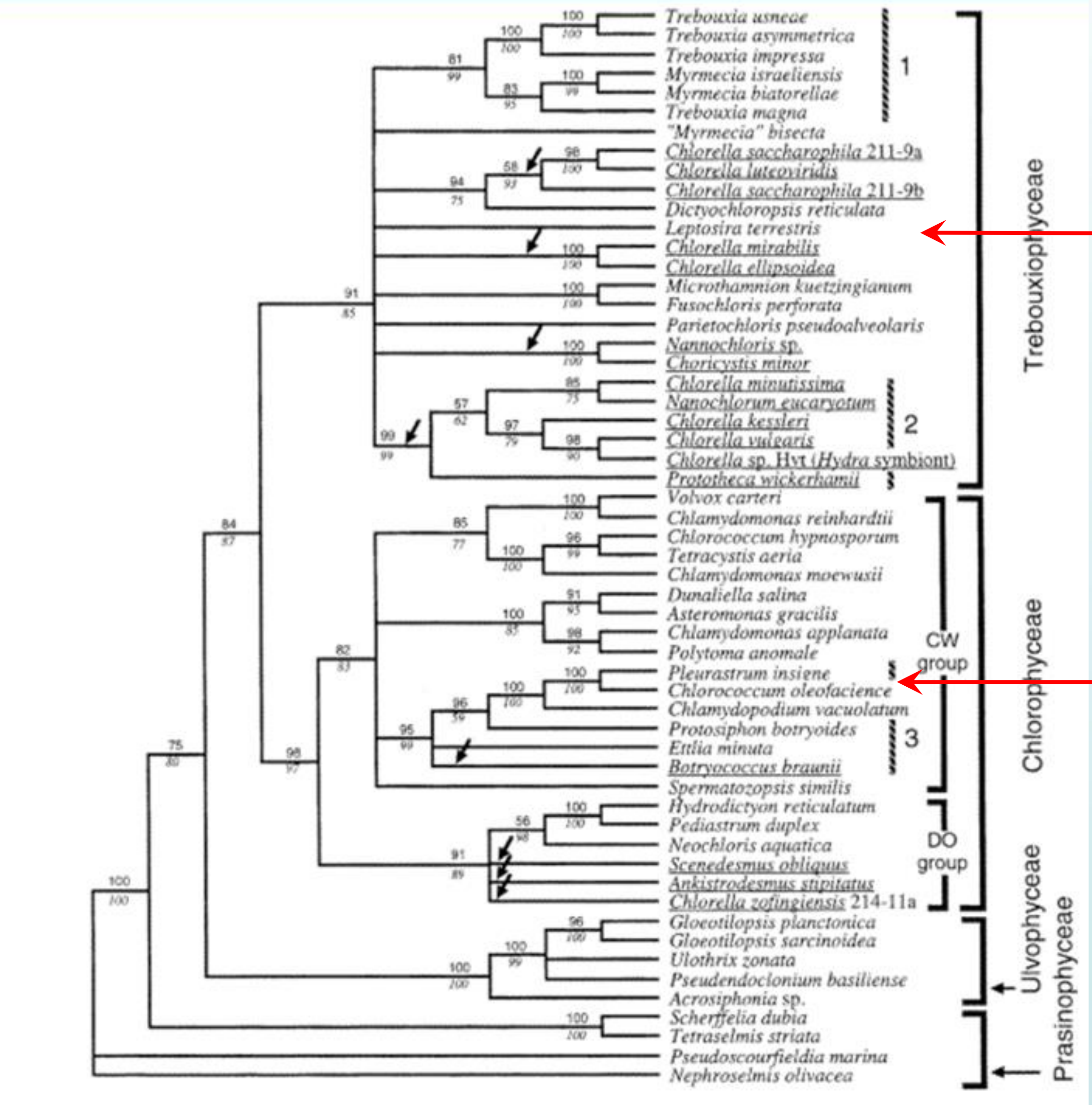
- the class was established in 1995
- unicellular and filamentous algae
- predominantly terrestrial, aerophytic
- a high proportion of symbiotic organisms





Mattox & Stewart (1984): Pleurastrophyceae (characterized by DO orientation of flagellar roots)

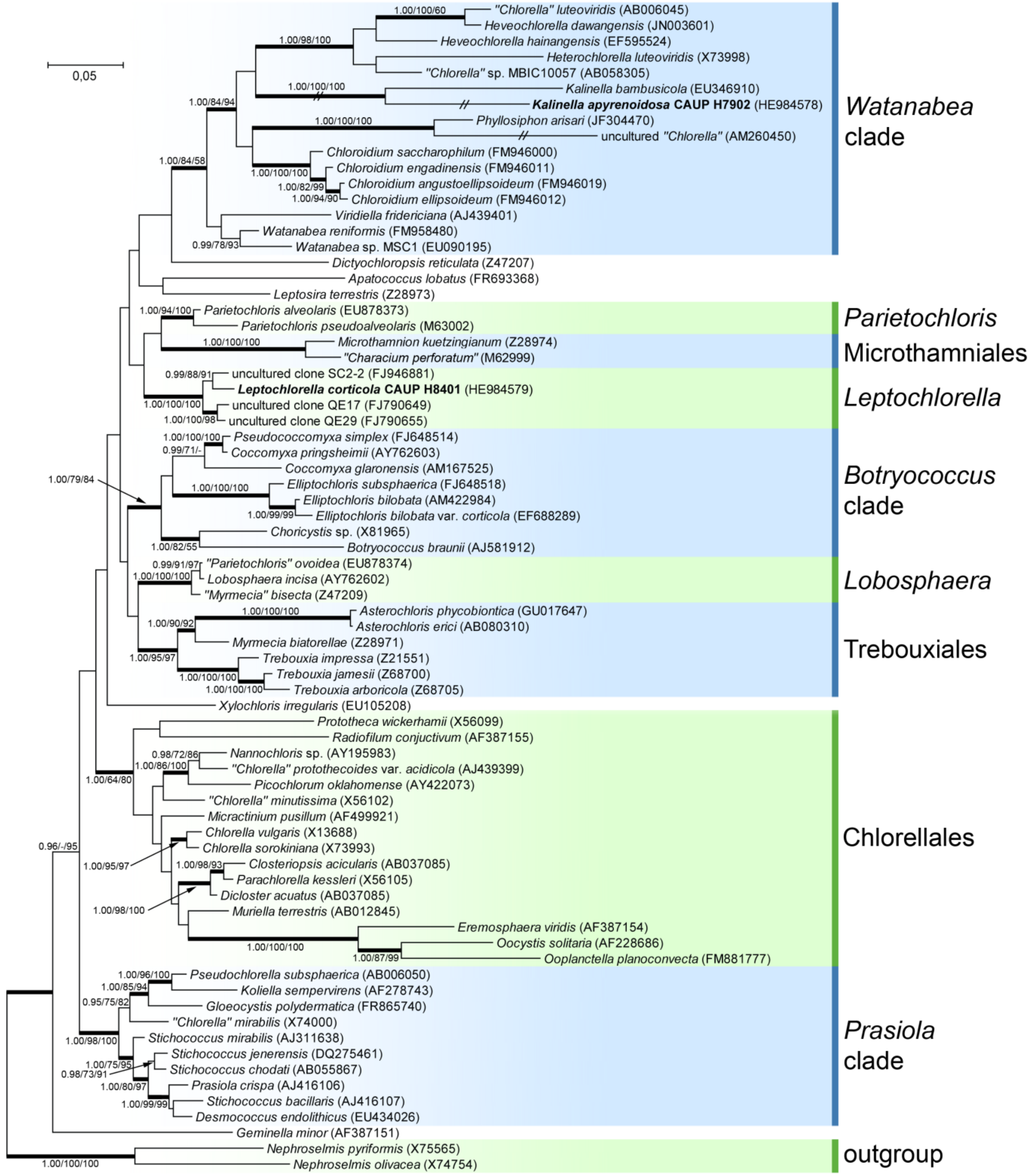
Friedl (1996): Trebouxiophyceae



„Pleurastrum“ terrestre

Pleurastrum insigne

Trebouxiophyceae

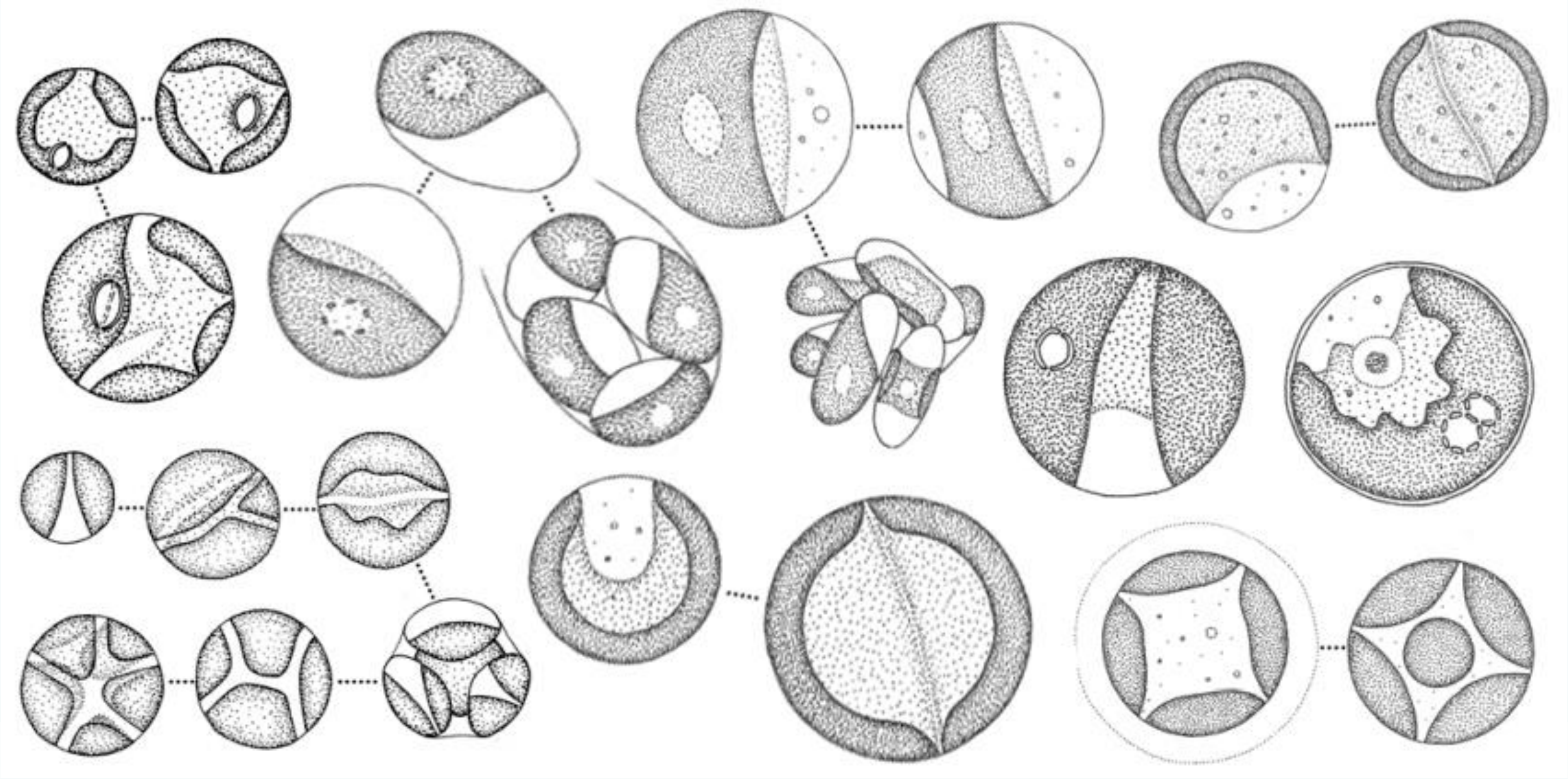


Trebouxiophyceae, *Chlorella*

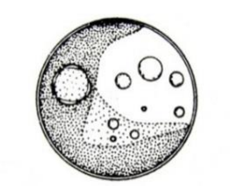
- Coccoid unicellular green algae with globular to oval cells that reproduce entirely by autospores
- Probably the most abundant and diversified group of aerophytic algae
- Beijerinck (1980):

„... ich werde unten die Algen derart beschreiben, dass jeder dieselben leicht erkennen kann.“

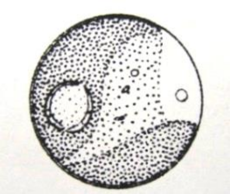
„... now I describe this alga in such a way that everybody will simply distinguish it... “



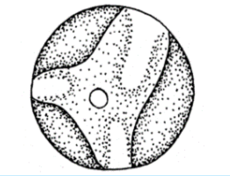
Trebouxiophyceae, *Chlorella*



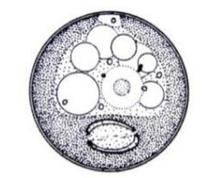
Chlorella vulgaris



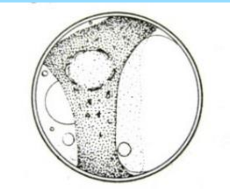
Chlorella sorokiniana



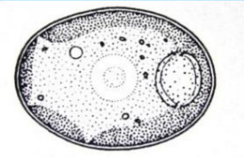
Chlorella lobophora



Chlorella kessleri

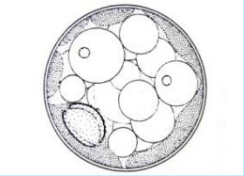


Chlorella luteoviridis

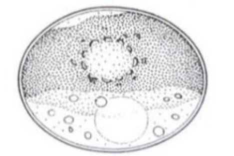


Chlorella fusca v. fusca

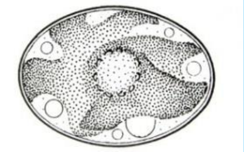
Chlorella fusca v. rubescens



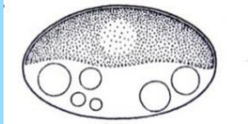
Chlorella fusca v. vacuolatus



Chlorella ellipsoidea



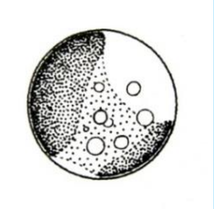
Chlorella trebouxioides



Chlorella saccharophila

Chlorella homosphaera

Chlorella zofingiensis

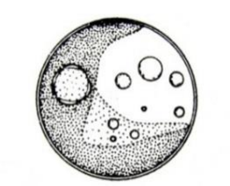


Chlorella protothecoides

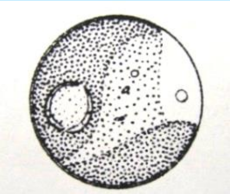
Chlorella minutissima

Trebouxiophyceae, *Chlorella*

glukosamin

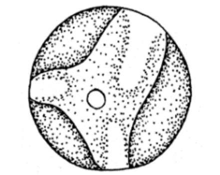


Chlorella vulgaris

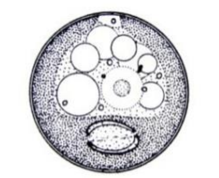


Chlorella sorokiniana

(Ch. vulgaris)



Chlorella lobophora

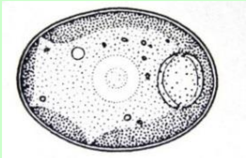


Parachlorella kessleri

(Ch. kessleri)

Heterochlorella luteoviridis

(Ch. luteoviridis)

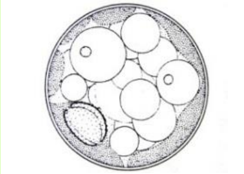


Desmodesmus abundans

(Ch. fusca, v. fusca)
(Scen. abundans)

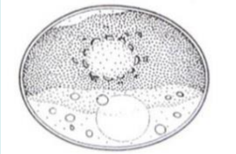
Scenedesmus rubescens

(Ch. fusca, v. rubescens)
(Halochlorella rubescens)



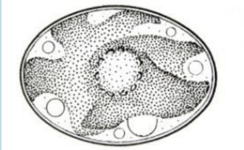
Scenedesmus vacuolatus

(Ch. fusca, v. vacuolata)
(Graesiella vacuolata)



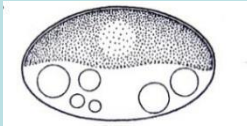
Chloroidium ellipsoideum

(Ch. ellipsoidea)



Chloroidium ellipsoideum

(Ch. trebouxioides)



Chloroidium saccharophilum

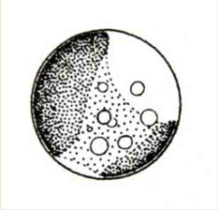
(Ch. saccharophila)

Mychonastes homosphaera

(Ch. homosphaera, Ch. minutissima)

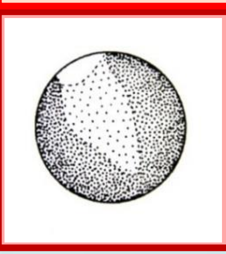
Chromochloris zofingiensis

(Ch. zofingiensis)



Auxenochlorella protothecoides

(Ch. protothecoides)



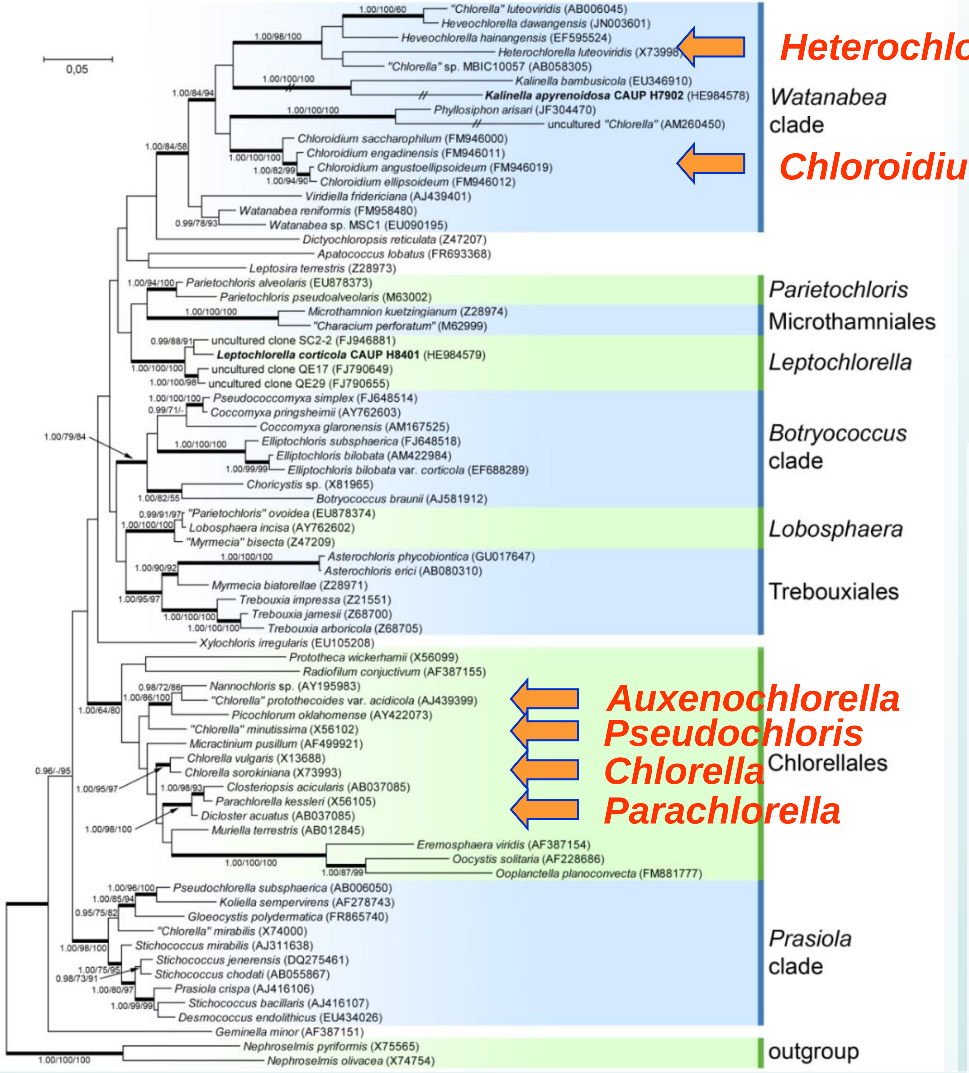
Pseudochloris wilhelmii

("Ch. minutissima")

An et al. (1999), Huss et al. (1999), Krienitz et al. (2004), Darienko et al. (2010), Neustupa et al. (2009), Fučíková & Lewis (2012), Somogyi et al. (2013)

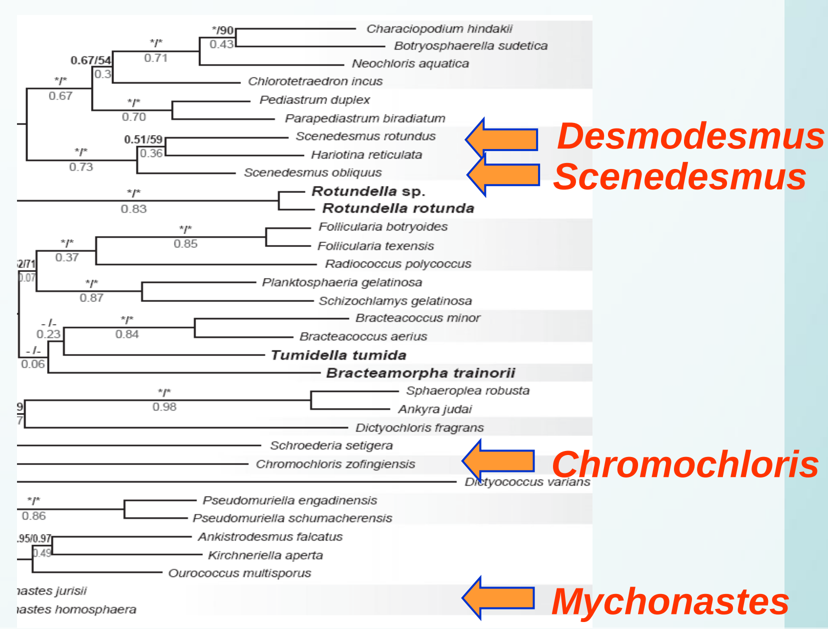
Trebouxiophyceae, *Chlorella*

Trebouxiophyceae:

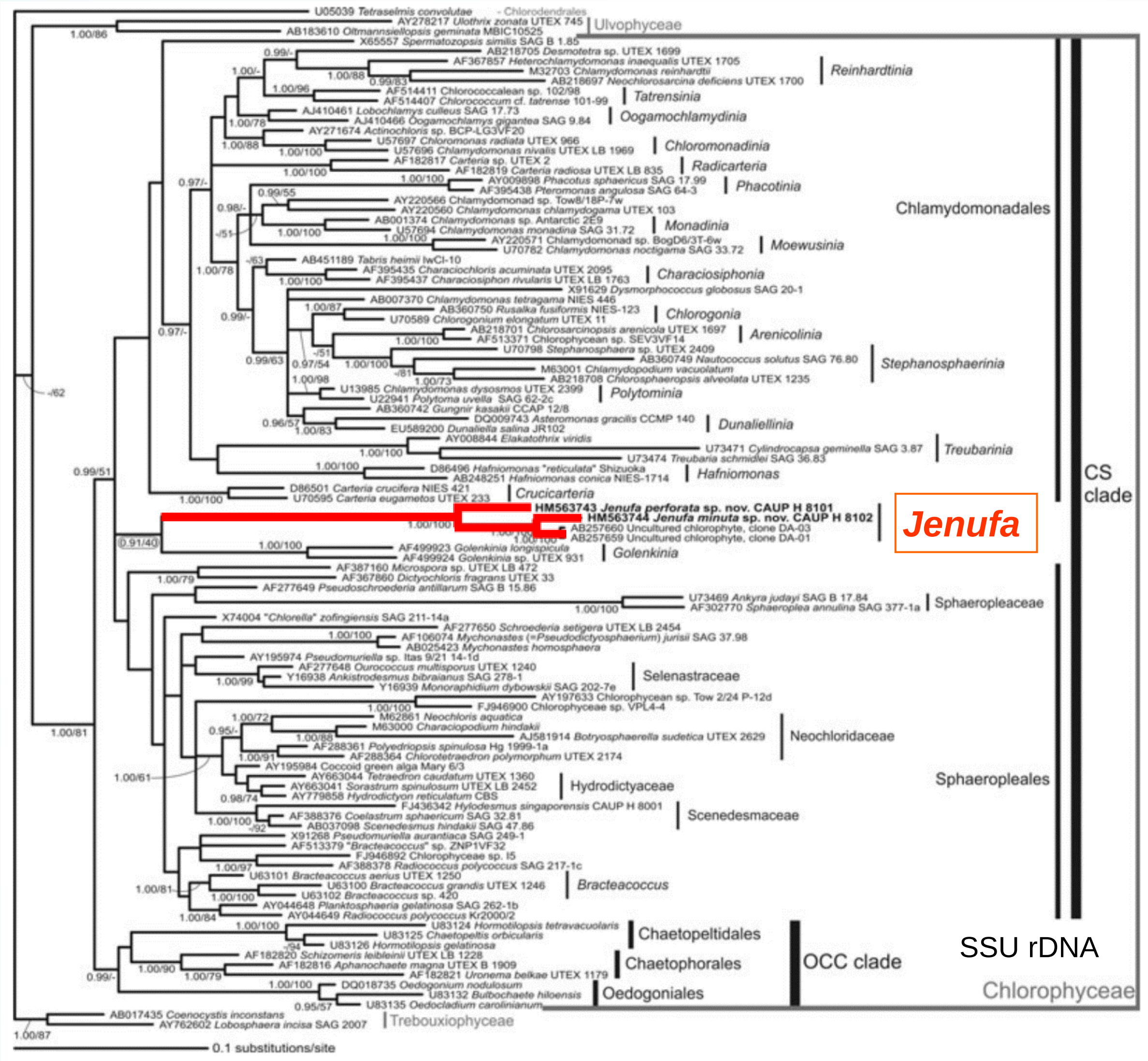


- In subaerial conditions, the drought stress drives selection towards the globular forms with low surface-to-volume ratio
- Traditionally circumscribed *Chlorella* species fall into at least 10 different lineages/genera

Chlorophyceae:



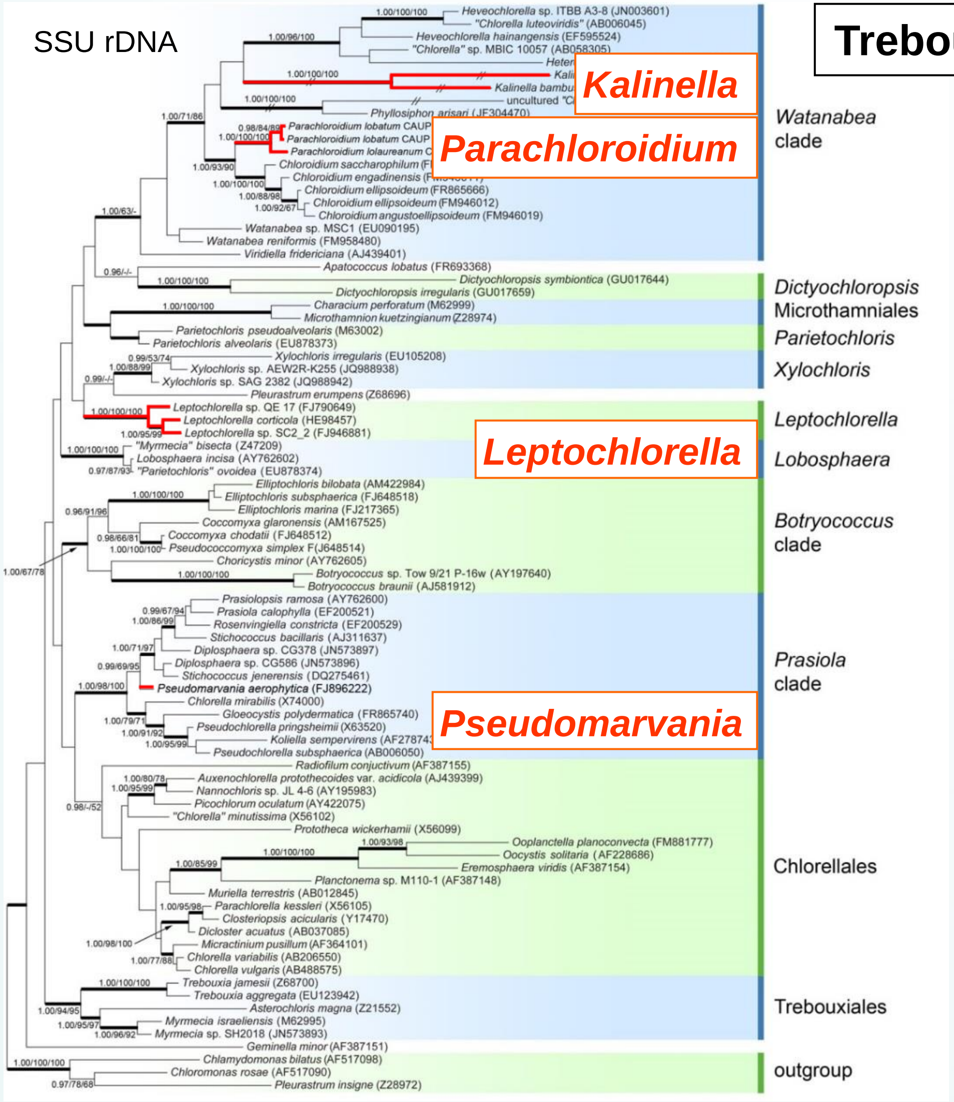
Trebouxiophyceae, *Chlorella* – cryptic genera



Chlorophyceae:

Němcová et al. (2011): *Journal of Phycology* **47**, 928-938

Trebouxiophyceae, *Chlorella* – cryptic genera

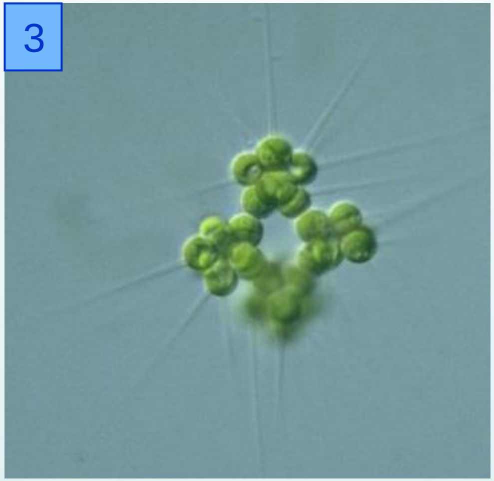


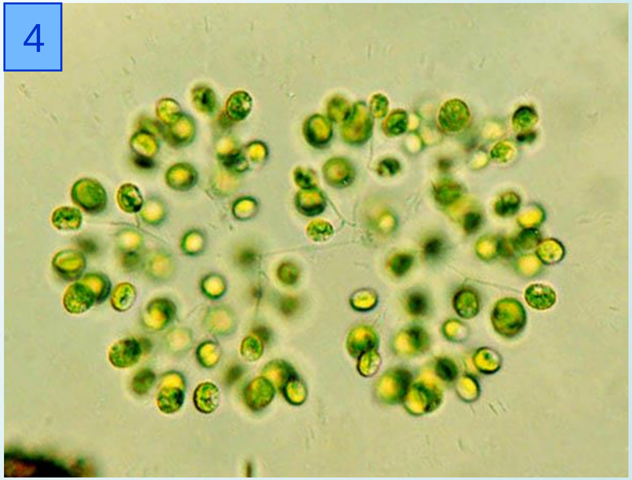
Trebouxiophyceae:

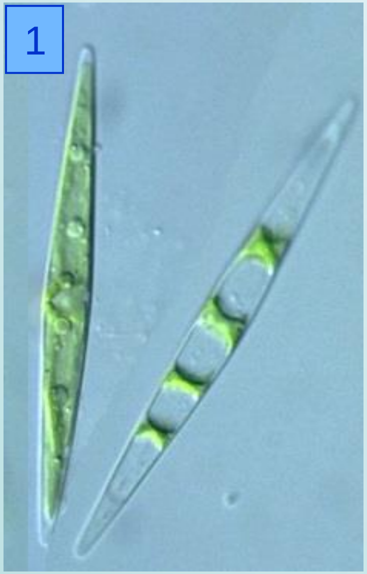
Neustupa et al. (2013): *Phycologia* **52**, 411-421; Neustupa et al. (2013): *IJSEM* **63**, 377-387 ; Neustupa et al. (2009): *Phycological Research* **57**, 159-169; Eliáš & Neustupa (2009): *Fottea* 9, 169-177

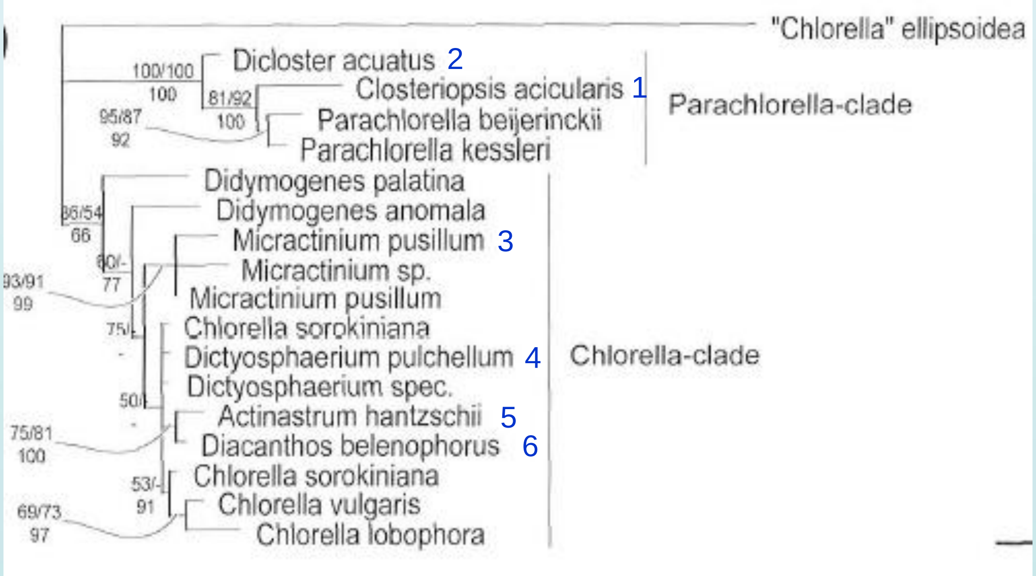
Trebouxiophyceae, Chlorellaceae

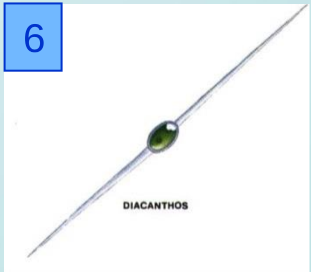
- morphologically distinct planktonic genera are close related to *Chlorella*







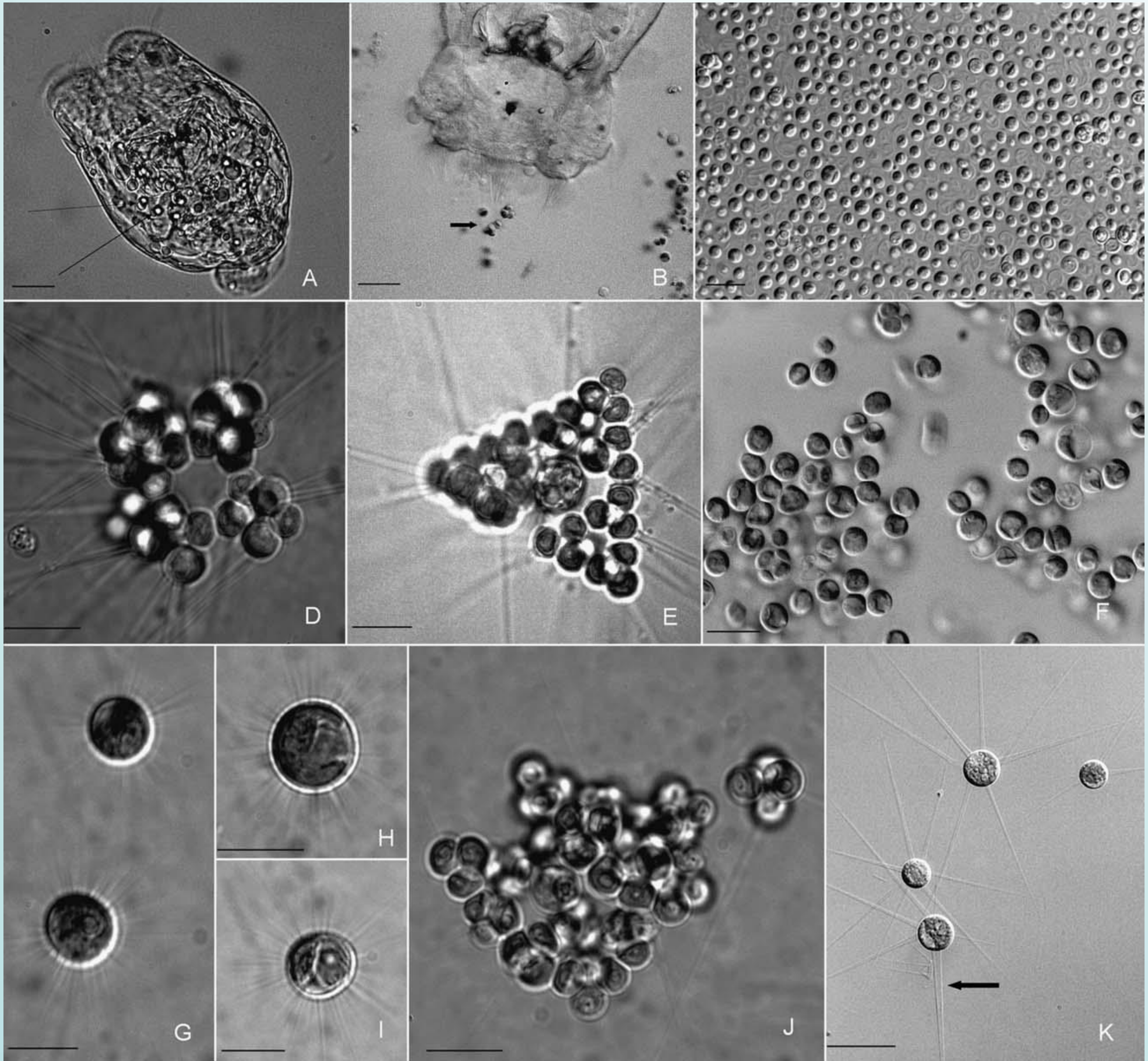


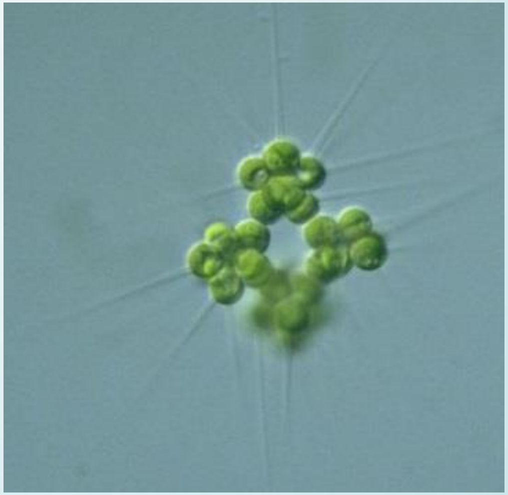


Krienitz et al. (2004): *Phycologia* **43**, 529-542

Trebouxiophyceae, Chlorellaceae

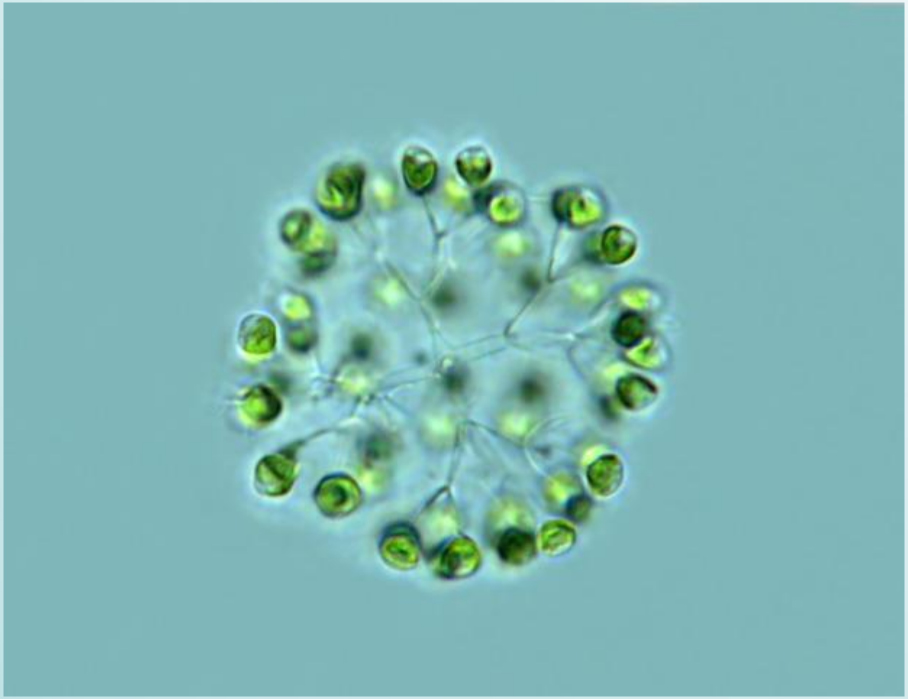
- Luo et al. (2006)
- production of spines in *Micractinium* as a result of predation pressure by *Brachionus*

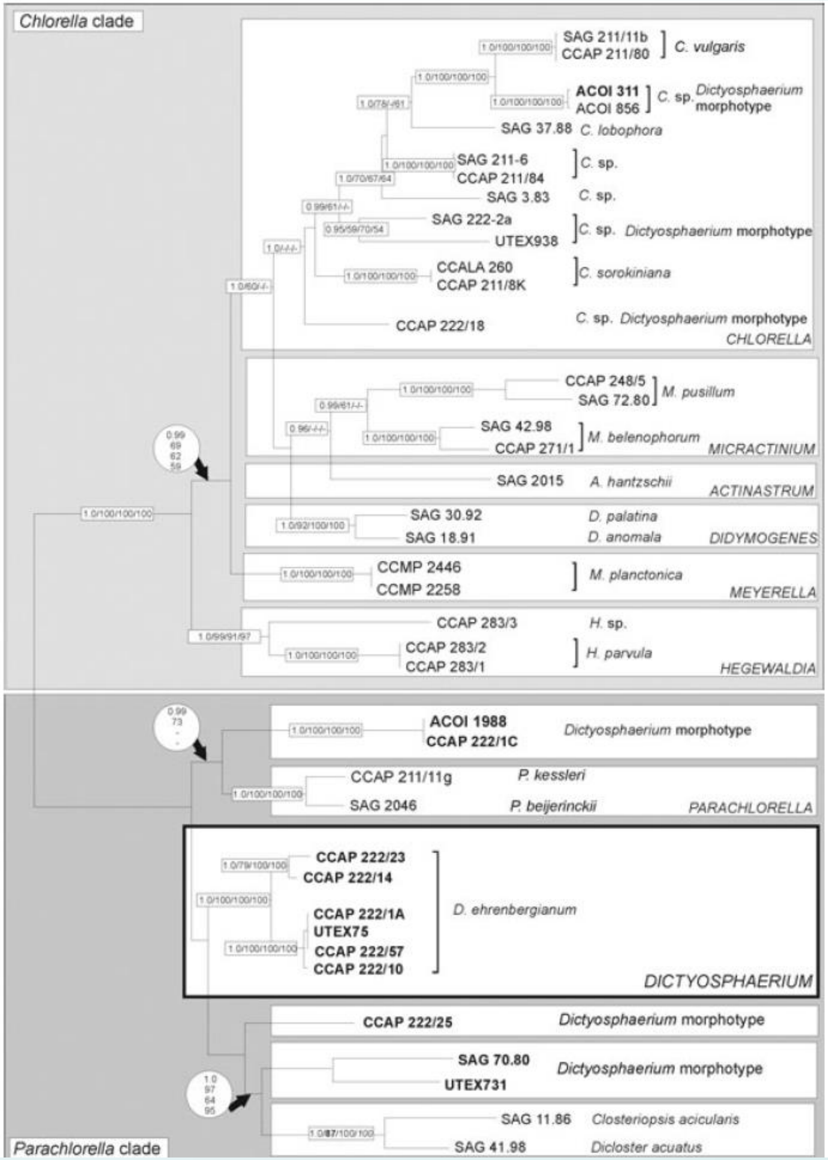




Trebouxiophyceae, Chlorellaceae

- Chlorella-clade + Parachlorella-clade
- *Dictyosphaerium* – highly polyphyletic genus

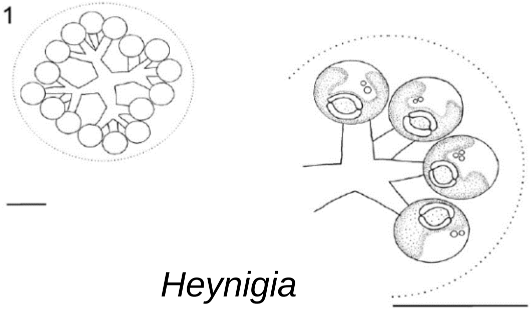




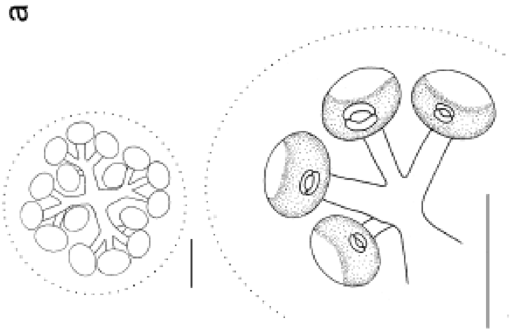
Krienitz et al. (2004): *Journal of Phycology* **46**, 559-563

Dictyosphaerium

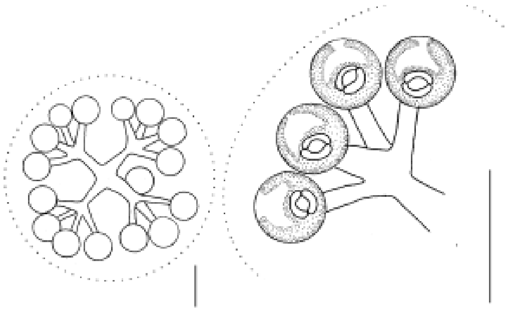
- 9 cryptic genera



Heynigia

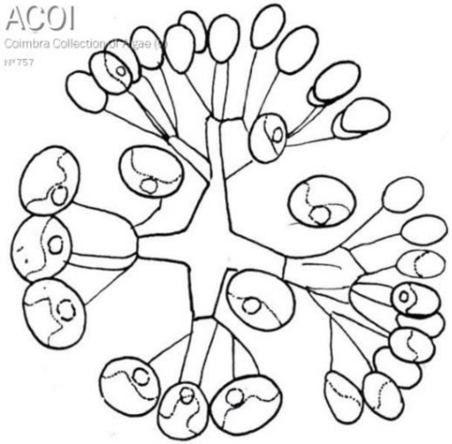


Dictyosphaerium

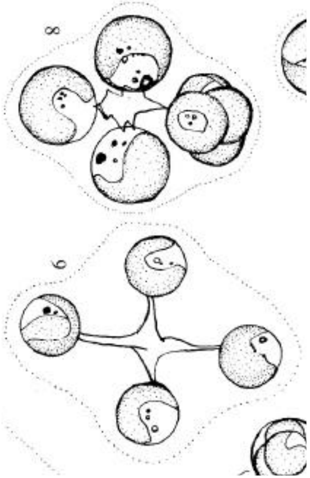


Mucidosphaerium

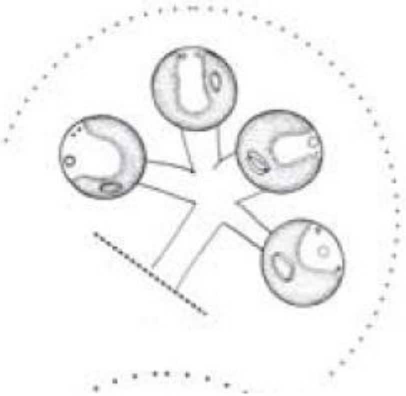
Hindakia



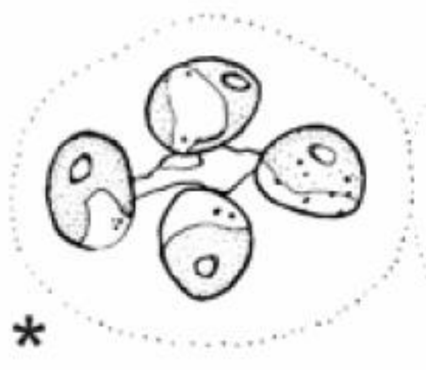
Mychonastes



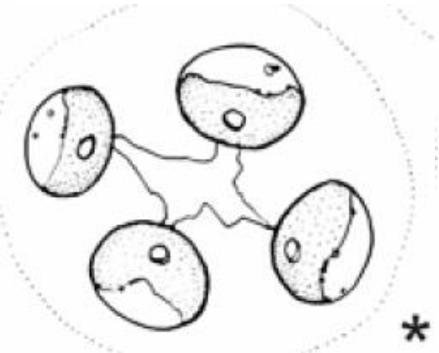
Chlorella



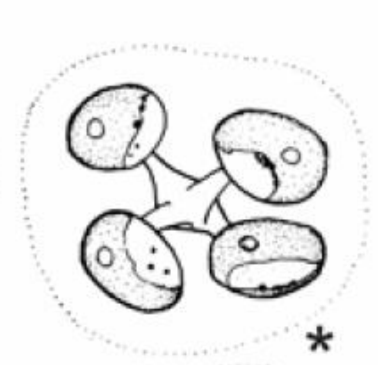
Compactochlorella



Kalenjinia



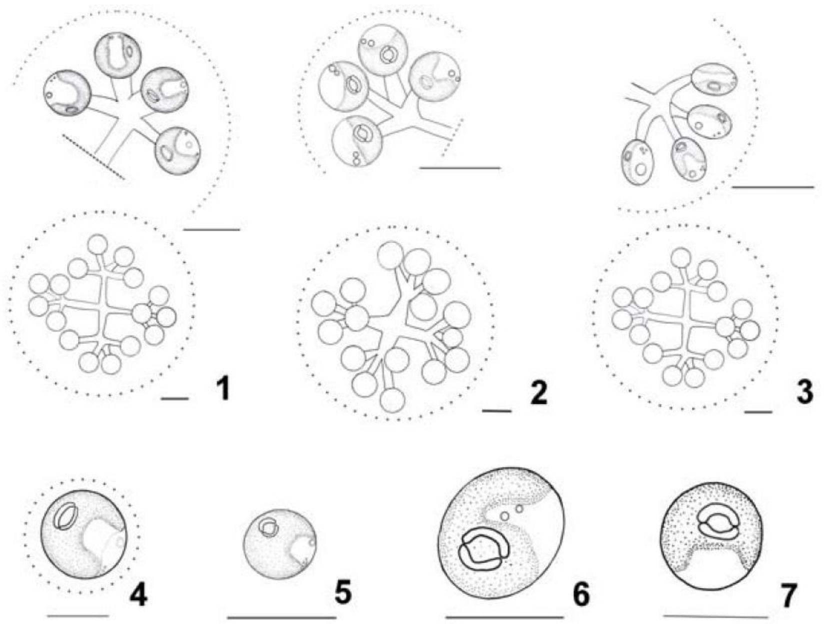
Masaia



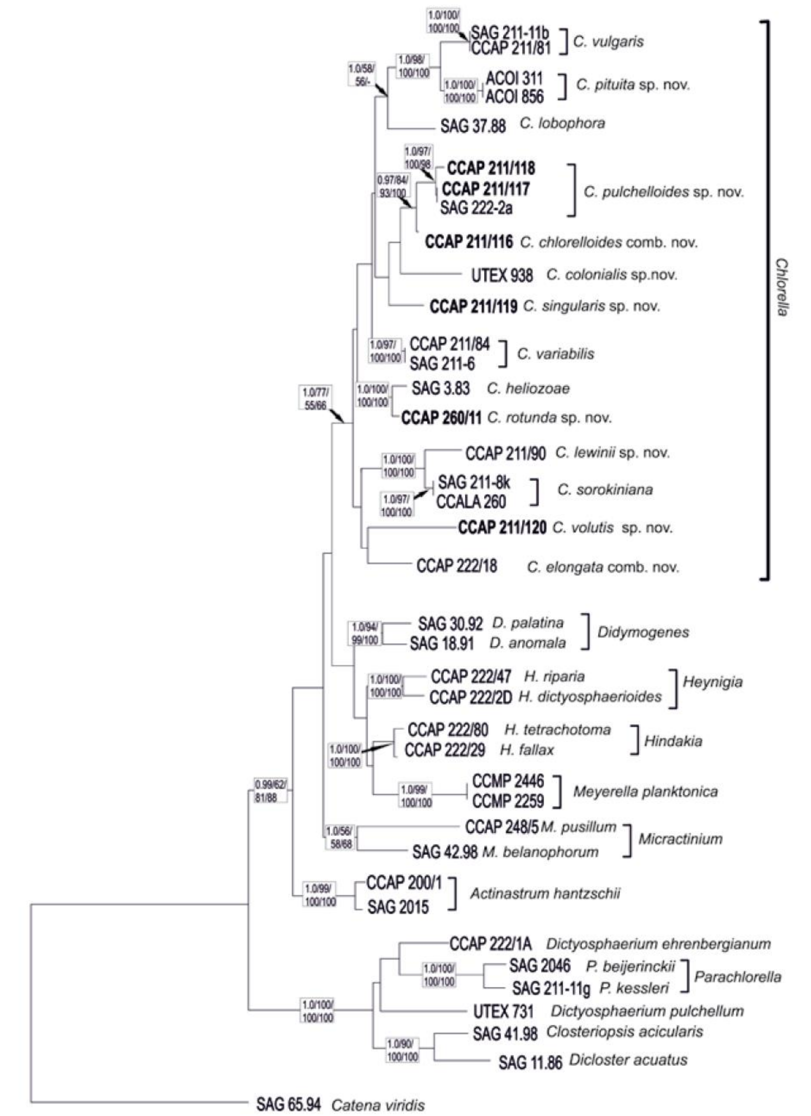
Krienitz et al. (2012): *Fottea* **12**, 231-253; Bock et al. (2010): *European Journal of Phycology* **45**, 267-277; Bock et al. (2011): *Journal of Phycology* **47**, 638-652; Krienitz et al. (2011): *Phycologia* **50**, 89-106

Trebouxiophyceae, Chlorellaceae

- Chlorella-clade
  - *Chlorella* – unicellular and colonial (*Dictyosphaerium*-like) species



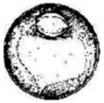
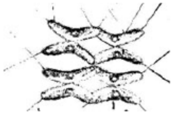
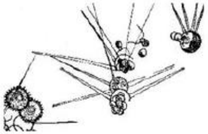
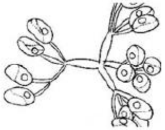
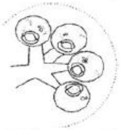
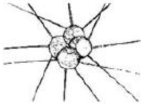
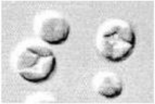
Figs 1–7. Drawings of light microscopical characters of *Chlorella* species. Iconotypes: (1) *Chlorella pituita*, authentic strain ACOI 311; (2) *Chlorella pulchelloides*, authentic strain CCAP 211/118; (3) *Chlorella coloniales*, authentic strain UTEX 938; (4) *Chlorella singularis*, authentic strain CCAP 211/119; (5) *Chlorella rotunda*, authentic strain CCAP 260/11; (6) *Chlorella lewinii*, authentic strain CCAP 211/90; (7) *Chlorella volutis*, authentic strain CCAP 211/120. Scale bars 10 µm.

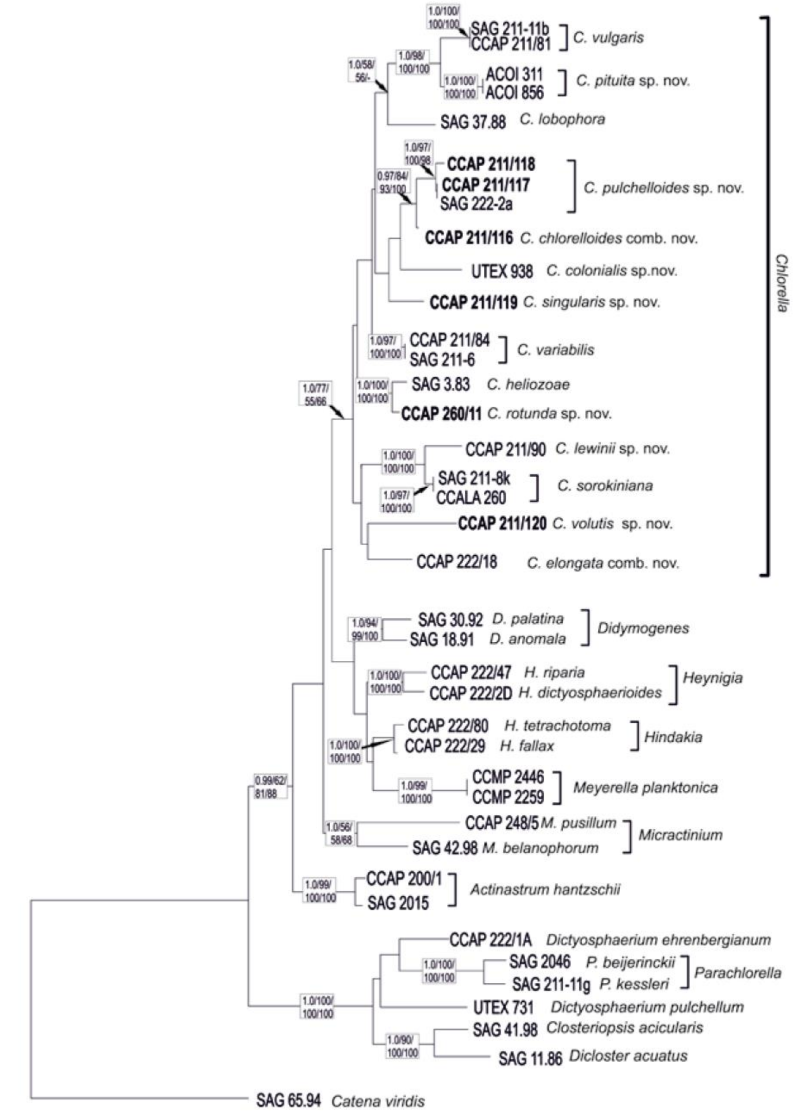


Bock et al. (2011): *Fottea* **11**, 293-312

Trebouxiophyceae, Chlorellaceae

- Chlorella-clade

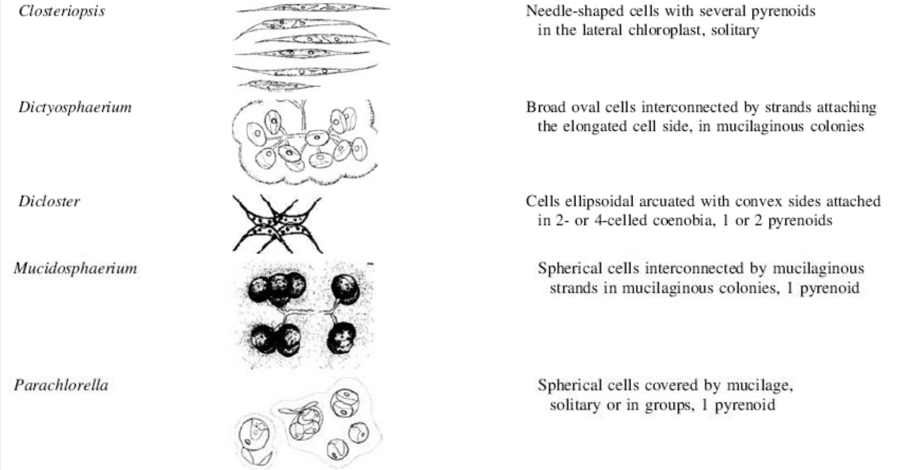
Genus	Drawing	Main diacritic morphology
Actinastrum		Cells rod-shaped, elongated, radially arranged in coenobia
Chlorella		Spherical or broad oval cells, with one pyrenoid, solitary or in mucilage covered colonies
Didymogenes		Cells cylindrical curved with convex side attached in 2-, 4- or 16-celled coenobia, one pyrenoid, spines
Hegewaldia		Spherical cells with or without bristles, solitary or in colonies, 1 pyrenoid, facultative oogamy
Hindakia		Broad oval cells interconnected by strands attaching the apical pole, in mucilaginous colonies, 1 pyrenoid
Heynigia		Spherical cells interconnected by mucilaginous strands in mucilaginous colonies, 1 pyrenoid
Micractinium		Spherical cells with long bristles, in colonies, 1 pyrenoid
Meyerella		Cells short cylindrical, small, without mucilage, solitary, pyrenoid missing



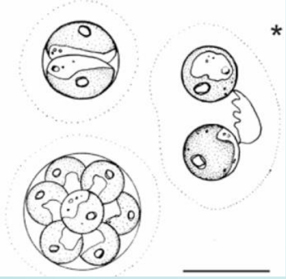
Krienitz & Bock (2012): *Hydrobiologia* **698**: 295 – 326

Trebouxiophyceae, Chlorellaceae

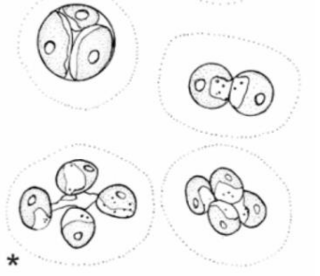
- Parachlorella-clade



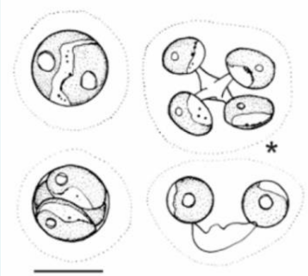
Closteriopsis	Needle-shaped cells with several pyrenoids in the lateral chloroplast, solitary
Dictyosphaerium	Broad oval cells interconnected by strands attaching the elongated cell side, in mucilaginous colonies
Dicloster	Cells ellipsoidal arcuated with convex sides attached in 2- or 4-celled coenobia, 1 or 2 pyrenoids
Mucidosphaerium	Spherical cells interconnected by mucilaginous strands in mucilaginous colonies, 1 pyrenoid
Parachlorella	Spherical cells covered by mucilage, solitary or in groups, 1 pyrenoid



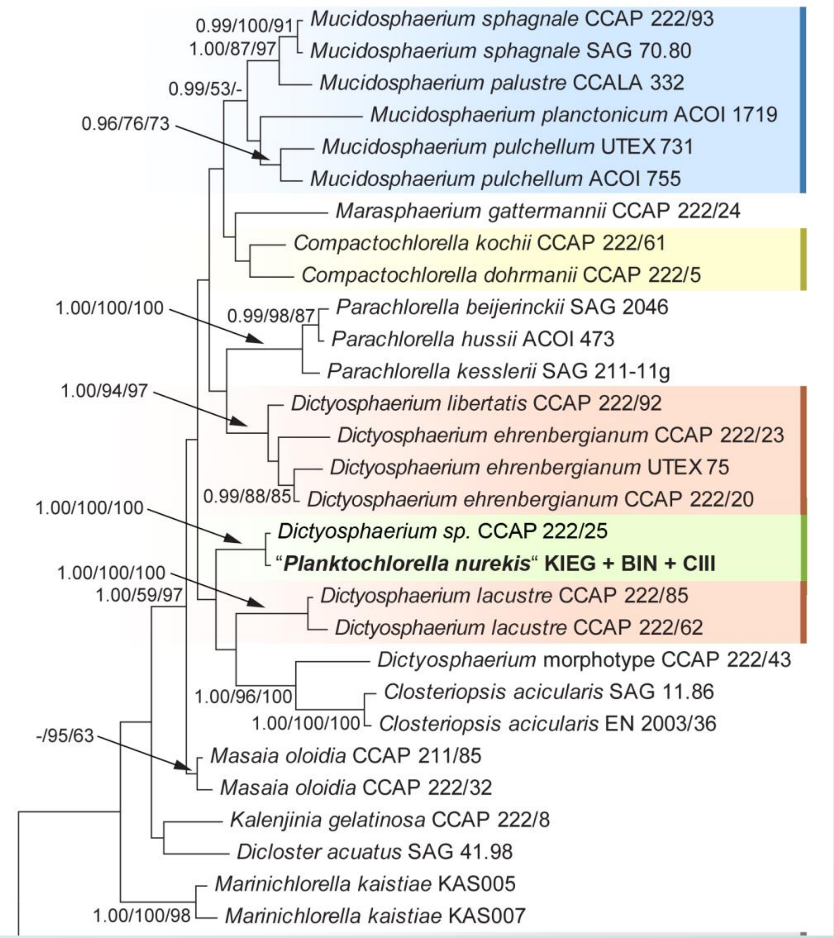
Marasphaerium

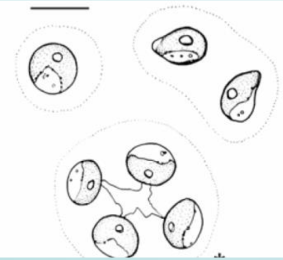


Compactochlorella

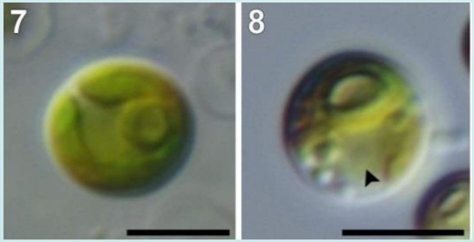


Masaia





Kalenjinia

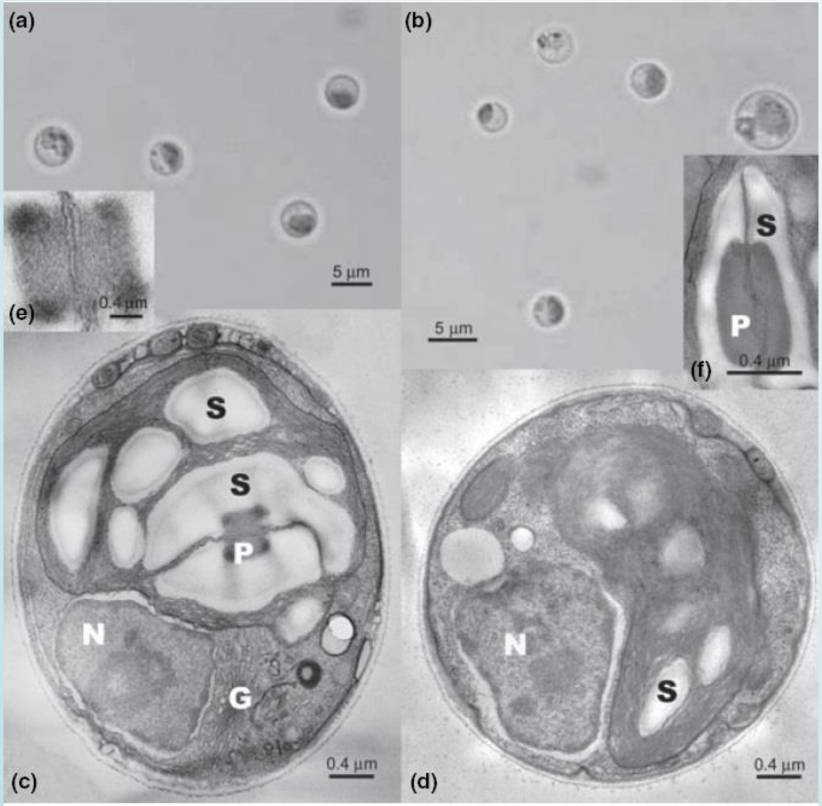


Planktochlorella

Krienitz & Bock (2012): *Hydrobiologia* **698**, 295 – 326; Krienitz et al. (2012): *Fottea* **12**, 231-253; Škaloud et al. (2014): *Fottea* **14**, 53-62

Trebouxiophyceae, Chlorellaceae

- Parachlorella-clade
    - *Marinichlorella kaistiae*



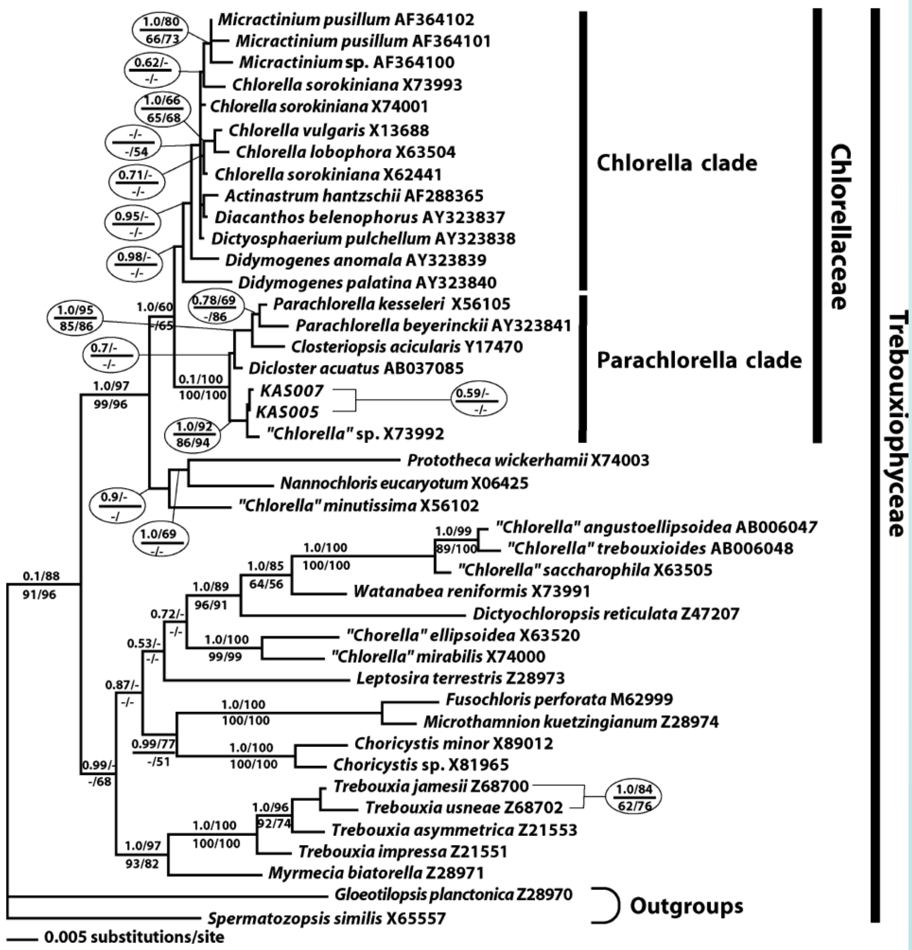


FIG. 2. Maximum-likelihood (ML) tree inferred from 18S rRNA gene sequences, with *Gloeotilopsis planctonica* and *Spermatozopsis similes* a outgroup taxa. The numbers above each branch show posterior probabilities (0.50 and higher) of Bayesian analysis (1,000,000 generations, left) and bootstrap values (50% or more) of ML (500 replicates, right). The numbers below each branch show bootstrap value (50% or more) of ML distance (1000 replicates, left) and maximum parsimony (1000 replicates, right). Some duplicate strains of som genera are not included in the tree because they have the same sequences. Branch lengths correspond to evolutionary distances. A distance of 0.005 is indicated by the scale.

Aslam et al. (2007): *Journal of Phycology* **43**, 576 – 584

Trebouxiophyceae, Chlorellles

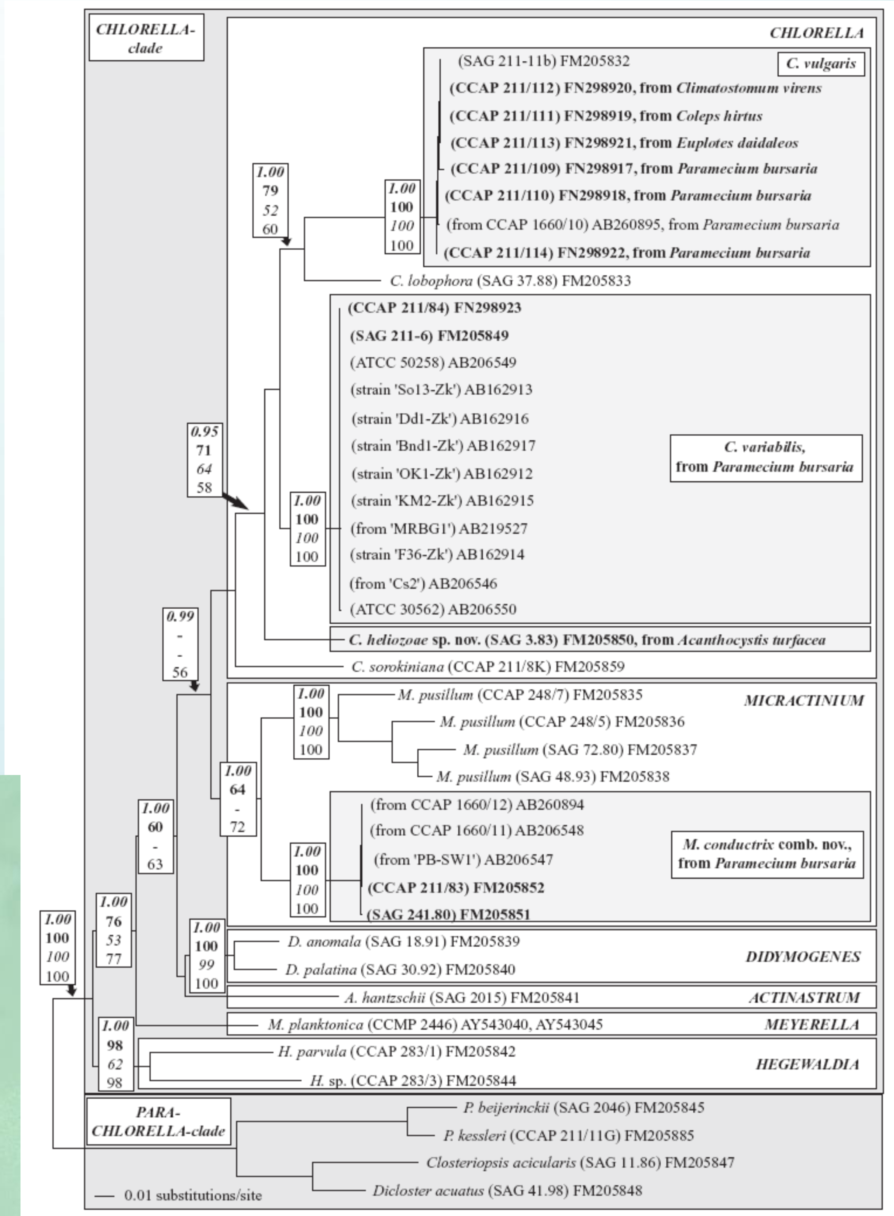
- ***Chlorella*-clade**
  - symbionts

environmental microbiology

society for applied microbiology sfam

Environmental Microbiology (2010) doi:10.1111/j.1462-2920.2010.02333.x

The systematics of *Zoochlorella* revisited employing an integrative approach



Chlorellales, practical use

- high growth rate – a popular model organism
- *Chlorella* has the highest chlorophyll content from al studied genera
- large scale cultivations

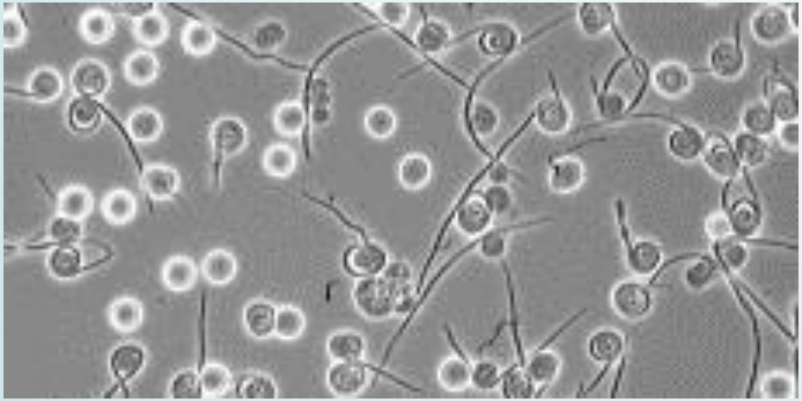
Chlorellales, practical use

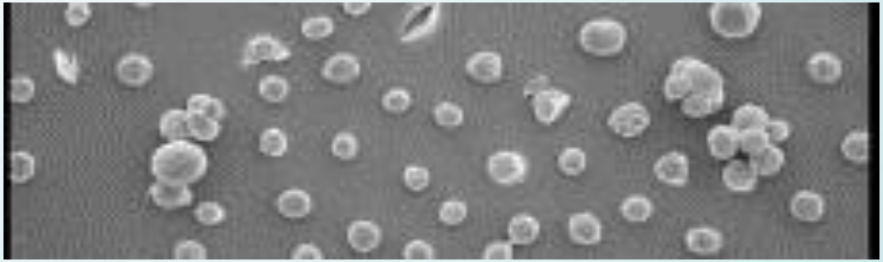
- **chlorophyll:**
  - anti-inflammatory effects, supportswound healing
  - elimination of heavy metals and toxins
  - anaemia therapy
  - anti-tumor activity
  - supports immune system
  - reducing high blood pressure

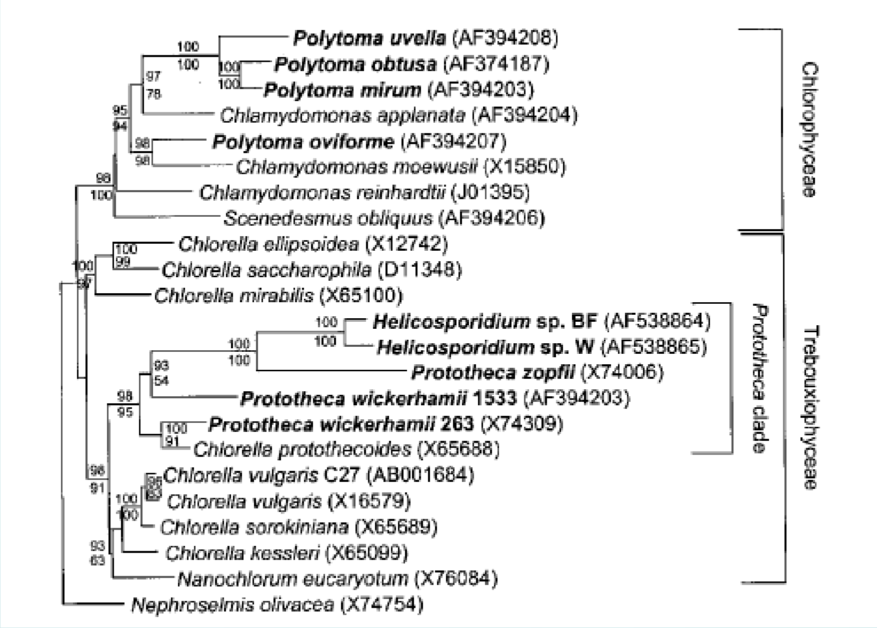
Chlorella tabs

Chlorellales, *Helicosporidium*

- parasitic organism, described from insect larvae (1921)
- classified to Protozoa, then Fungi
- 18S rRNA analysis – Trebouxiophyceae
- autosporogenesis

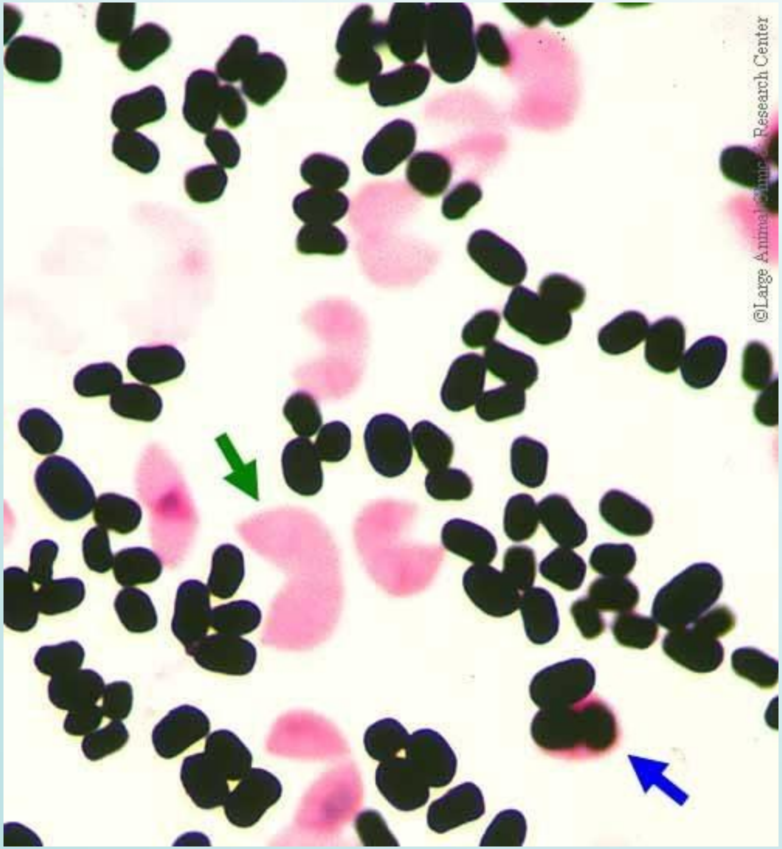






Chlorellales, *Prototheca*

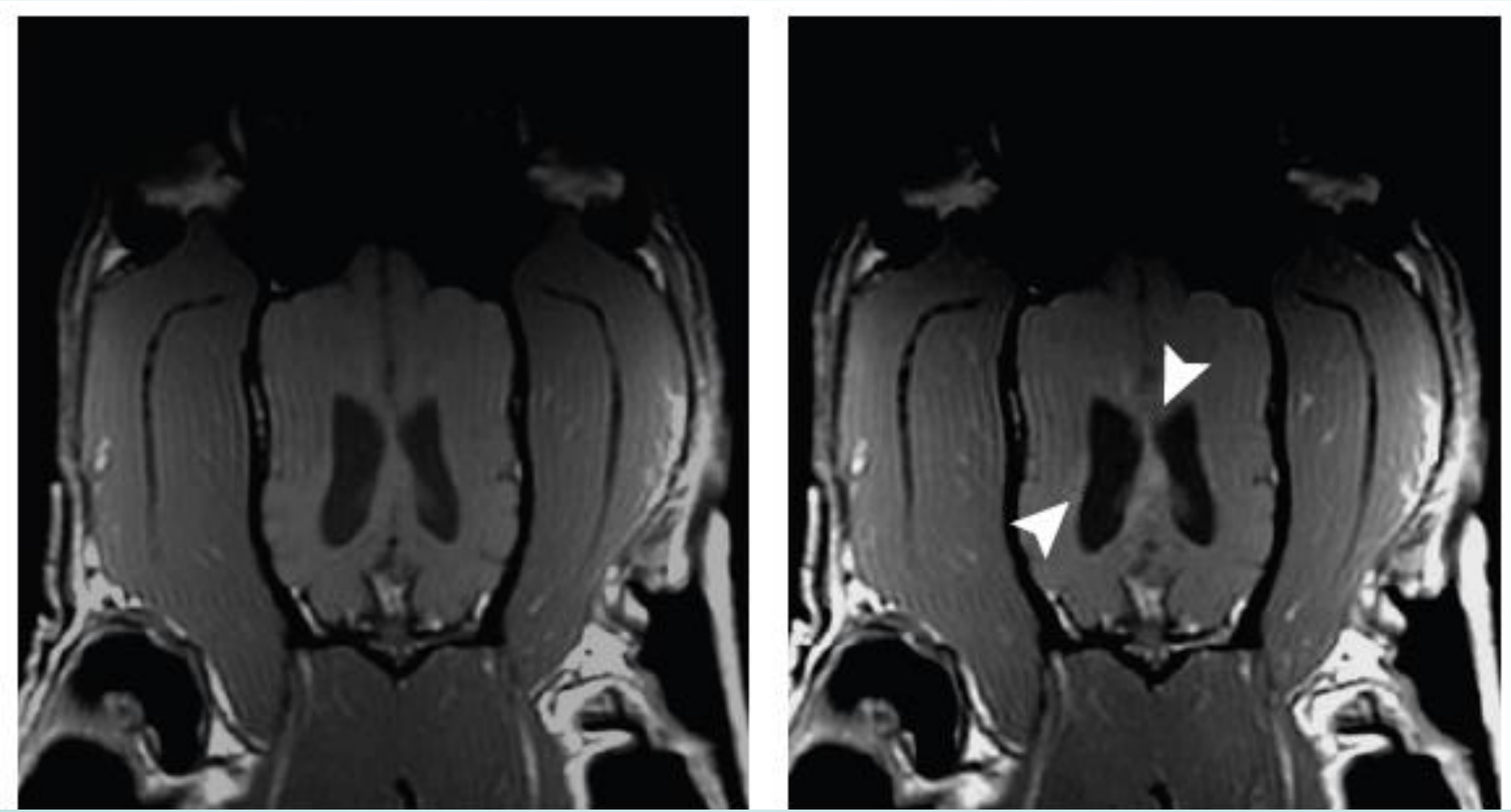
- heterotrophic, pathogenic organism
- *protothecosis*


©Large Animal Clinic & Research Center


©Large Animal Clinic & Research Center

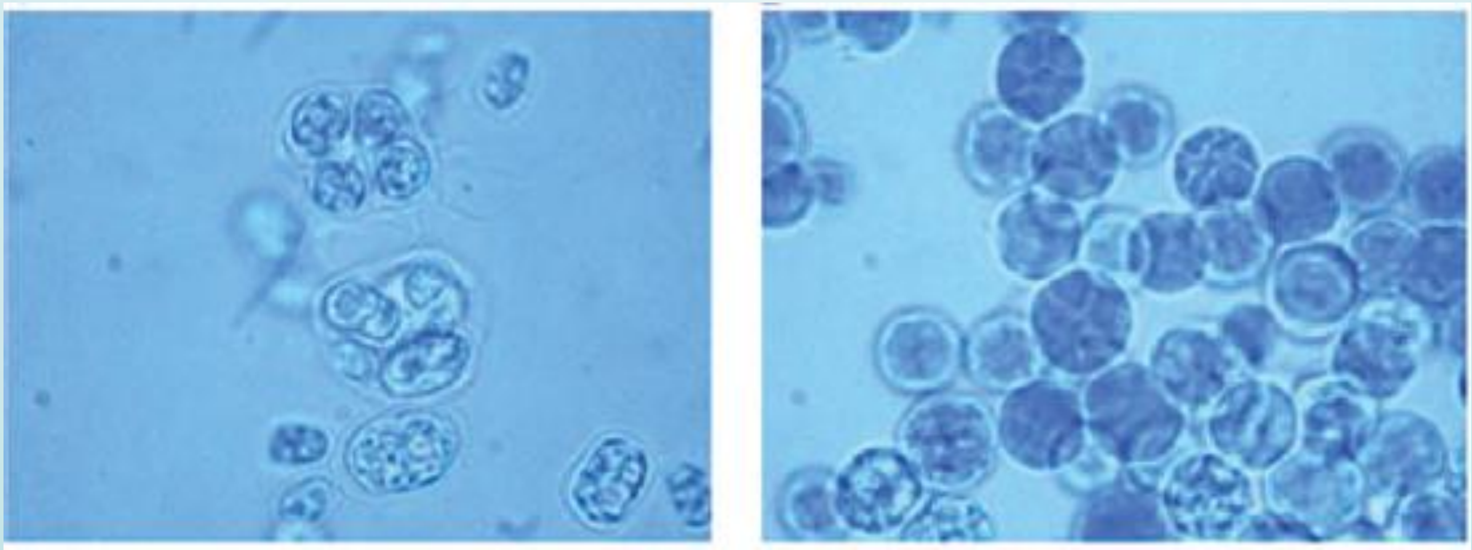
Protothecosis

- 6-year-old dog: malfunction of coordination
- surgery of cranial tendon prior the disease
- magnetic resonance – brain lysis (meningoencefalitis)
- the dog was put to death

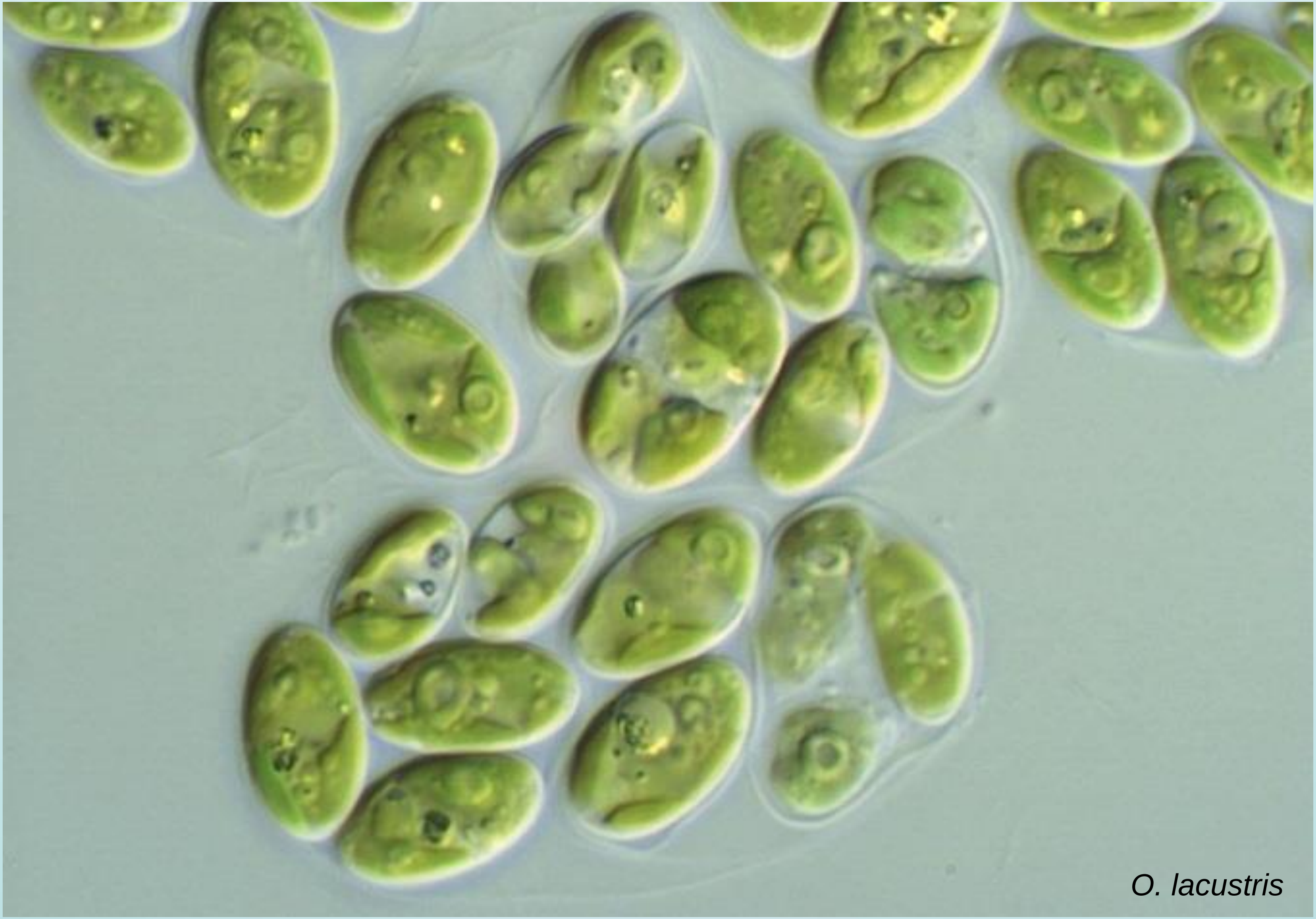


Protothecosis

- humans – infections from soil, water, ...
- skin at immunosupresive patients
- first incidence - 1964 (Sierra Leone – foot lysis)
- mortality 2,2%

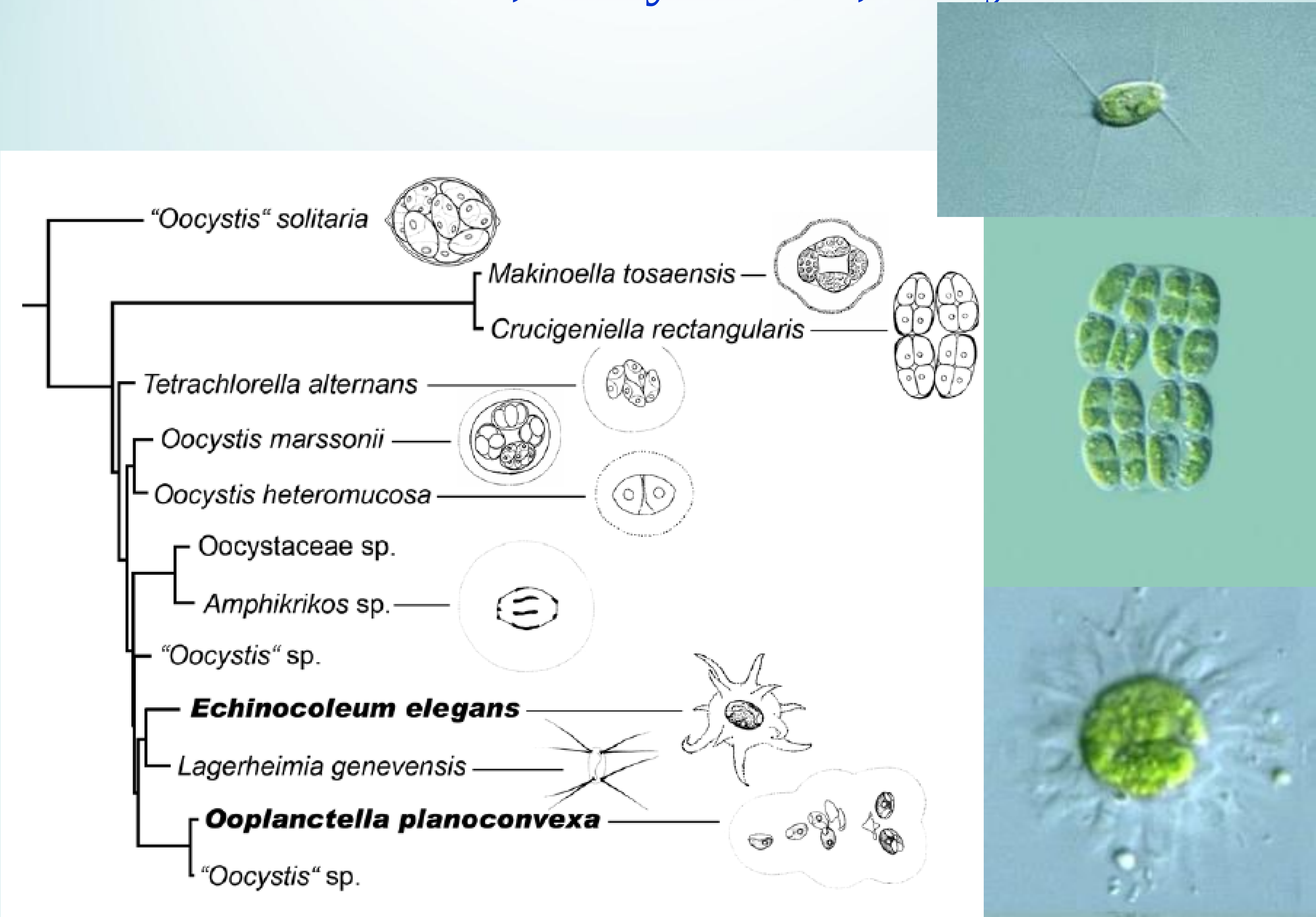


Chlorellales, Oocystaceae, *Oocystis*



O. lacustris

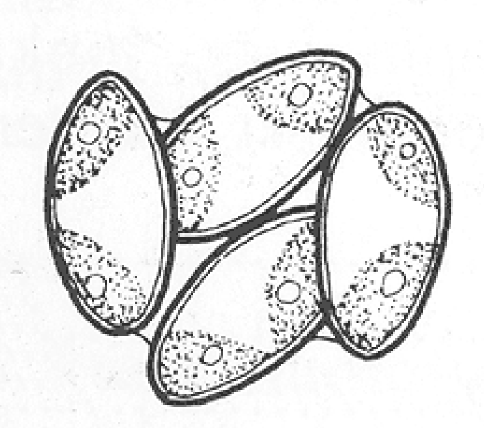
Chlorellales, Oocystaceae, *Oocystis*



Chlorellales, Oocystaceae

Makinoella

Crucigeniella

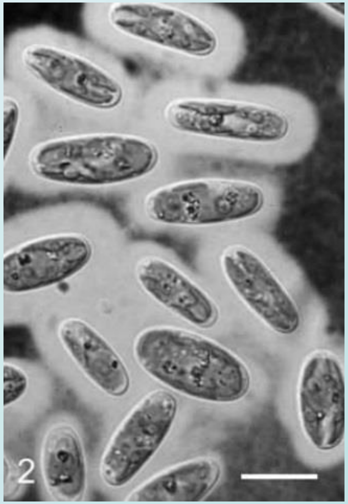


Tetrachlorella

Amphikrikos

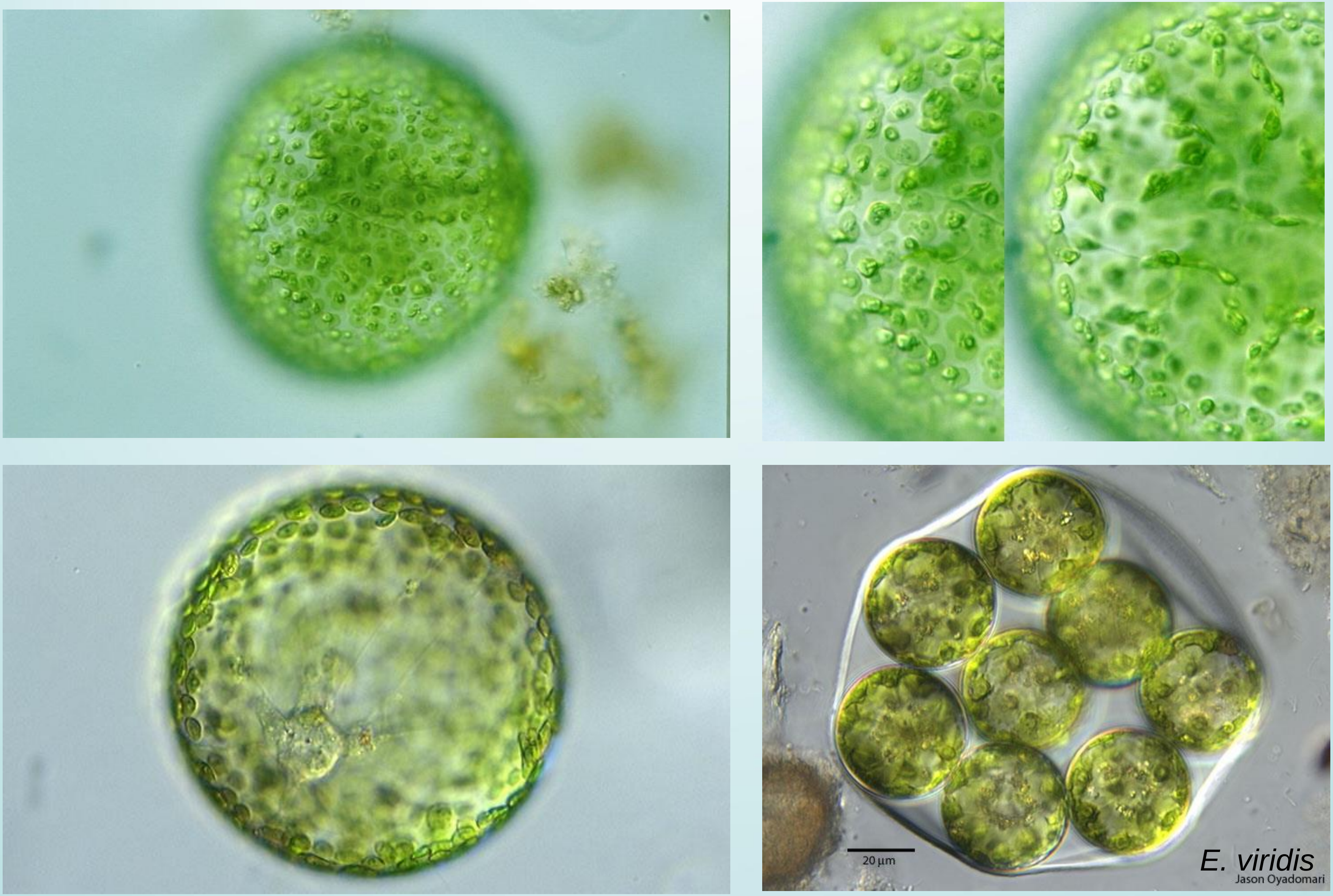
Lagerheimia

Echinocoleum



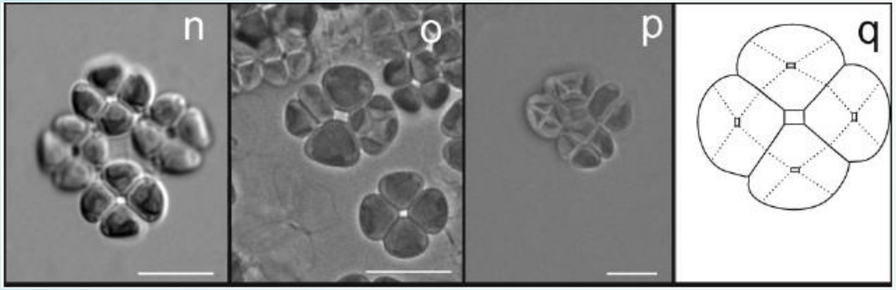
Elongatocystis

Chlorellales, Oocystaceae, *Eremosphaera*

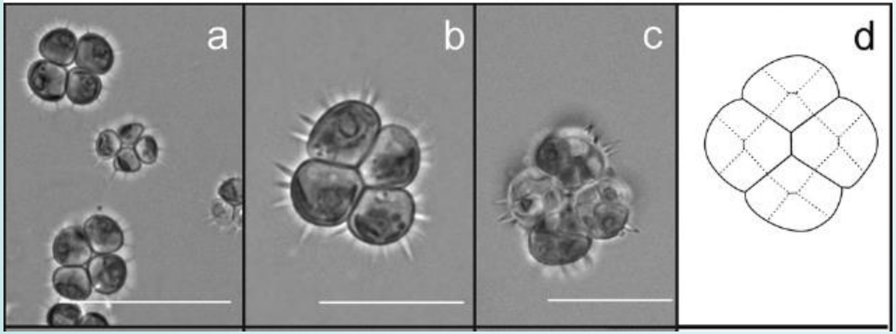


Trebouxiophyceae, tetraedrické kolonie

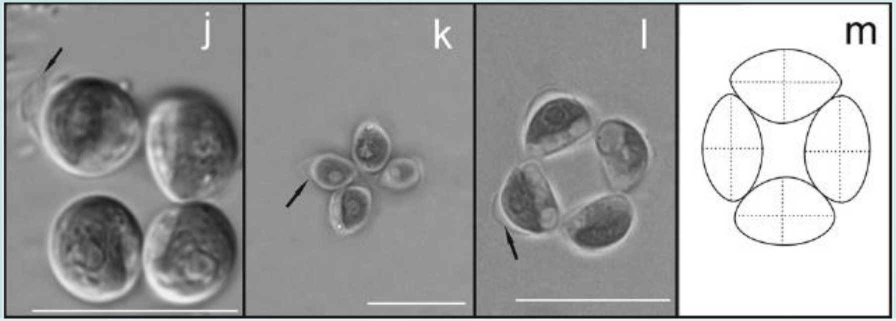
Lemmermannia – smooth colonies, small aperture

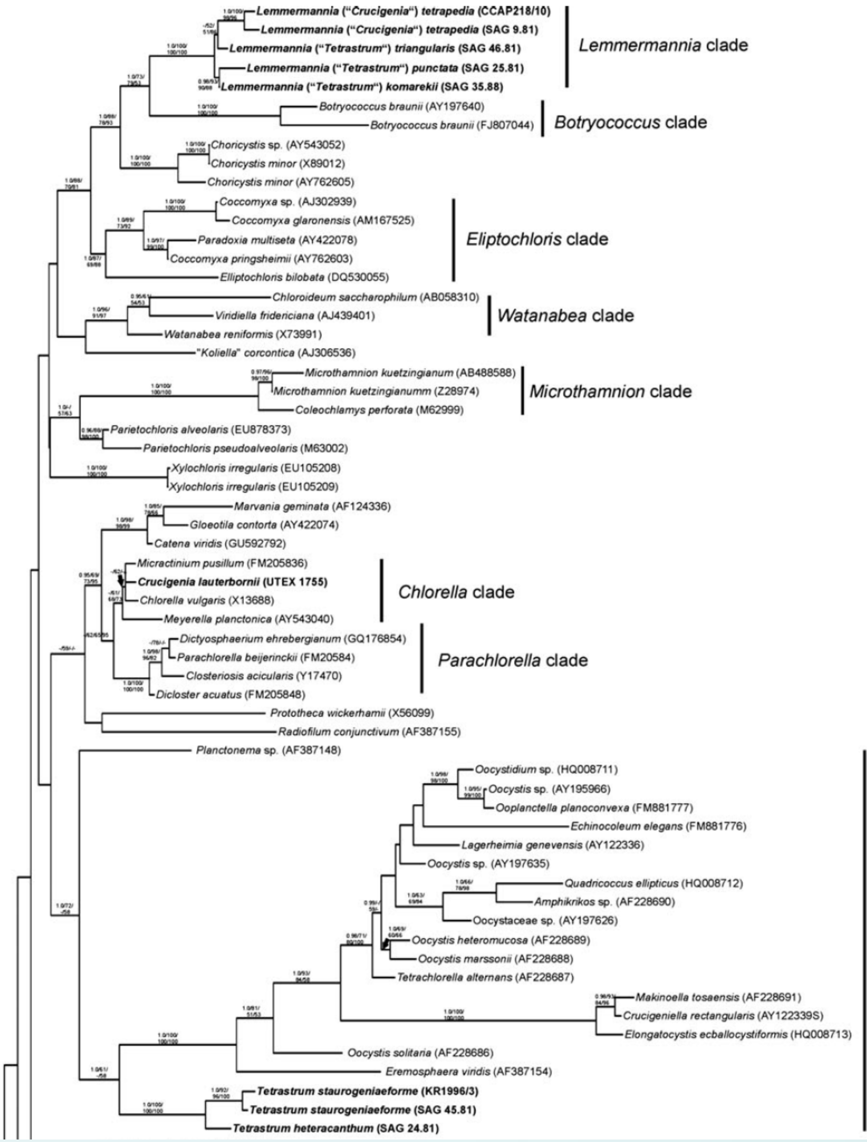


Tetrastrum – spiny colonies



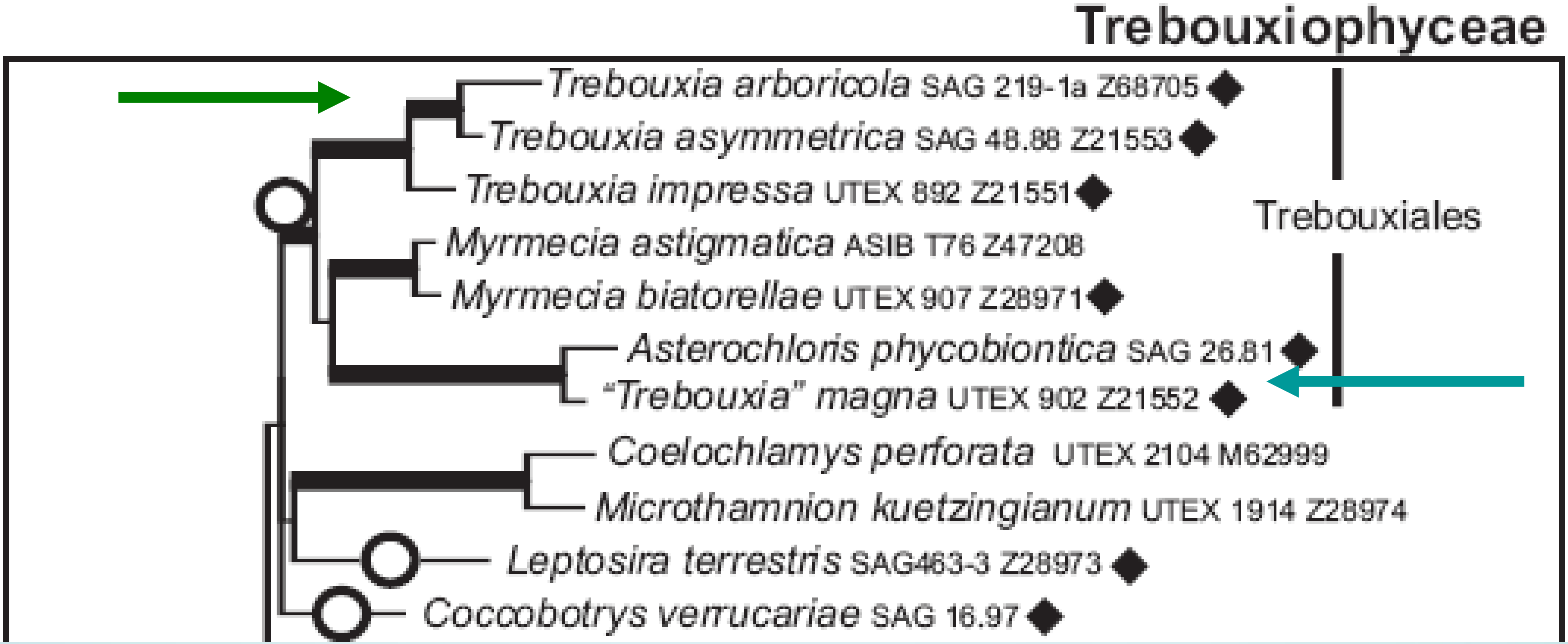
Crucigenia – smooth colonies, big aperture

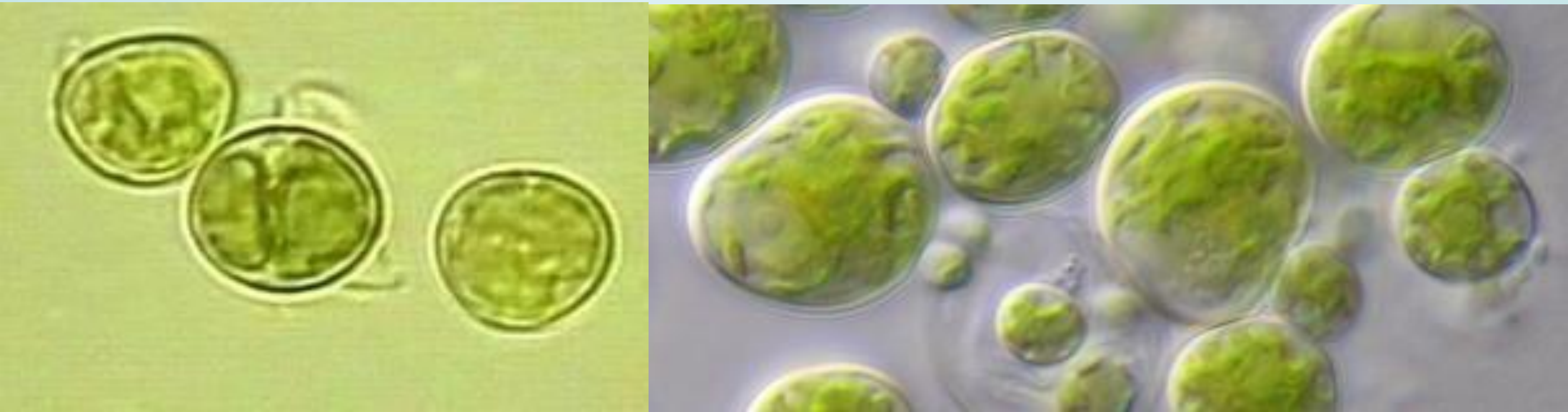




Bock et al. (2013): *Journal of Phycology* **49**, 329 – 339

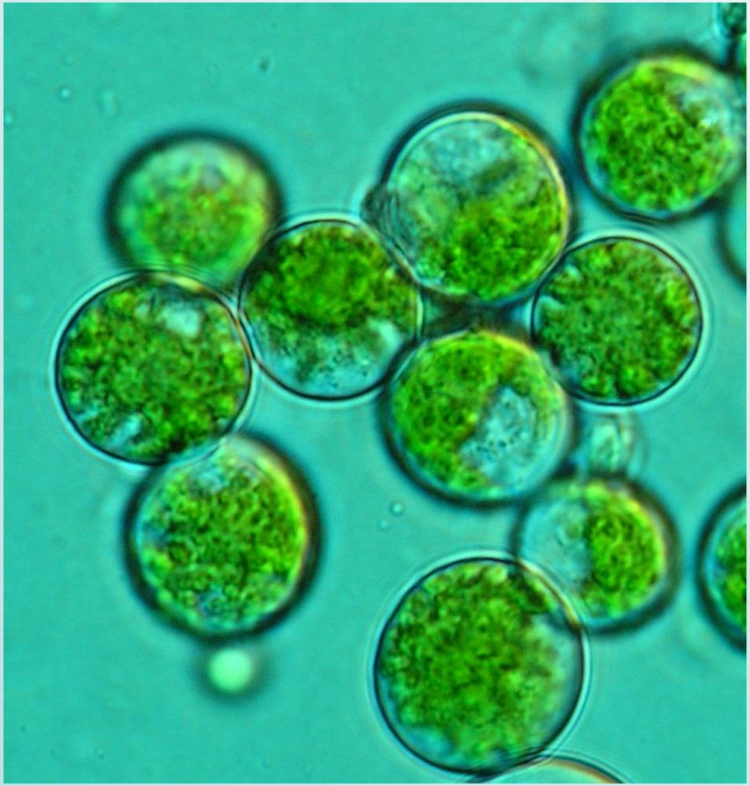
Trebouxiales

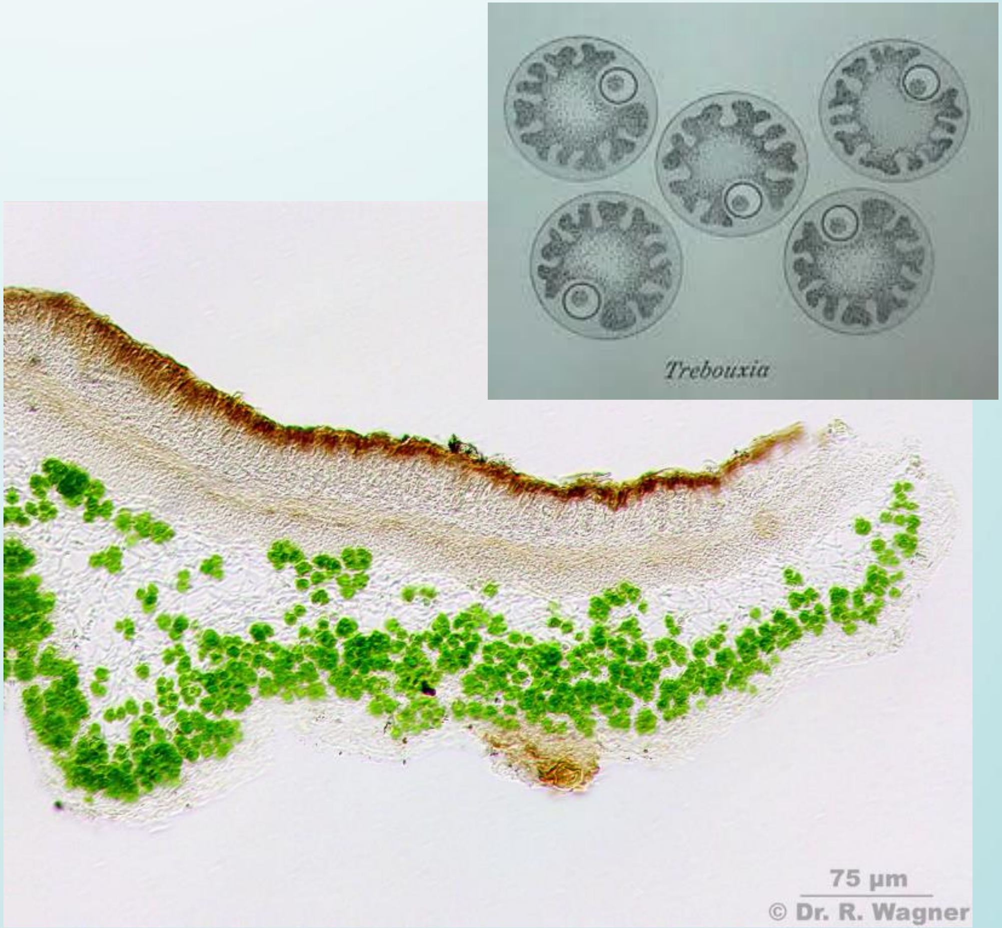




Trebouxiales, *Trebouxia*

- lichen endosymbiont, probably free-living, as well (bark)
- coccoid green alga with a central, asteroid plastid
- autospores, zoospores

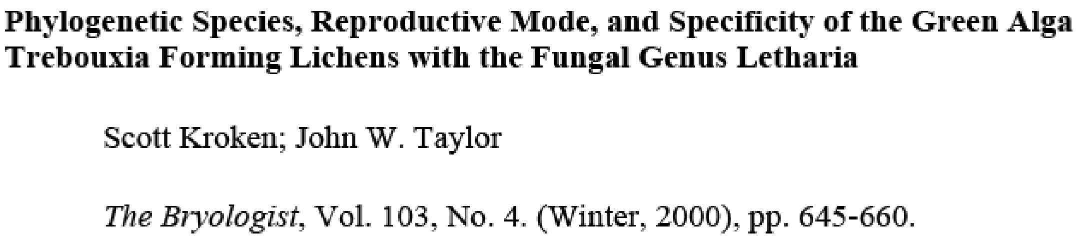




Trebouxiales, *Trebouxia*

© AJ Silverside

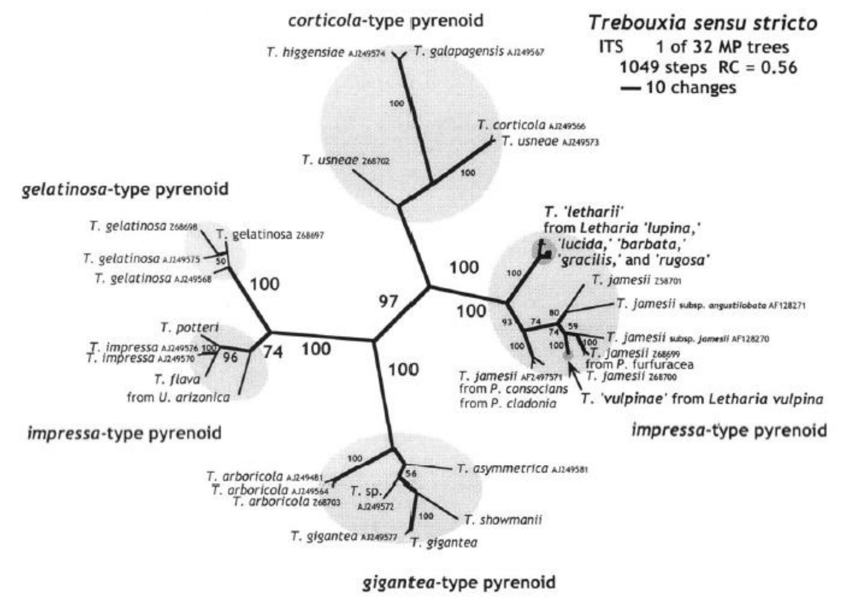
Trebouxiales, *Trebouxia*

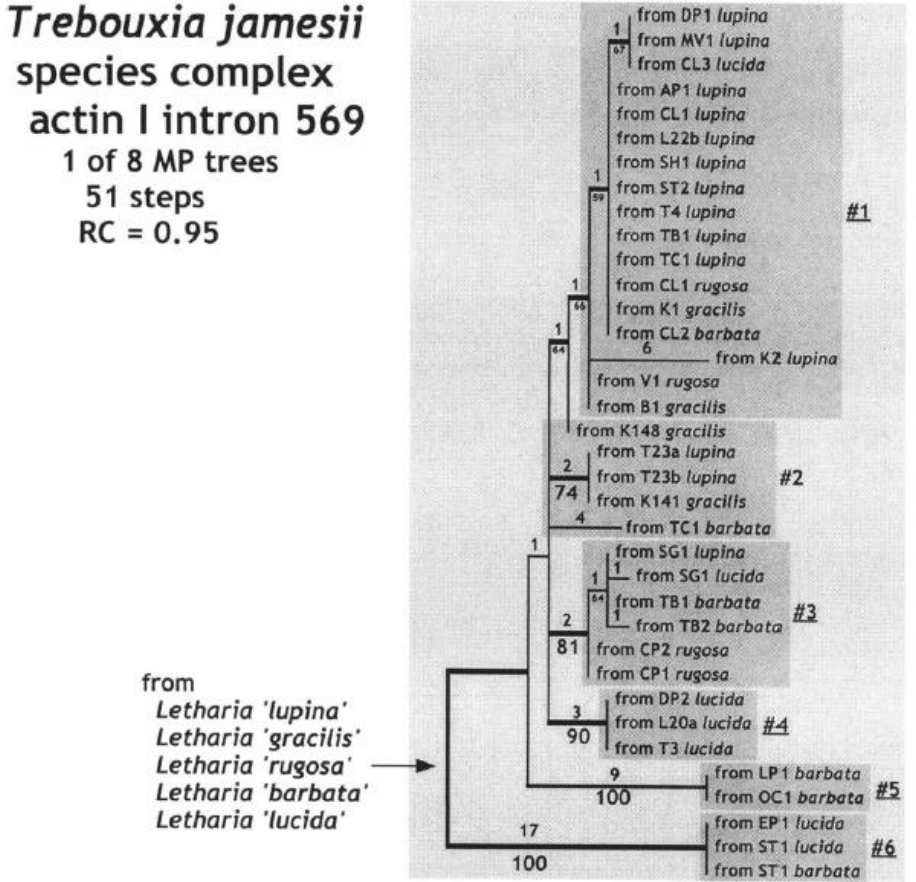


Phylogenetic Species, Reproductive Mode, and Specificity of the Green Alga Trebouxia Forming Lichens with the Fungal Genus Letharia

Scott Kroken; John W. Taylor

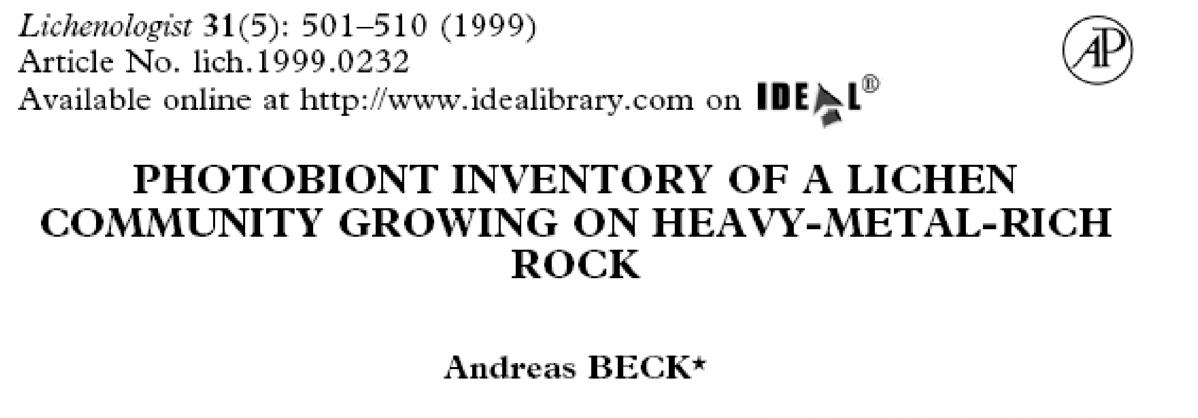
The Bryologist, Vol. 103, No. 4. (Winter, 2000), pp. 645-660.





Cryptic diversity* – e.g. *T. jamesii

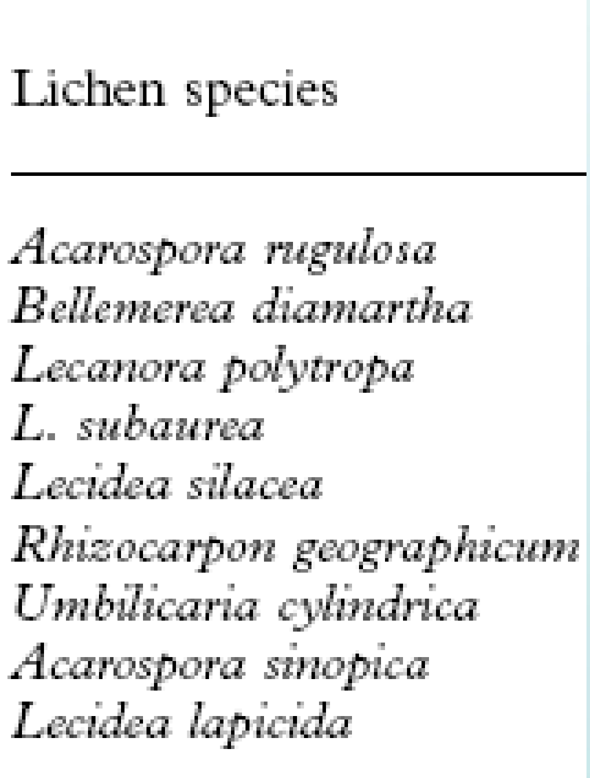
Trebouxiales, *Trebouxia*



Lichenologist **31**(5): 501–510 (1999)
Article No. lich.1999.0232
Available online at http://www.idealibrary.com on IDEAL®

PHOTOBIONT INVENTORY OF A LICHEN COMMUNITY GROWING ON HEAVY-METAL-RICH ROCK

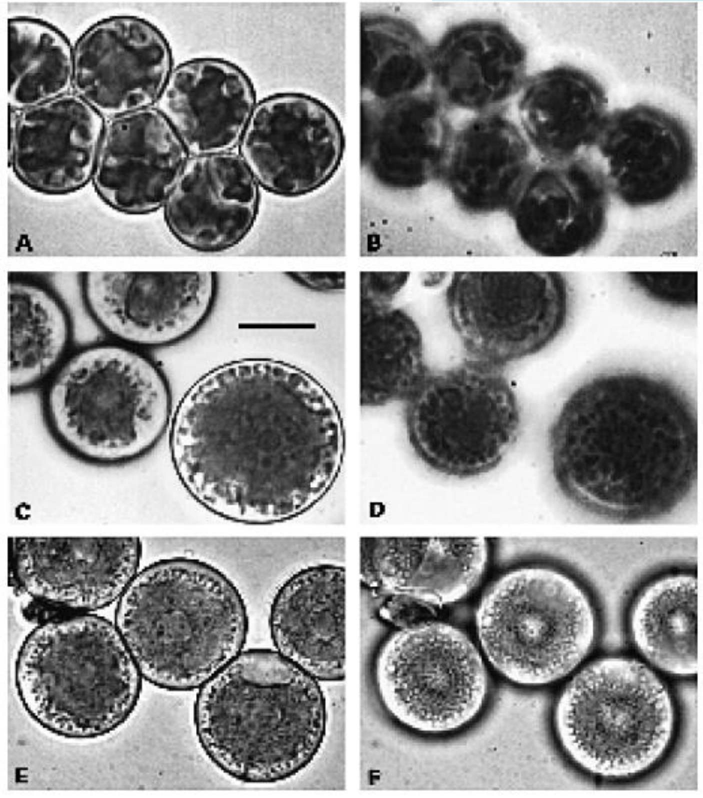
Andreas BECK*



Lichen species
Acarospora rugulosa
Bellemerea diamartha
Lecanora polytropa
L. subaurea
Lecidea silacea
Rhizocarpon geographicum
Umbilicaria cylindrica
Acarospora sinopica
Lecidea lapicida

symbiont population on a single rock:

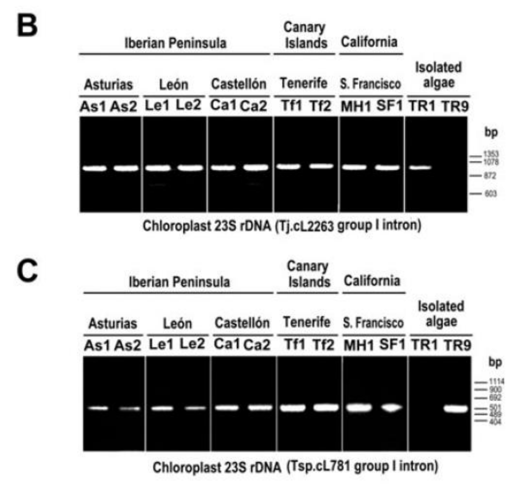
- **9 different lichens**
- **1 alga (*T. jamessii)***



Trebouxiales, *Trebouxia*

Casano et al. (2011): co-existence of two physiologically distinct algae

- TR1: cold-requiring
- TR9: warm-requiring (thermophilic)



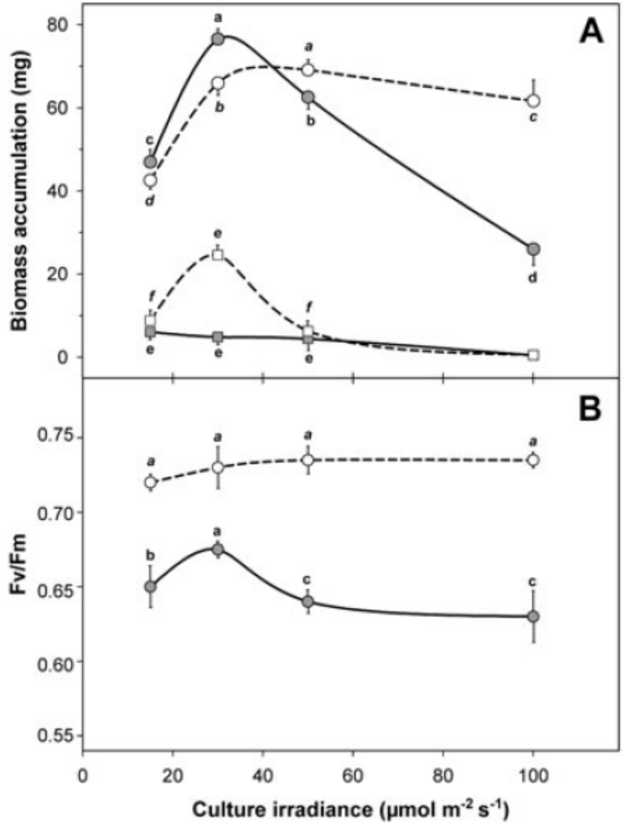
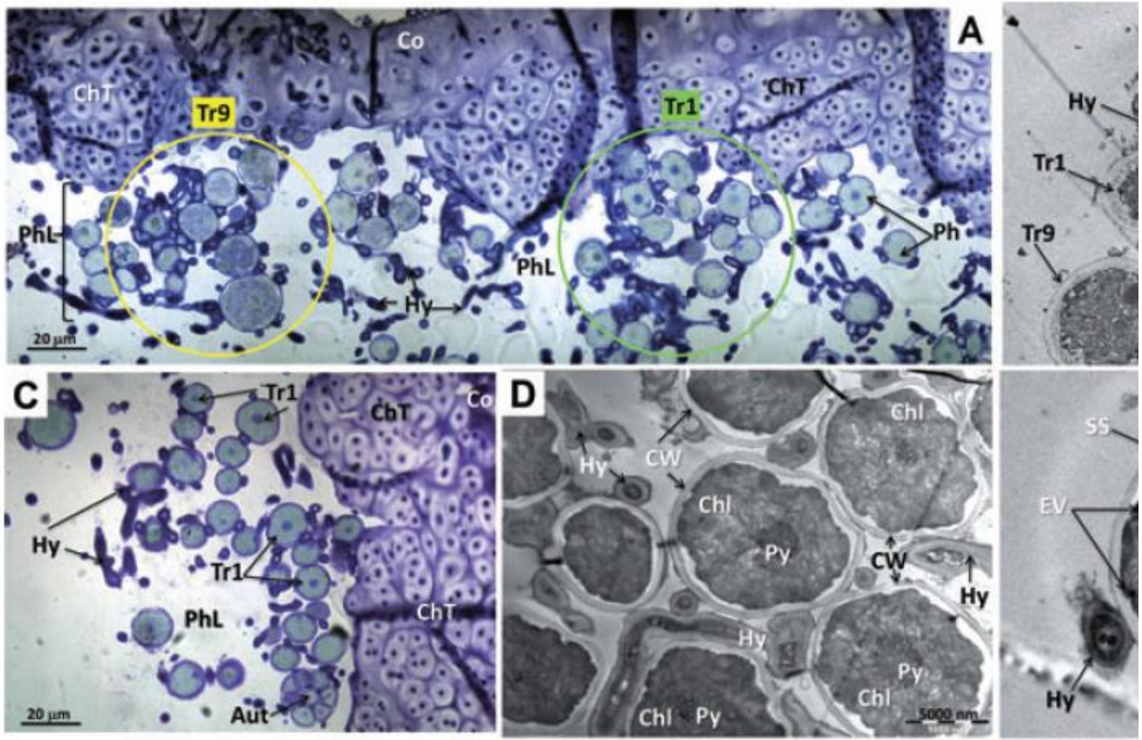
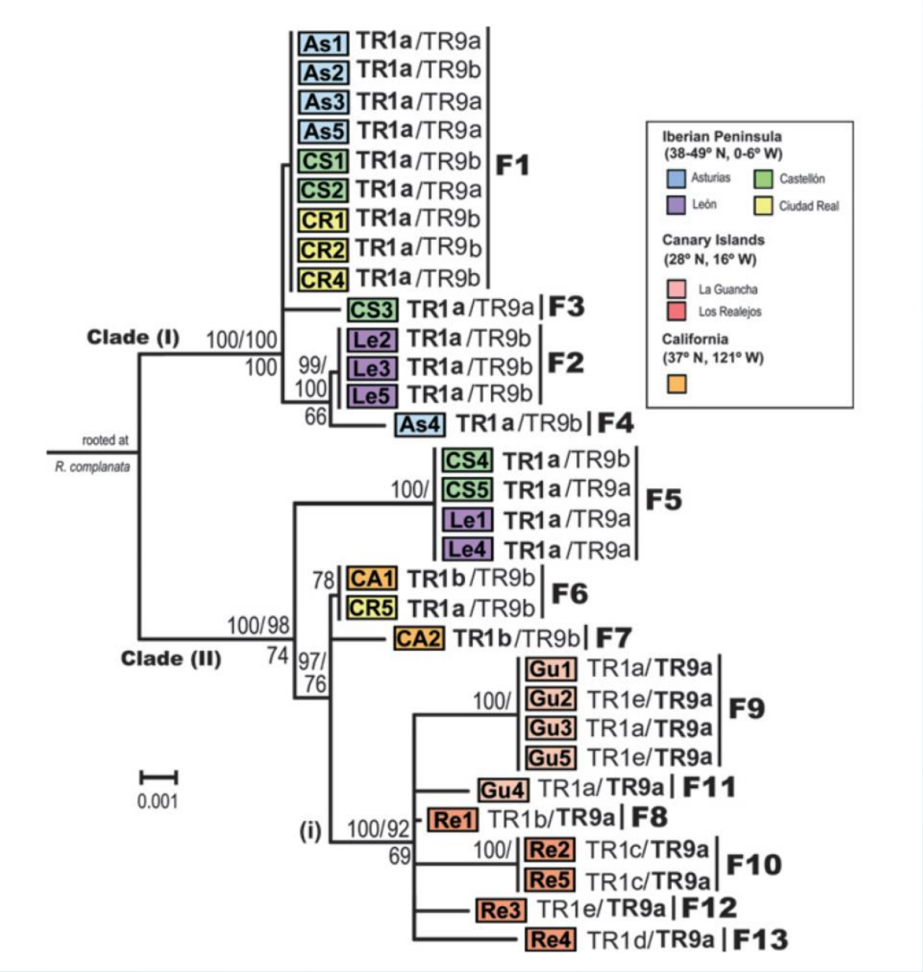


Fig. 4. Effects of temperature and irradiance during culture on growth and photosynthesis in isolated TR1 and TR9 phycobionts. A. TR9 and TR1 biomass accumulation after 30 days of culture at 17°C or 20°C and the indicated irradiances. Grey and white circles represent TR1 and TR9 phycobionts cultured at 17°C respectively. Grey and white squares represent TR1 and TR9 phycobionts cultured at 20°C respectively. Data are the mean values of five independent replicates (+ or –SD).
B. Maximum quantum yield of PSII (F_v/F_m) of TR1 and TR9 phycobionts cultured at 17°C and four different light intensities during 30 days. Data are the mean values of five independent replicates (± SD). Grey and white circles represent TR1 and TR9 phycobionts respectively. Different normal and italic letters indicate significant differences among culture conditions for TR1 and TR9 phycobionts respectively (LSD test).



Trebouxiales, *Trebouxia*

Del Campo et al (2013) – ecological speciation of mycobionts and photobionts



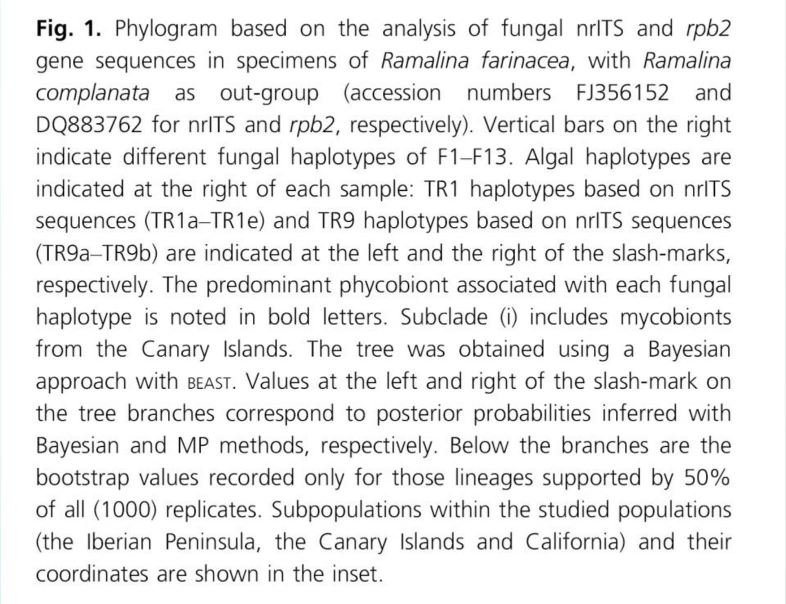


Fig. 1. Phylogram based on the analysis of fungal nrITS and *rpb2* gene sequences in specimens of *Ramalina farinacea*, with *Ramalina complanata* as out-group (accession numbers FJ356152 and DQ883762 for nrITS and *rpb2*, respectively). Vertical bars on the right indicate different fungal haplotypes of F1–F13. Algal haplotypes are indicated at the right of each sample: TR1 haplotypes based on nrITS sequences (TR1a–TR1e) and TR9 haplotypes based on nrITS sequences (TR9a–TR9b) are indicated at the left and the right of the slash-marks, respectively. The predominant phycobiont associated with each fungal haplotype is noted in bold letters. Subclade (i) includes mycobionts from the Canary Islands. The tree was obtained using a Bayesian approach with BEAST. Values at the left and right of the slash-mark on the tree branches correspond to posterior probabilities inferred with Bayesian and MP methods, respectively. Below the branches are the bootstrap values recorded only for those lineages supported by 50% of all (1000) replicates. Subpopulations within the studied populations (the Iberian Peninsula, the Canary Islands and California) and their coordinates are shown in the inset.

Trebouxiales, *Asterochloris*

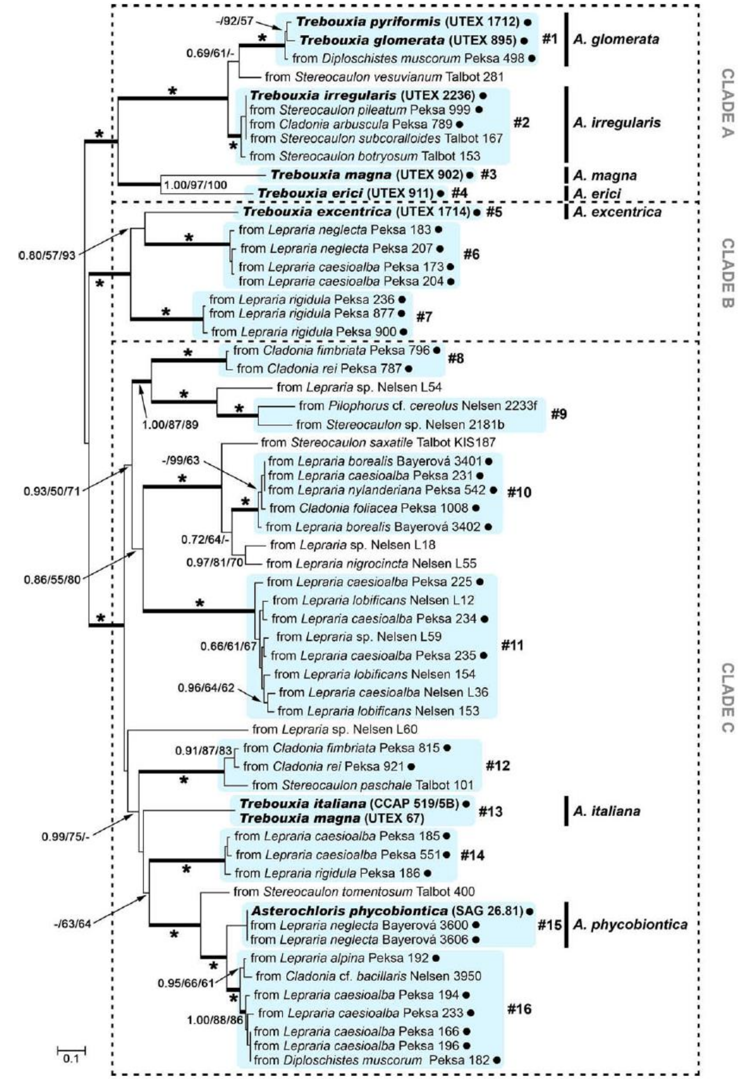
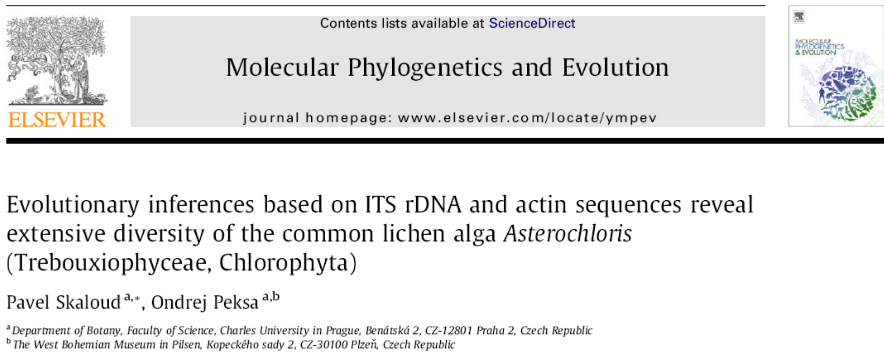


Fig. 3. Unrooted BI analysis based on the combined ITS + actin dataset using a GTR+Γ model for ITS1, K80+I+Γ model for ITS2, and JC model for 5.8 rRNA partition; and HKY+Γ model for the actin-intron 206, HKY+I model for the actin-intron 248, and K80+CP_{123}+I model for the actin-exon partition. The doublet model is applied for the ster regions in all ITS rDNA partitions. Values at the nodes indicate statistical support estimated by three methods – MrBayes posterior node probability (left), maximur likelihood bootstrap (in the middle) and maximum parsimony bootstrap (right). Full statistical support (1.00/100/100) is marked with an asterisk. Thick branches represen nodes receiving the highest PP support (1.00). Sequences determined in this study are marked by full circles. Authentic strains of *Asterochloris phycobiontica* and severa former *Trebouxia* species are given in bold. Strain affiliation to 16 lineages (#1–16) and three major clades (A–C) is indicated. Scale bar – substitutions per site.



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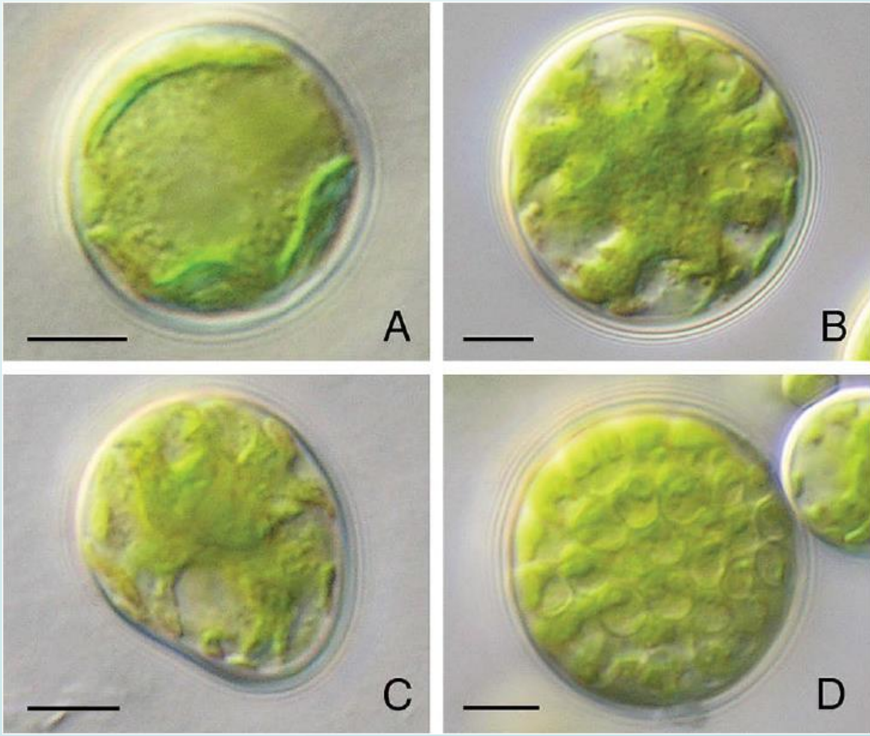
Evolutionary inferences based on ITS rDNA and actin sequences reveal extensive diversity of the common lichen alga *Asterochloris* (Trebouxiophyceae, Chlorophyta)

Pavel Skaloud [a,*], Ondrej Peksa [a,b]

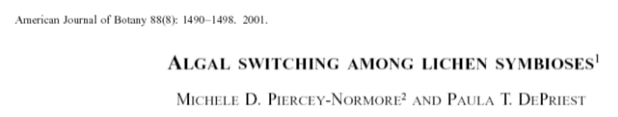
[a] Department of Botany, Faculty of Science, Charles University in Prague, Benátská 2, CZ-12801 Praha 2, Czech Republic
[b] The West Bohemian Museum in Pilsen, Kopeckého sady 2, CZ-30100 Plzeň, Czech Republic



Trebouxiales, *Asterochloris*

Trebouxiales, *Asterochloris*

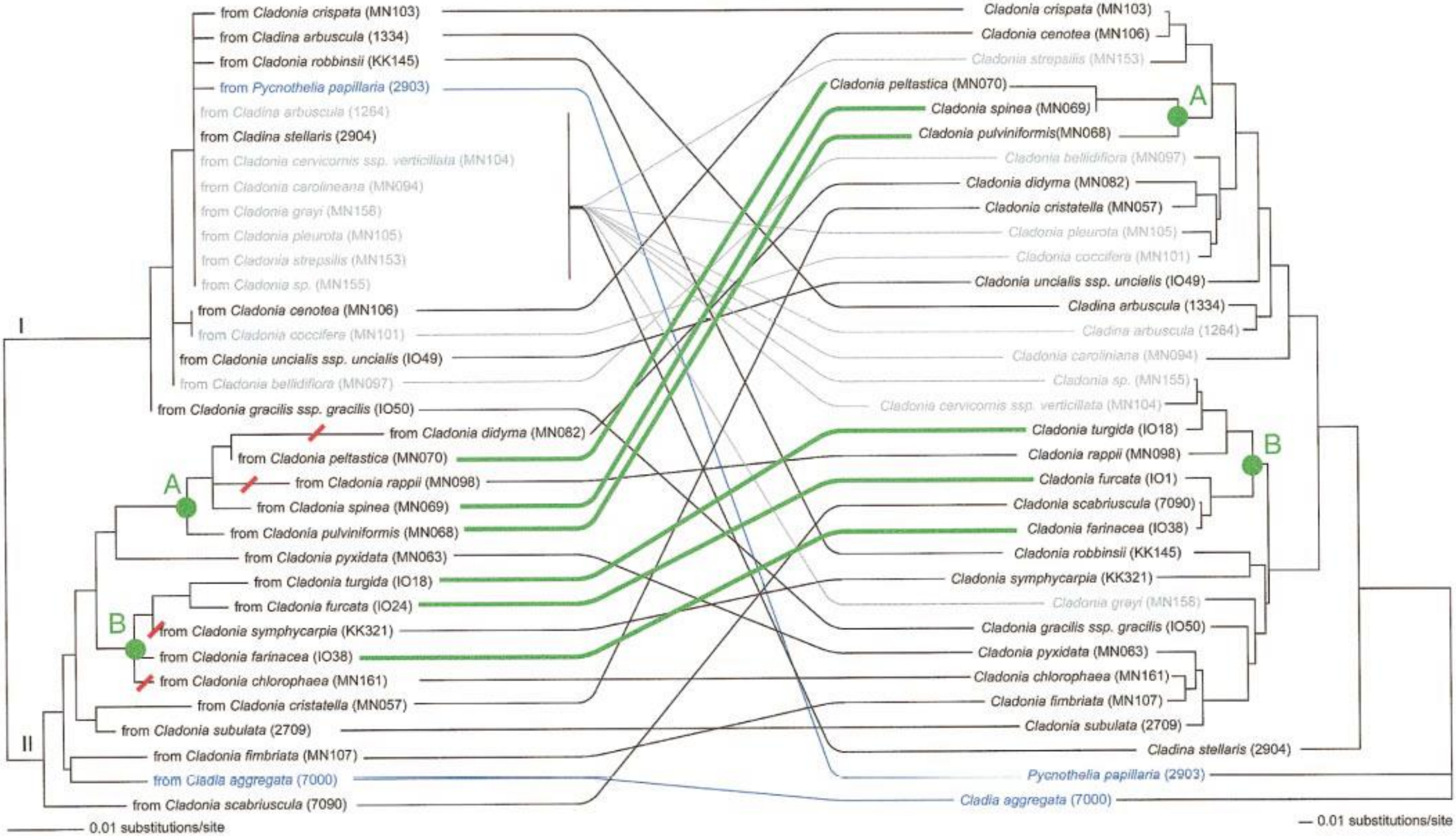
- incongruent evolution of algae and fungi
- algal domestication



American Journal of Botany 88(8): 1490–1498. 2001.

ALGAL SWITCHING AMONG LICHEN SYMBIOSES[1]

MICHELE D. PIERCEY-NORMORE[2] AND PAULA T. DEPRIEST



Trebouxiales, *Asterochloris*

MOLECULAR ECOLOGY

Molecular Ecology (2011) **20**, 3936–3948 doi: 10.1111/j.1365-294X.2011.05168.x

Do photobionts influence the ecology of lichens? A case study of environmental preferences in symbiotic green alga *Asterochloris* (Trebouxiophyceae)

ONDŘEJ PEKSA*† and PAVEL ŠKALOUD†
The West Bohemian Museum in Pilsen, Kopeckého sady 2, CZ-30100 Plzeň, Czech Republic, †Department of Botany, Faculty of Science, Charles University in Prague, Benátská 2, CZ-12801 Prague, Czech Republic

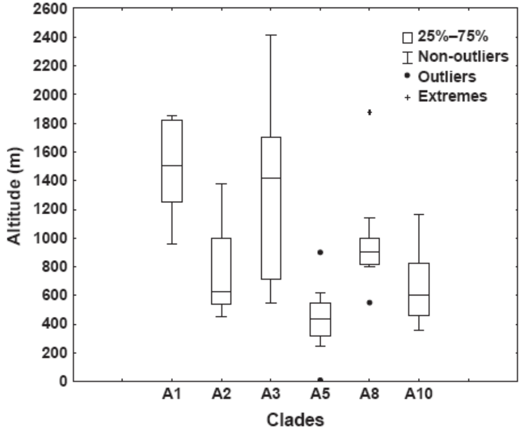


Fig. 3 Differences in the distribution of selected *Asterochloris* clades along the altitudinal gradient. Box and whisker plots are based on altitudinal data from six clades (only those represented by at least eight samples). All samples were collected in similar latitudes in Europe (43–58°N, i.e. somewhere in the temperate belt). The approximate upper borders of vertical vegetation belts for central Europe are as follows: 200 m a.s.l.—lowland, 600 m—colline, 1000 m—submontane, 1400 m—montane, 1800 m—subalpine, 2400 m—alpine.

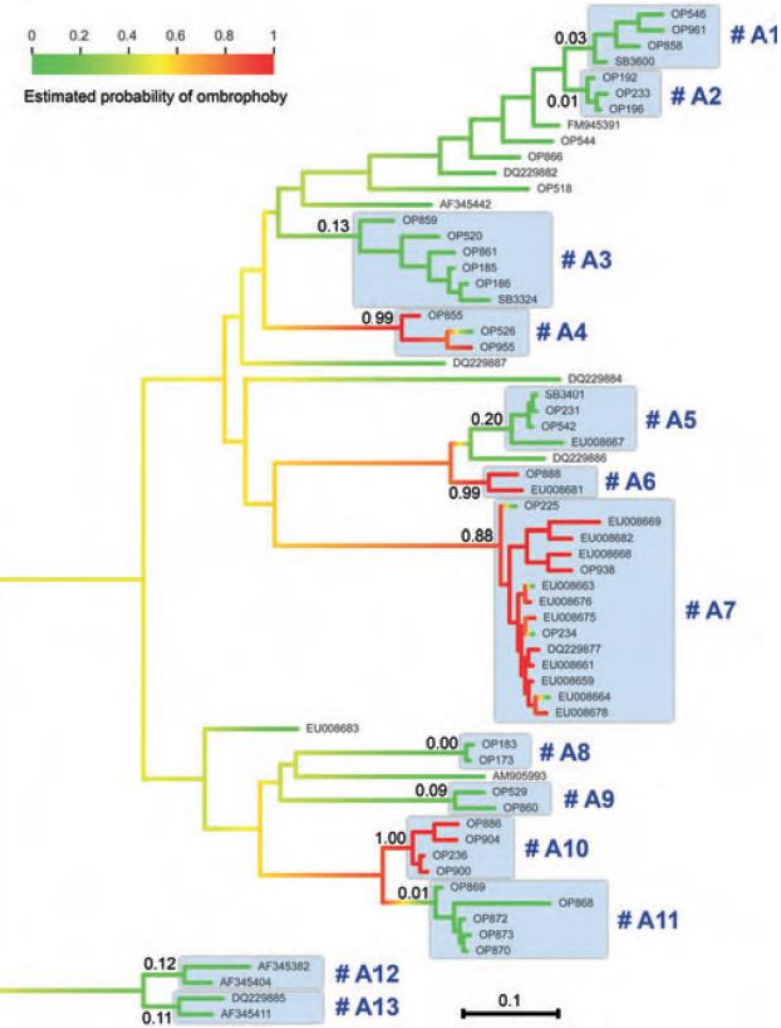
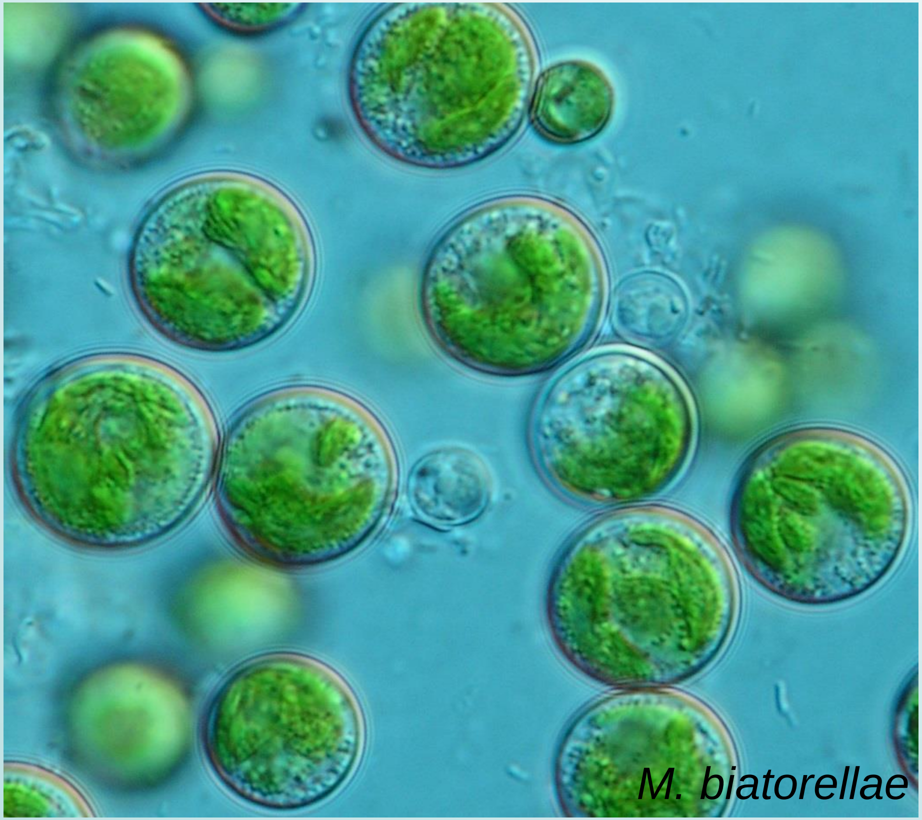


Fig. 2 The evolution of the selected ecological character—the ombrophoby (ombrophily) of lichens—mapped onto the photobiont phylogenetic tree. Colours are used to visualize estimated probabilities of the presence of ombrophoby along the phylogenetic tree. Red indicates a high probability of ombrophoby, whereas green denotes a low probability of ombrophobic preference. The estimated probabilities for ombrophoby are indicated for ancestors of each significantly supported clade (see Fig. 1). The topology of the tree corresponds completely to the topology of the phylogenetic tree in Fig. 1.

Trebouxiales, *Myrmecia*

- terrestrial, aerophytic
- lichen symbiont

Bacidia

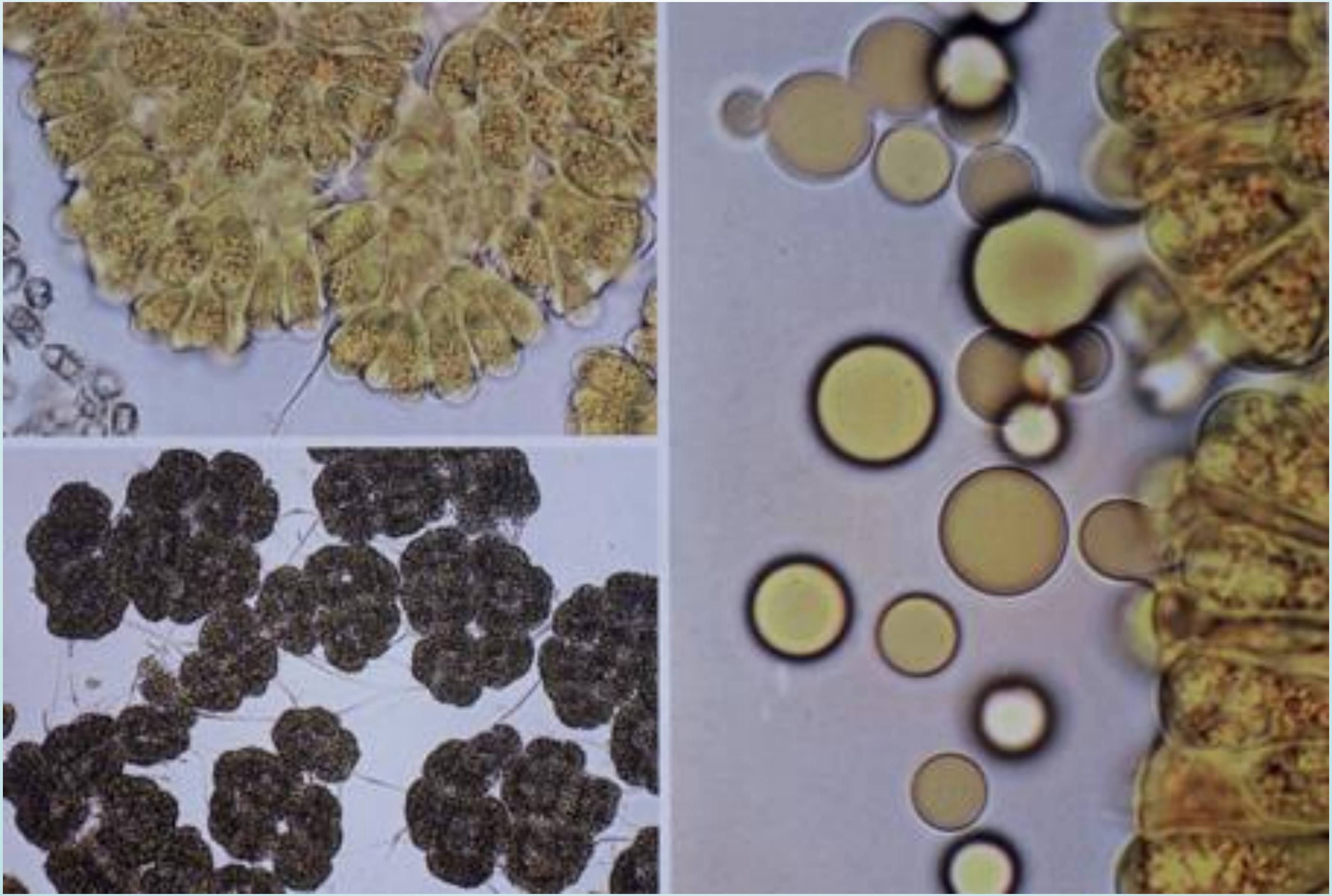


M. biatorellae

M. bisecta

Botryococcus-clade, *Botryococcus*

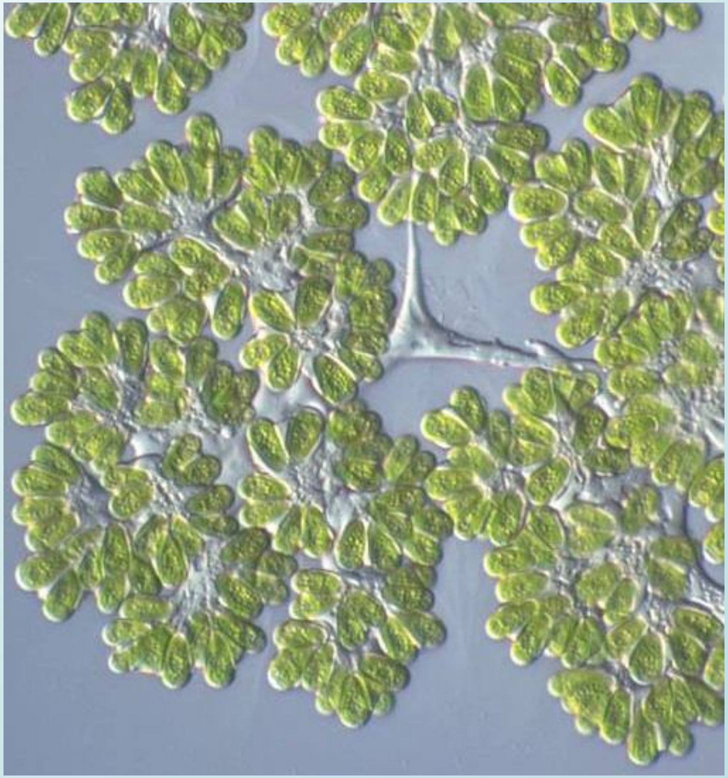
- *Botryococcus braunii* – colonial green alga



Botryococcus-clade, *Botryococcus*

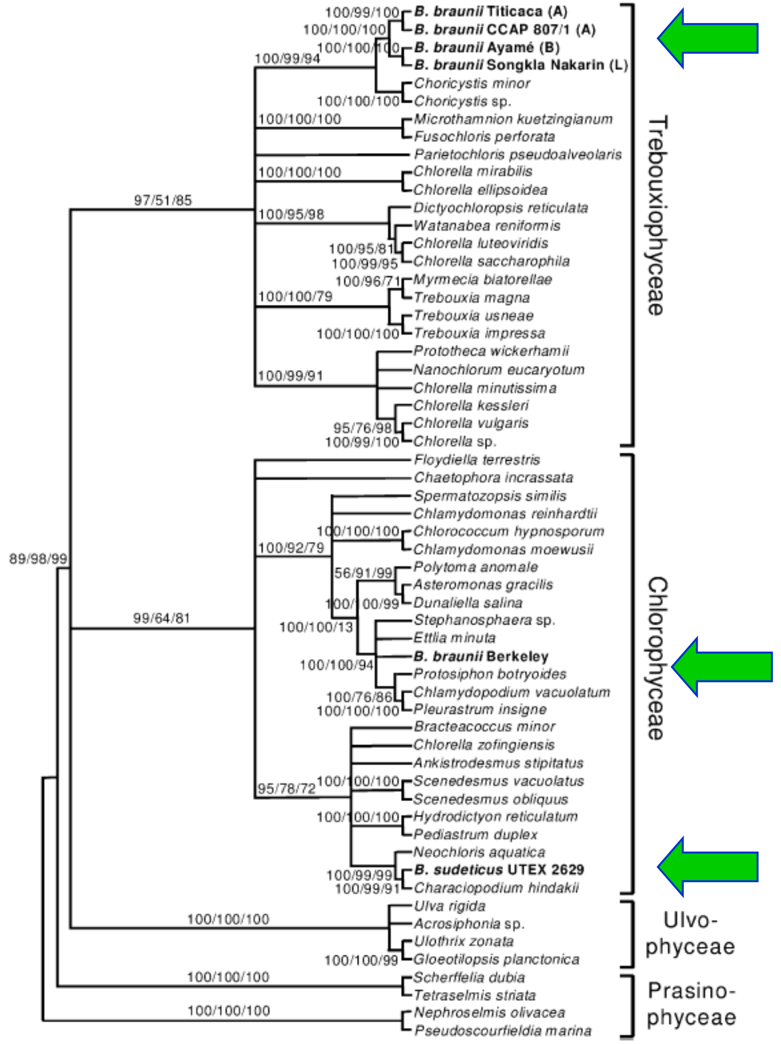
- water blooms
- botryococcen = hydrocarbon, 35% of the dry weight
- fuel?

©2003 Tamar Zohary



Botryococcus-clade, *Botryococcus*

- Senousy et al. (2004) – polyphyletic *Botryococcus*



B. braunii

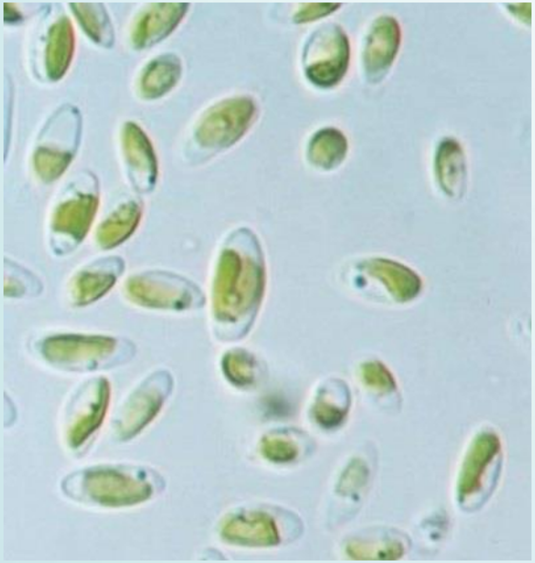
kontaminace ?

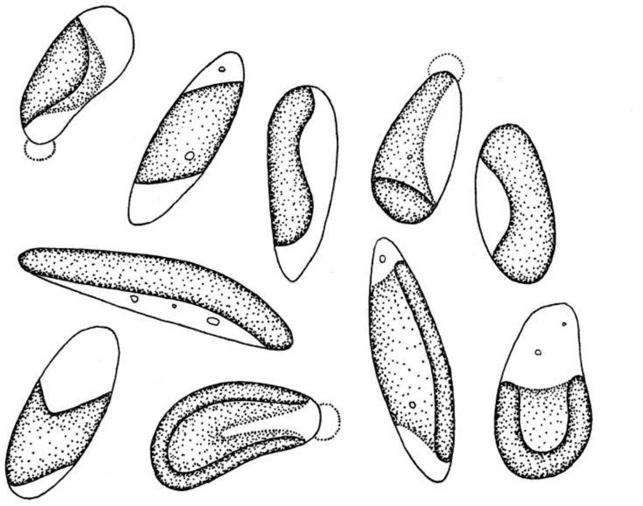
„B“. sudeticus
= Botryosphaerella

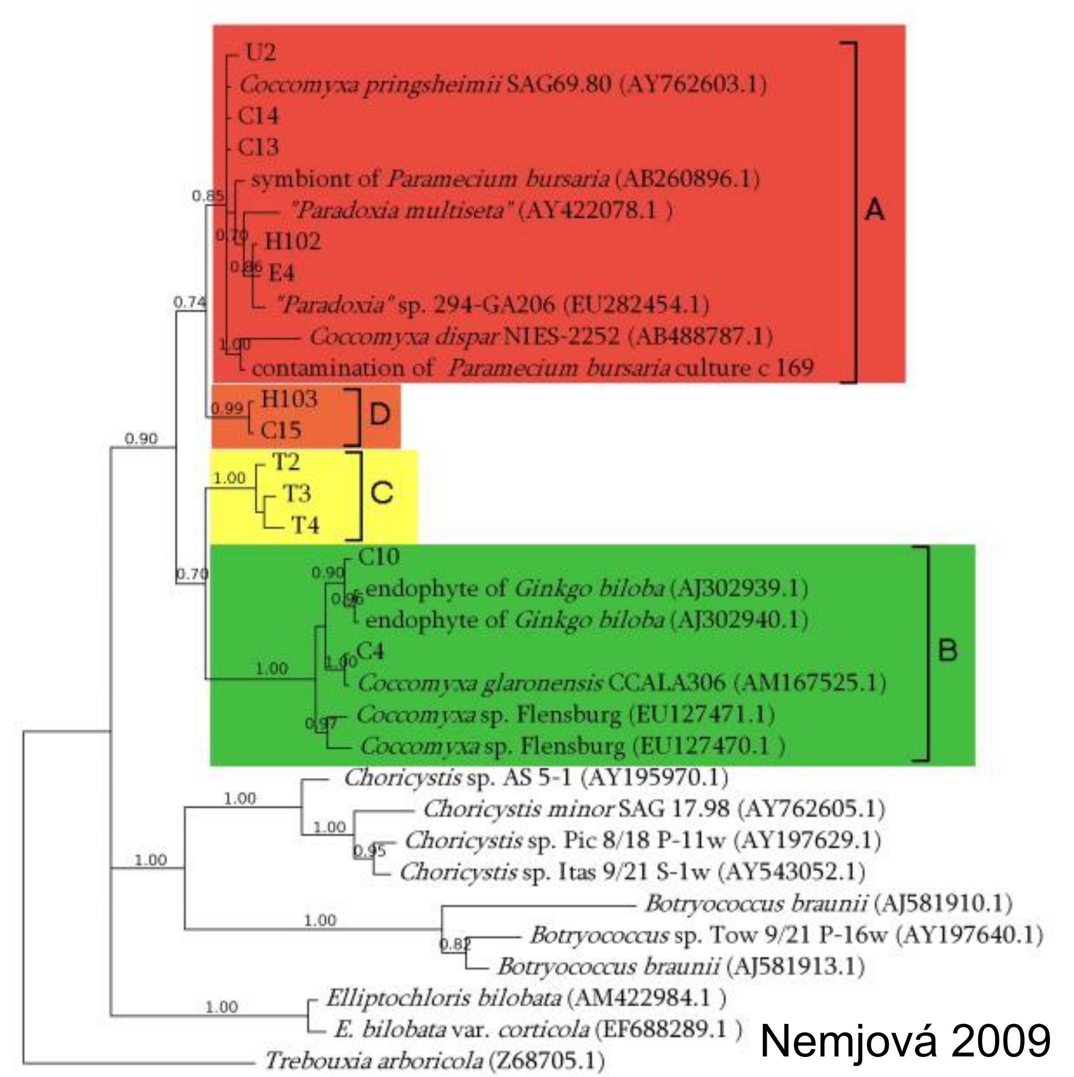
FIG. 3. Consensus tree from trees inferred with different methods of analysis. The numbers shown at the branches are credibility percentages determined using Bayesian inference (left) and bootstrap values determined using weighted parsimony (middle) and minimum evolution (right). Taxa shown in bold letters are the isolates whose 18S rRNA sequences were determined in this study.

Botryococcus-clade, *(Pseudo-)Coccomyxa*

- ellipsoid cells, frequent in aerophytic substrate







Nemjová 2009

Botryococcus-clade, *(Pseudo-)Coccomyxa*

- lichen photobionts

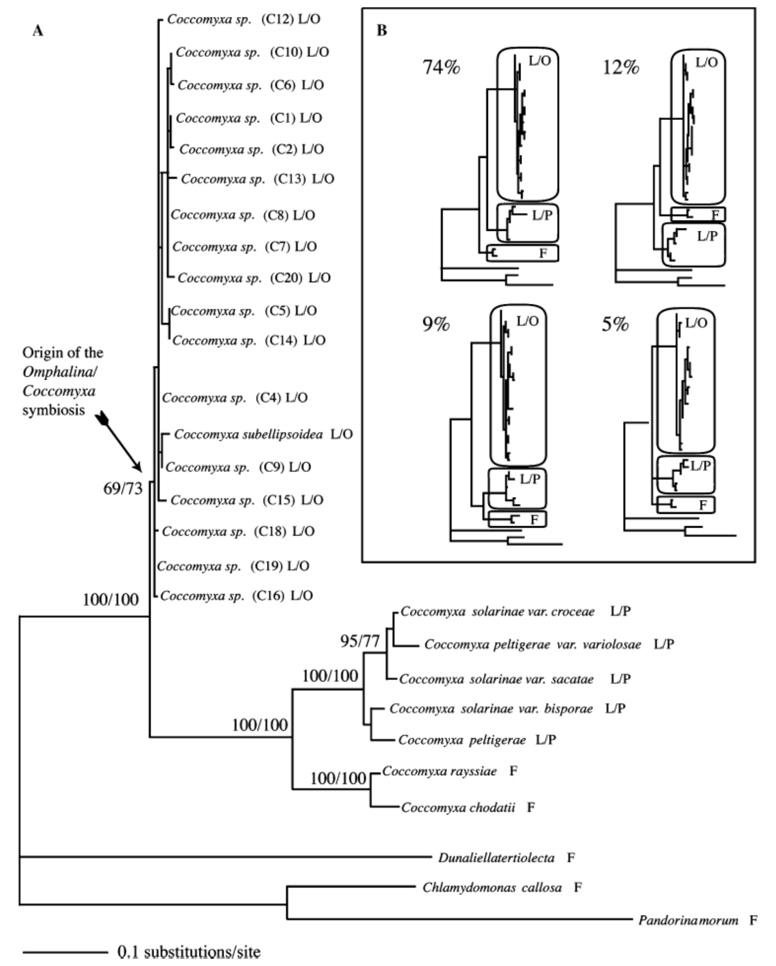
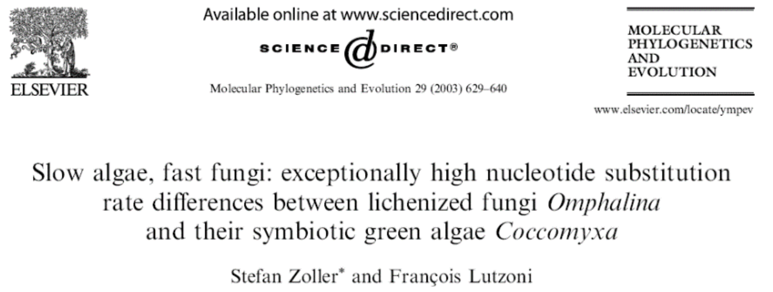


Fig. 3. Phylogenetic relationships among lichenized and non-lichenized *Coccomyxa* algae (dataset AC) as revealed by an ML search using ITS (ITS1-5.8S-ITS2) sequences. *Coccomyxa* isolated from lichenized *Omphalina* species (Basidiomycota) are denoted by a bold L/O after the name. *Coccomyxa* isolated from members of the Peltigerales (Ascomycota) are annotated with a bold L/P. Free-living species are denoted by a bold F. (A) Single most likely tree with maximum parsimony and maximum likelihood bootstrap support values greater than 50% given above internal branches, before and after the backslash, respectively. (B) Frequency of the four topologies recovered by the ML analysis from 100 simulated datasets. The topology under which the data were simulated (monophyly of the lichenized *Coccomyxa* species) was recovered only 74% of the times (top left).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Molecular Phylogenetics and Evolution 29 (2003) 629–640
MOLECULAR PHYLOGENETICS AND EVOLUTION
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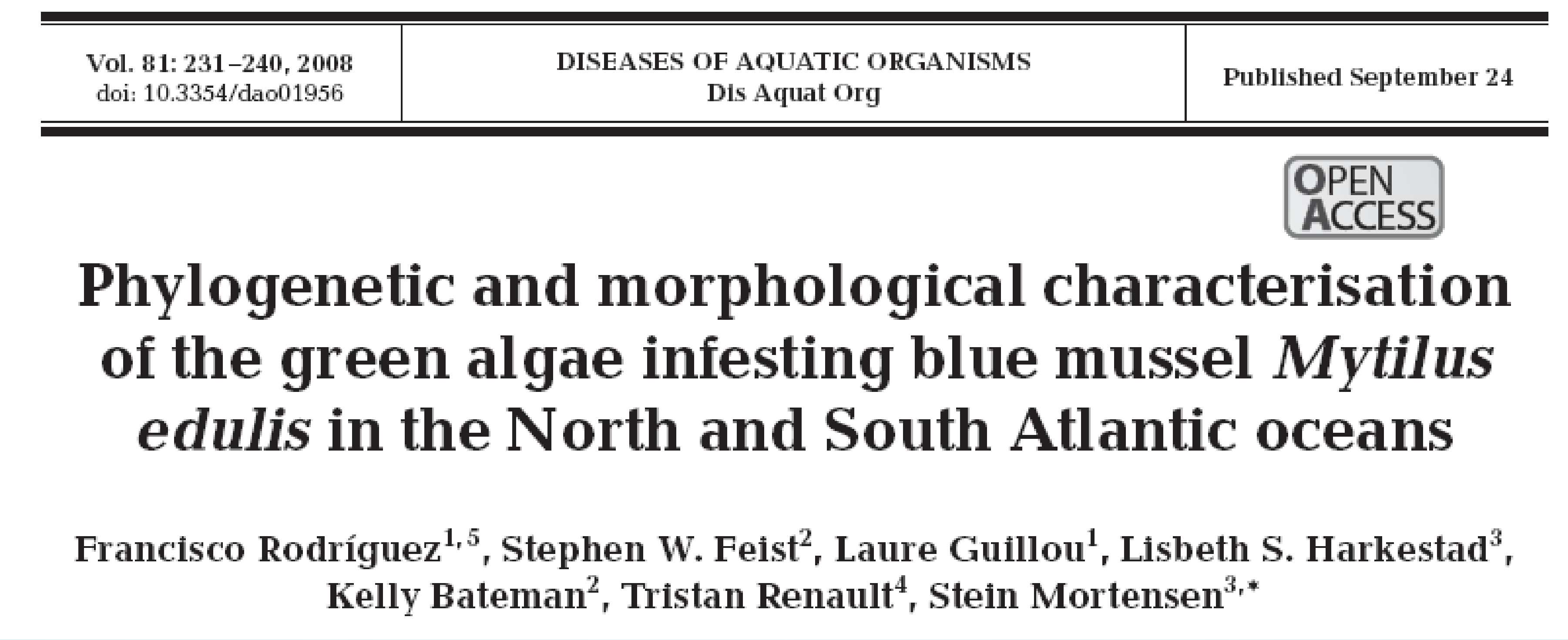
Slow algae, fast fungi: exceptionally high nucleotide substitution rate differences between lichenized fungi *Omphalina* and their symbiotic green algae *Coccomyxa*

Stefan Zoller* and François Lutzoni

Botryococcus-clade, *(Pseudo-)Coccomyxa*



Vol. 81: 231–240, 2008
doi: 10.3354/dao01956

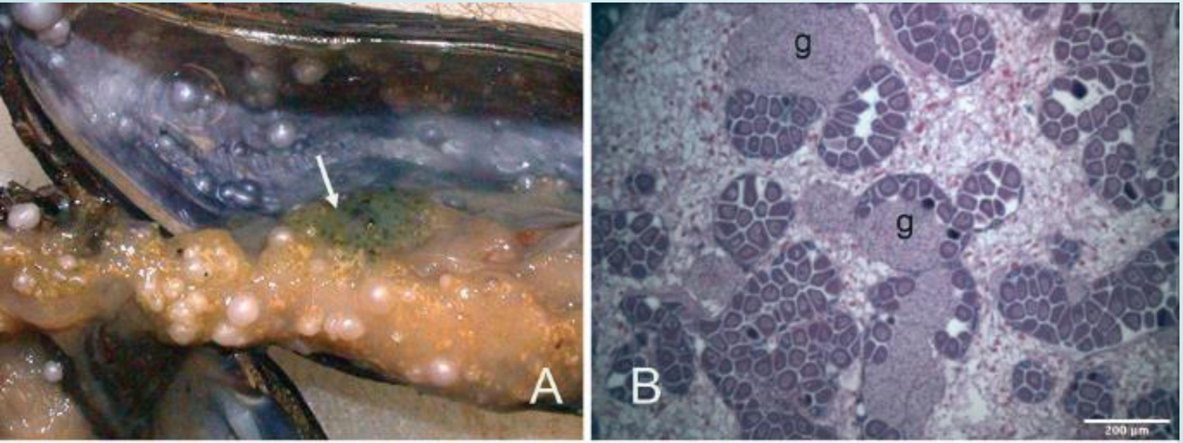
DISEASES OF AQUATIC ORGANISMS
Dis Aquat Org

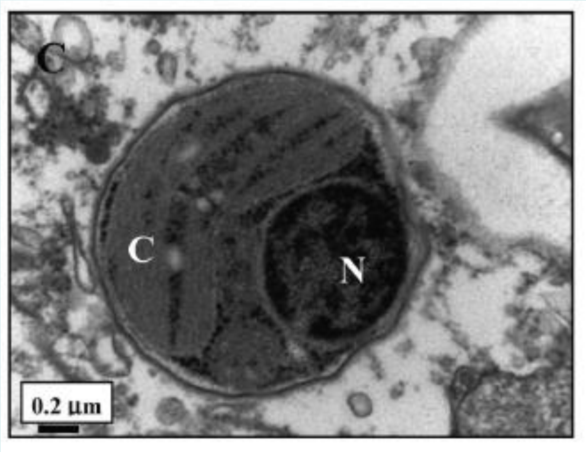
Published September 24

OPEN ACCESS

Phylogenetic and morphological characterisation of the green algae infesting blue mussel *Mytilus edulis* in the North and South Atlantic oceans

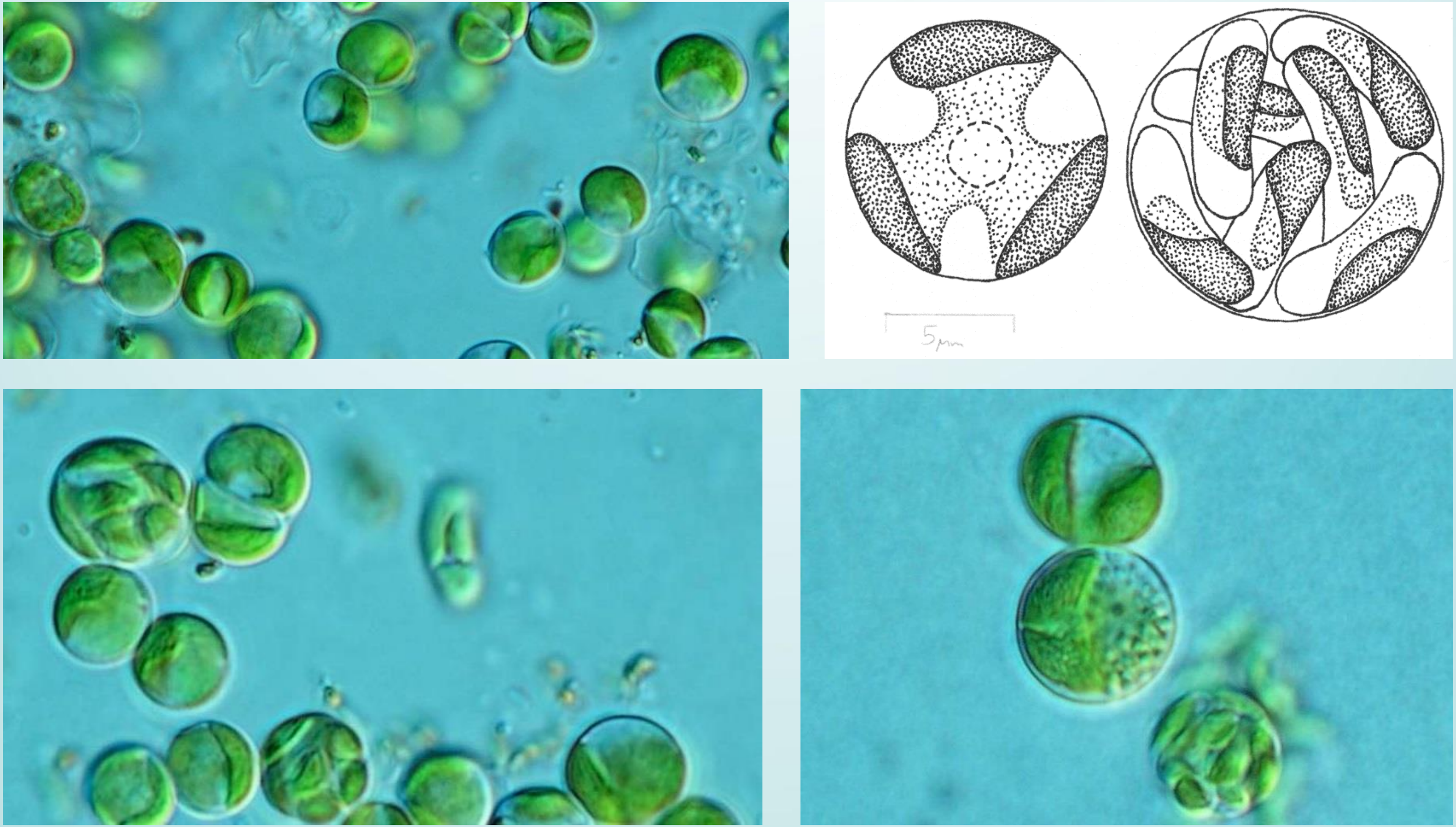
Francisco Rodríguez[1,5], Stephen W. Feist[2], Laure Guillou[1], Lisbeth S. Harkestad[3], Kelly Bateman[2], Tristan Renault[4], Stein Mortensen[3,*]





Botryococcus-clade, *Elliptochloris*

- 2 autospore types

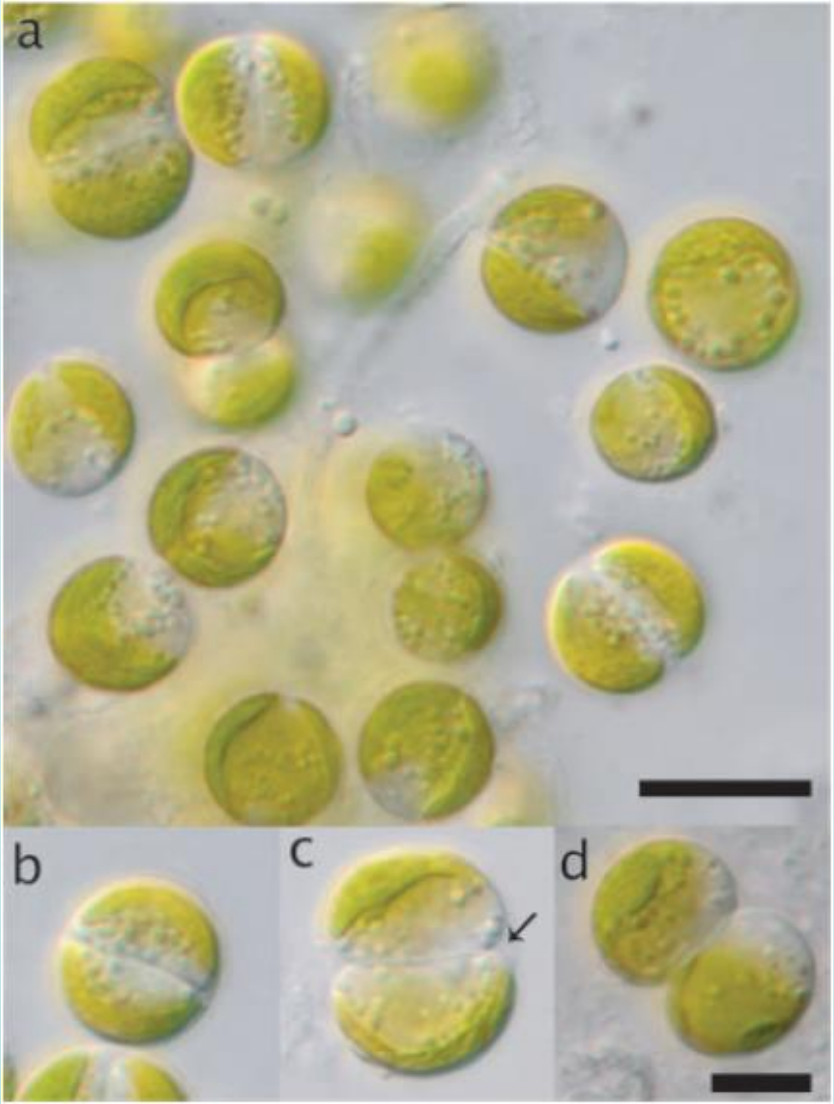


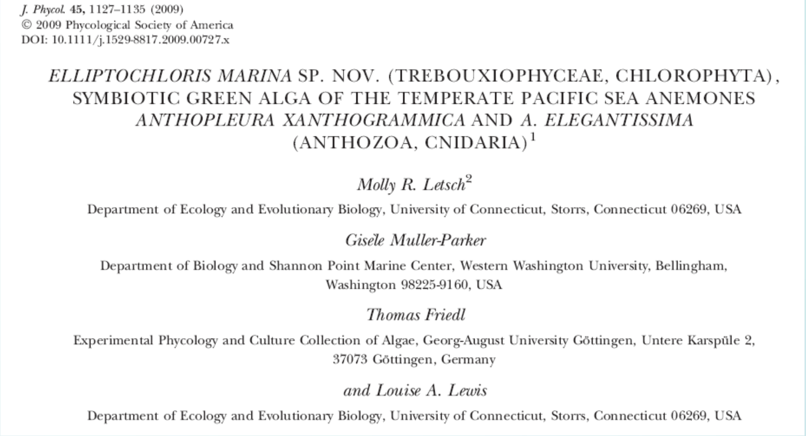
Botryococcus-clade, *Elliptochloris*

- symbiont of lichens (*Baeomyces*, *Catolechia*), sea anemones (*Anthopleura*)

Botryococcus-clade, *Elliptochloris*

- symbiont of lichens (*Baeomyces*, *Catolechia*), sea anemones (*Anthopleura*)




J. Phycol. **45,** 1127–1135 (2009)
© 2009 Phycological Society of America
DOI: 10.1111/j.1529-8817.2009.00727.x

ELLIPTOCHLORIS MARINA SP. NOV. (TREBOUXIOPHYCEAE, CHLOROPHYTA), SYMBIOTIC GREEN ALGA OF THE TEMPERATE PACIFIC SEA ANEMONES *ANTHOPLEURA XANTHOGRAMMICA* AND *A. ELEGANTISSIMA* (ANTHOZOA, CNIDARIA)[1]

Molly R. Letsch[2]
Department of Ecology and Evolutionary Biology, University of Connecticut, Storrs, Connecticut 06269, USA

Gisèle Muller-Parker
Department of Biology and Shannon Point Marine Center, Western Washington University, Bellingham, Washington 98225-9160, USA

Thomas Friedl
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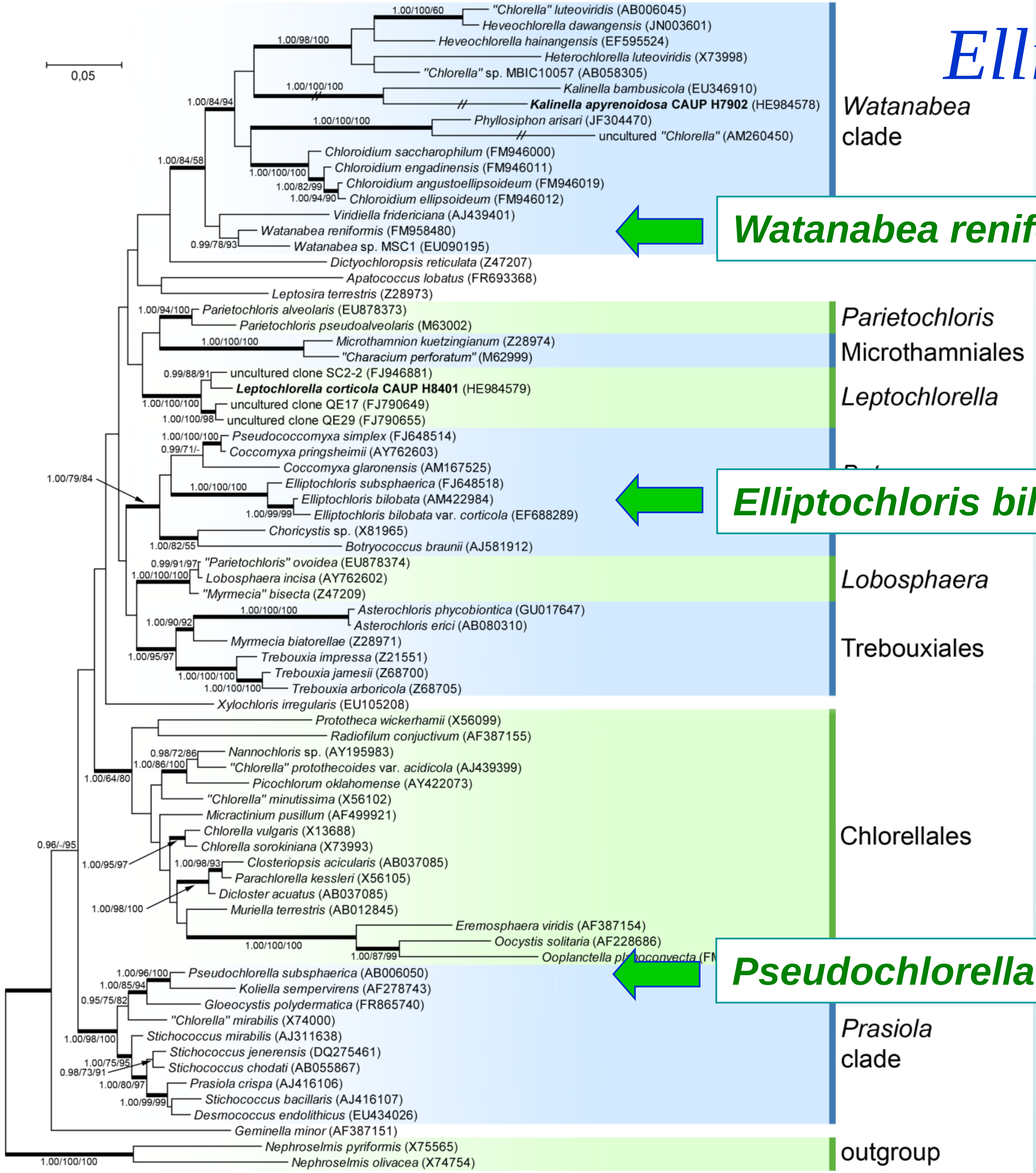
and Louise A. Lewis
Department of Ecology and Evolutionary Biology, University of Connecticut, Storrs, Connecticut 06269, USA

Elliptochloris



Watanabea reniformis

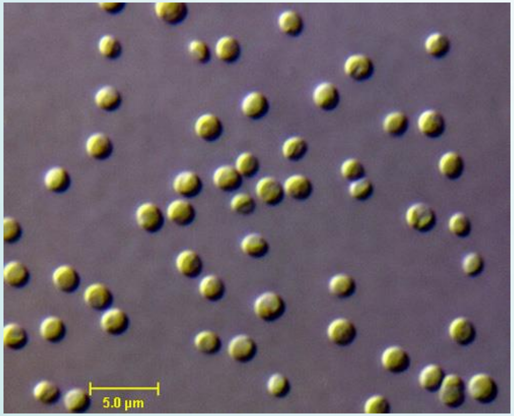
Elliptochloris bilobata

Pseudochlorella subsphaerica

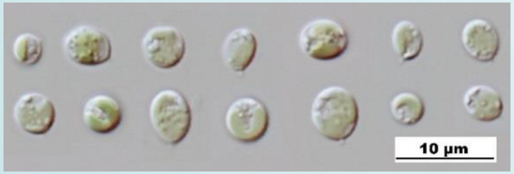
Trebouxiophyceae, picoplankton

- green balls up to 3 μm in diameter

Nannochloris

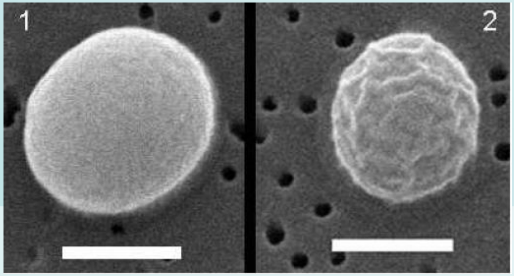


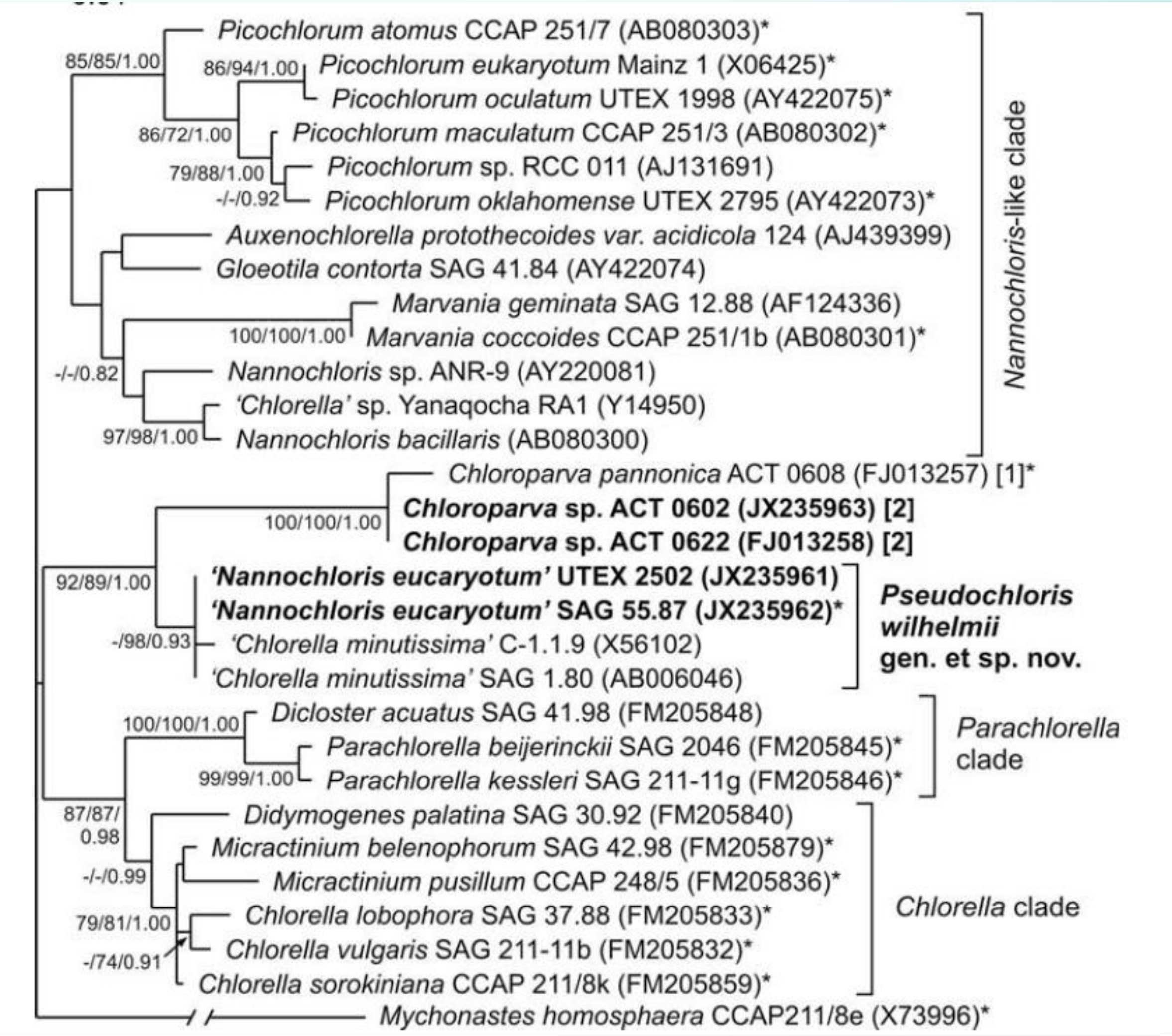
Picochlorum



Pseudochloris

Chloroparva

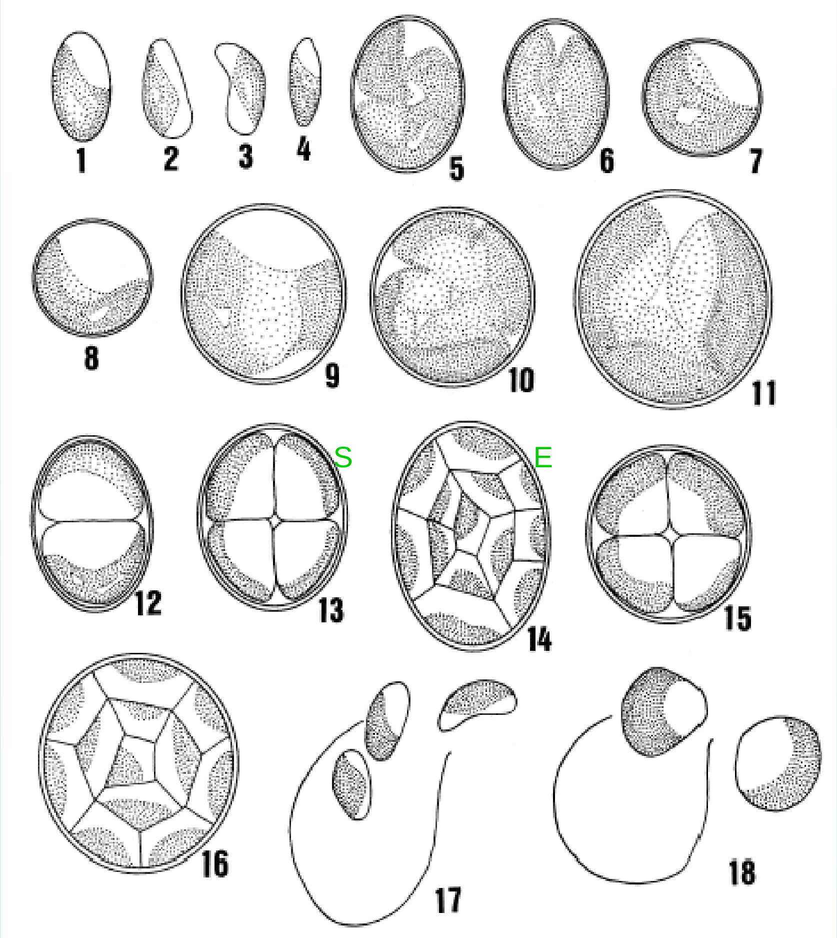


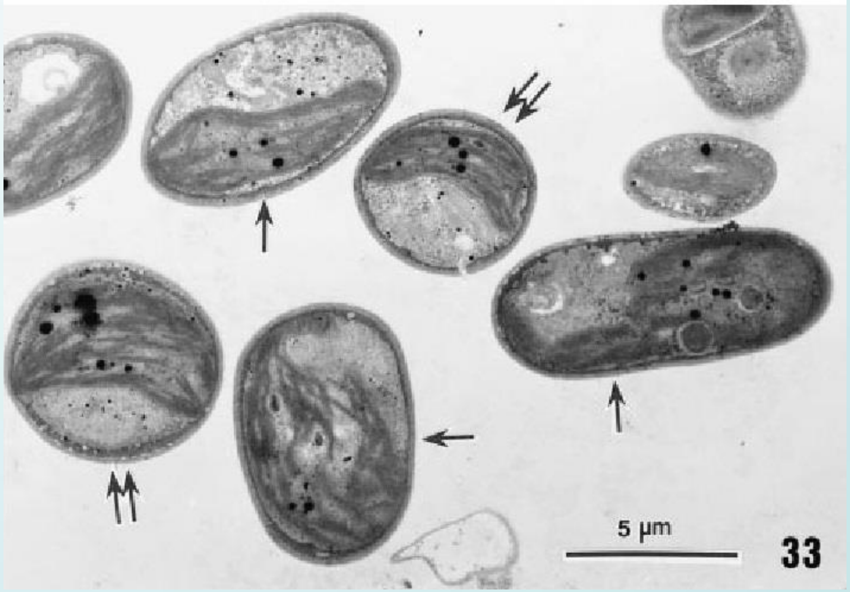


Somogyi et al. (2013): European Journal of Phycology 48, 427-36

Watanabea-clade, *Watanabea*

- *W. reniformis* (Hanagata et al., 1998) – 2 autospore types
- characteristic cell wall (different from *Elliptochloris*)





- unilayered CW (*Elliptochloris* – trilaminar CW)

Watanabea-clade, *Chloroidium*

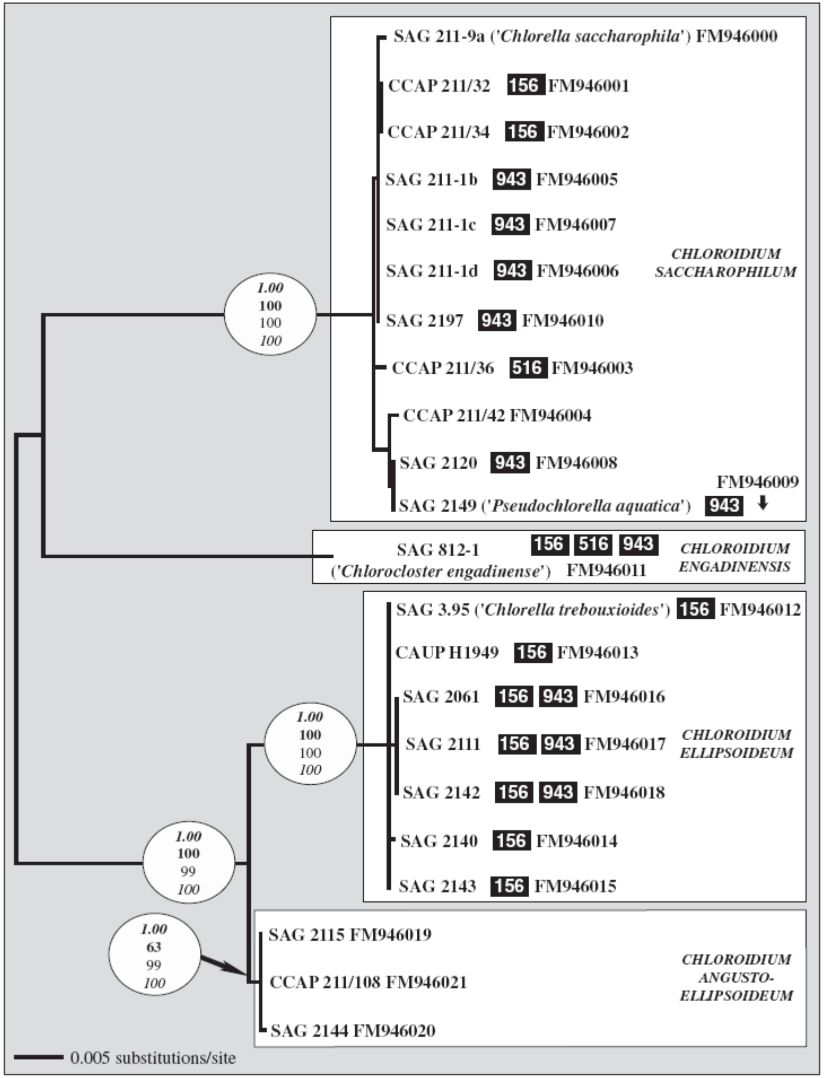
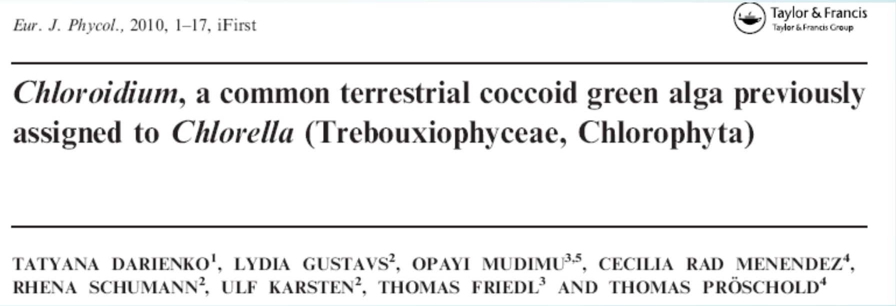


Fig. 2. Molecular phylogeny of *Chloroidium* based on SSU and ITS rDNA sequences, inferred by maximum likelihood (ML) based on a data set of 2500 aligned positions of 22 taxa using PAUP 4.0b10, using GTR model, with proportion of invariable sites I = 0.86. Bayesian values (>0.95; bold italic) using the covarion model (5 million generations) and bootstrap values (>50%) of the ML (using the GTR + I model, 100 replicates; bold), neighbor-joining (using the GTR + I model, 1000 replicates; not bold), and maximum parsimony (1000 replicates; italic) are shown in boxes on the tree. Strains marked in bold are new sequences, and strain and accession numbers, as well as intron position (white number in black box), are given.



Eur. J. Phycol., 2010, 1–17, iFirst

Taylor & Francis
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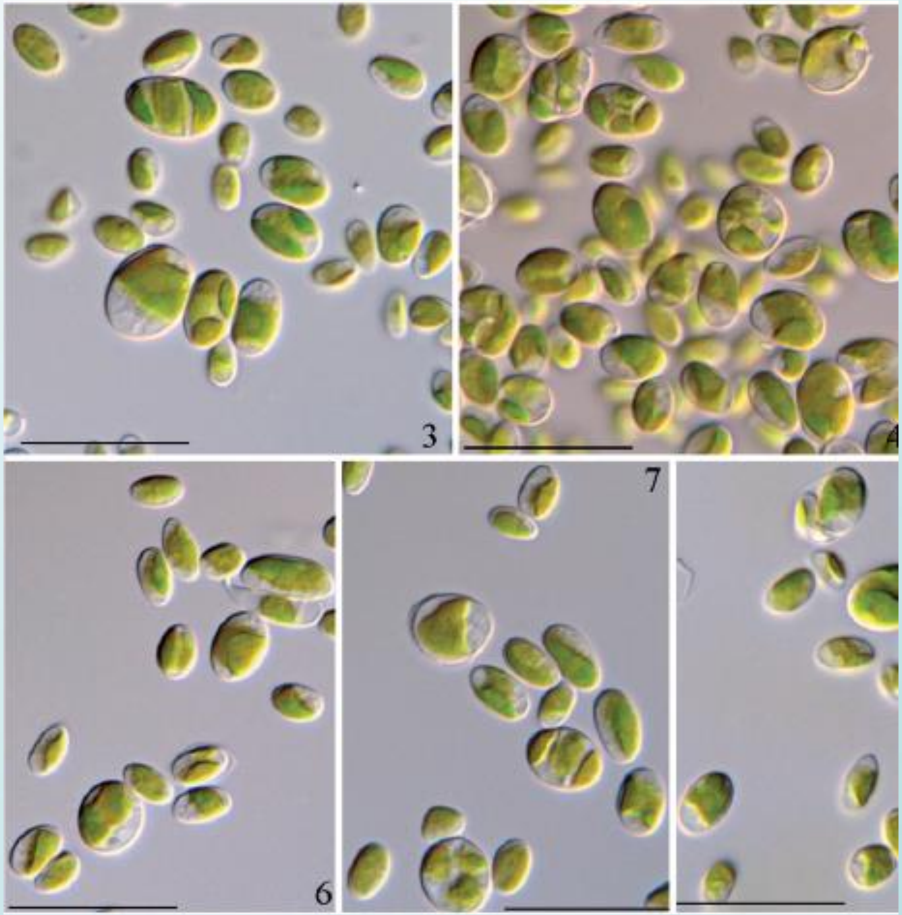
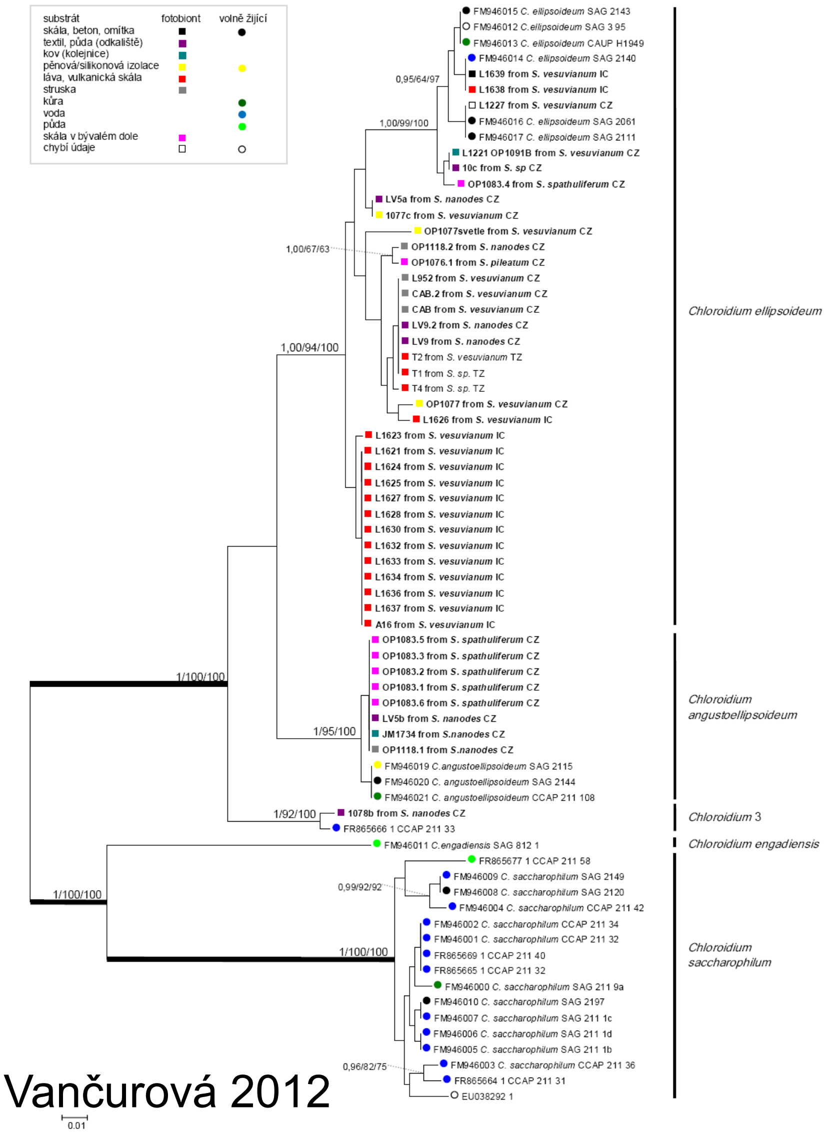
Chloroidium, a common terrestrial coccoid green alga previously assigned to Chlorella (Trebouxiophyceae, Chlorophyta)

TATYANA DARIENKO[1], LYDIA GUSTAVS[2], OPAYI MUDIMU[3,5], CECILIA RAD MENENDEZ[4], RHENA SCHUMANN[2], ULF KARSTEN[2], THOMAS FRIEDL[3] AND THOMAS PRÖSCHOLD[4]



Watanabea-clade, *Chloroidium*

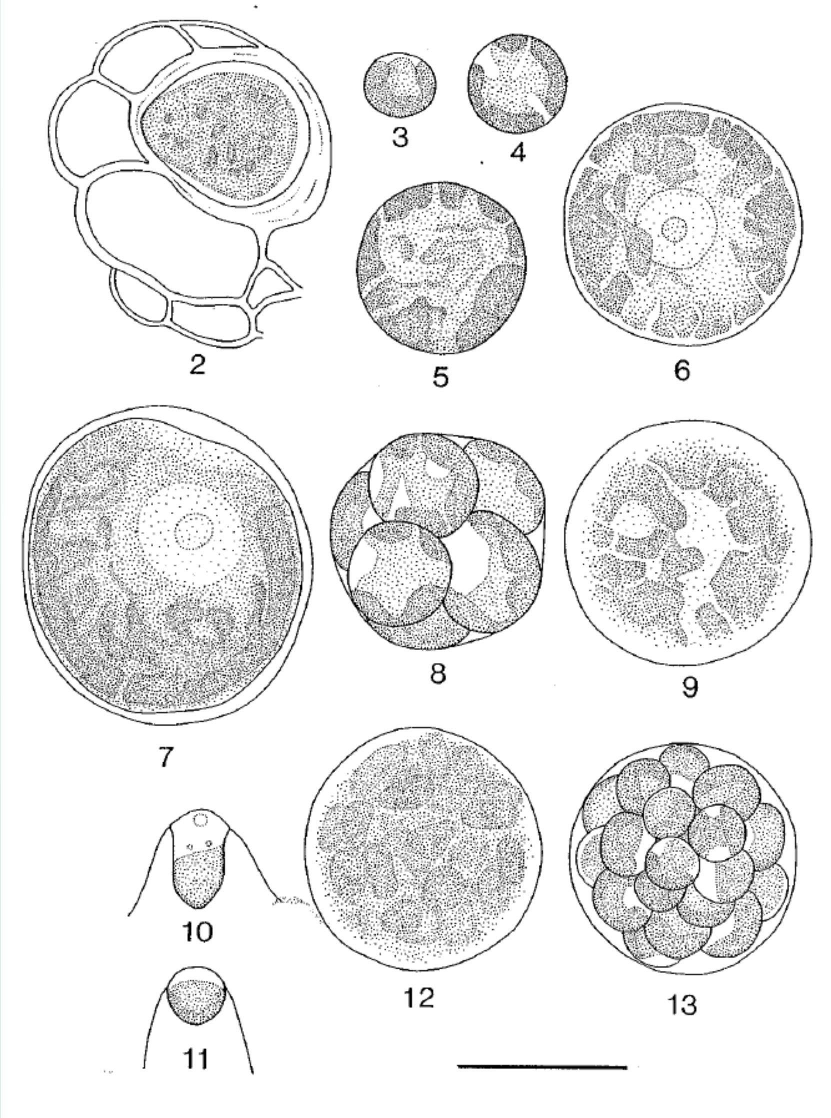


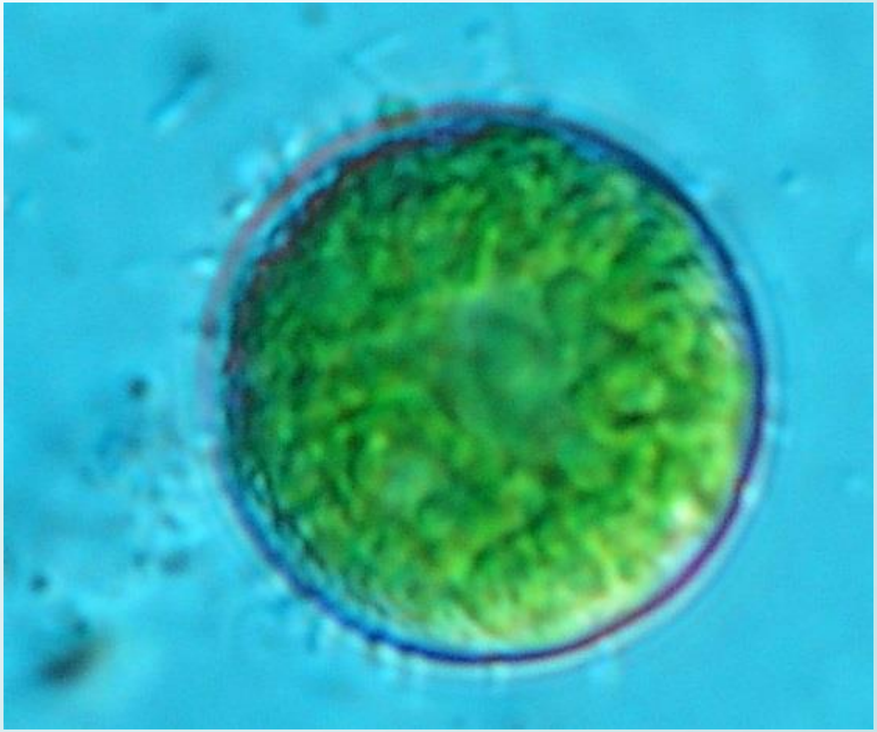
Vančurová 2012

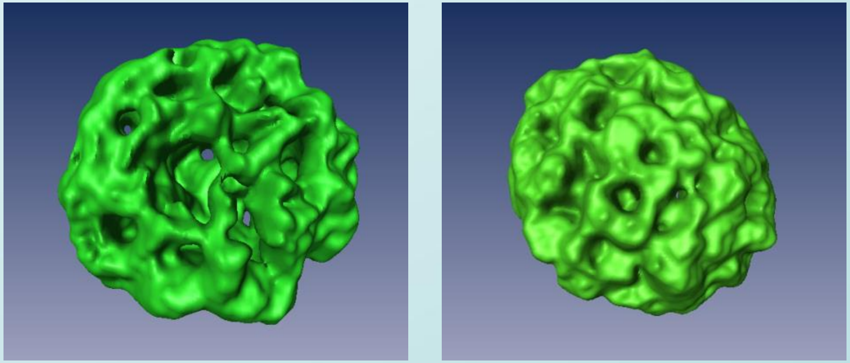
Obrázek 15: Nezakořeněný BI fylogenetický strom založený úseku ITS rDNA. Hodnoty v uzlech vyjadřují statistickou podporu určenou třemi metodami: MrBayes posteriorní pravděpodobnost/maximum likelihood bootstrap/maximum parsimony bootstrap. Zobrazeny jsou pouze hodnoty >0,89 pro BI a >49 pro ML/MP. Popisky sekvencí fotobiontů obsahují označení DNA, druh mykobionta a geografický původ (CZ – Česká republika, IC – Kanárské ostrovy, TZ – Tanzánie). Popisky sekvencí volně žijících zástupců obsahují číslo sekvence v GenBanku, druh dle (Darienko et al., 2010) a číslo sbírkového kmene.

Watanabea-clade, *Dictyochloropsis*

- aerophytic alga, lichen symbiont

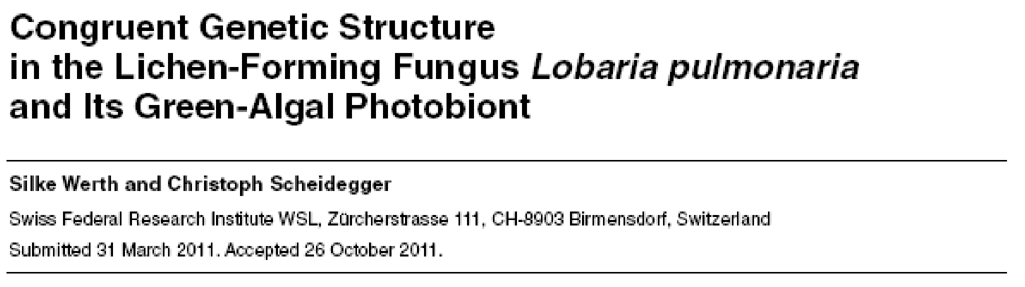






Watanabea-clade, *Dictyochloropsis*

- aerophytic alga, lichen symbiont

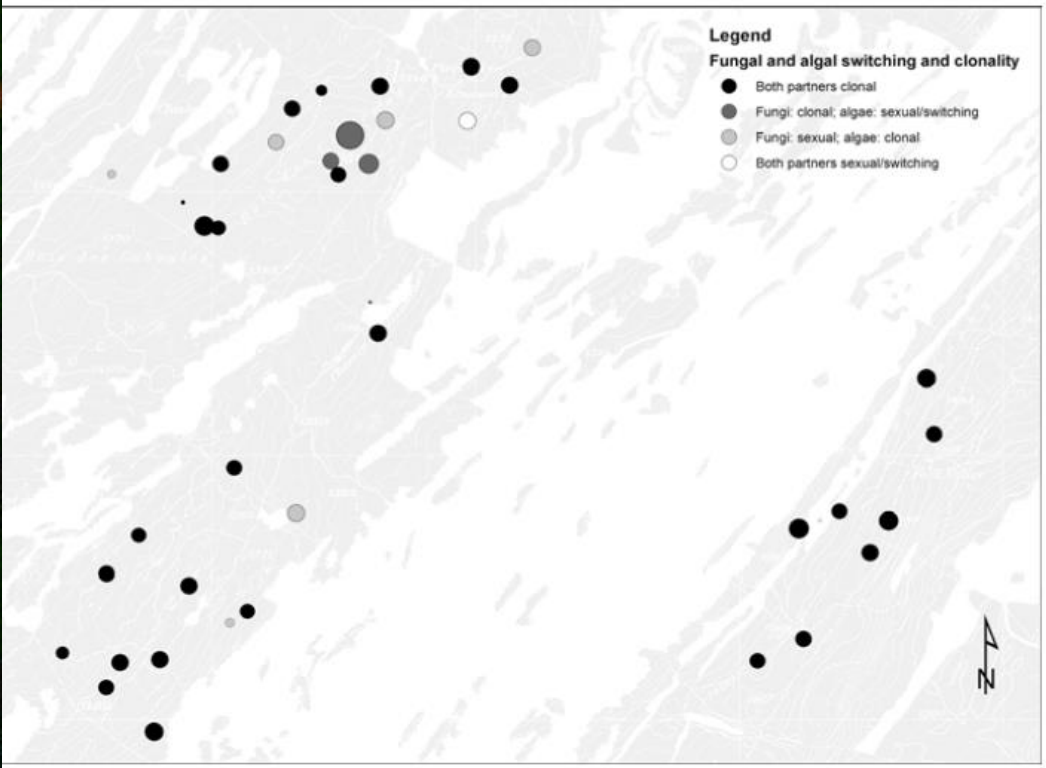


Congruent Genetic Structure in the Lichen-Forming Fungus *Lobaria pulmonaria* and Its Green-Algal Photobiont

Silke Werth and Christoph Scheidegger

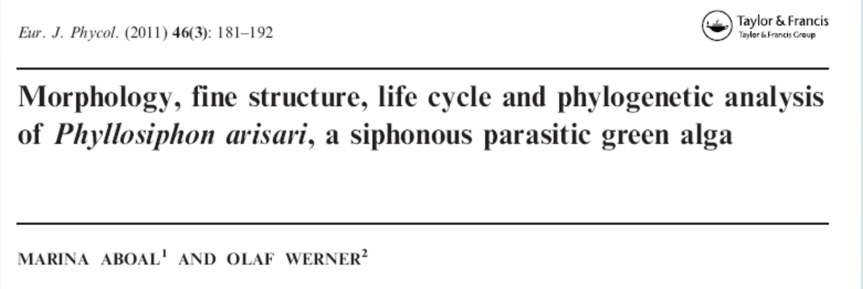
Swiss Federal Research Institute WSL, Zürcherstrasse 111, CH-8903 Birmensdorf, Switzerland

Submitted 31 March 2011. Accepted 26 October 2011.



Watanabea-clade, *Phylosiphon*

- sifonal parasitic alga
- leaves of *Arisarum*



Eur. J. Phycol. (2011) **46**(3): 181–192

Taylor & Francis
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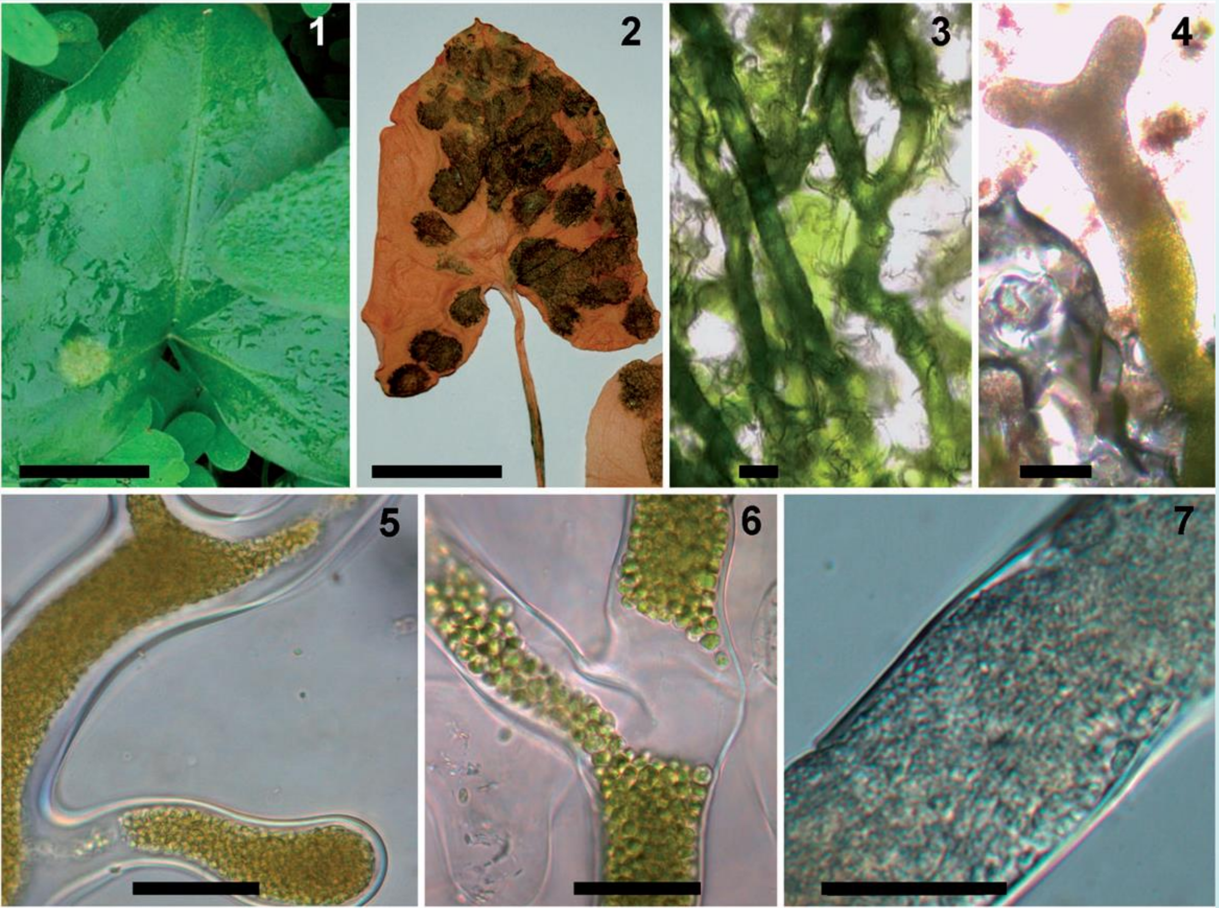
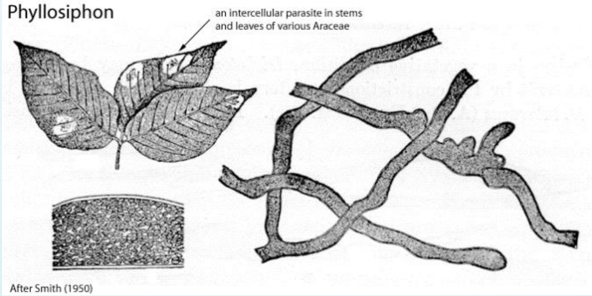
Morphology, fine structure, life cycle and phylogenetic analysis of *Phyllosiphon arisari*, a siphonous parasitic green alga

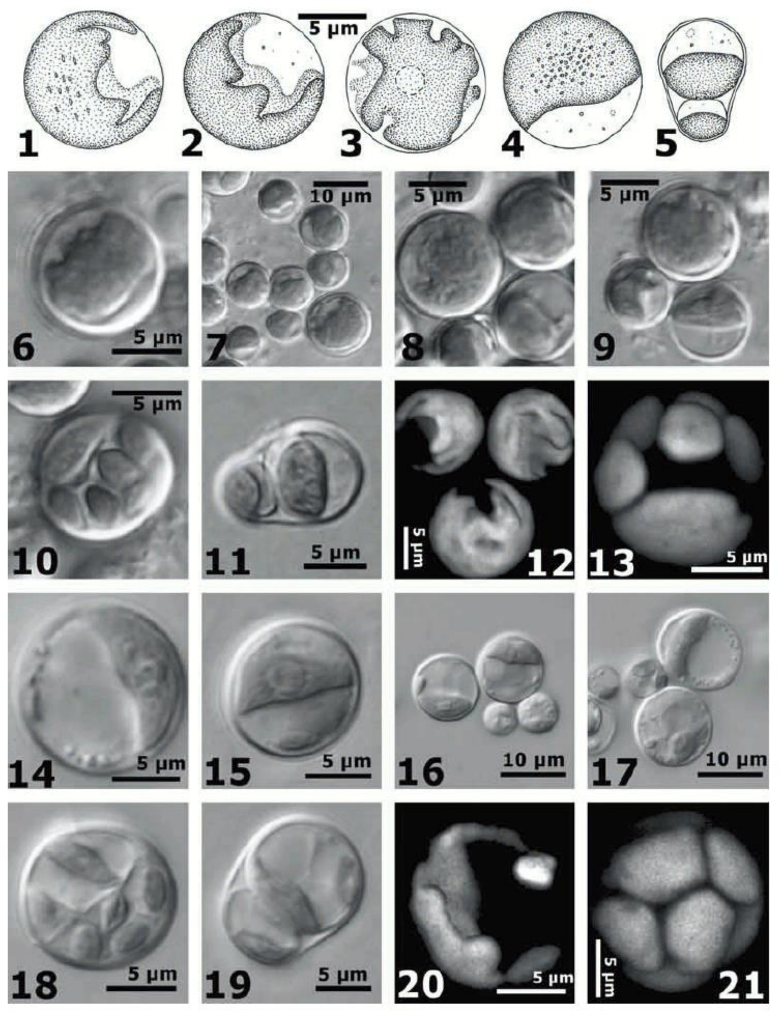
MARINA ABOAL[1] AND OLAF WERNER[2]

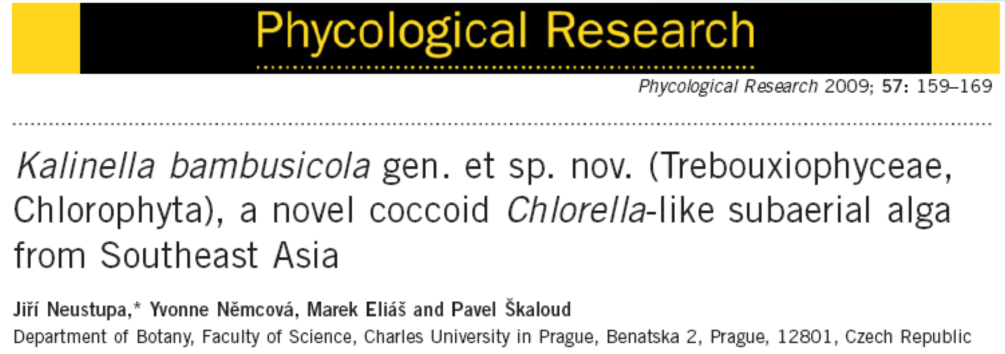




After Smith (1950)

Watanabea-clade, *Kalinella*

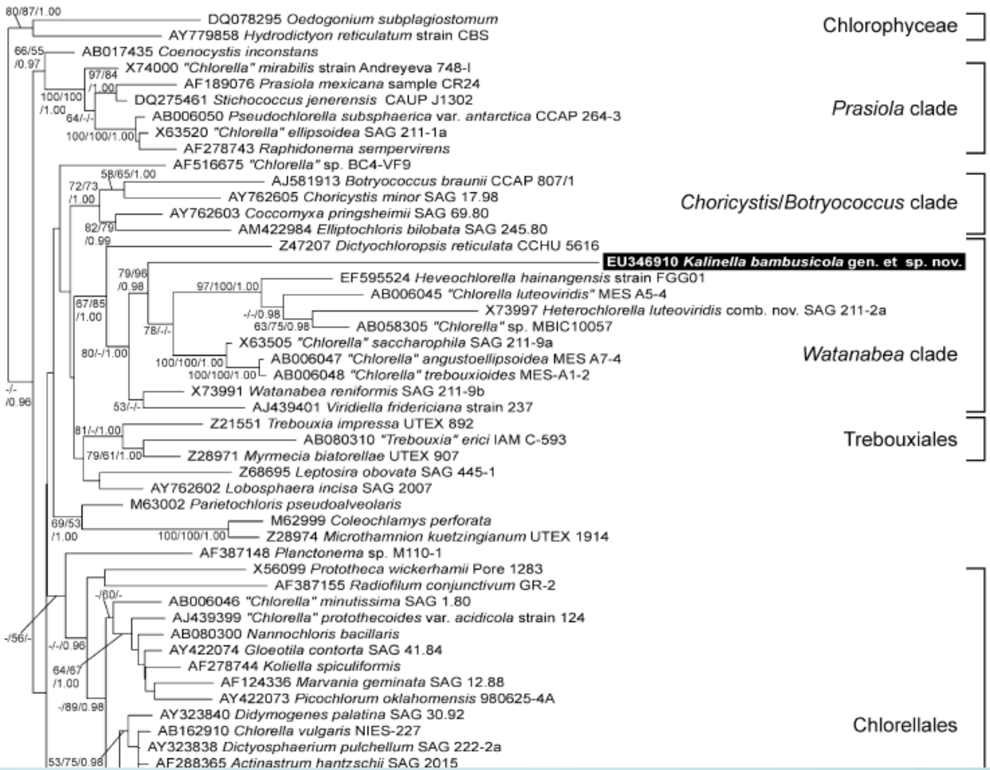



Phycological Research

Phycological Research 2009; **57:** 159–169

Kalinella bambusicola gen. et sp. nov. (Trebouxiophyceae, Chlorophyta), a novel coccoid *Chlorella*-like subaerial alga from Southeast Asia

Jiří Neustupa,* Yvonne Němcová, Marek Eliáš and Pavel Škaloud
Department of Botany, Faculty of Science, Charles University in Prague, Benatska 2, Prague, 12801, Czech Republic

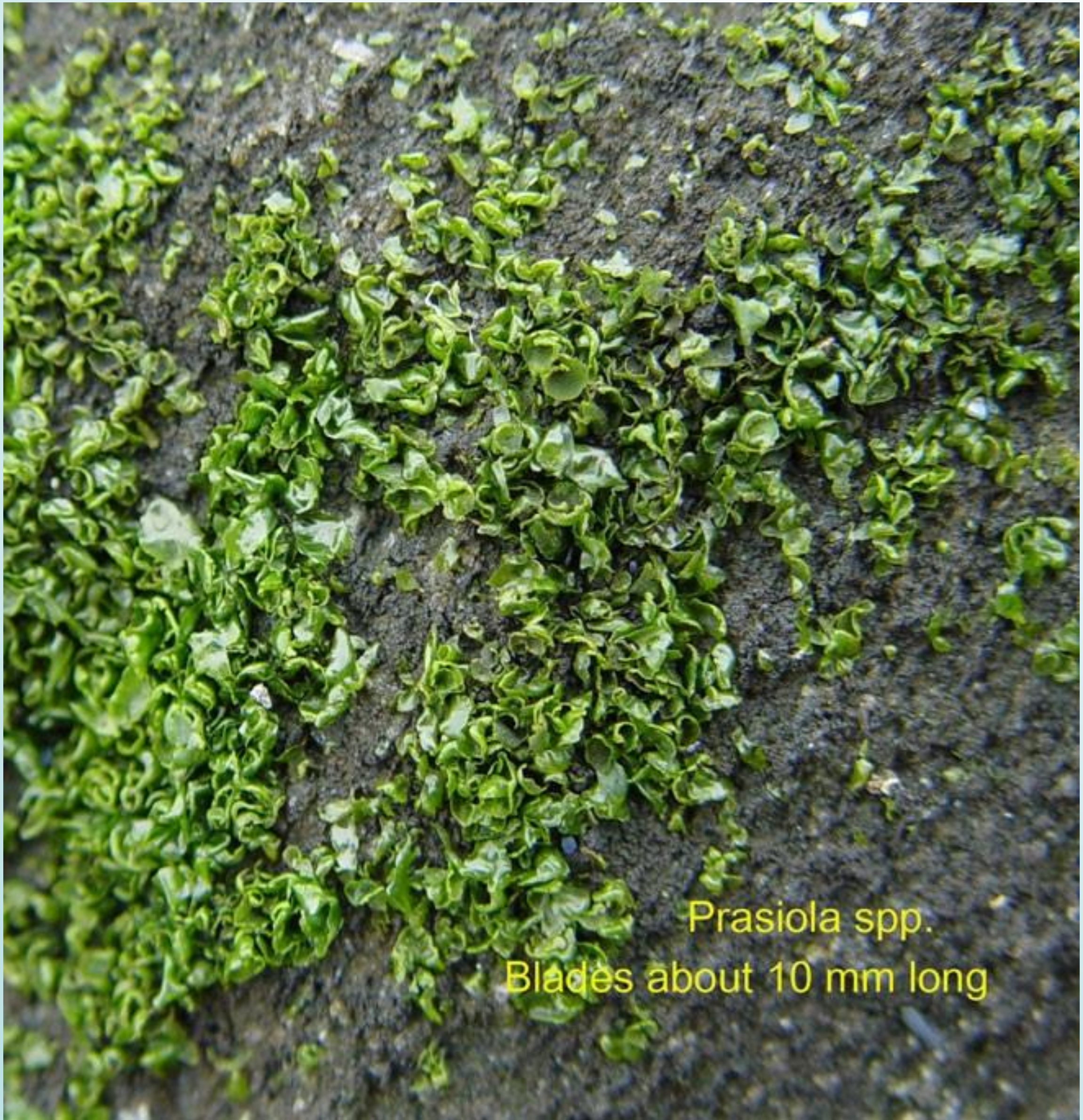


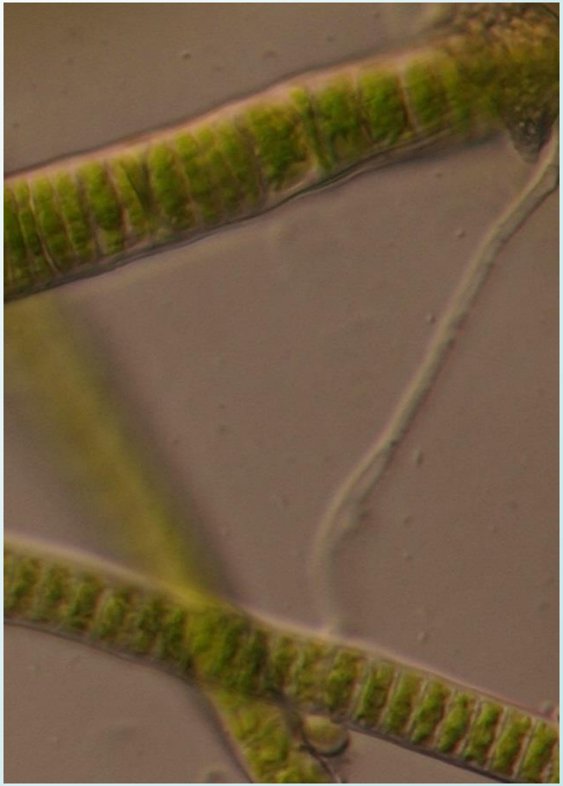
Apatococcus

Microthamniales, *Microthamnion*

M. kuetzingianum

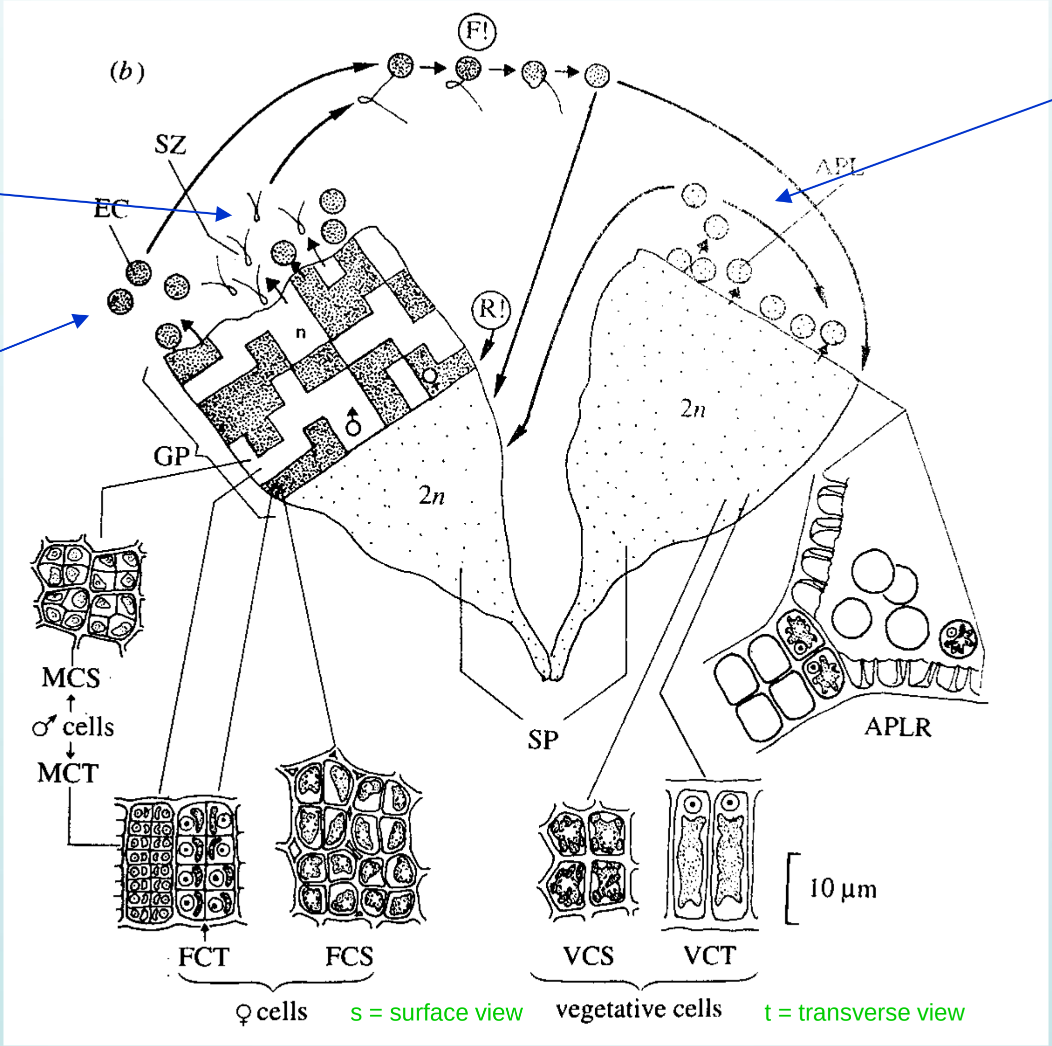
Prasiolales, *Prasiola*





Prasiolales, *Prasiola*

- mosaic sexual reproduction



s = surface view

t = transverse view

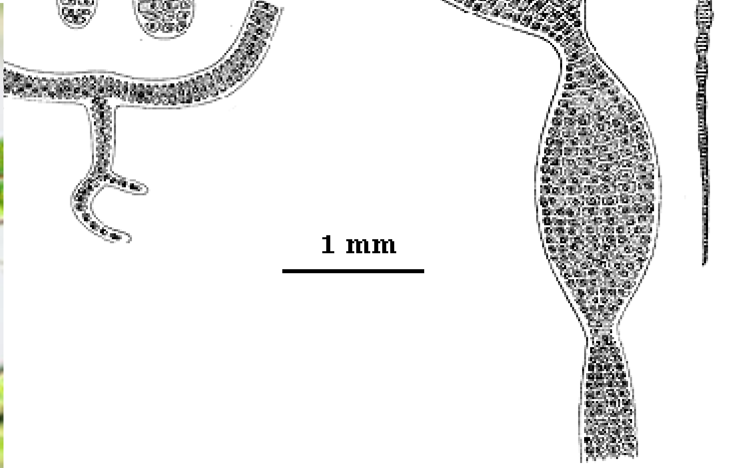
spermatozoids

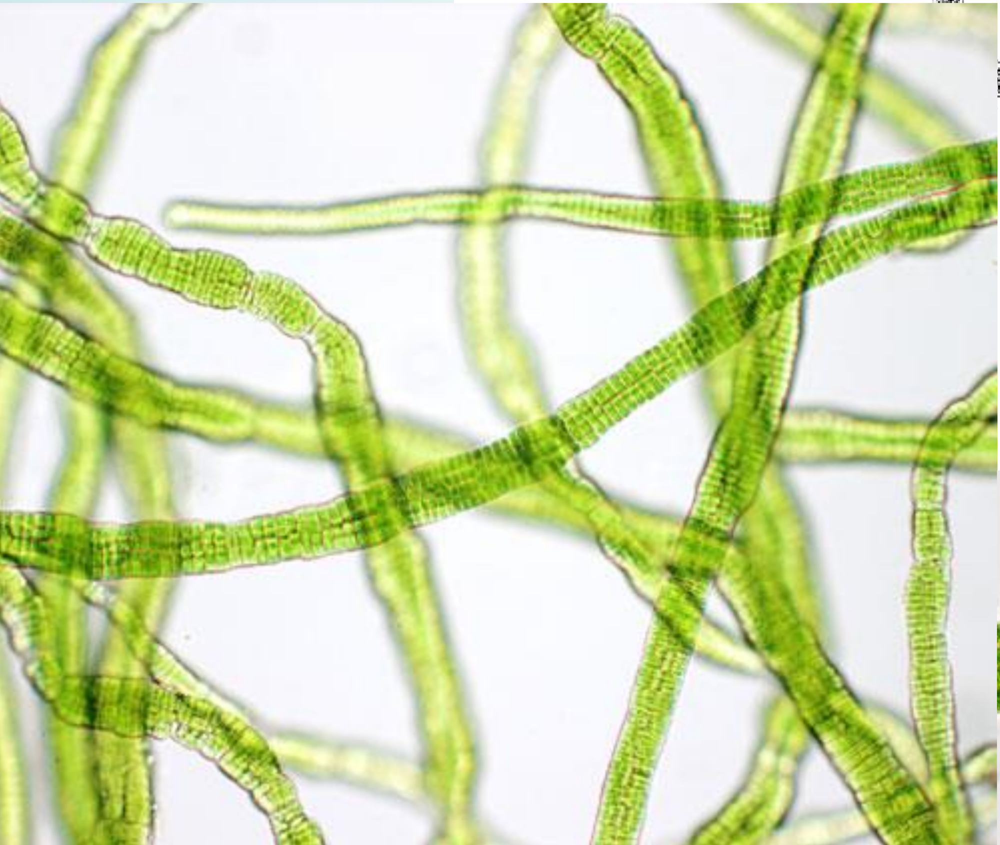
egg cells

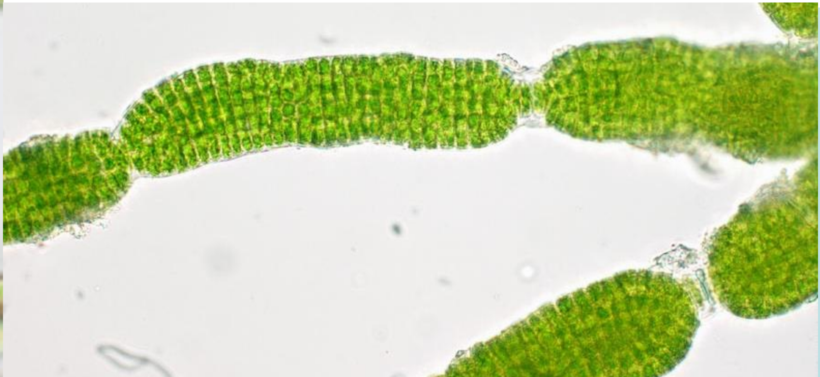
aplanospores (asexual reproduction)

Prasiolales, *Rosenvingiella*

haploid thallus,
zygotic meiosis







Prasiolales

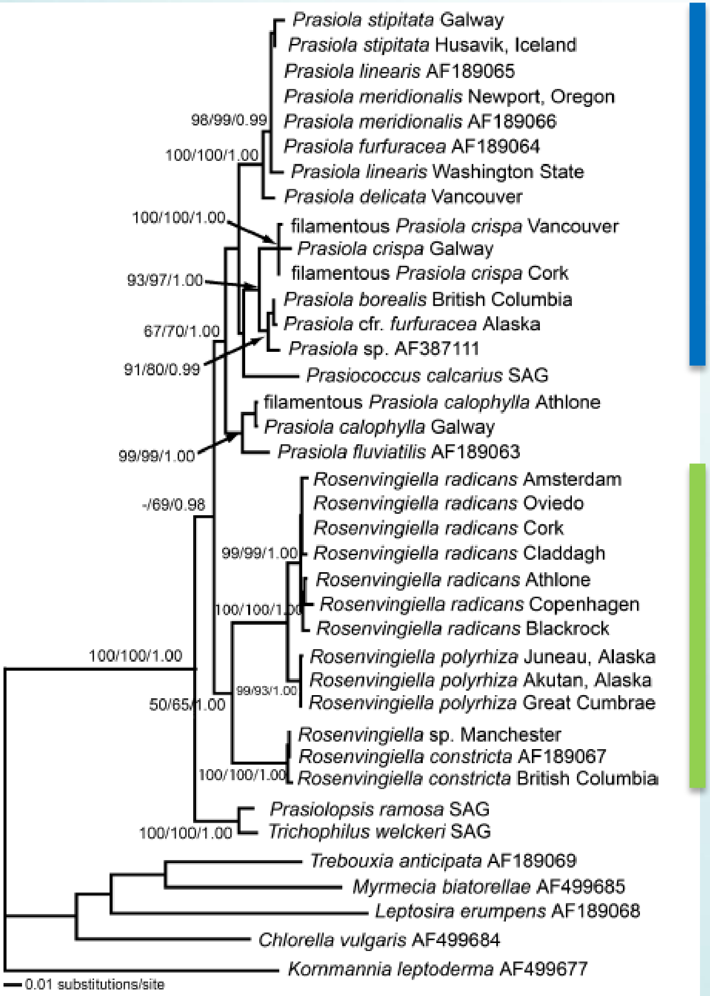
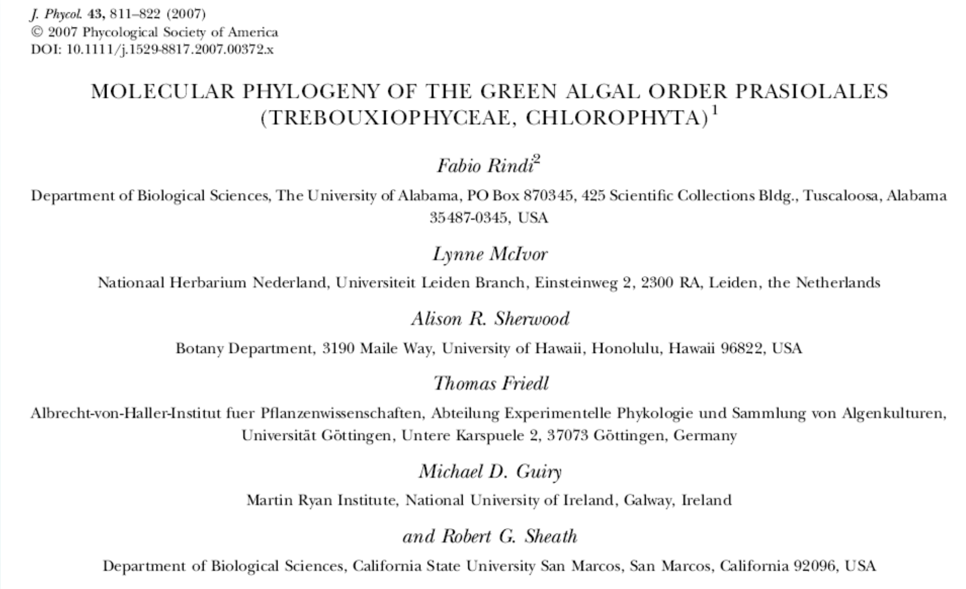


FIG. 1. Phylogenetic tree inferred from maximum-likelihood (ML) analysis of *rbc*L gene sequence data for the Prasiolales and outgroup taxa, with bootstrap support (BP) and posterior probabilities (PP) indicated at the nodes. Left number from maximum parsimony, middle from ML, and right from Bayesian analyses. The BP values lower than 50% and PP values lower than 0.95 are not shown. Branch lengths are drawn proportional to the amount of sequence change.



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MOLECULAR PHYLOGENY OF THE GREEN ALGAL ORDER PRASIOLALES (TREBOUXIOPHYCEAE, CHLOROPHYTA)[1]

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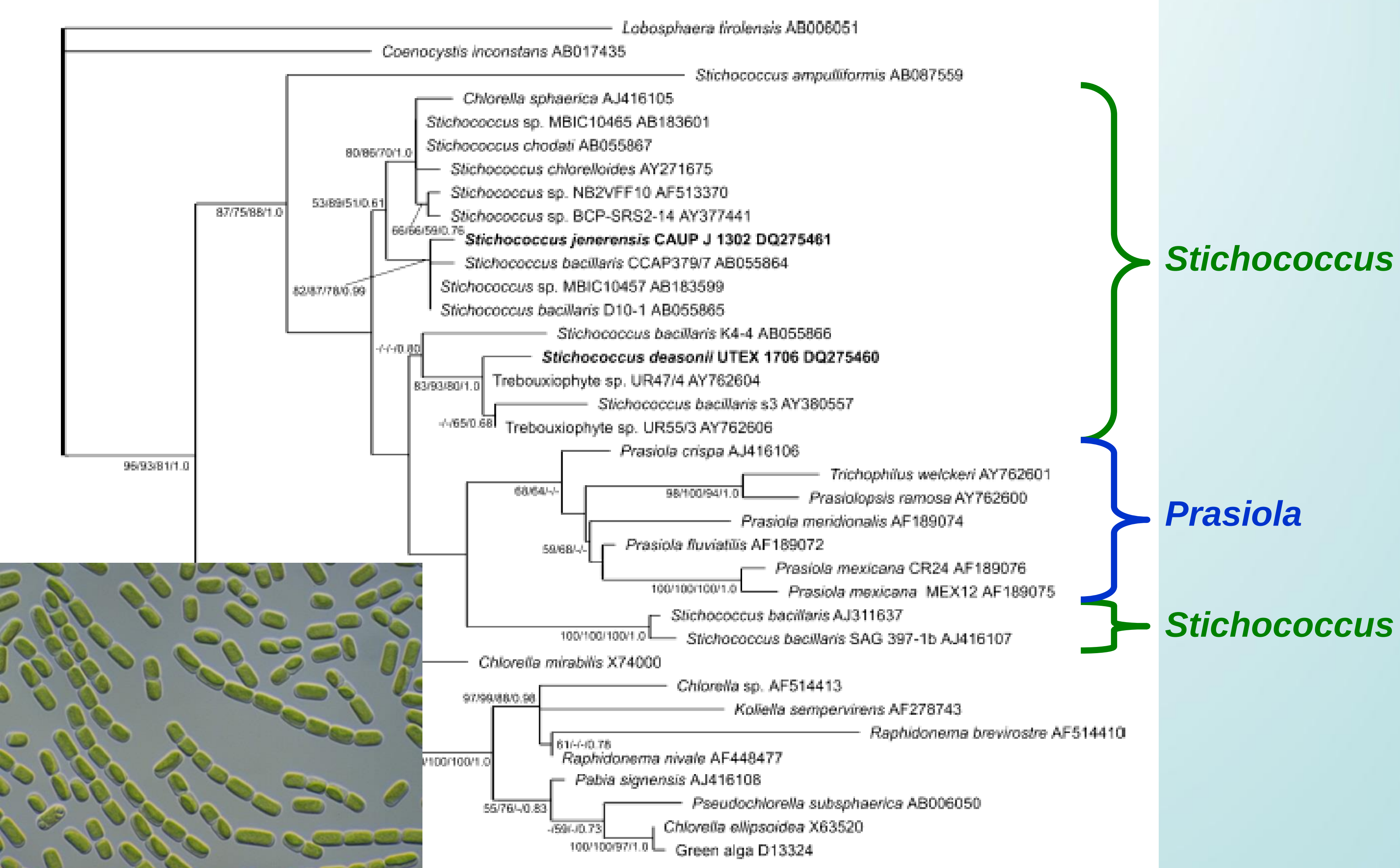
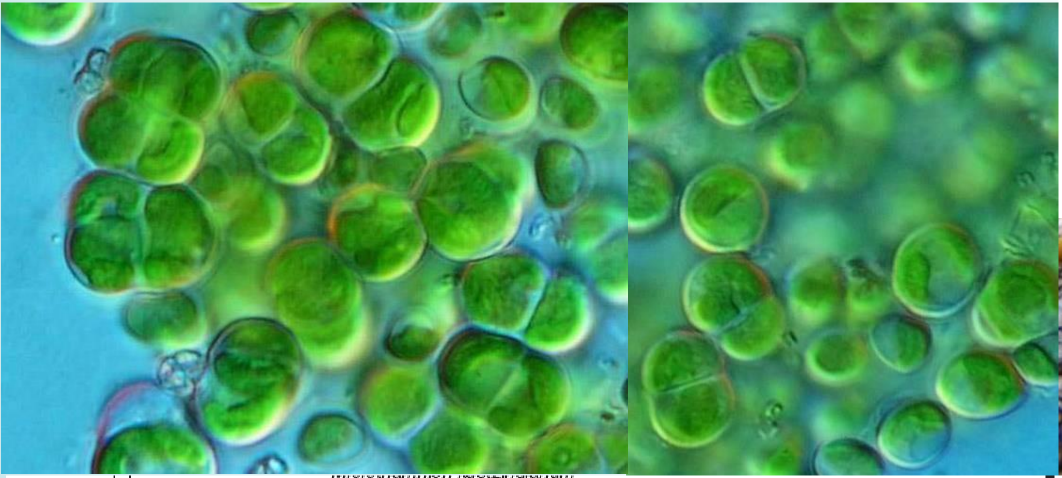
Prasiolales, *Stichococcus*

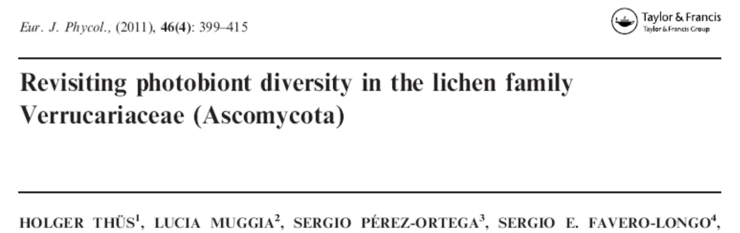
- *Prasiola* – crown group in *Stichococcus* lineage



Prasiolales, *Diplosphaera*

- free living, lichen photobiont





Eur. J. Phycol., (2011), **46(4)**: 399–415

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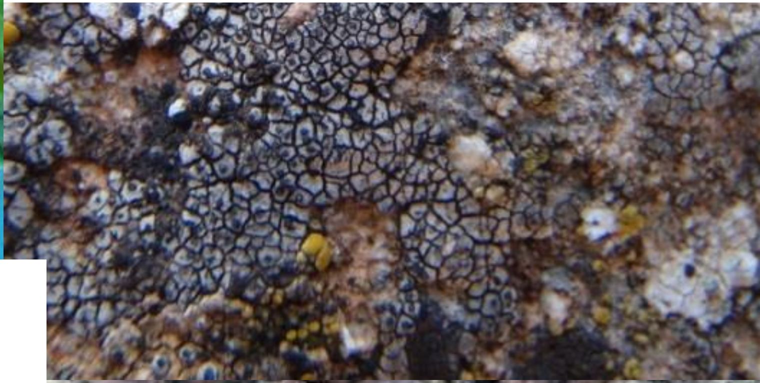
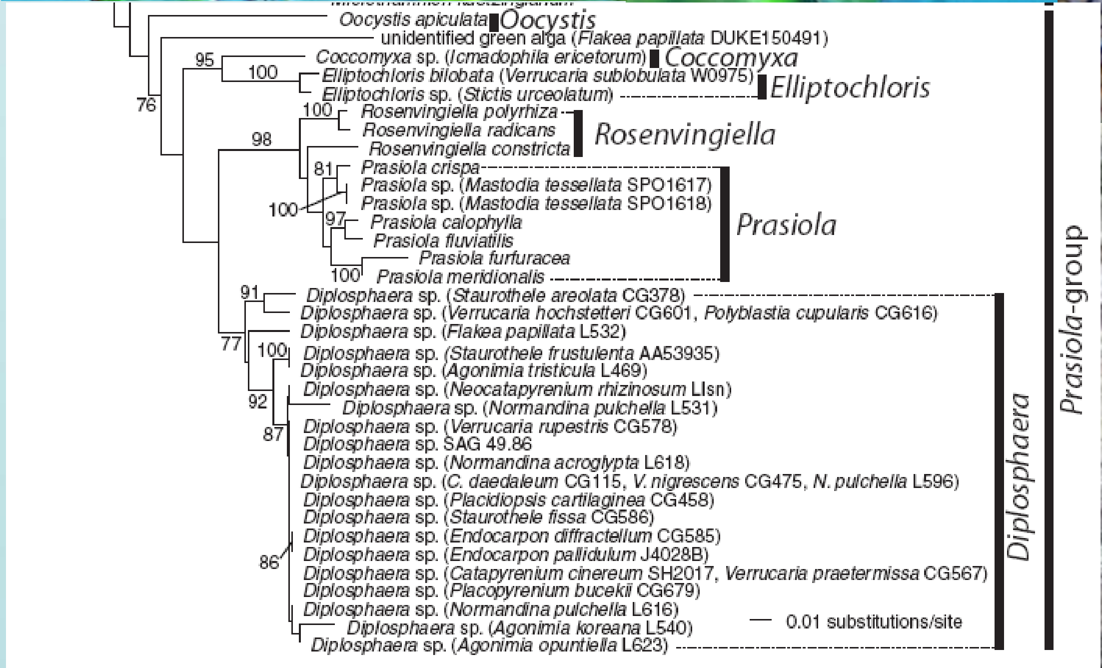
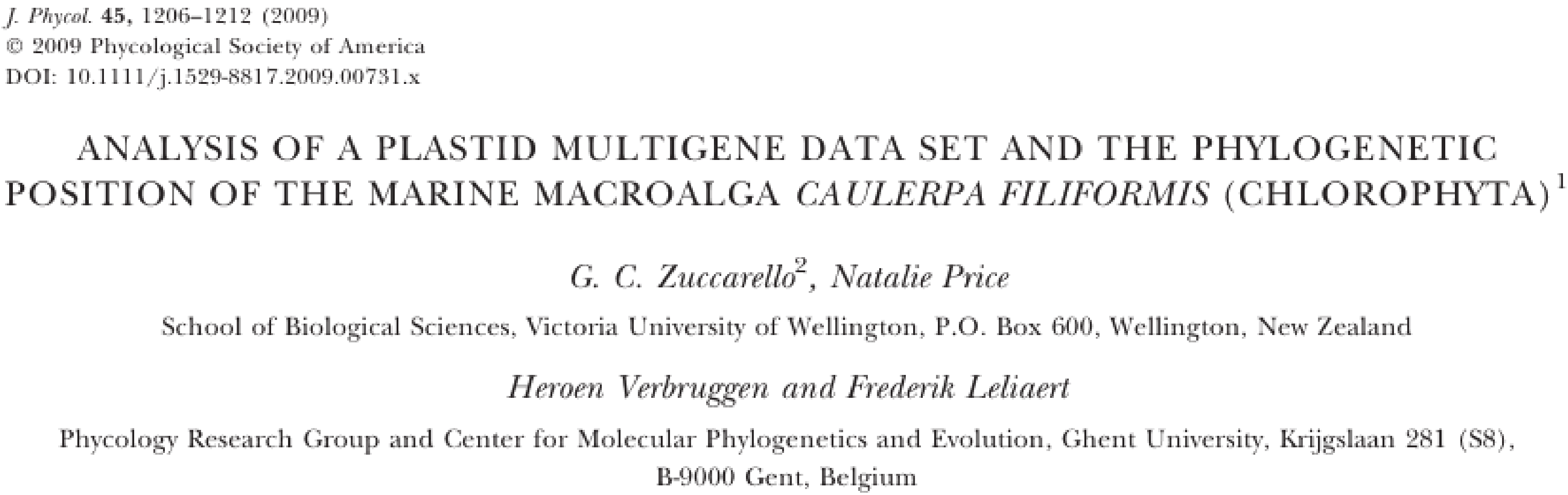
Revisiting photobiont diversity in the lichen family Verrucariaceae (Ascomycota)

HOLGER THÜS[1], LUCIA MUGGIA[2], SERGIO PÉREZ-ORTEGA[3], SERGIO E. FAVERO-LONGO[4], SUZANNE JONESON[5], HEATH O'BRIEN[6], MATTHEW P. NELSEN[7,8], RHINAIXA DUQUE-THÜS[1], MARTIN GRUBE[2], THOMAS FRIEDL[9], JULIET BRODIE[1], CARRIE J. ANDREW[7,10], ROBERT LÜCKING[7], FRANÇOIS LUTZONI[11] AND CÉCILE GUEIDAN[1]





Monophyly of Trebouxiophyceae



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DOI: 10.1111/j.1529-8817.2009.00731.x

ANALYSIS OF A PLASTID MULTIGENE DATA SET AND THE PHYLOGENETIC POSITION OF THE MARINE MACROALGA *CAULERPA FILIFORMIS* (CHLOROPHYTA)[1]

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Phycology Research Group and Center for Molecular Phylogenetics and Evolution, Ghent University, Krijgslaan 281 (S8),
B-9000 Gent, Belgium

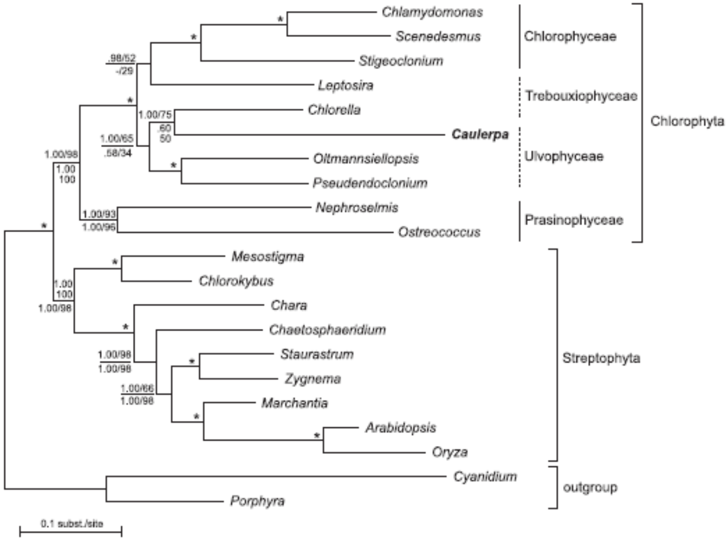


FIG. 2. Phylogenetic tree resulting from Bayesian inference (BI) of 23 chloroplast genes at the amino acid level, showing the position of *Caulerpa filiformis* among the Ulvophyceae+Trebouxiophyceae+Chlorophyceae (UTC) taxa. Values above branches indicate BI posterior probabilities and maximum-likelihood (ML) bootstrap support from the analyses of protein data under a CpREV+G8 model; values below branches indicate BI posterior probabilities and ML bootstrap support from the analyses of nucleotide data (1st and 2nd codon position) under a GTR+G8 model. The nodes that received full support in BI and ML analyses of both protein and nucleotide data are denoted by asterisks. Solid brackets on the right indicate monophyletic taxa; dashed brackets indicate nonmonophyletic taxa. GTR, general time reversible.

Monophyly of Trebouxiophyceae

The Chloroplast Genomes of the Green Algae *Pedinomonas minor, Parachlorella kessleri*, and *Oocystis solitaria* Reveal a Shared Ancestry between the Pedinomonadales and Chlorellales

Monique Turmel, Christian Otis, and Claude Lemieux
Département de Biochimie et de Microbiologie, Université Laval, Québec (Québec) Canada

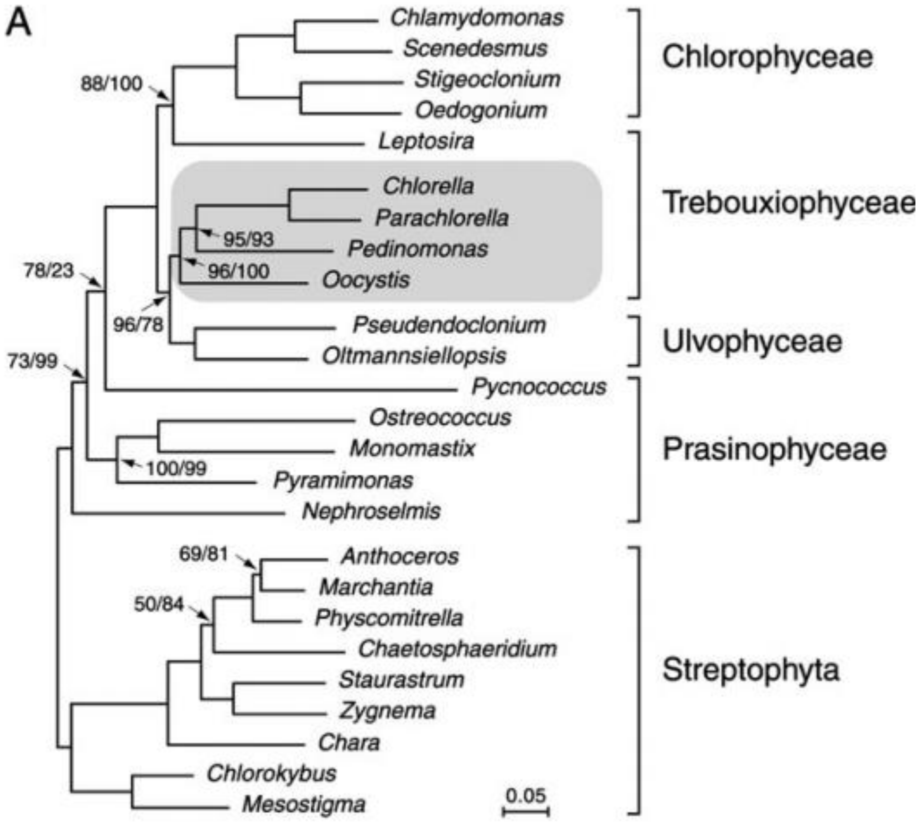
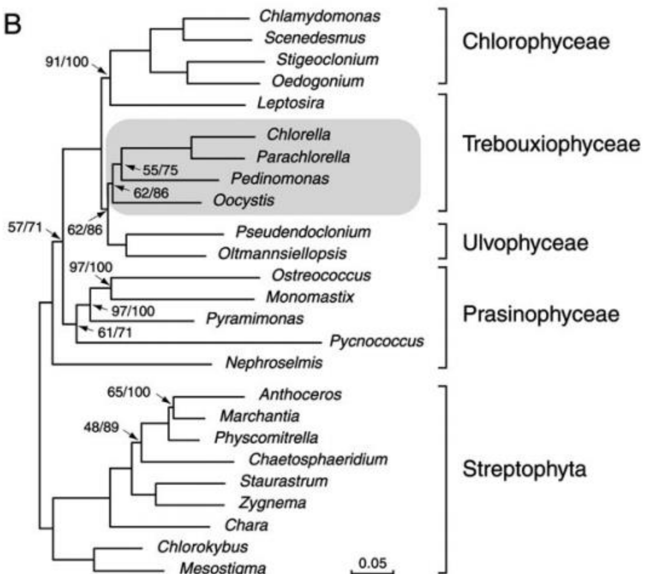
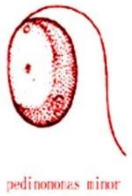


FIG. 4.—Phylogenies inferred from 71 concatenated chloroplast protein-coding genes (first two codon positions) and their deduced amino acid sequences. (*A*) Best ML tree inferred from the amino acid data set. (*B*) Best ML tree inferred from the nucleotide data set. Support values indicate ML bootstrap values/Bayesian posterior probabilities. When both values were 100%, they are not shown. The clade containing *Chlorella* and the three taxa newly investigated in the present study is highlighted in gray.





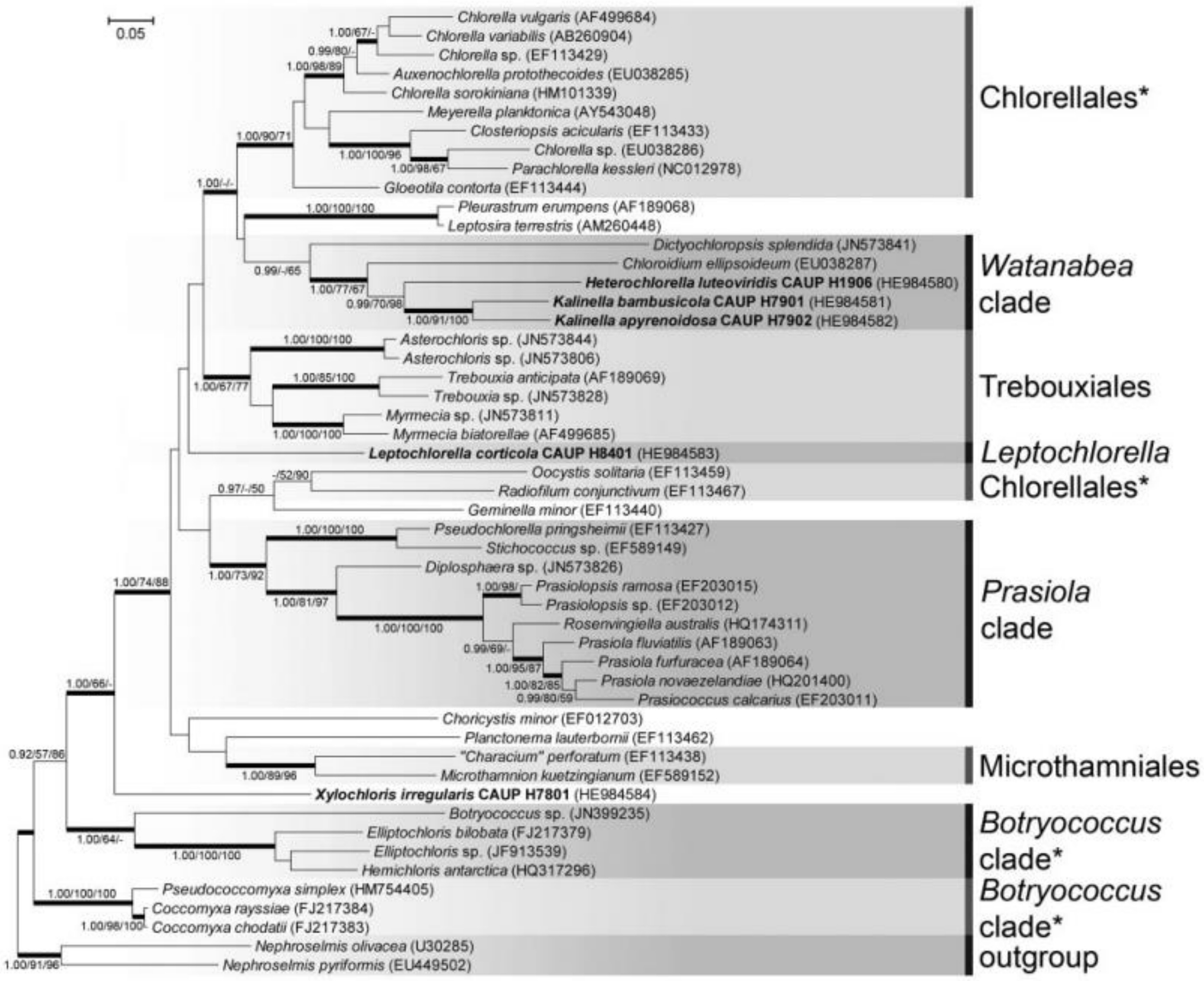
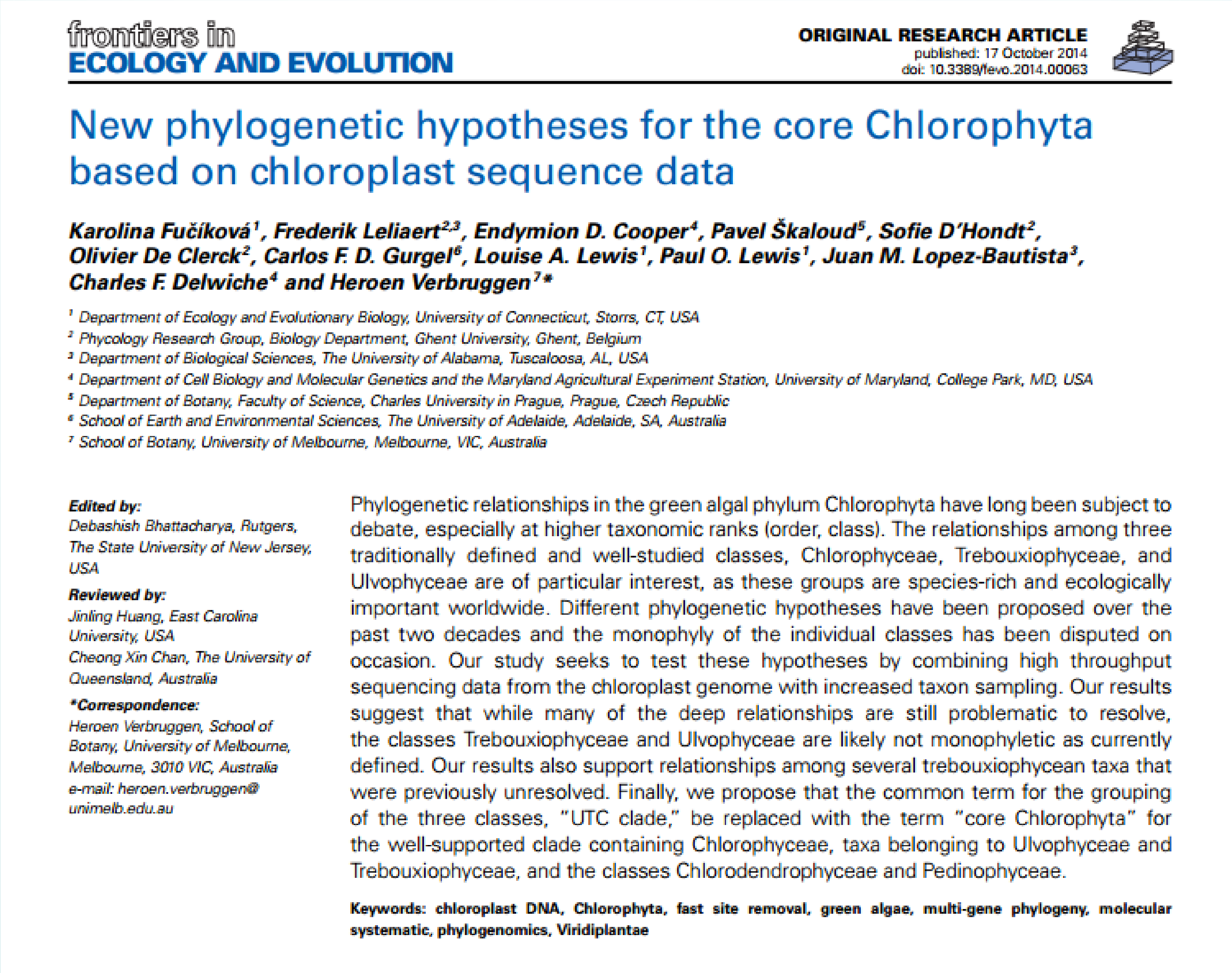


Fig. 4. Phylogenetic position of the investigated microalgae within the class Trebouxiophyceae (Chlorophyta) based on *rbcL* sequences. The tree was inferred using MrBayes. Three partitions were analysed separately using the GTR+G+I model for the 1st and 3rd codon positions, and the JC+G+I model for the 2nd codon position. The tree was arbitrarily rooted with strains of

Monophyly of Trebouxiophyceae



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ORIGINAL RESEARCH ARTICLE
published: 17 October 2014
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New phylogenetic hypotheses for the core Chlorophyta based on chloroplast sequence data

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Phylogenetic relationships in the green algal phylum Chlorophyta have long been subject to debate, especially at higher taxonomic ranks (order, class). The relationships among three traditionally defined and well-studied classes, Chlorophyceae, Trebouxiophyceae, and Ulvophyceae are of particular interest, as these groups are species-rich and ecologically important worldwide. Different phylogenetic hypotheses have been proposed over the past two decades and the monophyly of the individual classes has been disputed on occasion. Our study seeks to test these hypotheses by combining high throughput sequencing data from the chloroplast genome with increased taxon sampling. Our results suggest that while many of the deep relationships are still problematic to resolve, the classes Trebouxiophyceae and Ulvophyceae are likely not monophyletic as currently defined. Our results also support relationships among several trebouxiophycean taxa that were previously unresolved. Finally, we propose that the common term for the grouping of the three classes, "UTC clade," be replaced with the term "core Chlorophyta" for the well-supported clade containing Chlorophyceae, taxa belonging to Ulvophyceae and Trebouxiophyceae, and the classes Chlorodendrophyceae and Pedinophyceae.

Keywords: chloroplast DNA, Chlorophyta, fast site removal, green algae, multi-gene phylogeny, molecular systematic, phylogenomics, Viridiplantae

Monophyly of Trebouxiophyceae

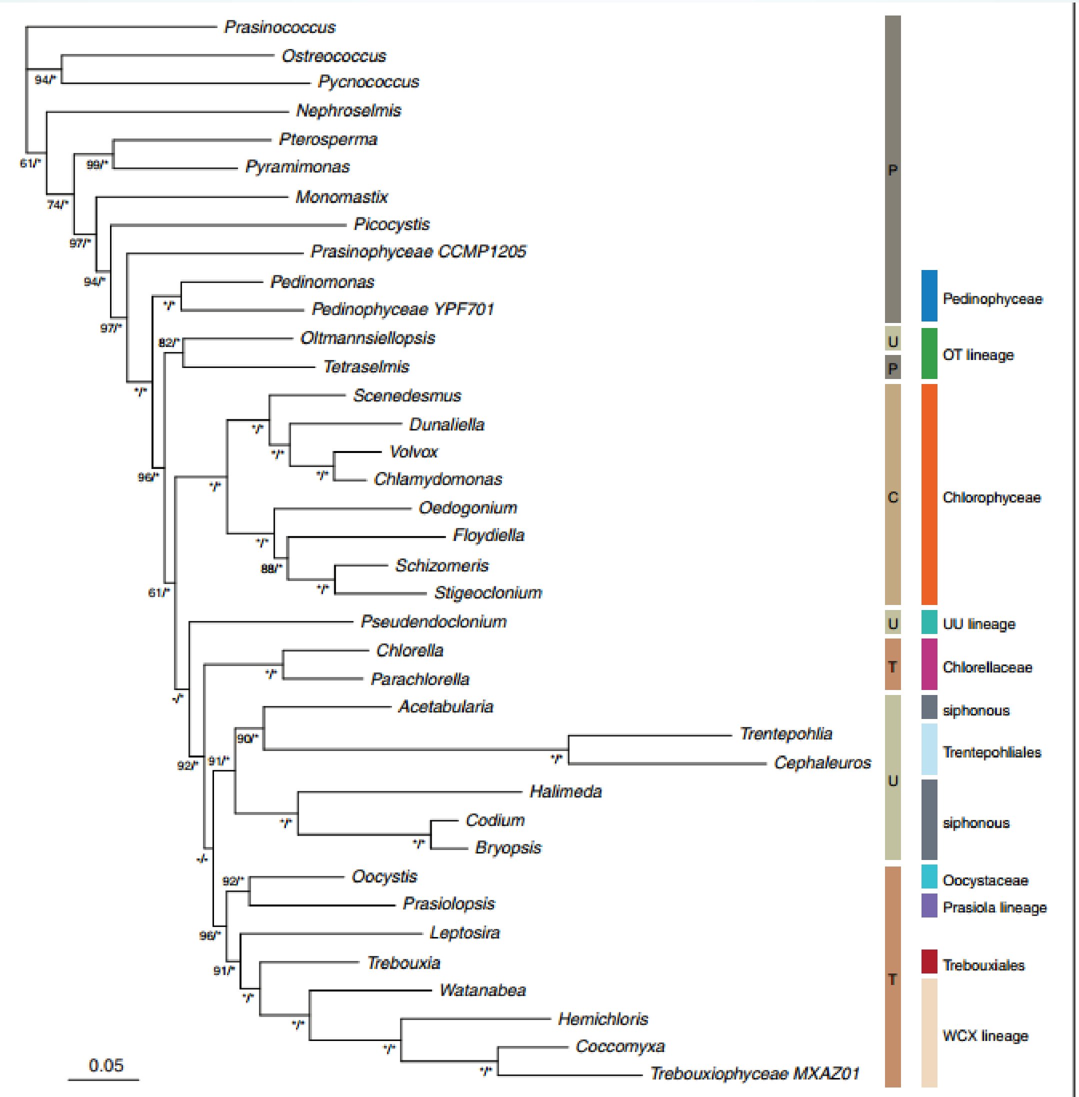
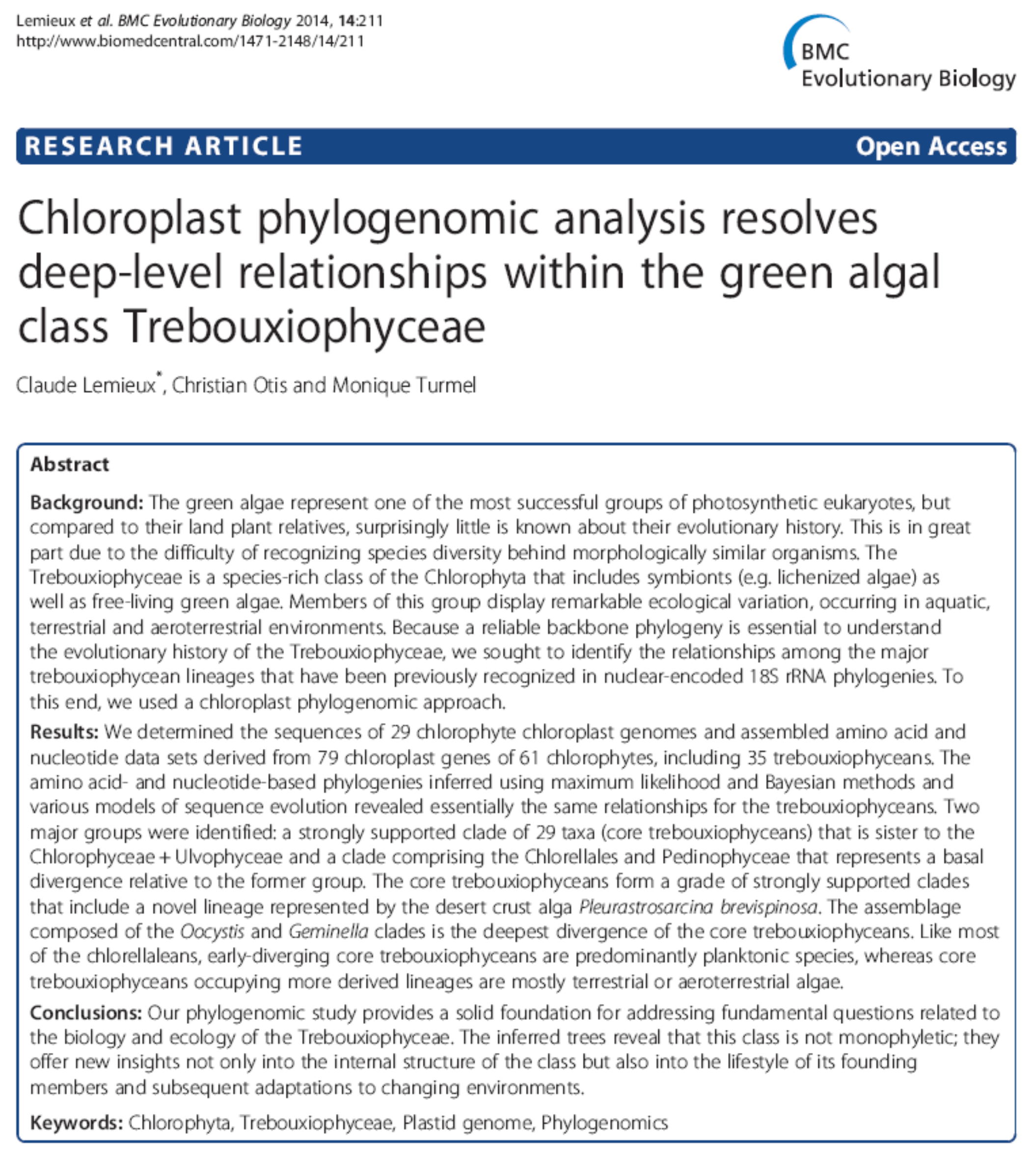


FIGURE 3 | Maximum likelihood phylogeny inferred from the genome-scale alignment (80% slowest sites). Bootstrap percentages and Bayesian posterior probabilities (MrBayes) are indicated along branches. The classical classification into Prasinophyceae (P), Chlorophyceae (C), Ulvophyceae (U) and Trebouxiophyceae (T) as well as the lineage-based classification discussed in the present paper are indicated to the right of the phylogeny. Values under 60 BS and 0.90 BPP are indicated as -, values of 100 BS and 1.00 BPP as *.

Monophyly of Trebouxiophyceae



Lemieux *et al. BMC Evolutionary Biology* 2014, **14**:211
http://www.biomedcentral.com/1471-2148/14/211

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RESEARCH ARTICLE **Open Access**

Chloroplast phylogenomic analysis resolves deep-level relationships within the green algal class Trebouxiophyceae

Claude Lemieux*, Christian Otis and Monique Turmel

Abstract

Background: The green algae represent one of the most successful groups of photosynthetic eukaryotes, but compared to their land plant relatives, surprisingly little is known about their evolutionary history. This is in great part due to the difficulty of recognizing species diversity behind morphologically similar organisms. The Trebouxiophyceae is a species-rich class of the Chlorophyta that includes symbionts (e.g. lichenized algae) as well as free-living green algae. Members of this group display remarkable ecological variation, occurring in aquatic, terrestrial and aeroterrestrial environments. Because a reliable backbone phylogeny is essential to understand the evolutionary history of the Trebouxiophyceae, we sought to identify the relationships among the major trebouxiophycean lineages that have been previously recognized in nuclear-encoded 18S rRNA phylogenies. To this end, we used a chloroplast phylogenomic approach.

Results: We determined the sequences of 29 chlorophyte chloroplast genomes and assembled amino acid and nucleotide data sets derived from 79 chloroplast genes of 61 chlorophytes, including 35 trebouxiophyceans. The amino acid- and nucleotide-based phylogenies inferred using maximum likelihood and Bayesian methods and various models of sequence evolution revealed essentially the same relationships for the trebouxiophyceans. Two major groups were identified: a strongly supported clade of 29 taxa (core trebouxiophyceans) that is sister to the Chlorophyceae + Ulvophyceae and a clade comprising the Chlorellales and Pedinophyceae that represents a basal divergence relative to the former group. The core trebouxiophyceans form a grade of strongly supported clades that include a novel lineage represented by the desert crust alga *Pleurastrosarcina brevispinosa*. The assemblage composed of the *Oocystis* and *Geminella* clades is the deepest divergence of the core trebouxiophyceans. Like most of the chlorellaleans, early-diverging core trebouxiophyceans are predominantly planktonic species, whereas core trebouxiophyceans occupying more derived lineages are mostly terrestrial or aeroterrestrial algae.

Conclusions: Our phylogenomic study provides a solid foundation for addressing fundamental questions related to the biology and ecology of the Trebouxiophyceae. The inferred trees reveal that this class is not monophyletic; they offer new insights not only into the internal structure of the class but also into the lifestyle of its founding members and subsequent adaptations to changing environments.

Keywords: Chlorophyta, Trebouxiophyceae, Plastid genome, Phylogenomics

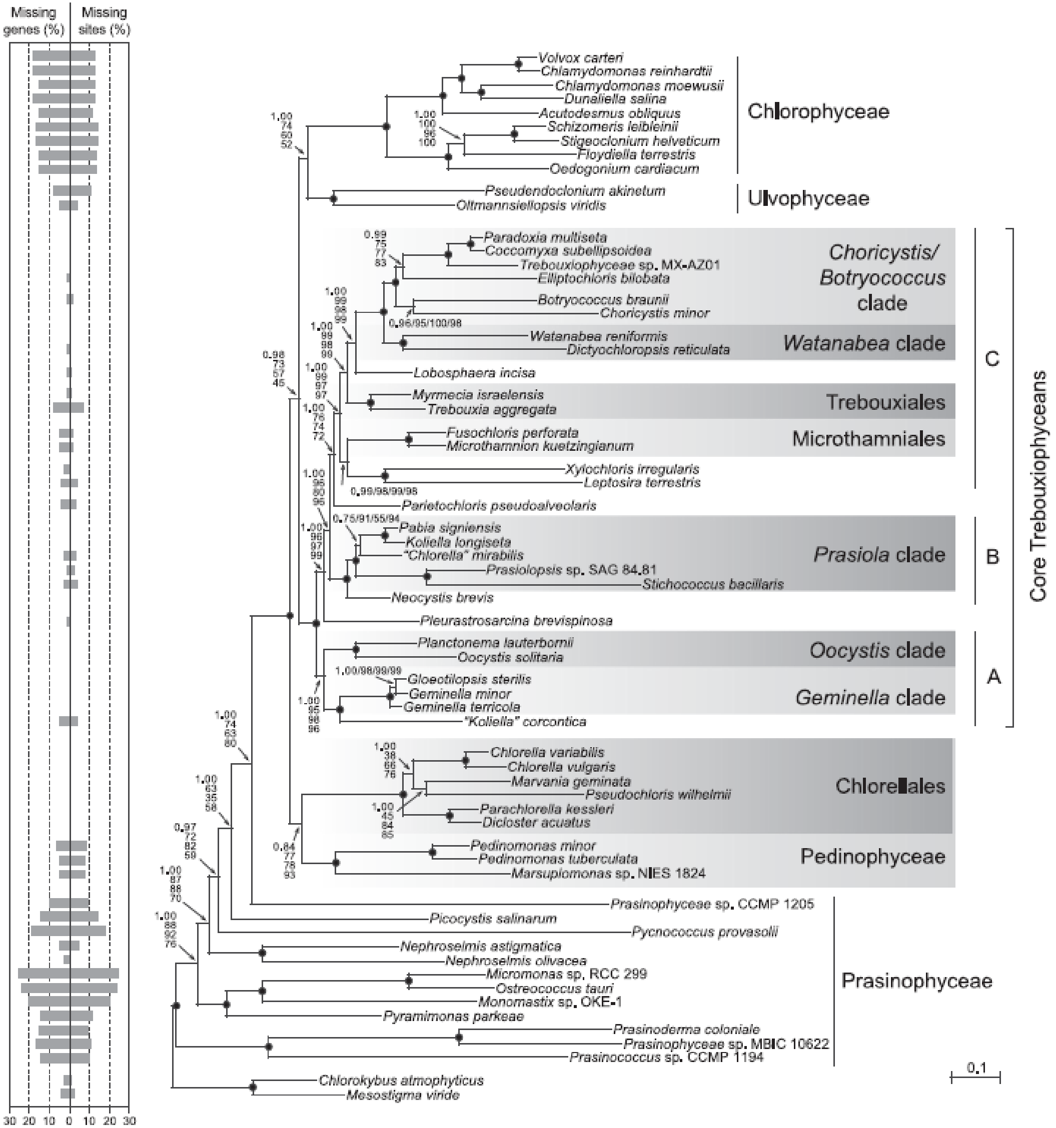

Figure 1 Phylogeny of 61 chlorophytes inferred using a data set of 15,549 positions assembled from 79 cpDNA-encoded proteins. The tree presented here is the best-scoring ML tree inferred under the GTR + Γ4 model. Support values are reported on the nodes: from top to bottom, or from left to right, are shown the posterior probability (PP) values for the PhyloBayes CATGTR + Γ4 analyses and the bootstrap support (BS) values for the RAxML GTR + Γ4, LG4X and gcpREV + Γ4 analyses. Black dots indicate that the corresponding branches received BS and PP values of 100% in all four analyses. Shaded areas identify the clades that are well supported in 18S rDNA phylogenies. The histograms on the left indicate the proportion of missing data for each taxon. The scale bar denotes the estimated number of amino acid substitutions per site.

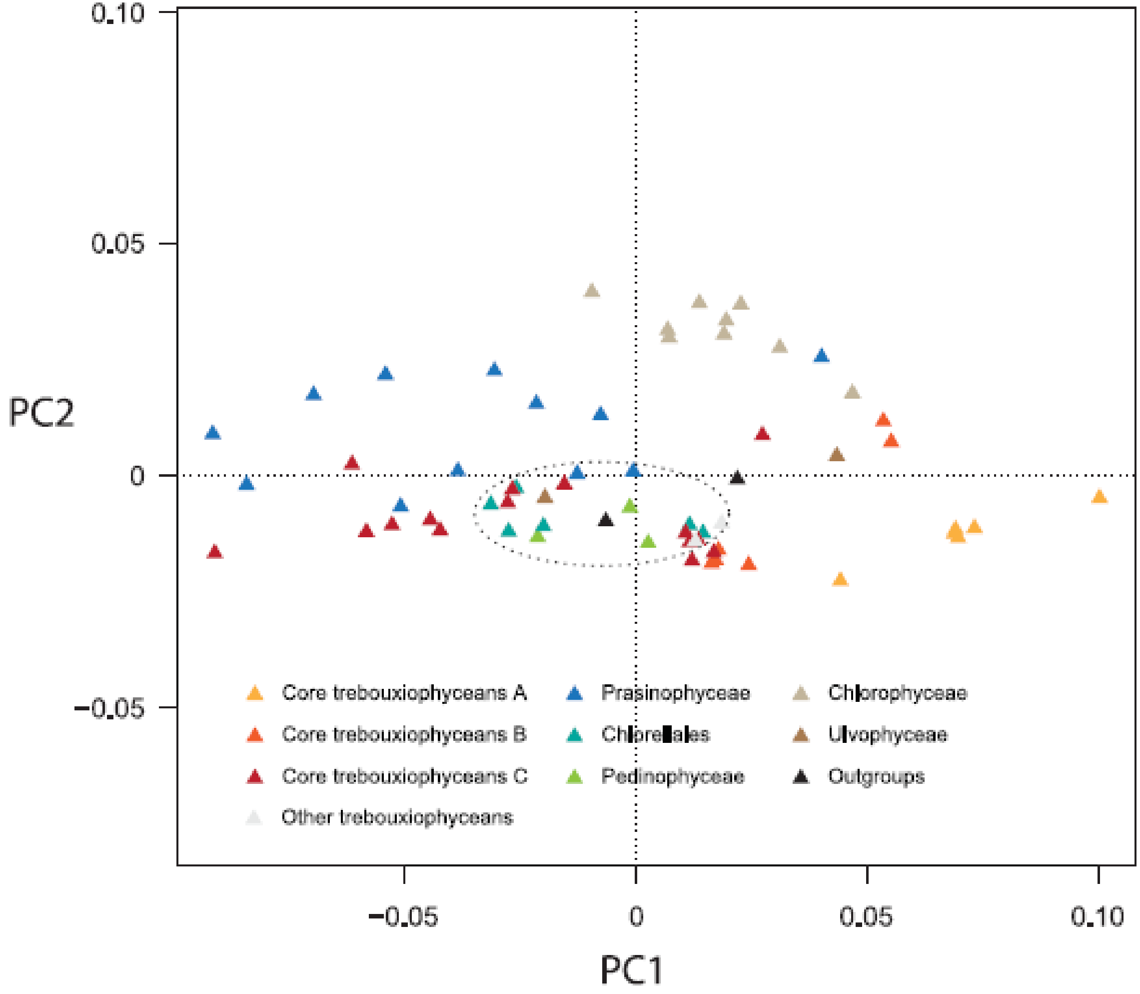

Figure 2 Correspondence analysis of amino acid usage in the data set of 15,549 positions. The members of the Chlorellales and Pedinophyceae are found within the circled area.

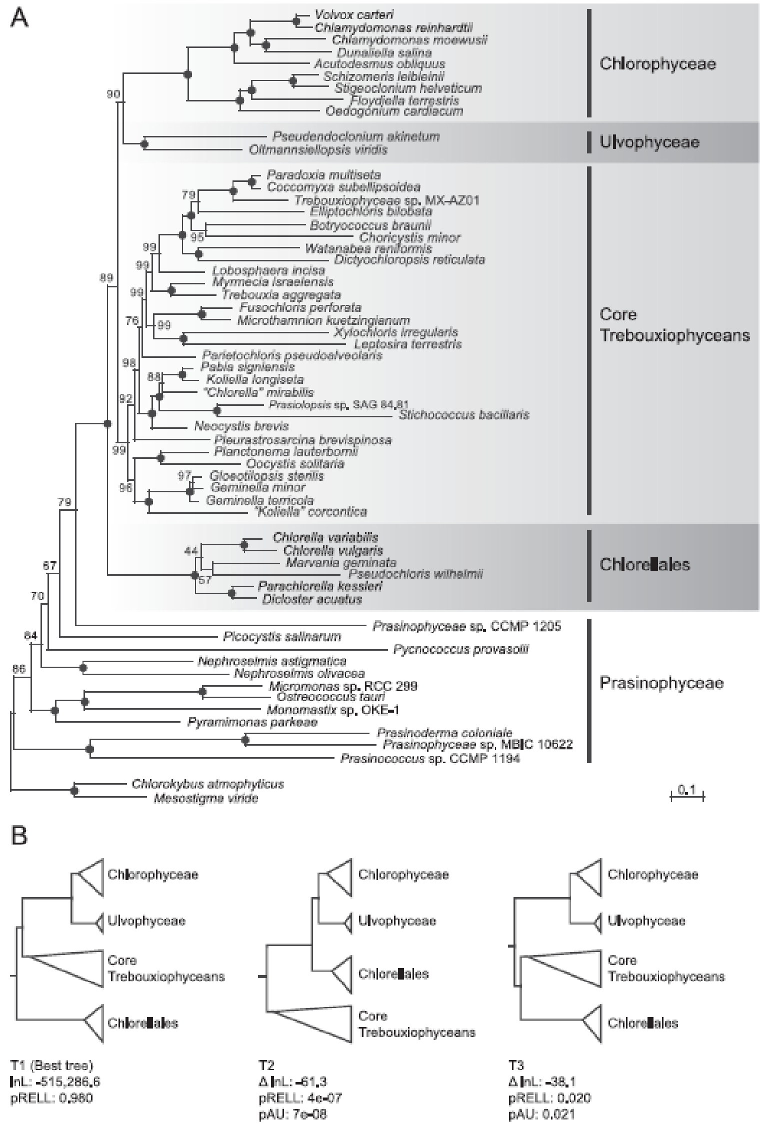

Figure 3 Influence of the Pedinophyceae on the placement of the Chlorellales. (A) Phylogeny of chlorophytes inferred under the GTR + Γ4 model using the amino acid data set of 15,549 positions after exclusion of the Pedinophyceae. The best-scoring RAxML tree is presented and support values are reported on the nodes, with black dots indicating 100% BS values. The scale bar denotes the estimated number of amino a cid substitutions per site. **(B)** Confidence assessment of the three possible topologies (T1, T2 and T3) for the placement of the Chlorellales under the GTR + Γ4 model. The ΔlnL value indicates the difference in log likelihood relative to the best tree (T1). Local bootstrap probabilities were estimated by resampling of the estimated log-likelihood (RELL). pAU, *P* value for the approximately unbiased (AU) test [60] as implemented in CONSEL 0.20 [61].