

Kingdom: Archaeplastida

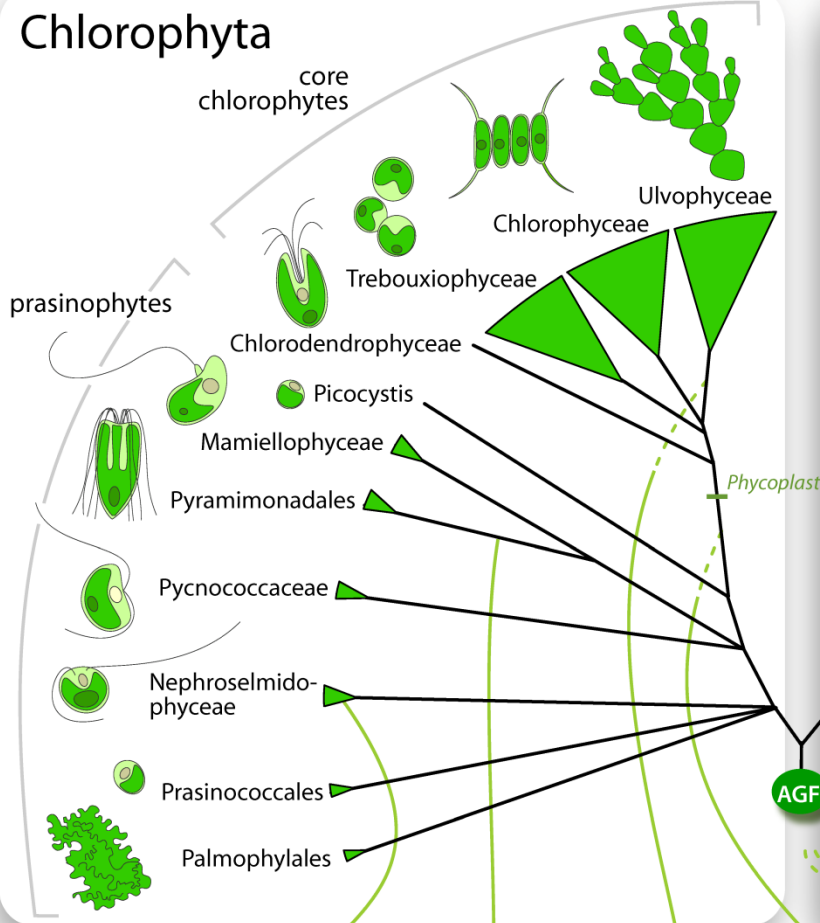
Order: Chlorophyta

Class: Trebouxiophyceae



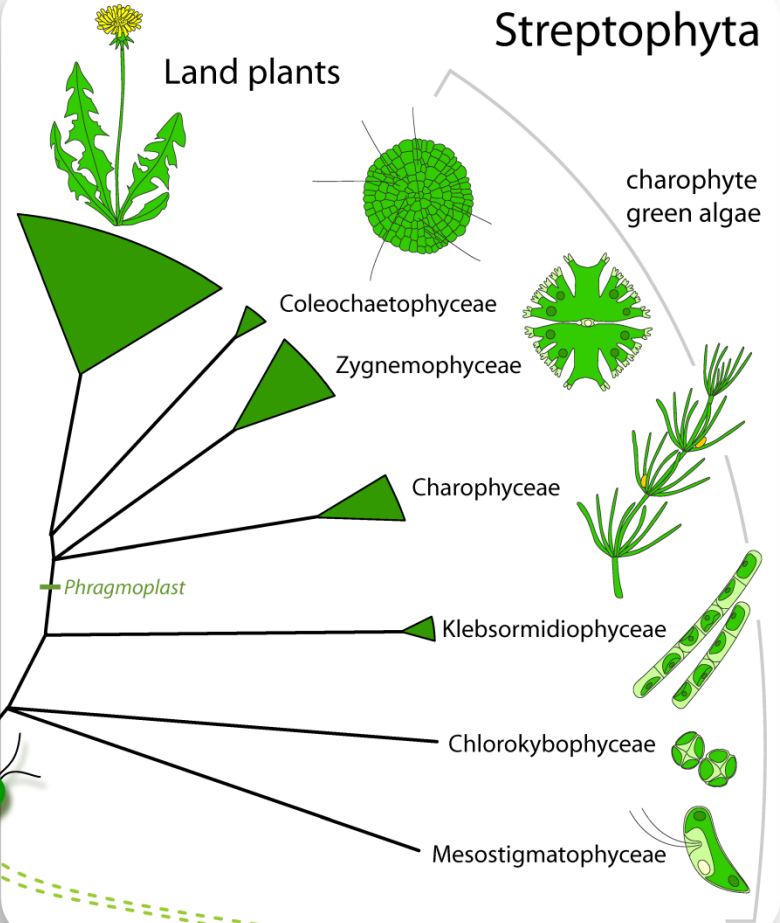
Chlorophyta

core
chlorophytes



Streptophyta

Land plants



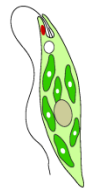
*Putative secondary
symbiosis in progress*

*Hatena
(Katablepharids)*

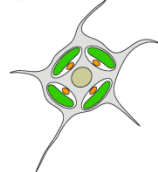


*Secondary
endosymbiosis*

Euglenophytes



*Chlorarachnio-
phytes*



*Serial secondary
endosymbiosis*

Green dinoflagellates



Lepidodinium

*Putative ancient
endosymbioses*

Chromalveolates



Diatom

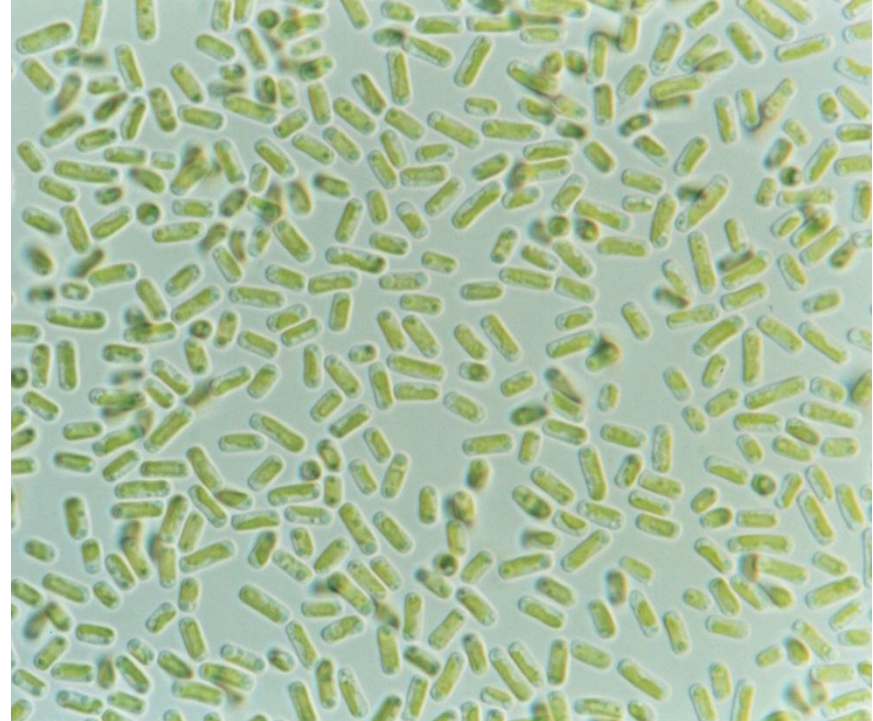
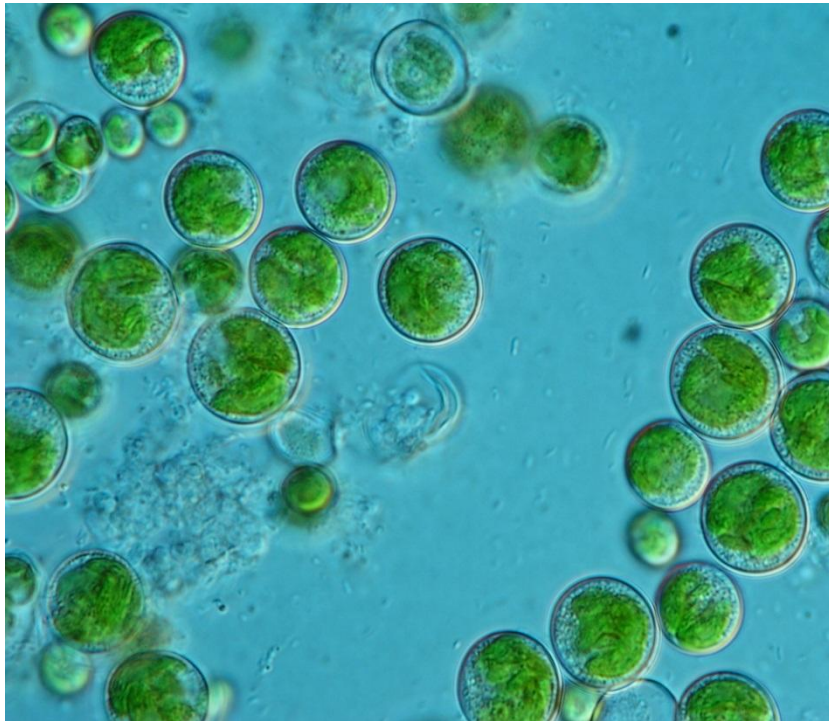
Choanoflagellates



Monosiga

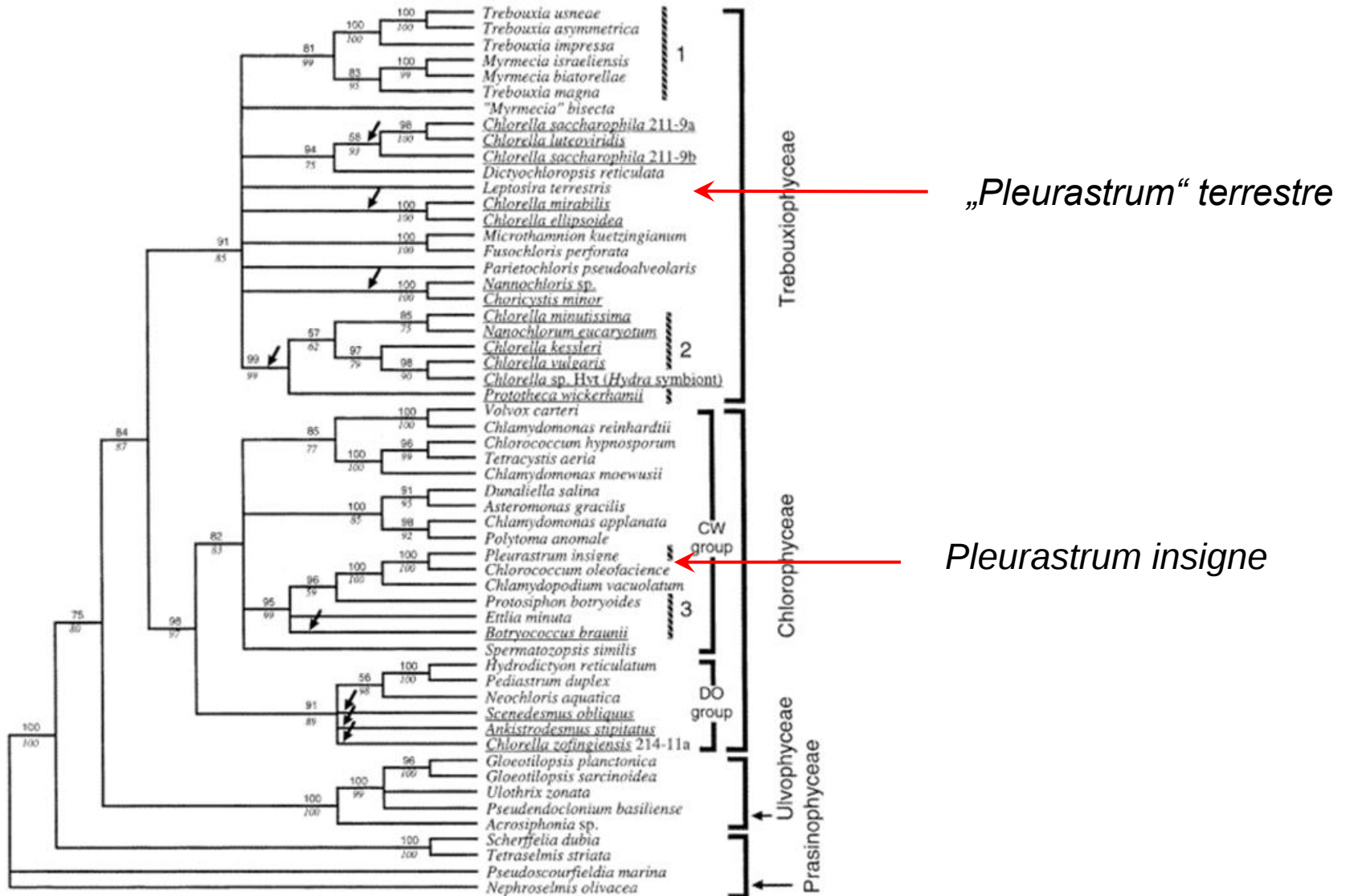
General features

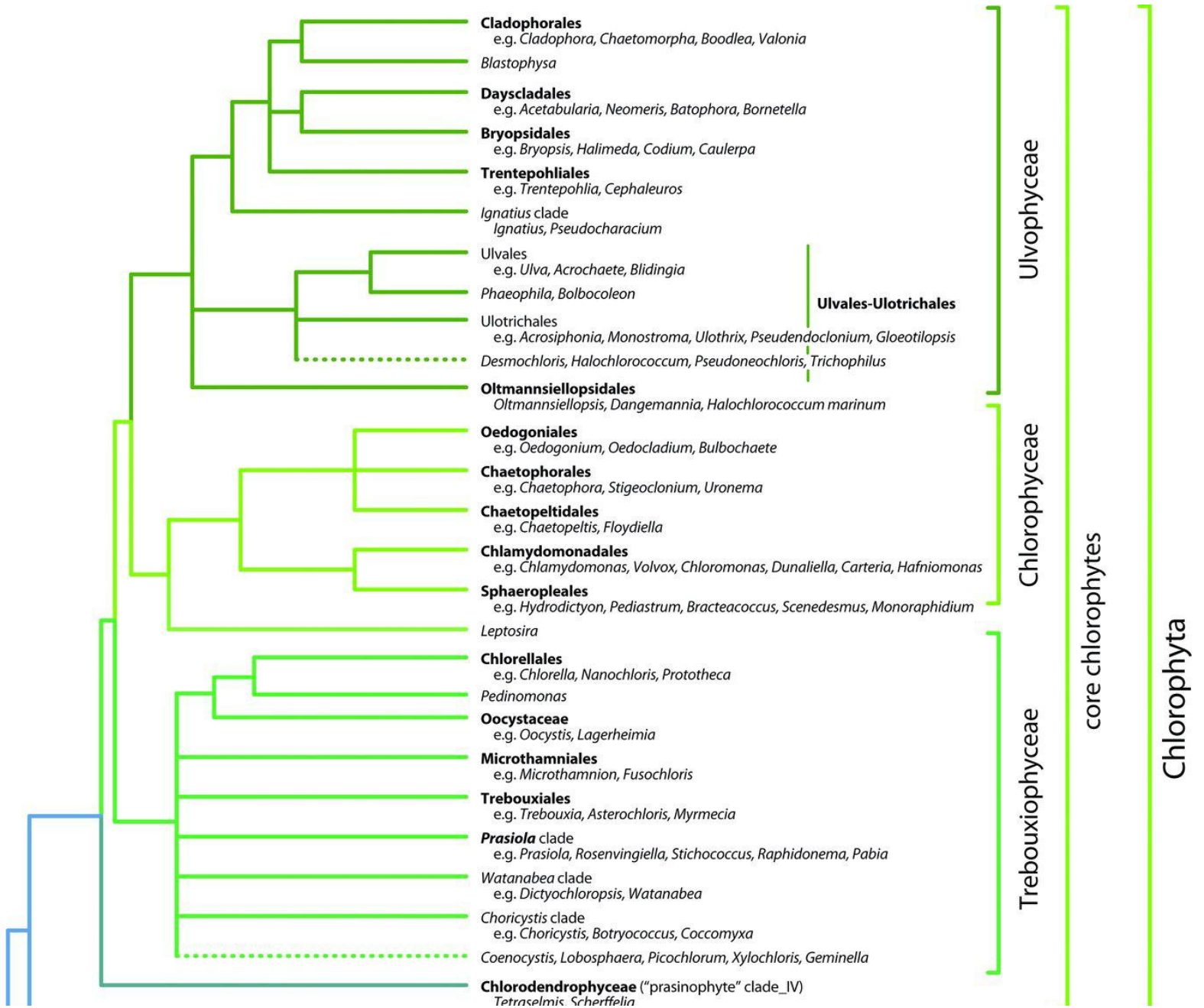
- unicellular and filamentous algae
- predominantly terrestrial, aerophytic
- a high proportion of symbiotic organisms



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

Friedl (1996): Trebouxiophyceae



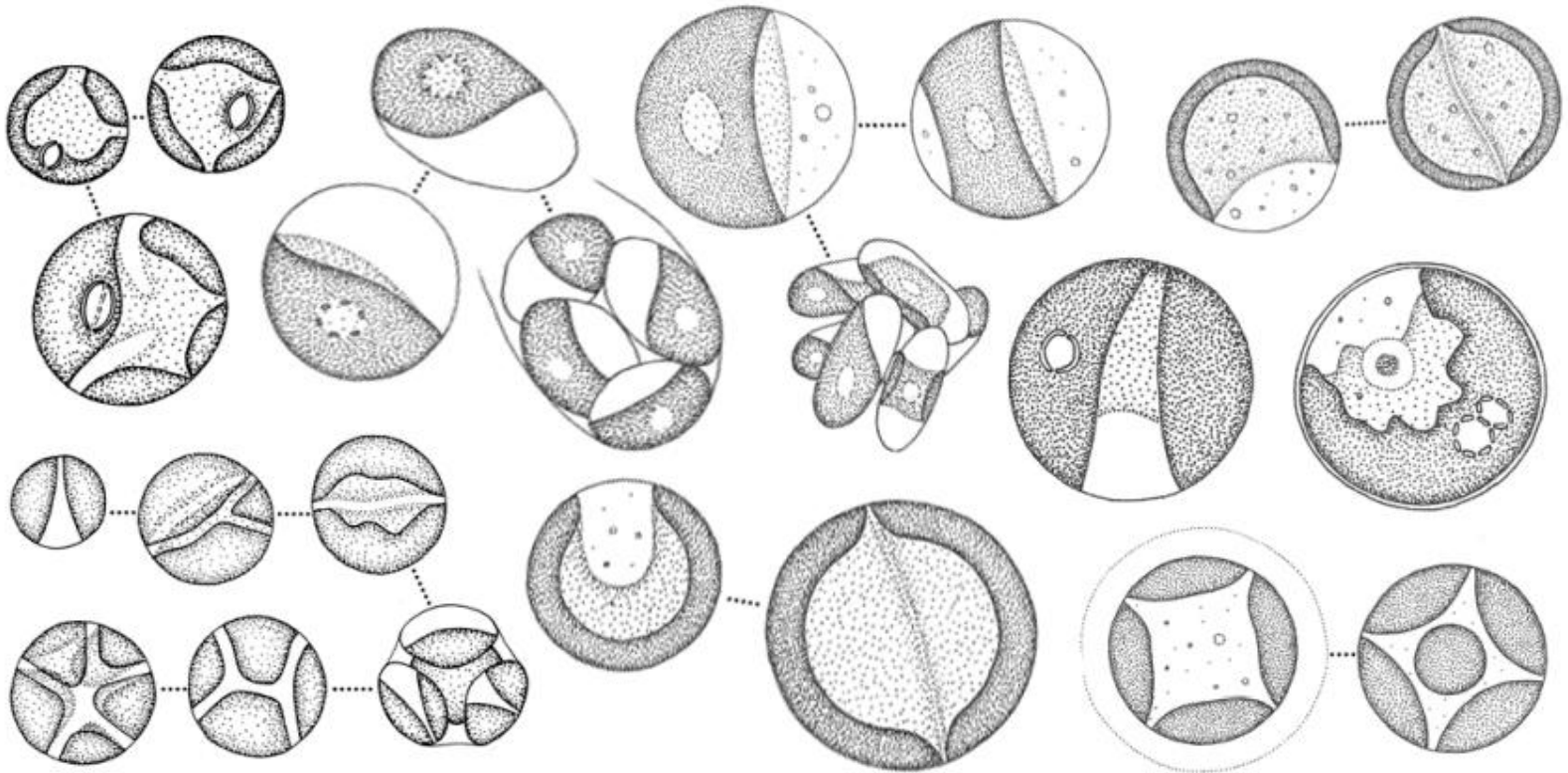


Trebouxiophyceae, *Chlorella*

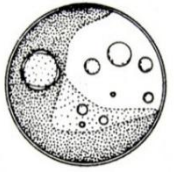
- Coccoid unicellular green algae with globular to oval cells that reproduce entirely by autospores
- Probably the most abundant and diversified group of aerophytic algae
- Beijerinck (1890):

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

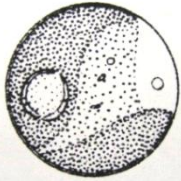
„... now I describe this alga in such a way that everybody will simply distinguish it... “



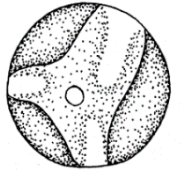
Trebouxiophyceae, *Chlorella*



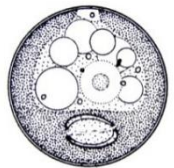
Chlorella vulgaris



Chlorella sorokiniana



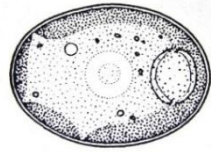
Chlorella lobophora



Chlorella kessleri



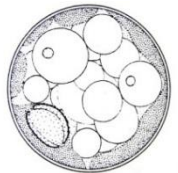
Chlorella luteoviridis



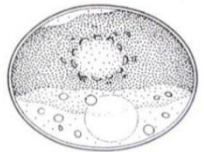
Chlorella fusca
v. fusca



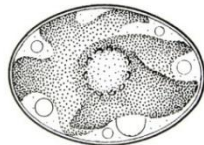
Chlorella fusca
v. rubescens



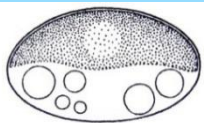
Chlorella fusca
v. vacuolatus



Chlorella ellipsoidea



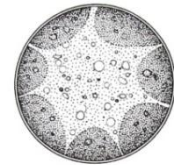
Chlorella trebouxioides



Chlorella saccharophila



Chlorella homosphaera



Chlorella zofingiensis

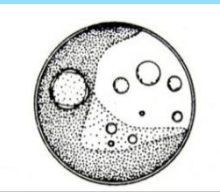
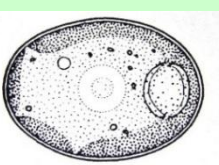
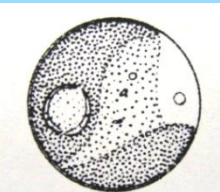
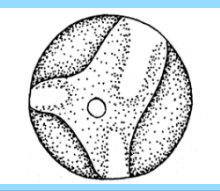
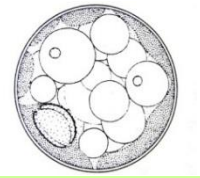
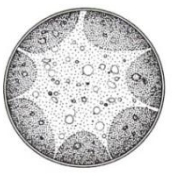
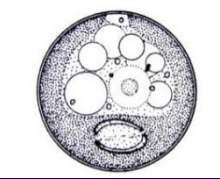
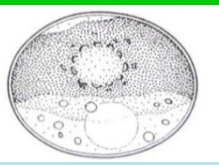
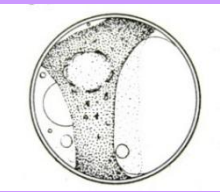
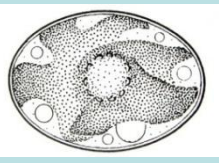
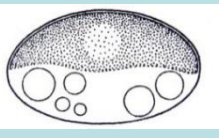
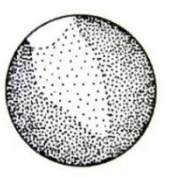


Chlorella protothecoides



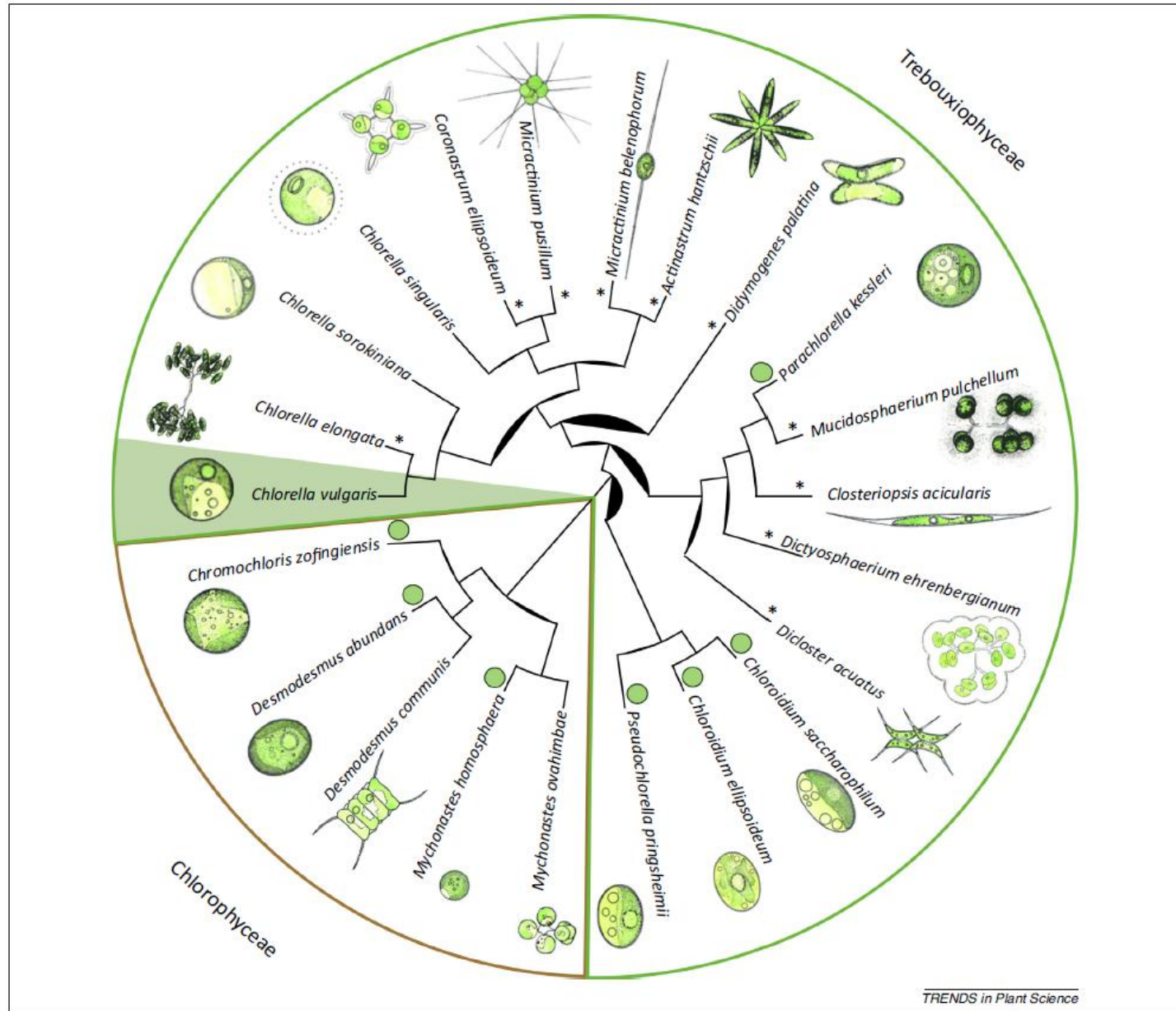
Chlorella minutissima

Trebouxiophyceae, *Chlorella*

	glukosamin <i>Chlorella vulgaris</i>		<i>Desmodesmus abundans</i> (<i>Ch. fusca</i> , v. <i>fusca</i>) (<i>Scen. abundans</i>)		<i>Mychonastes homosphaera</i> (<i>Ch. homosphaera</i> , <i>Ch. minutissima</i>)
	<i>Chlorella sorokiniana</i> (<i>Ch. vulgaris</i>)		<i>Scenedesmus rubescens</i> (<i>Ch. fusca</i> , v. <i>rubescens</i>) (<i>Halochlorella rubescens</i>)		
	<i>Chlorella lobophora</i>		<i>Scenedesmus vacuolatus</i> (<i>Ch. fusca</i> , v. <i>vacuolata</i>) (<i>Graesiella vacuolata</i>)		<i>Chromochloris zofingiensis</i> (<i>Ch. zofingiensis</i>)
	<i>Parachlorella kessleri</i> (<i>Ch. kessleri</i>)		<i>Chloroidium ellipsoideum</i> (<i>Ch. ellipsoidea</i>)		<i>Auxenochlorella protothecoides</i> (<i>Ch. protothecoides</i>)
	<i>Jaagichlorella luteoviridis</i> (<i>Ch. luteoviridis</i>)		<i>Chloroidium ellipsoideum</i> (<i>Ch. trebouxiioides</i>)		
			<i>Chloroidium saccharophilum</i> (<i>Ch. saccharophila</i>)		<i>Pseudochloris wilhelmii</i> (“ <i>Ch. minutissima</i> ”)

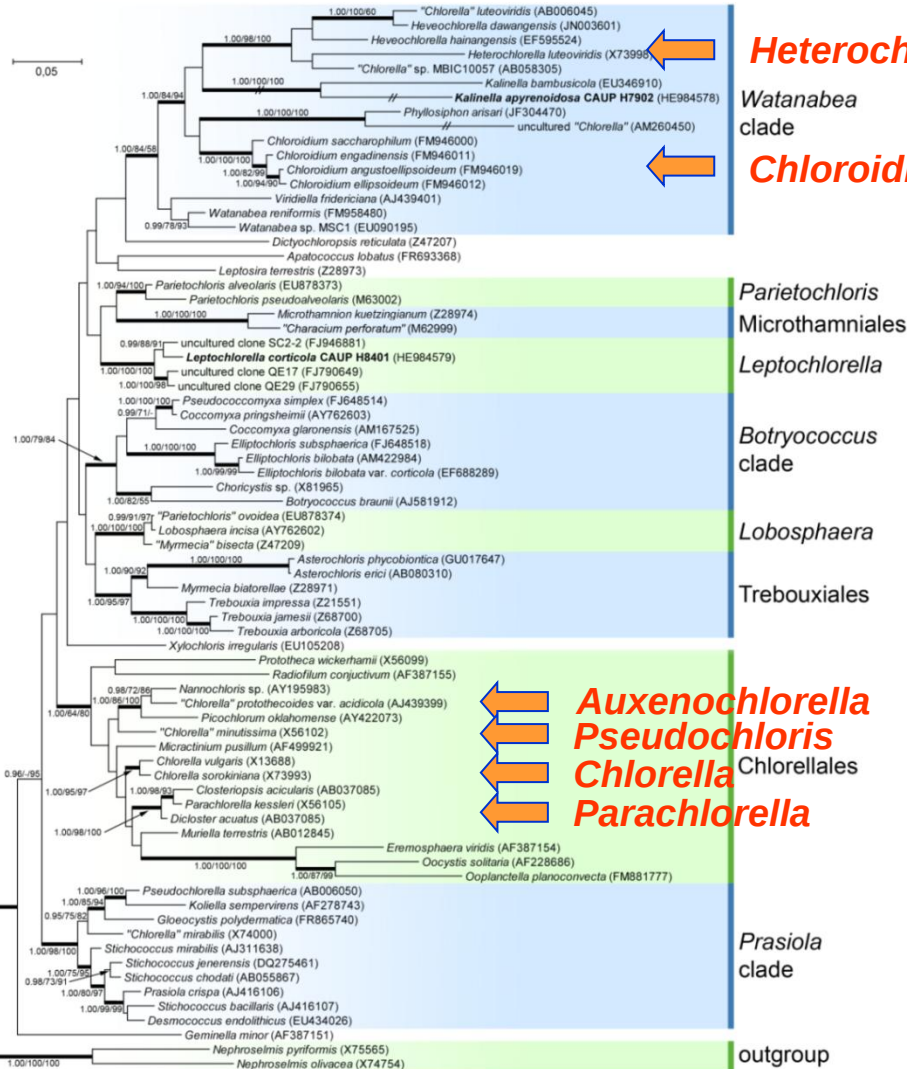
An et al. (1999), Huss et al. (1999), Krienitz et al. (2004), Darienko et al. (2010), Neustupa et al. (2009), Fučíková & Lewis (2012), Somogyi et al. (2013)

Trebouxiophyceae, *Chlorella*



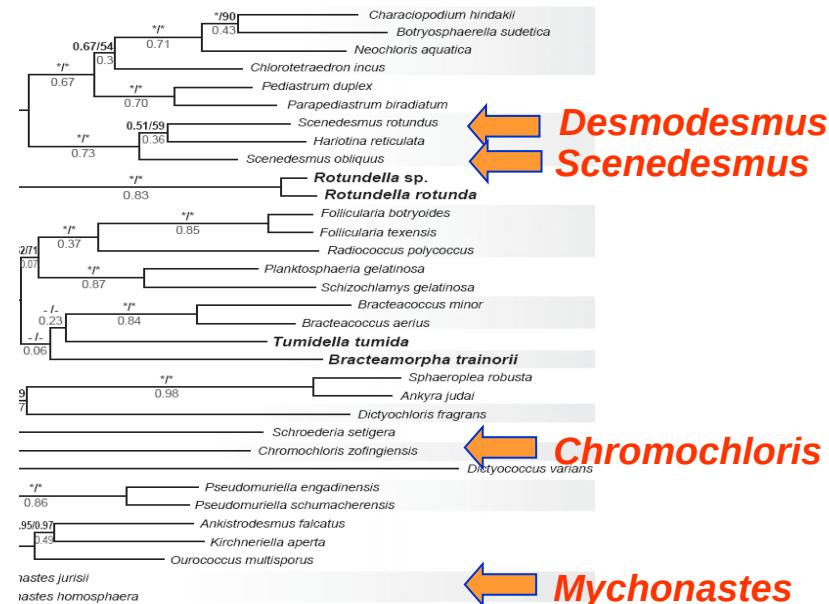
Trebouxiophyceae, *Chlorella*

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:



CS clade

Jenufa

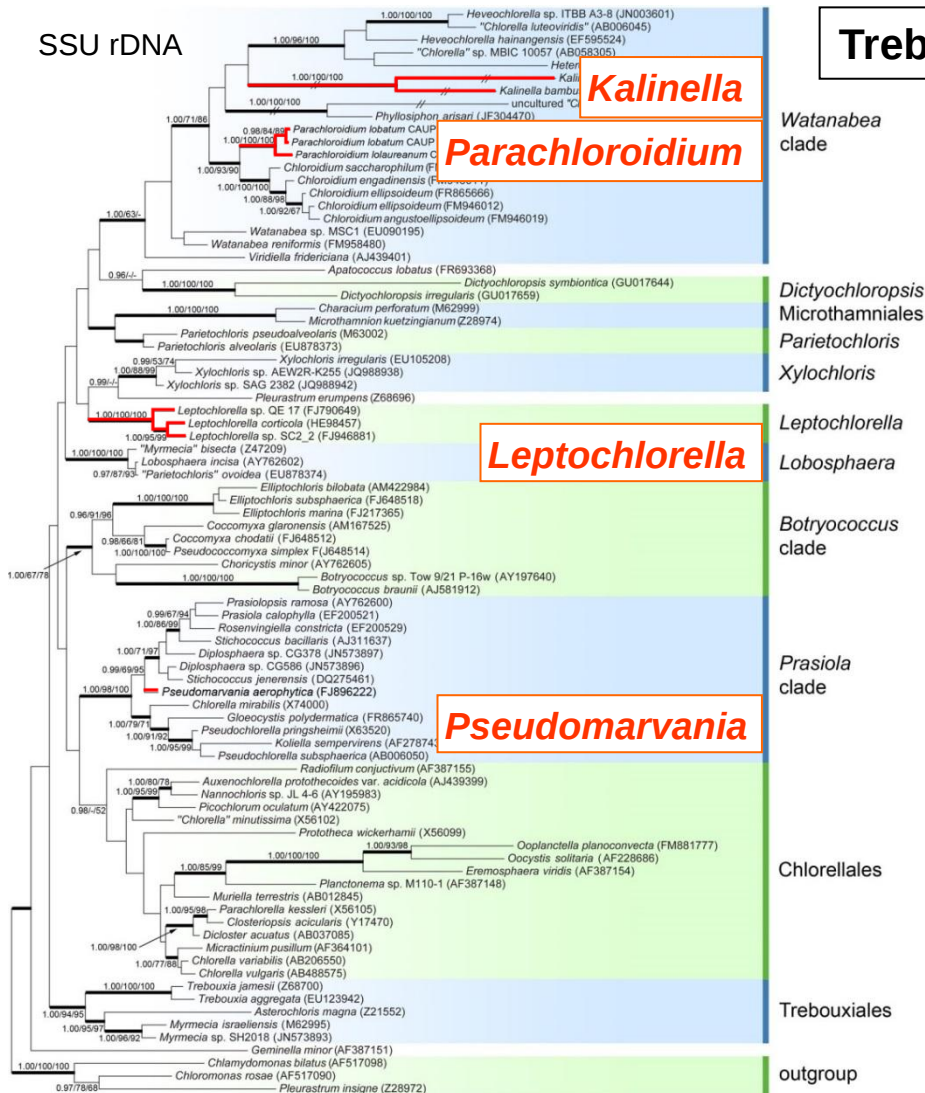
SSU rDNA

OCC clade

Chlorophyceae

Trebouxiophyceae, *Chlorella* – cryptic genera

SSU rDNA



Trebouxiophyceae:

Watanabea
clade

Dictyochloropsis
Microthamniales
Parietochloris
Xylochloris

Leptochlorella
Lobosphaera

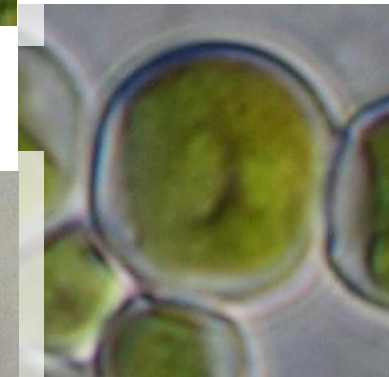
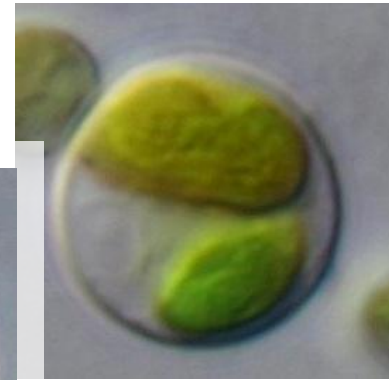
Botryococcus
clade

Prasiola
clade

Chlorellales

Trebouxiales

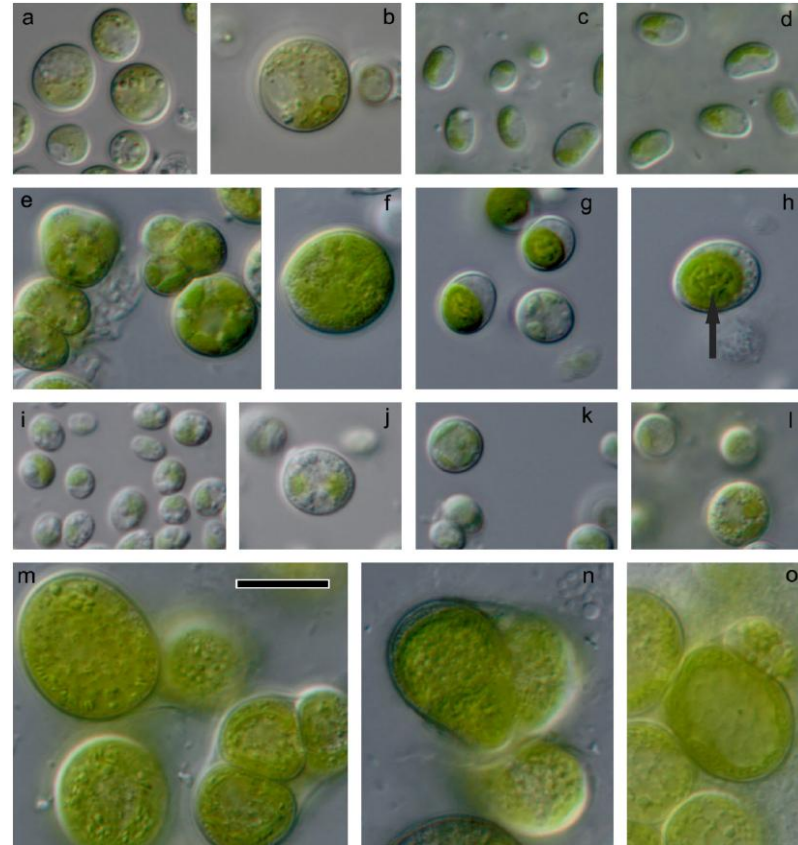
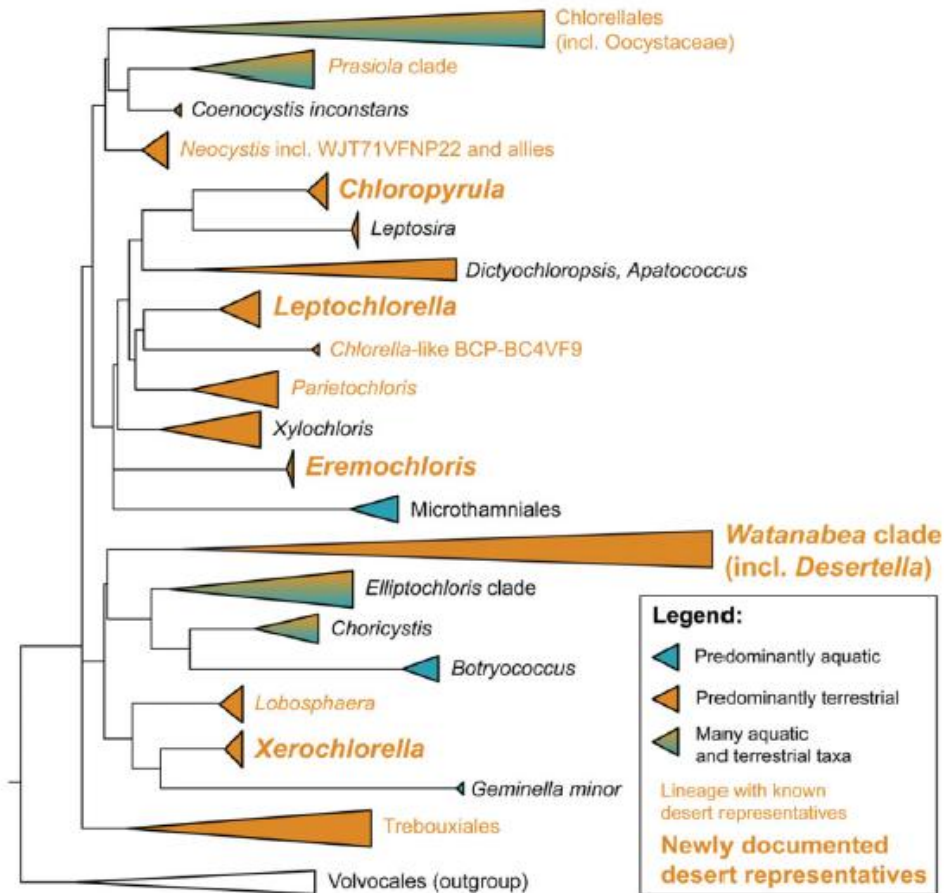
outgroup



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

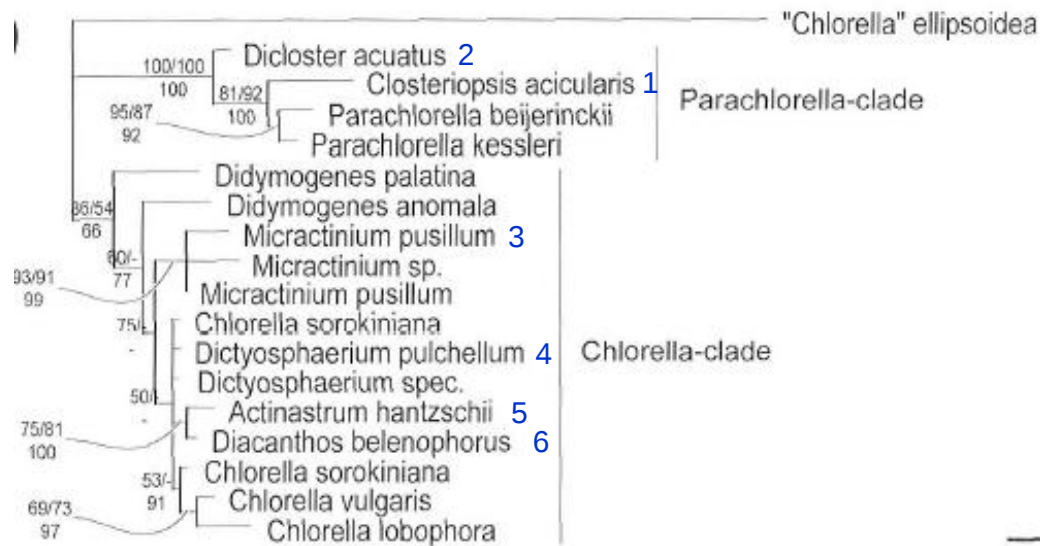
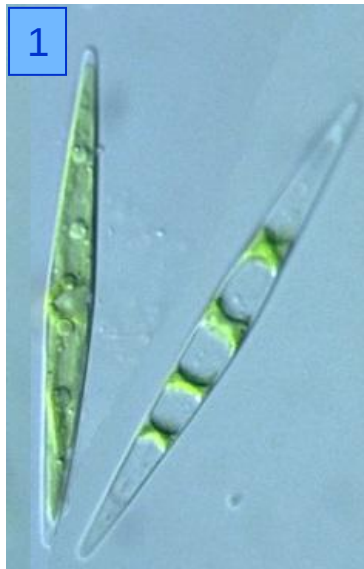
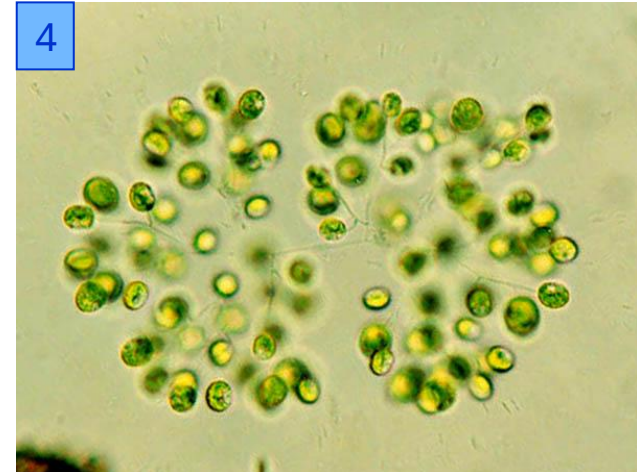
Trebouxiophyceae, cryptic genera

– Fučíková et al. (2014) – desert Trebouxiophyceae



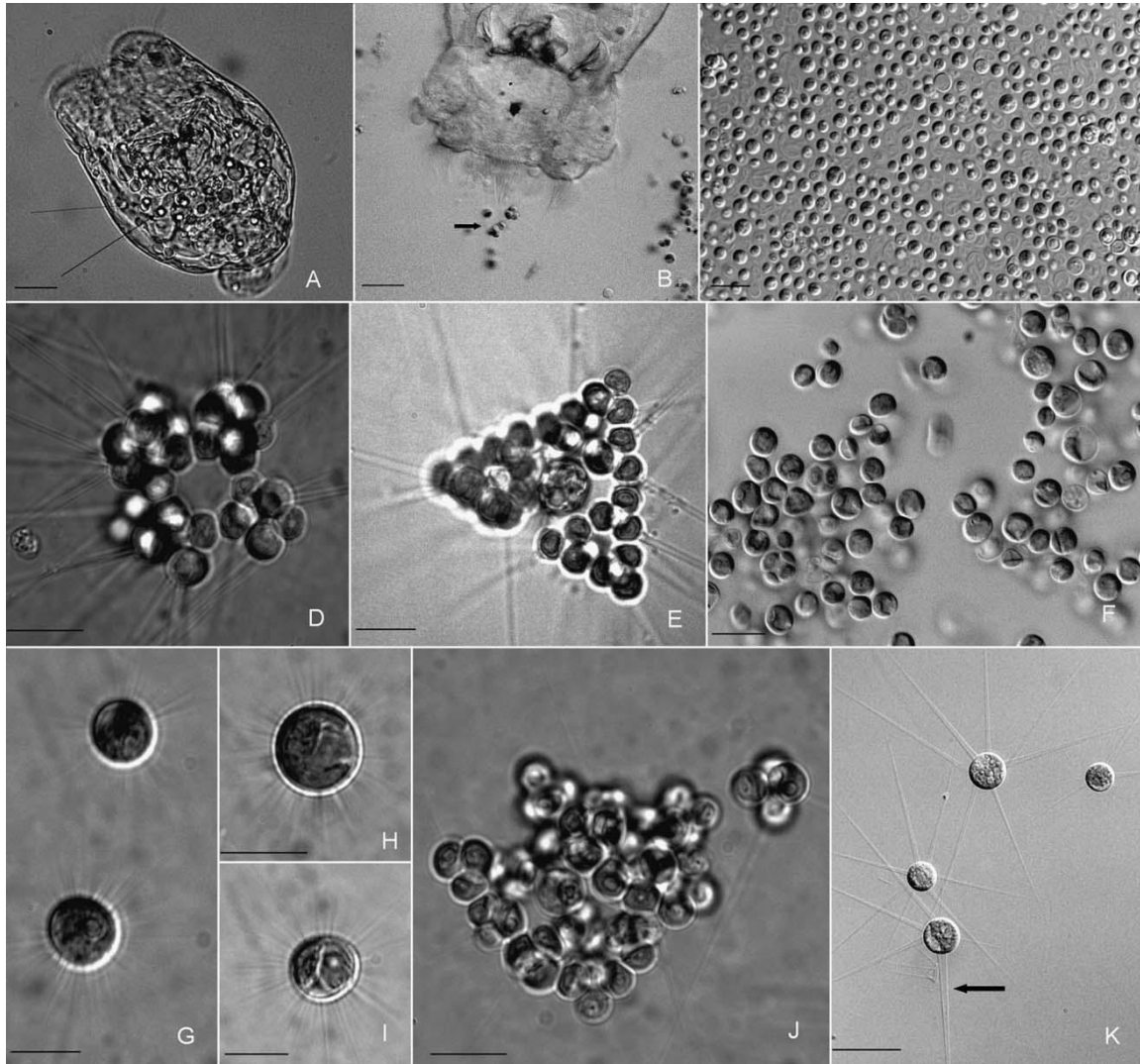
Trebouxiophyceae, Chlorellales

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



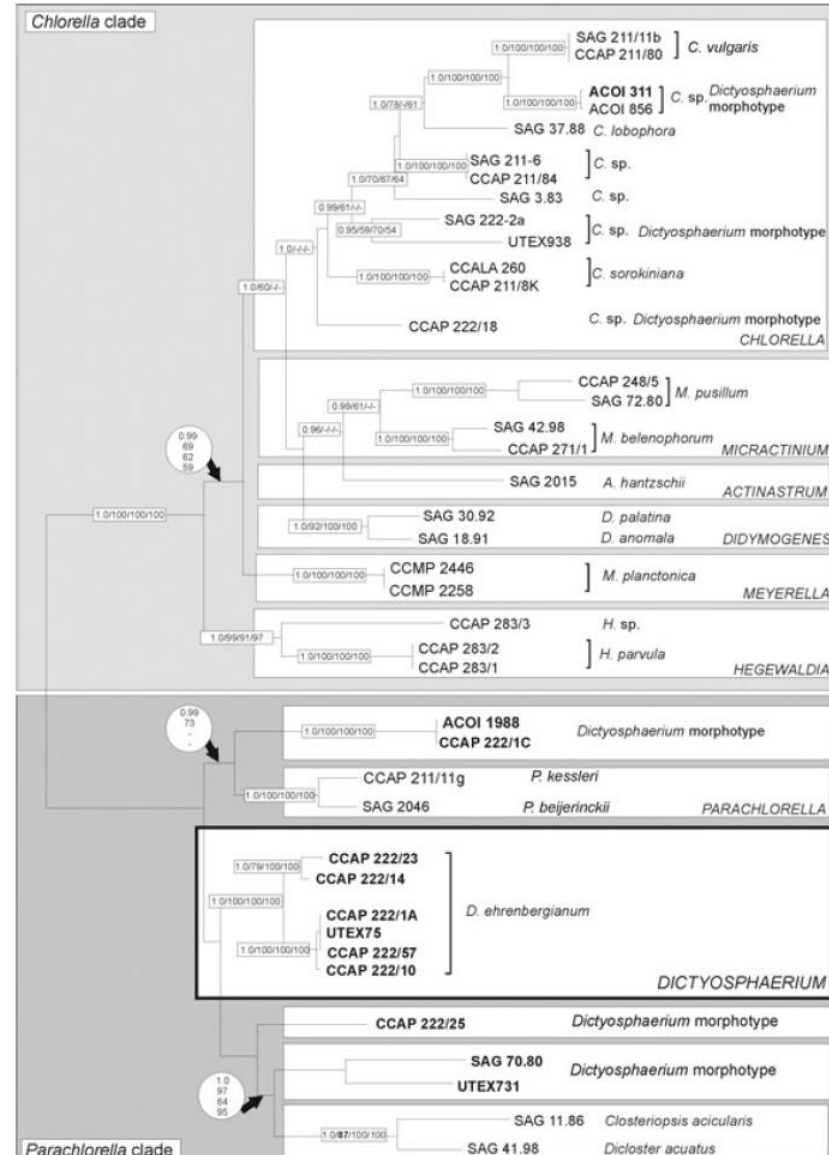
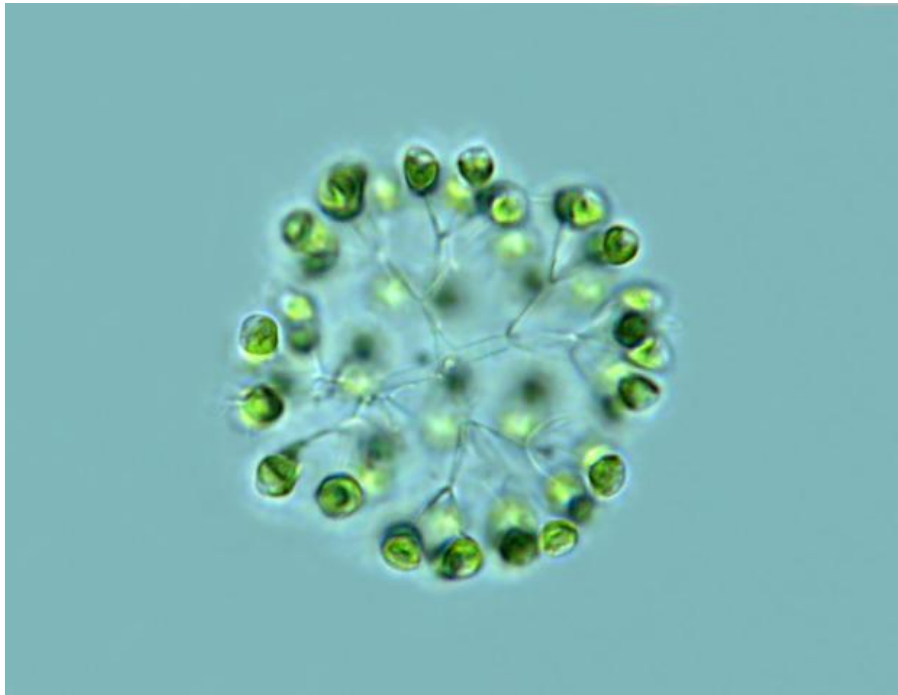
Trebouxioiophyceae, Chlorellales

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



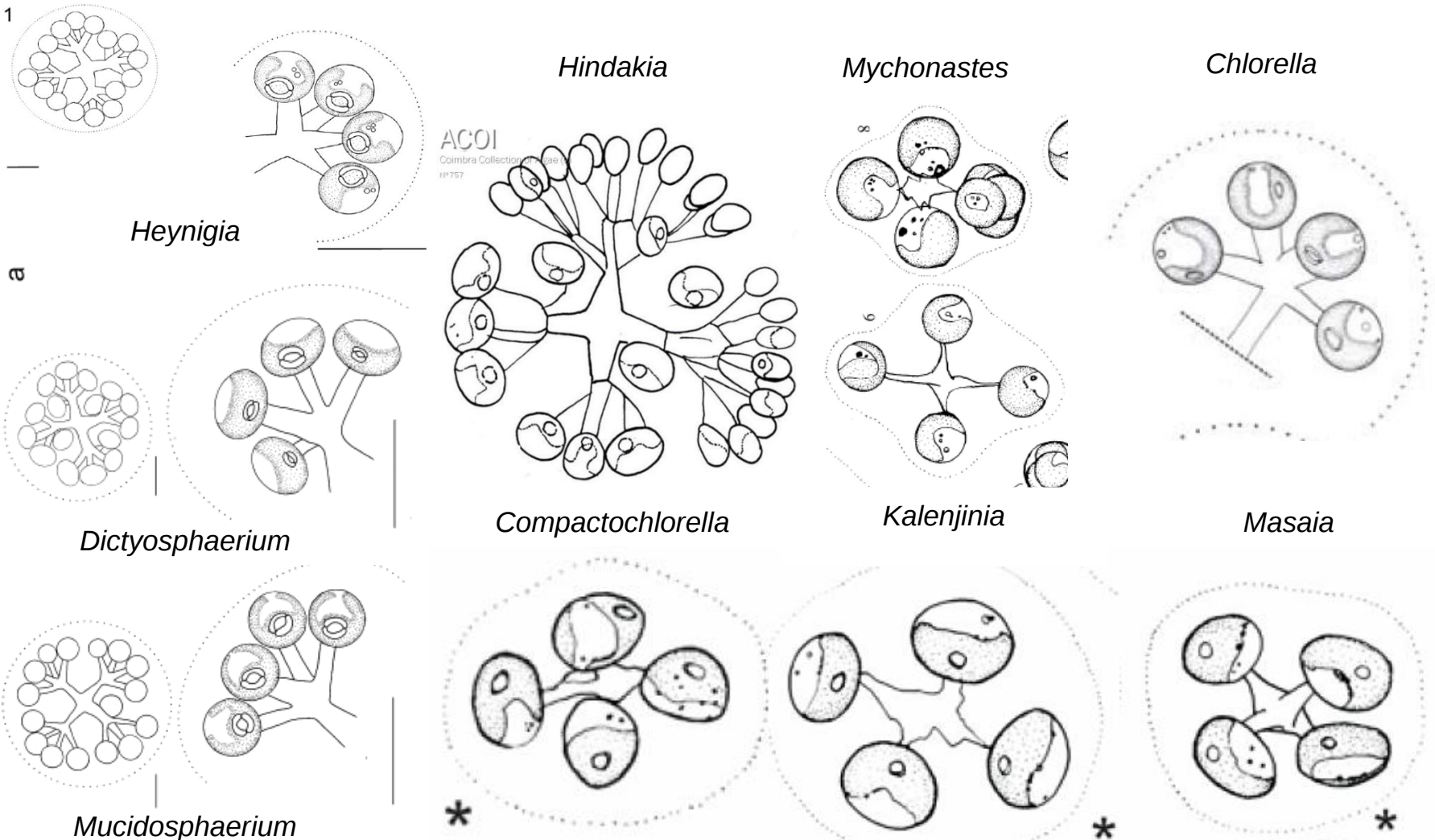
Trebouxioiophyceae, Chlorellales

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



Dictyosphaerium

- 9 cryptic genera

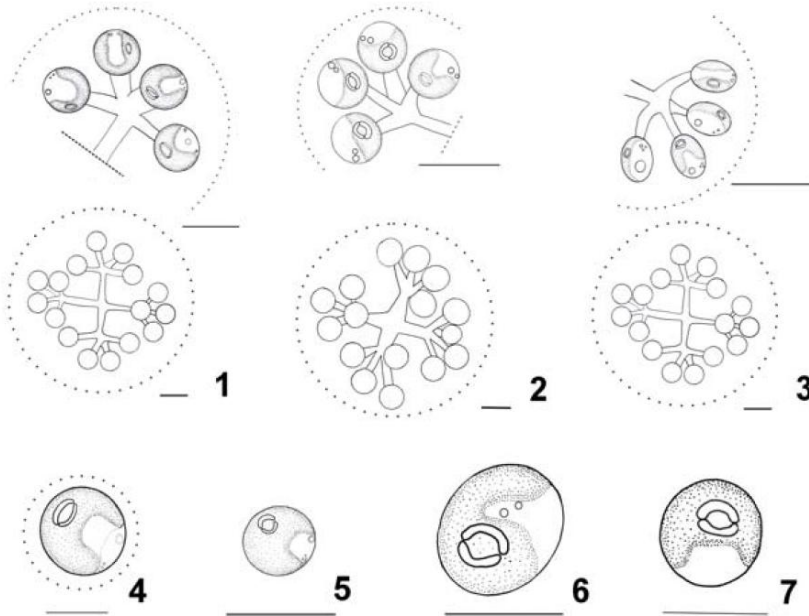


Krienitz et al. (2012): *Fottea* **12**, 231-253; Bock et al. (2010): *European Journal of Phycology* **45**, 267-277;
Bock et al. (2011): *Journal of Phycology* **47**, 638-652; Krienitz et al. (2011): *Phycologia* **50**, 89-106

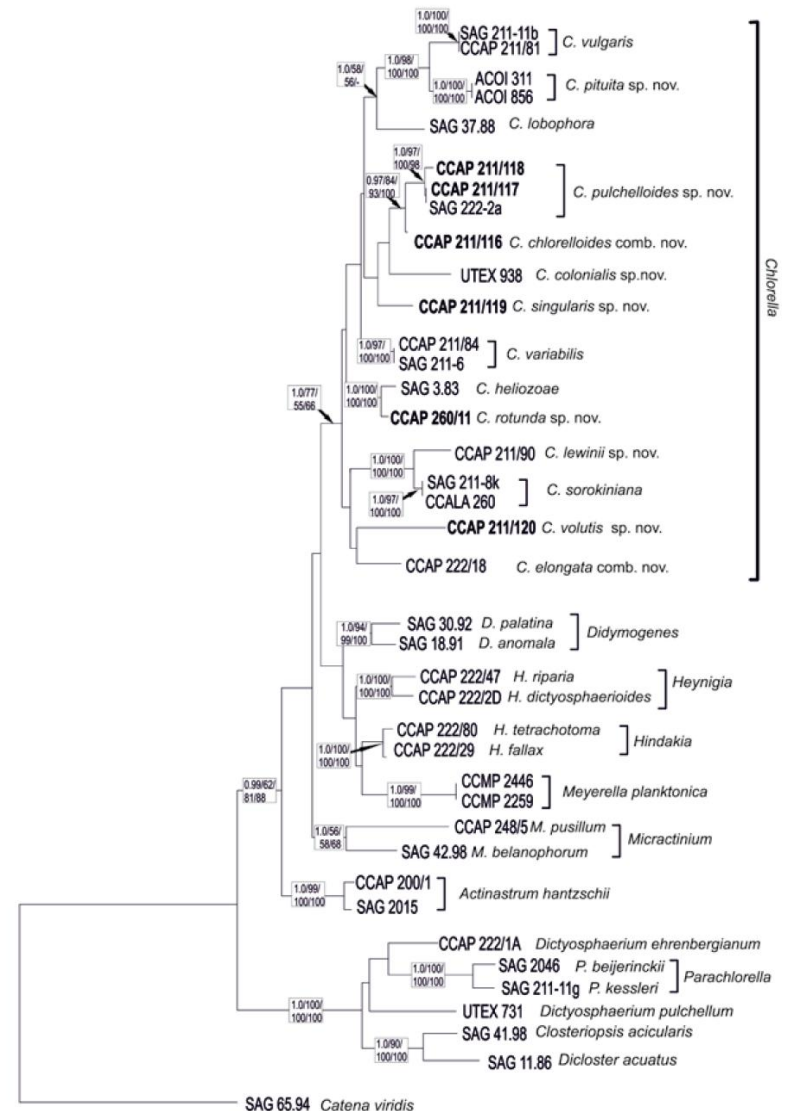
Trebouxiophyceae, Chlorellales

- Chlorella-clade

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

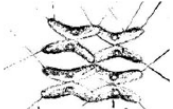
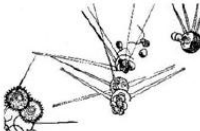
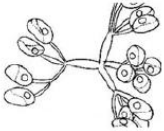
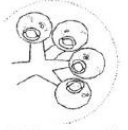
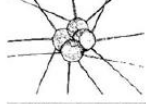


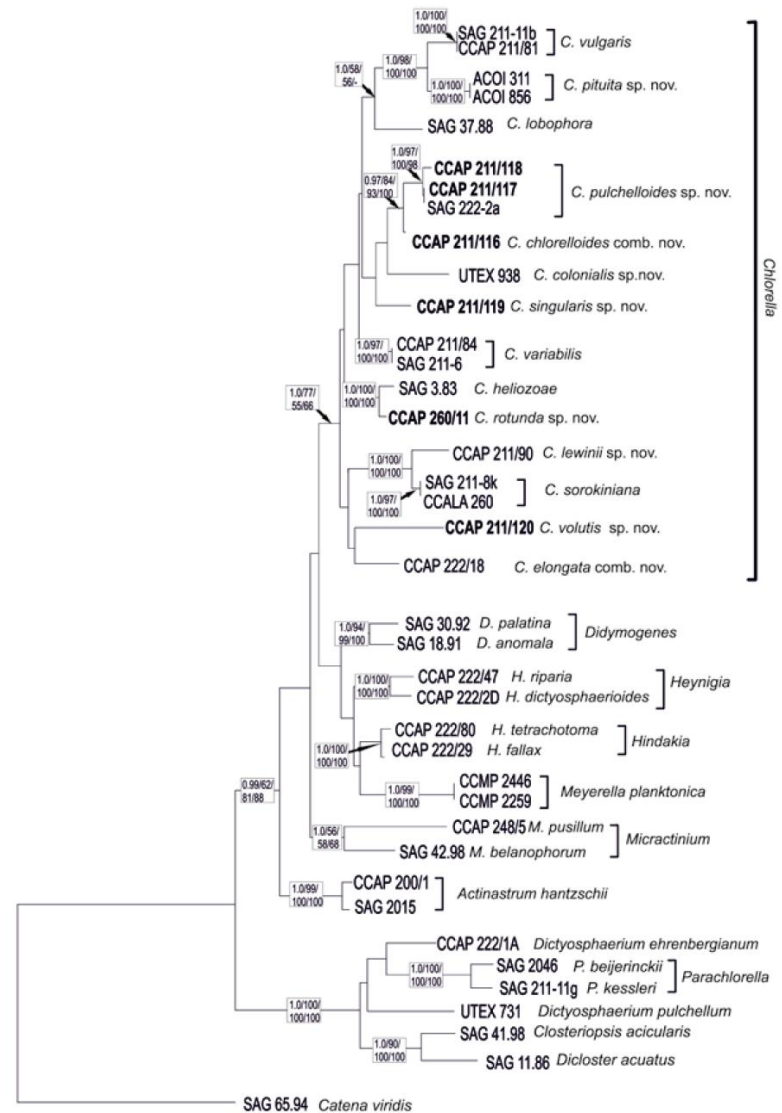
Figs 1–7. Drawings of light microscopical characters of *Chlorella* species. Iconotypes: (1) *Chlorella pituita*, authentic strain ACOI 311; (2) *Chlorella pulchelloides*, authentic strain CCAP 211/118; (3) *Chlorella coloniales*, authentic strain UTEX 938; (4) *Chlorella singularis*, authentic strain 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.



Trebouxioiophyceae, Chlorellales

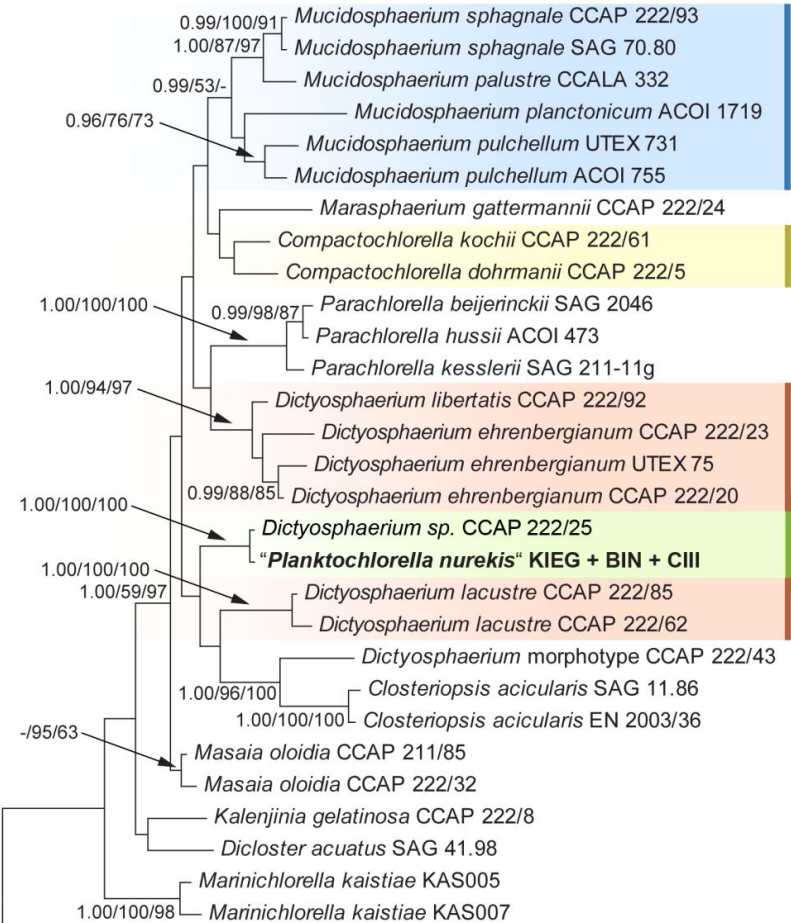
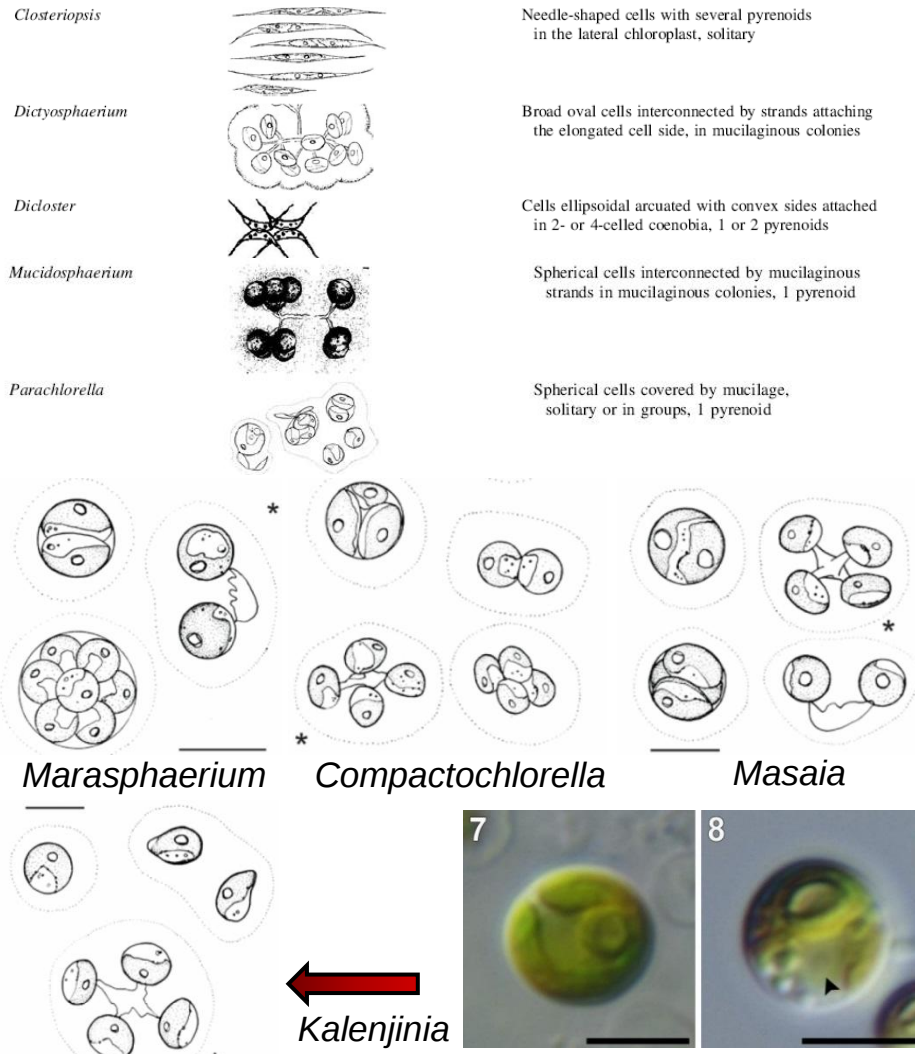
- Chlorella-clade

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



Trebouxiophyceae, Chlorellales

• Parachlorella-clade



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

Trebouxioiophyceae, Chlorellales

- Chlorella-clade**

- symbionts

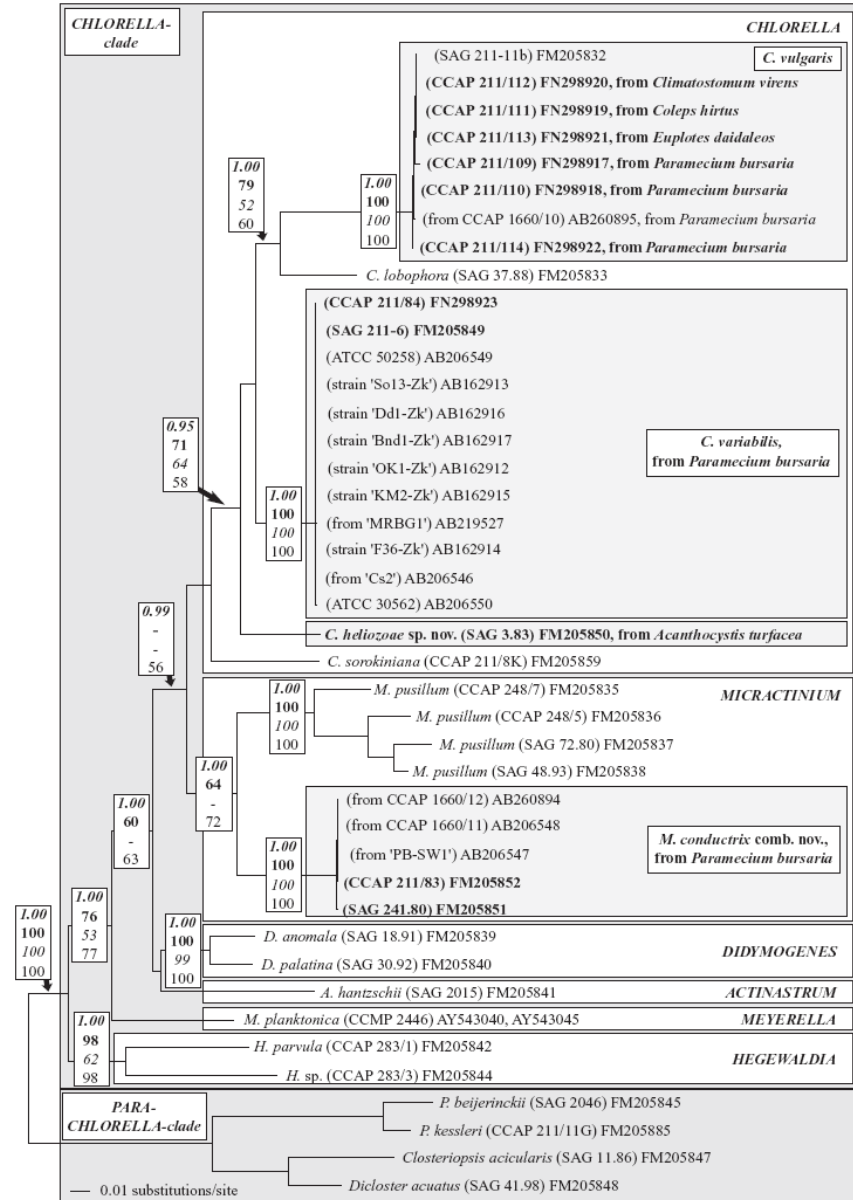
environmental
microbiology



Environmental Microbiology (2010)

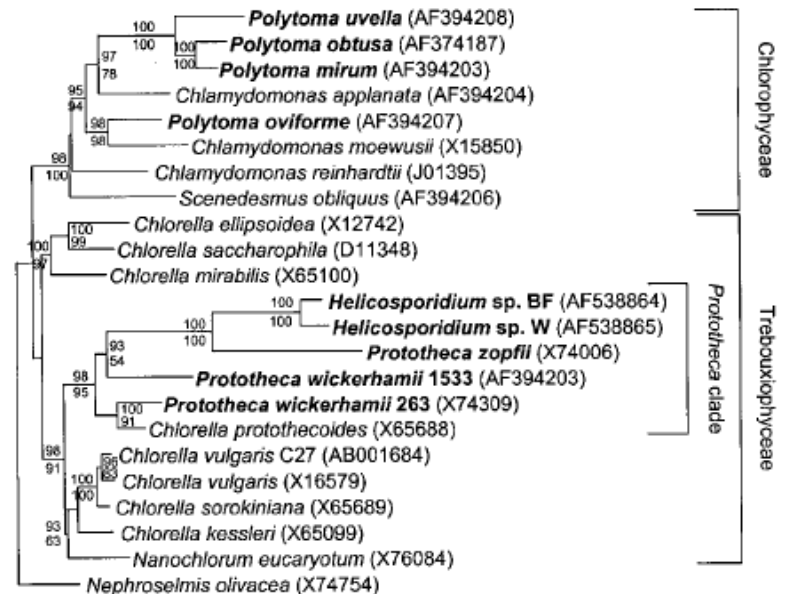
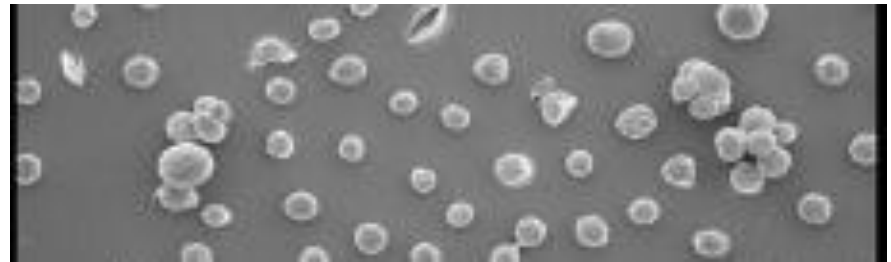
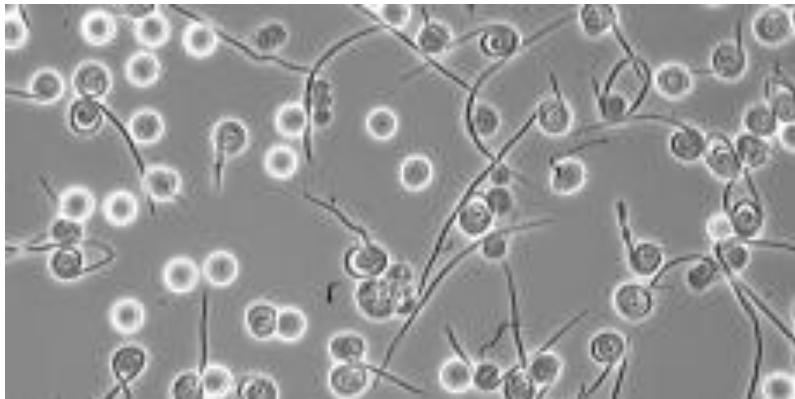
doi:10.1111/j.1462-2920.2010.02333.x

The systematics of *Zoochlorella* revisited employing an integrative approach



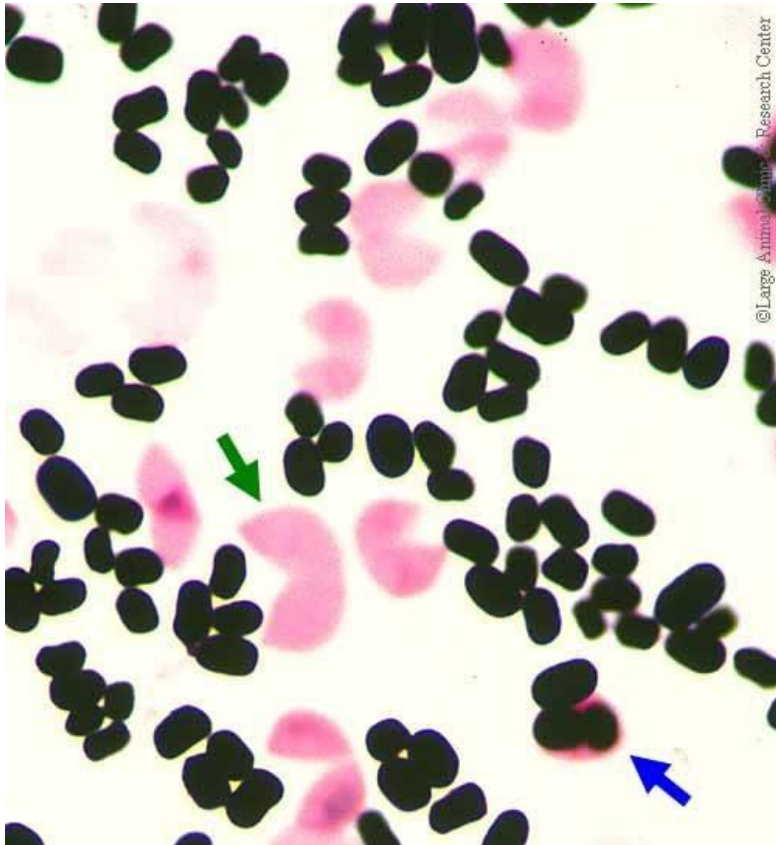
Chlorellales, *Helicosporidium*

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



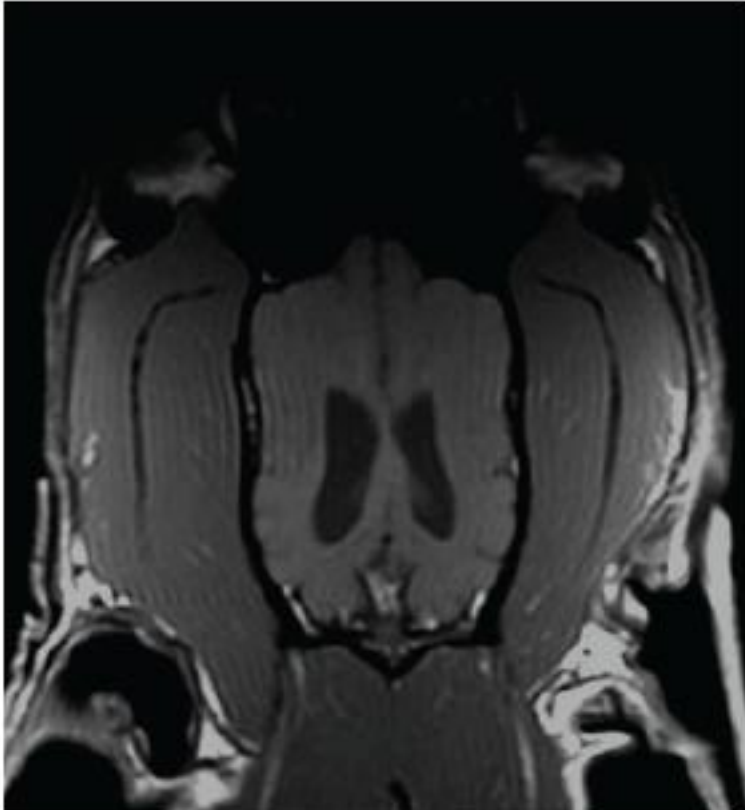
Chlorellales, *Prototheca*

- heterotrophic, pathogenic organism
- *protothecosis*



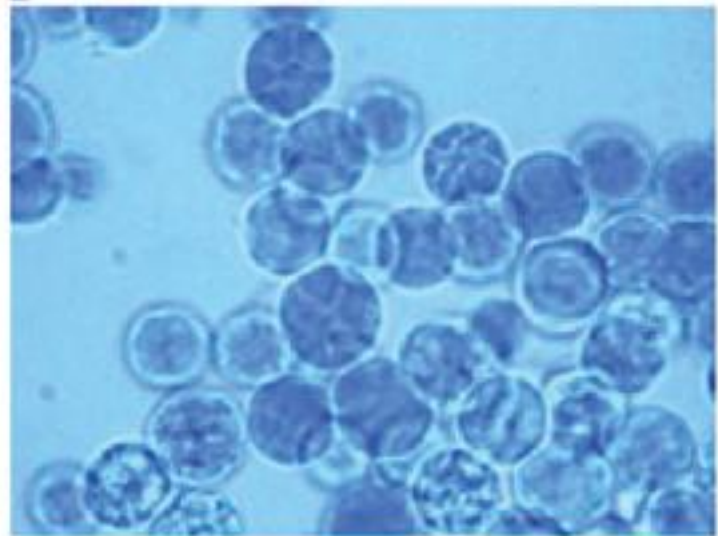
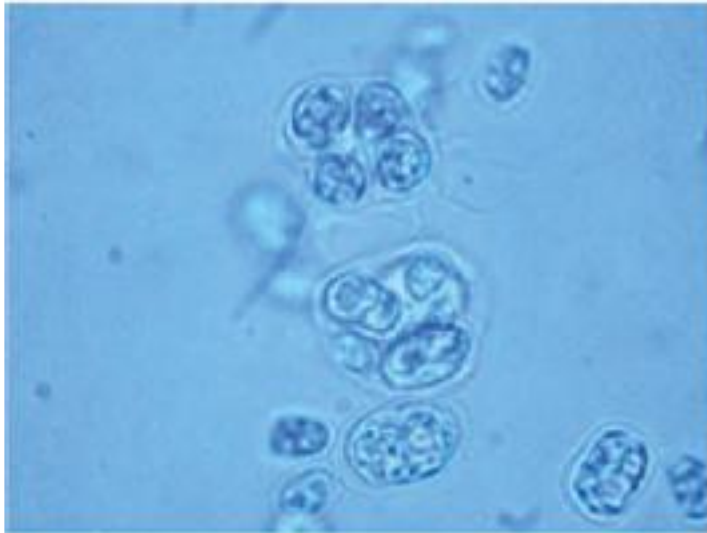
Protothecosis

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



Protothecosis

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



Chlorellales, practical use

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



Chlorellales, practical use

- **chlorophyll:**

- anti-inflammatory effects, support wound healing
- elimination of heavy metals and toxins
- anaemia therapy
- anti-tumor activity
- supports immune system
- reducing high blood pressure

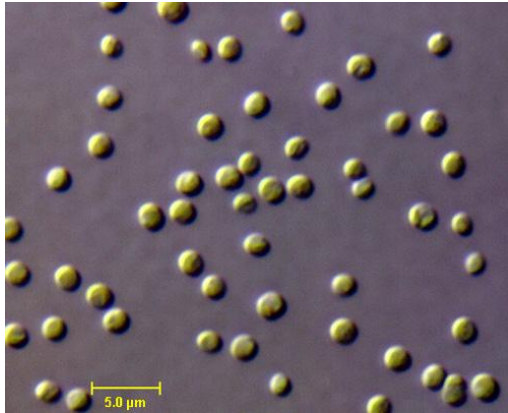


Chlorella tabs

Trebouxiophyceae, picoplankton

- green balls up to 3 μm in diameter

Nannochloris

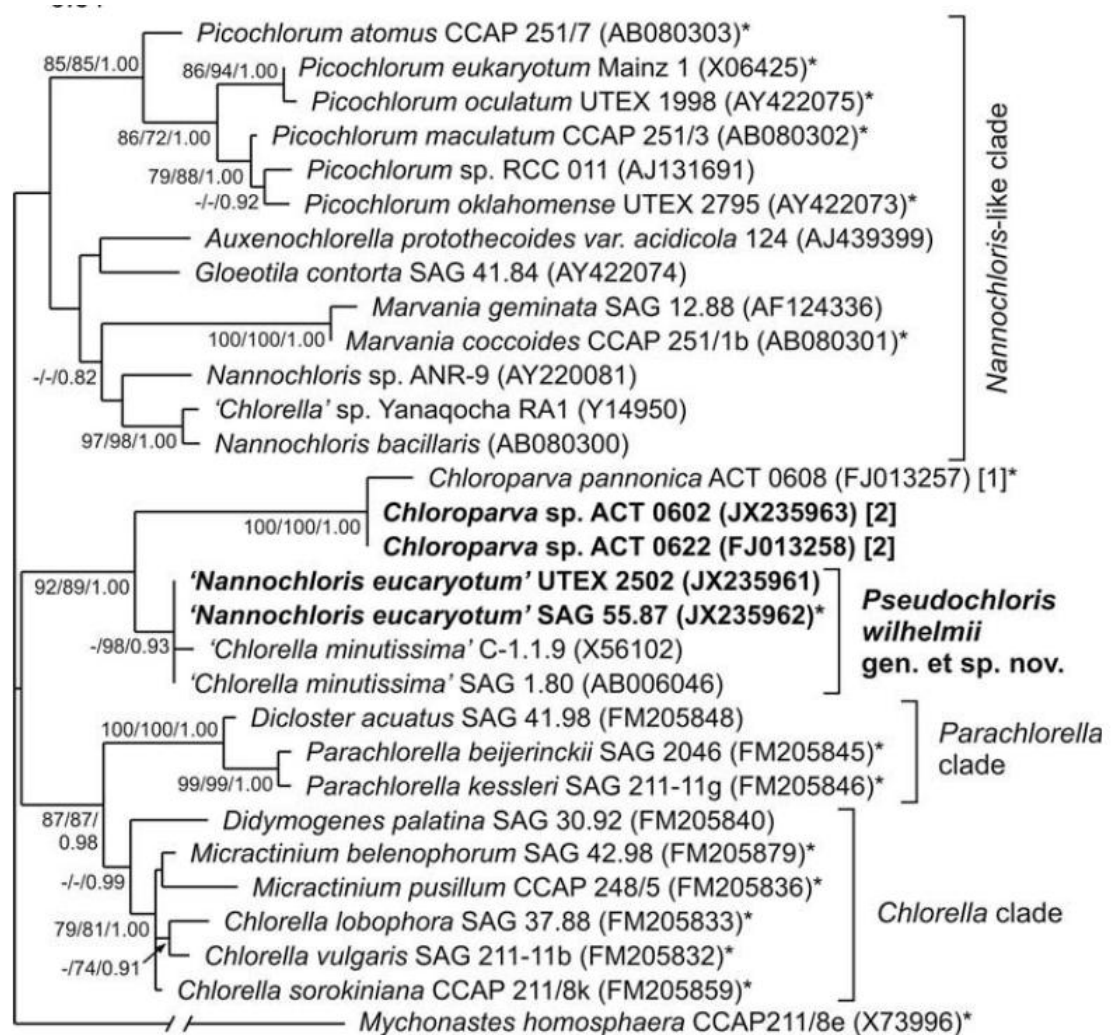
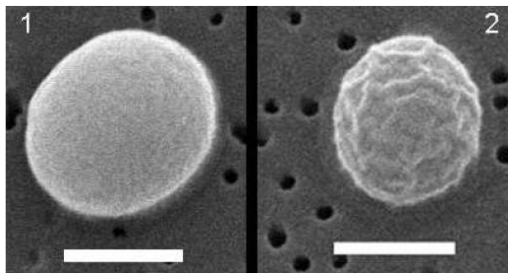


Picochlorum

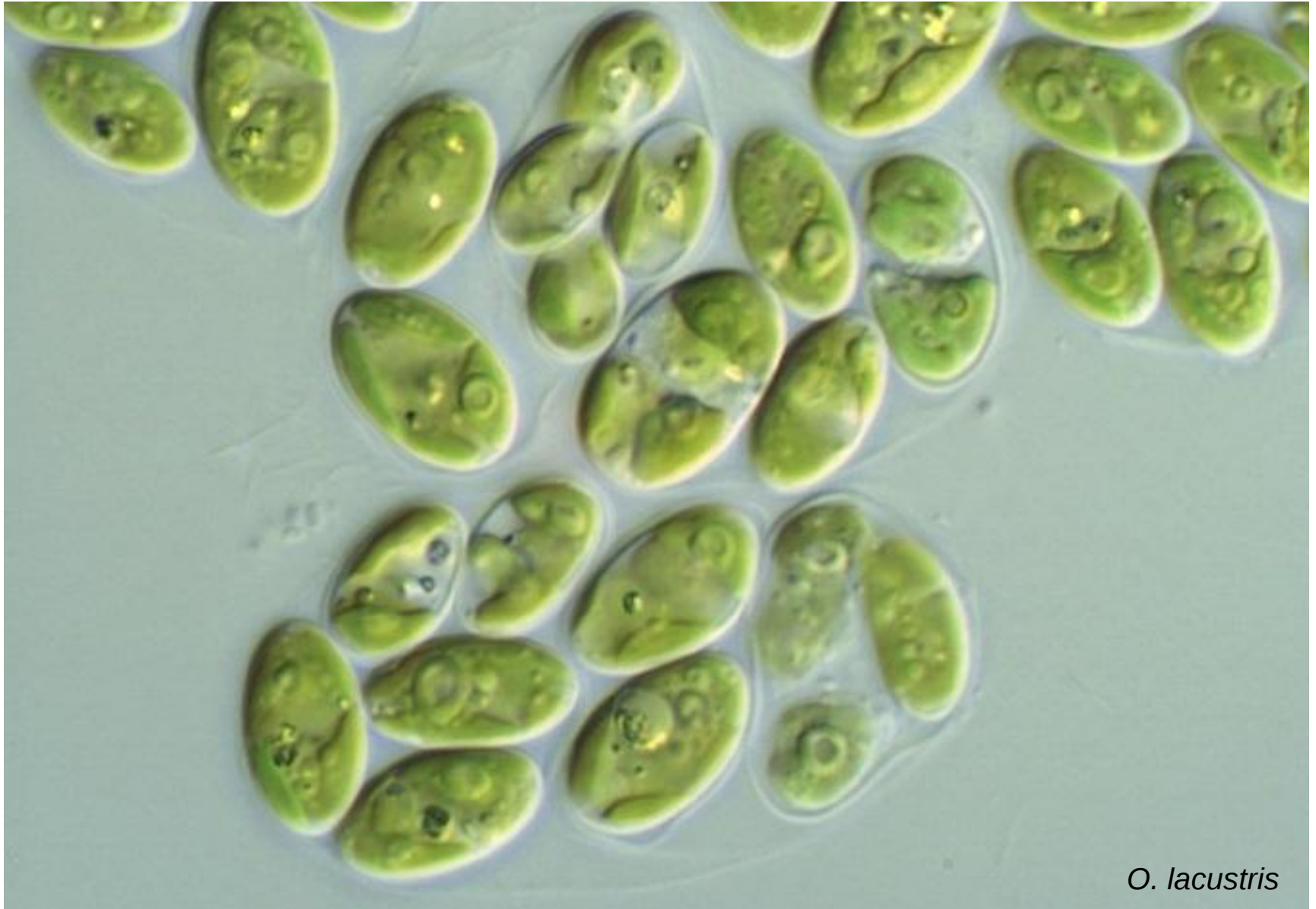


Pseudochloris

Chloroparva

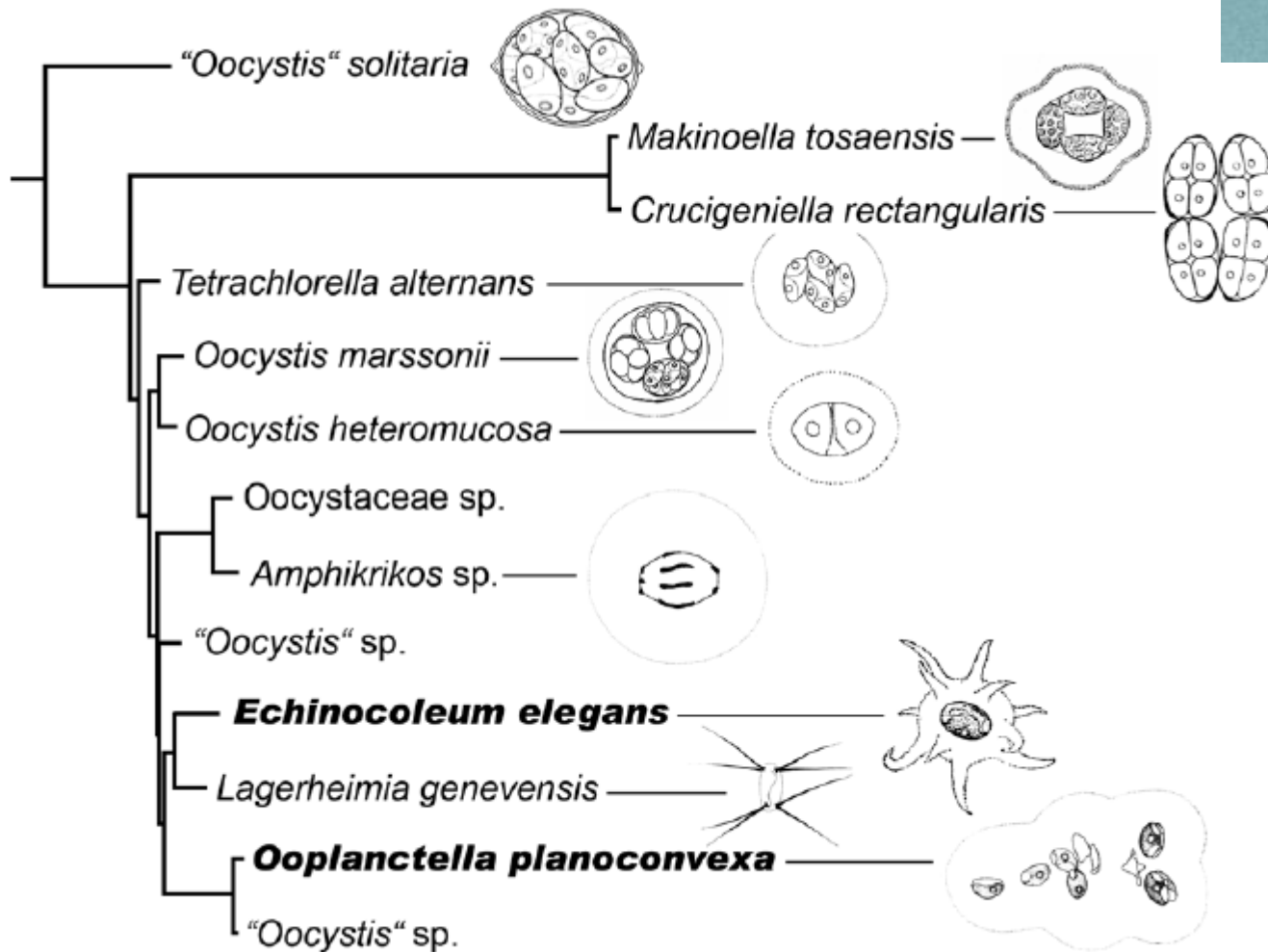


Chlorellales, Oocystaceae, *Oocystis*



O. lacustris

Chlorellales, Oocystaceae, Oocystis



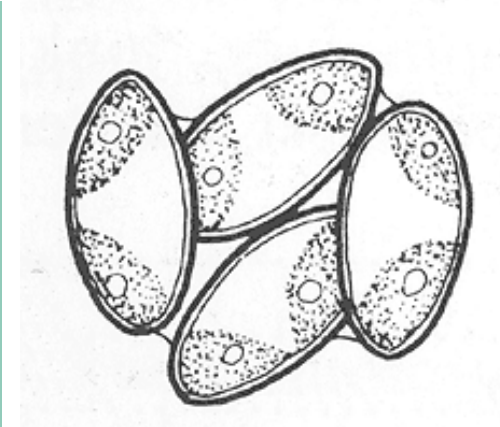
Chlorellales, Oocystaceae



Makinoella



Crucigeniella



Tetrachlorella



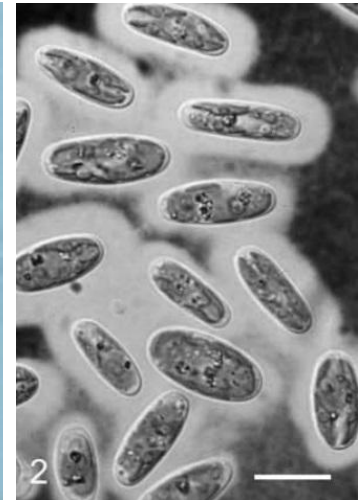
Amphikrikos



Lagerheimia

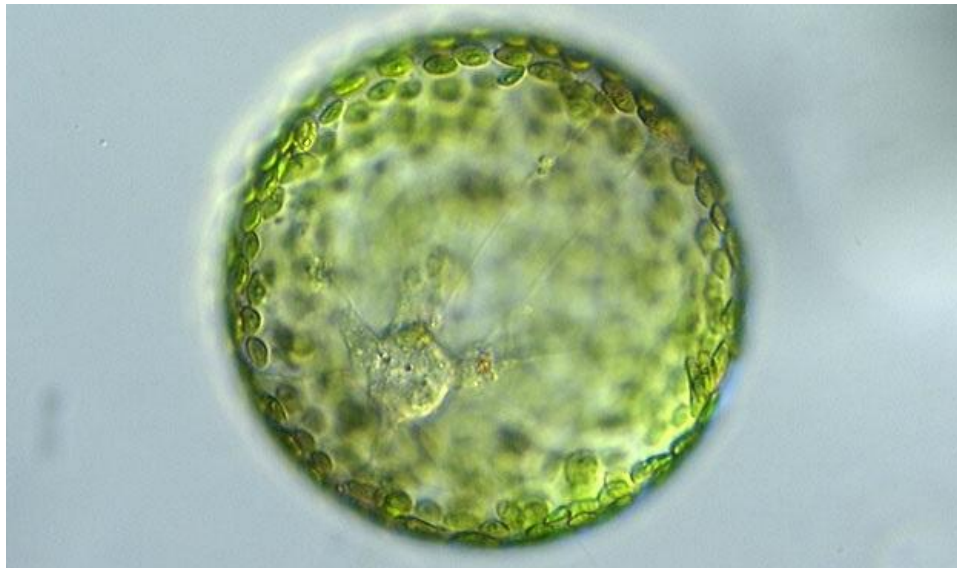
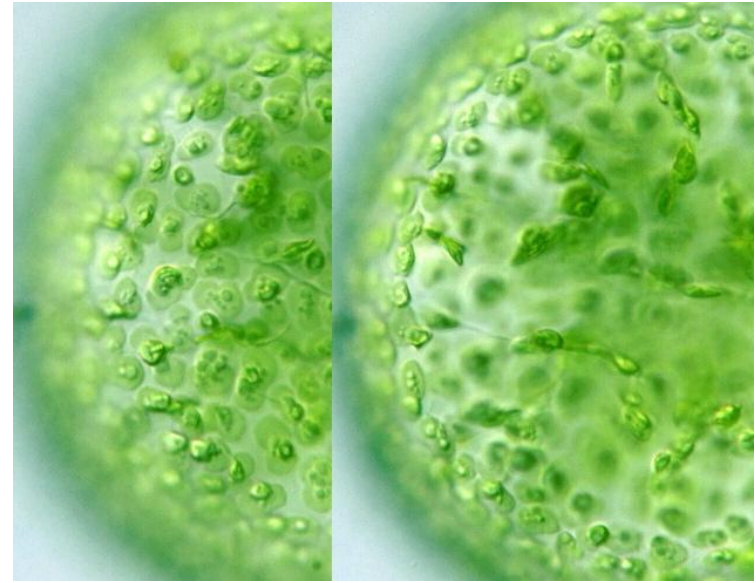


Echinocoleum



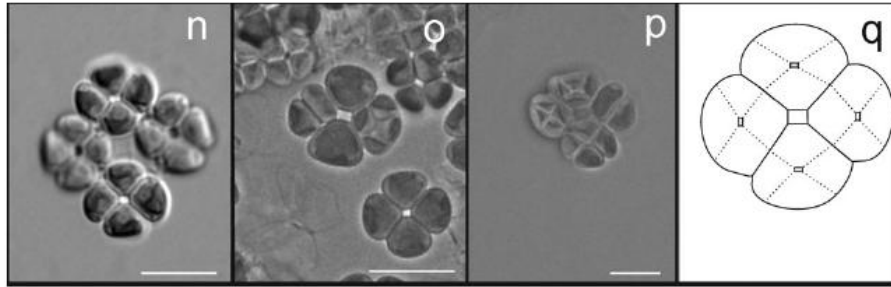
Elongatocystis

Chlorellales, Oocystaceae, *Eremosphaera*

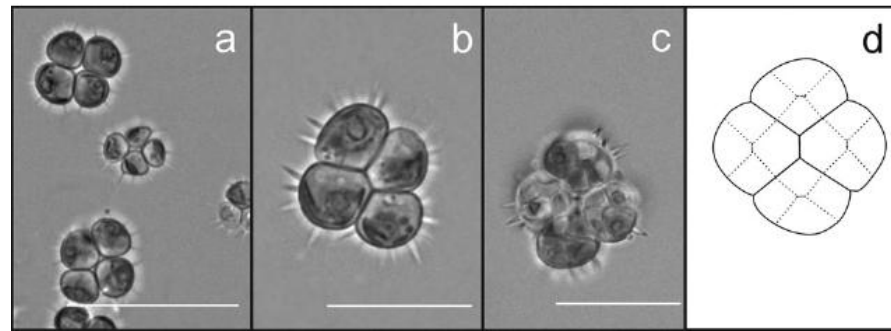


Trebouxioiophyceae, tetrahedric colonies

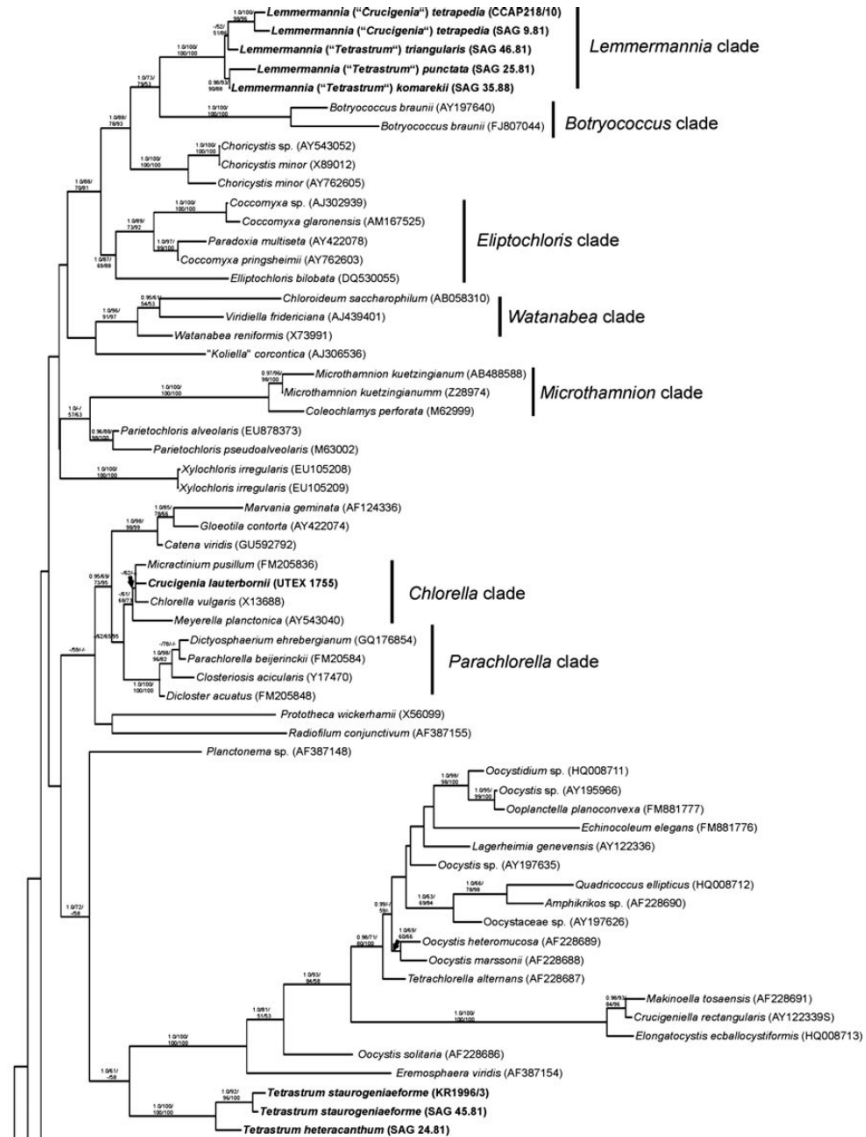
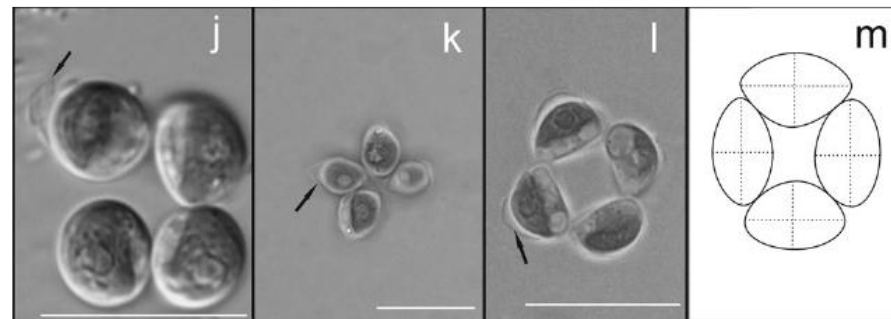
Lemmermannia – smooth colonies, small aperture



Tetrastrum – spiny colonies

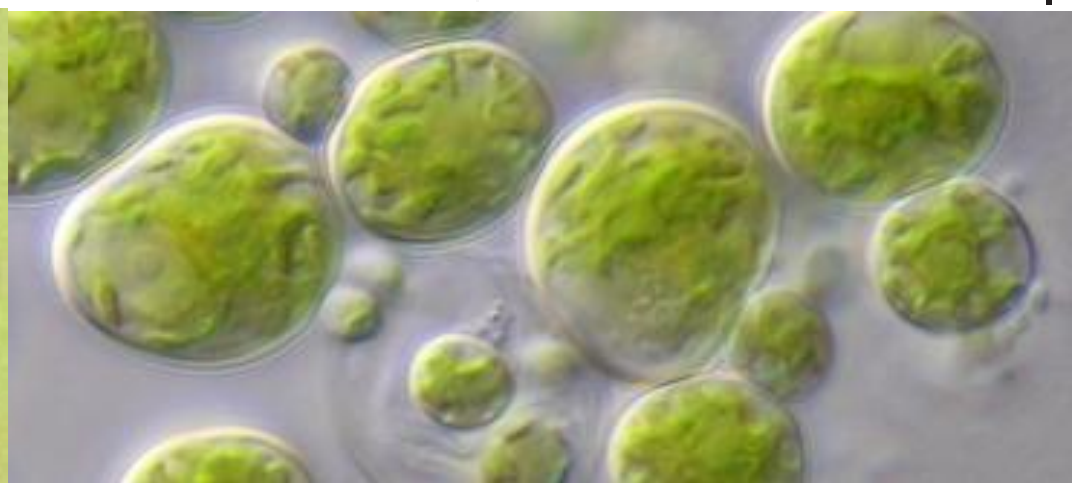
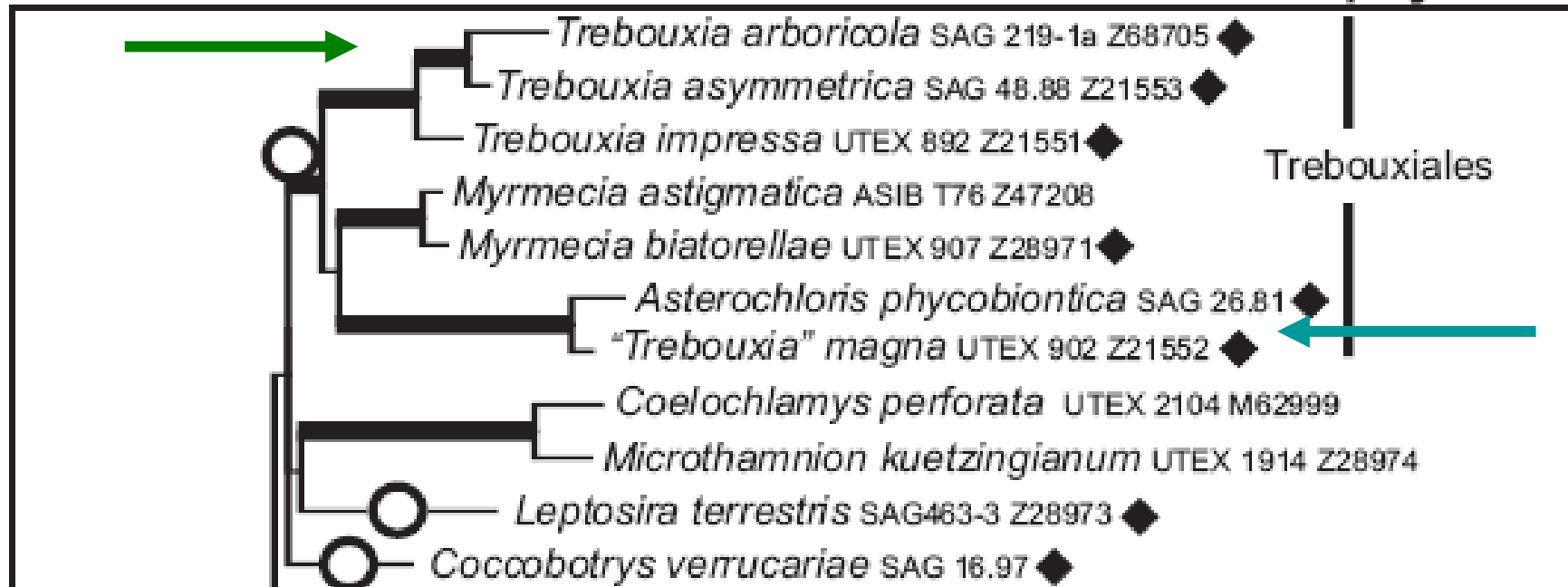


Crucigenia – smooth colonies, big aperture



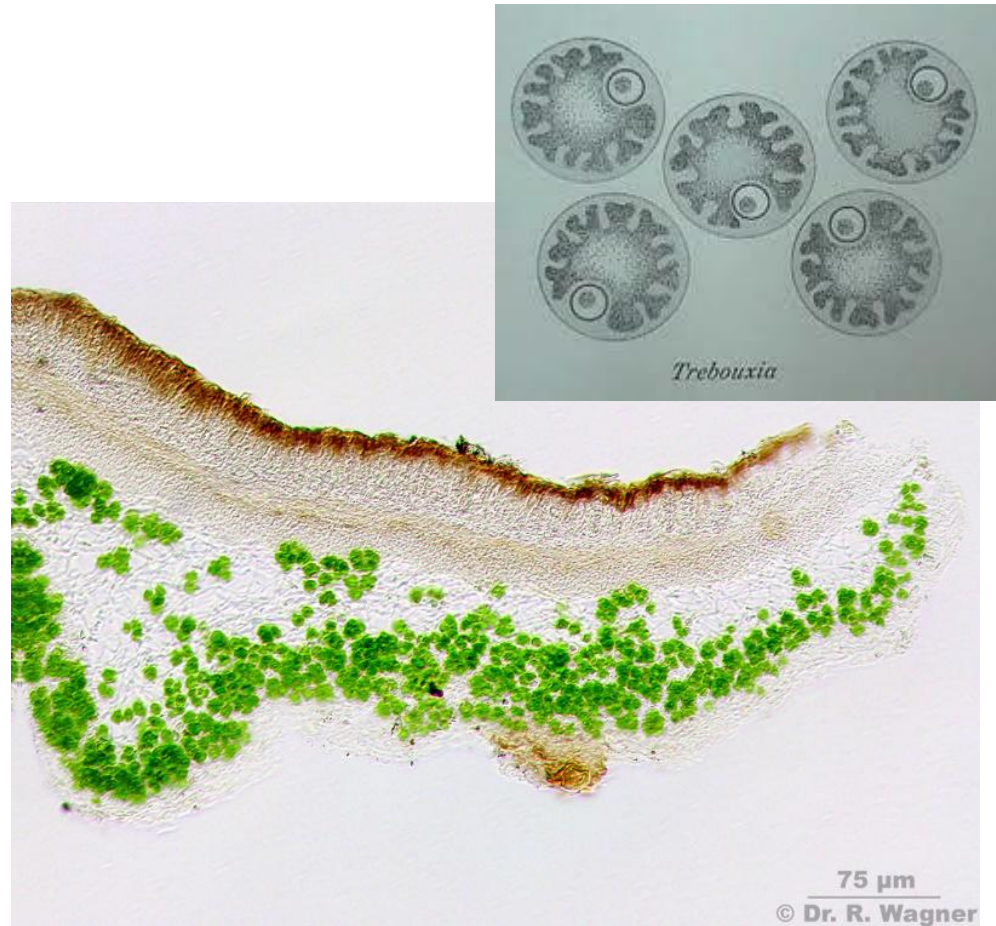
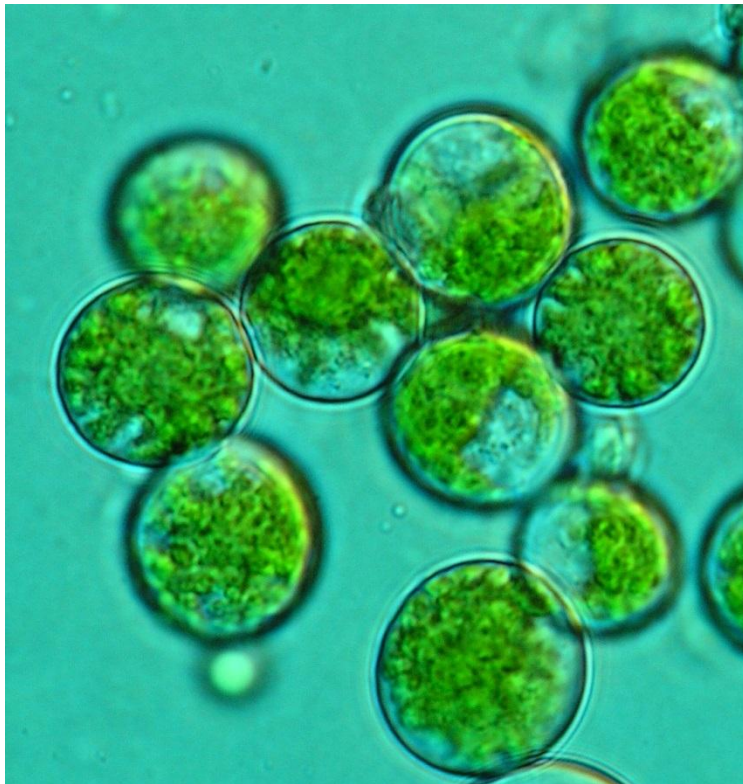
Trebouxiales

Trebouxiophyceae



Trebouxiales, *Trebouxia*

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



Trebouxiales, *Trebouxia*



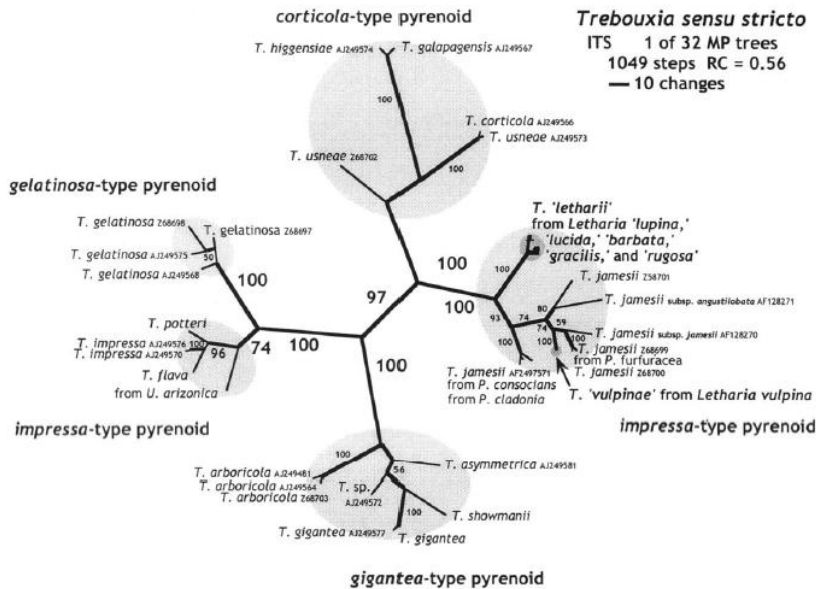
Trebouxiales, *Trebouxia*



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

Scott Kroken; John W. Taylor

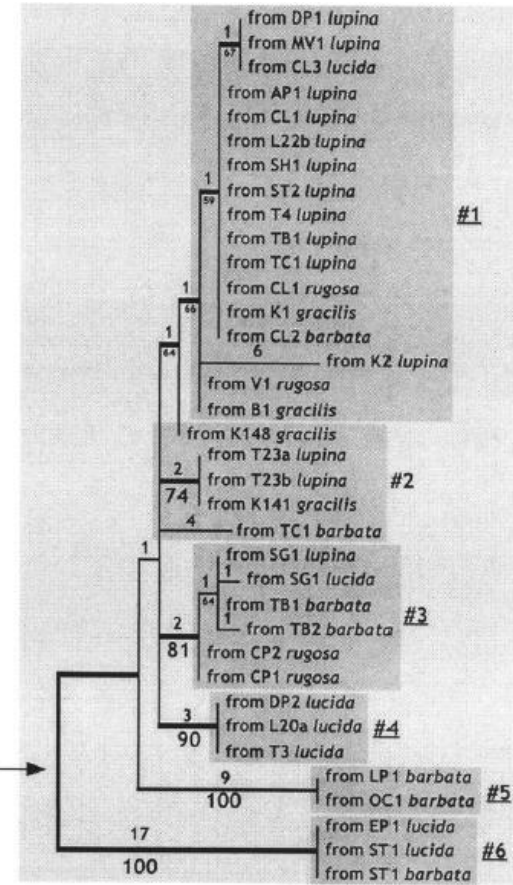
The Bryologist, Vol. 103, No. 4. (Winter, 2000), pp. 645-660.



***Trebouxia jamesii* species complex**
actin I intron 569
1 of 8 MP trees
51 steps
RC = 0.95

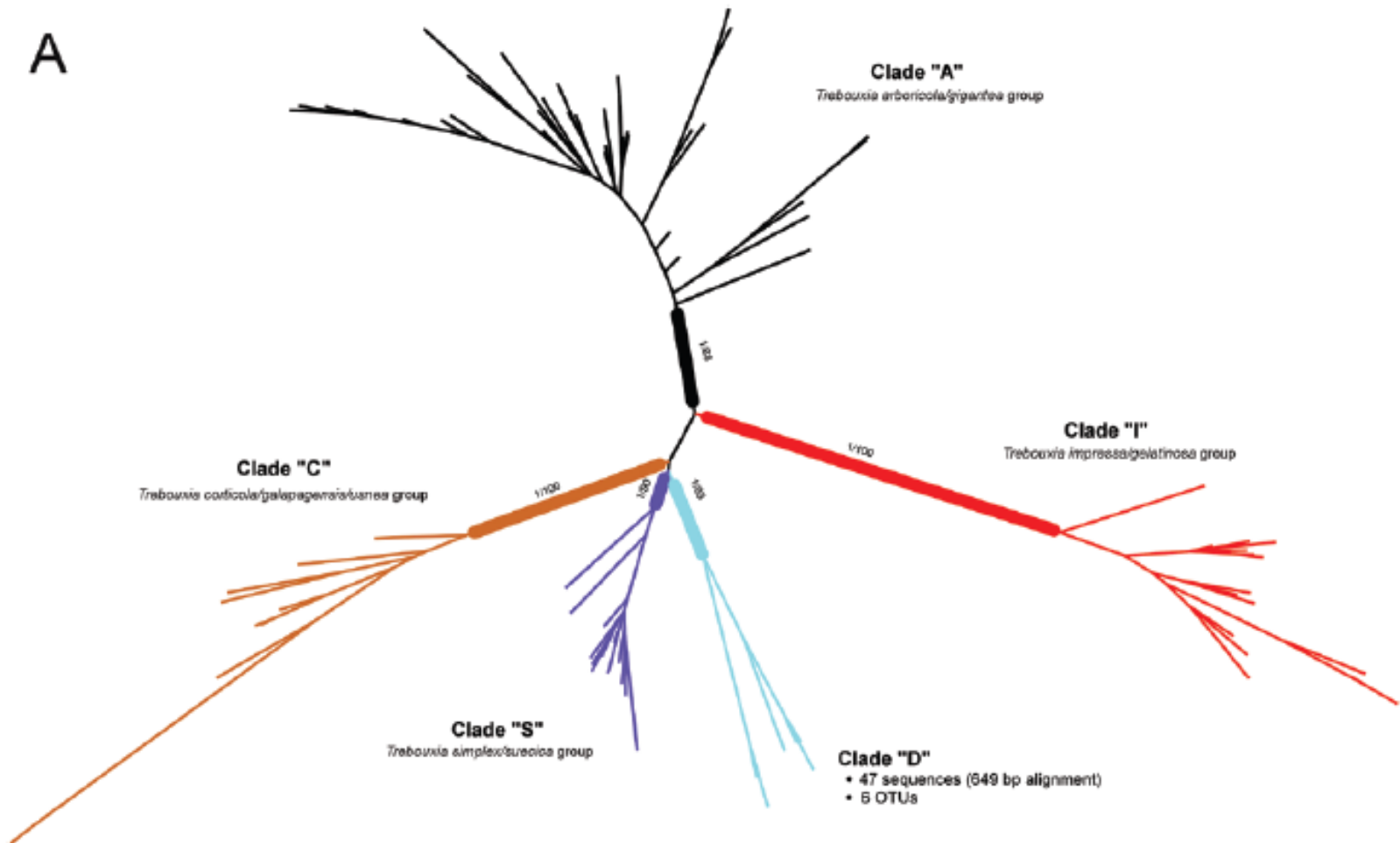
Cryptic diversity – e.g. *T. jamesii*

from
Letharia 'lupina'
Letharia 'gracilis'
Letharia 'rugosa'
Letharia 'barbata'
Letharia 'lucida'



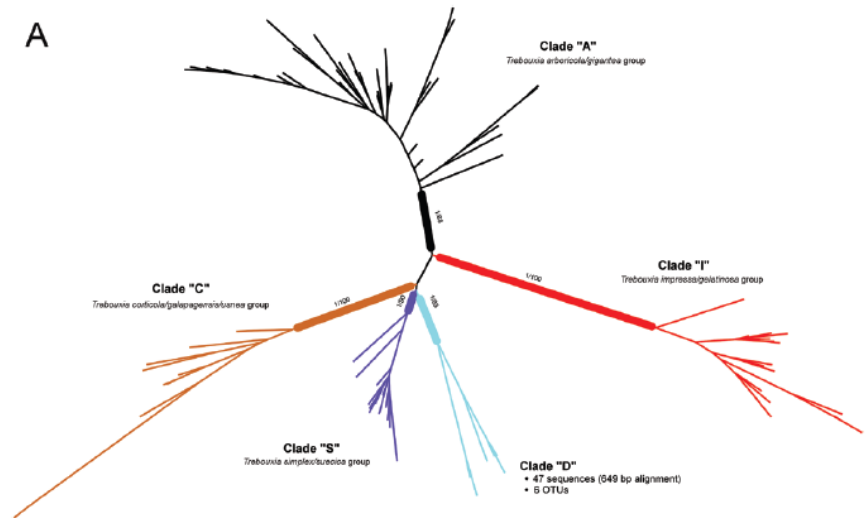
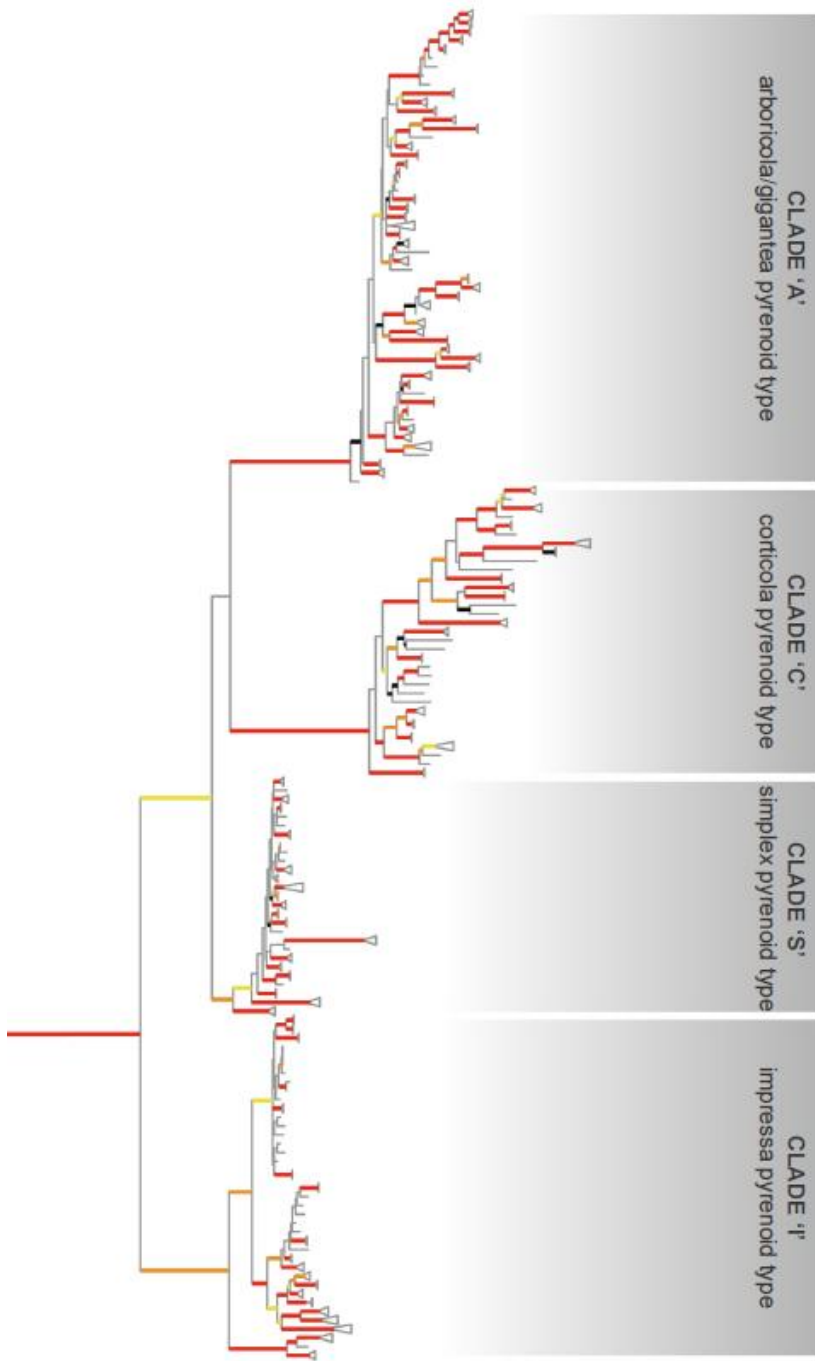
Trebouxiales, *Trebouxia*

A



Trebouxiales, *Trebouxia*

- 29 species described so far
- in reality, there is at least 111 species-level lineages



Muggia et al. (2020): *Molecular Phylogenetics and Evolution* **149**

Trebouxiales, *Trebouxia*

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

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

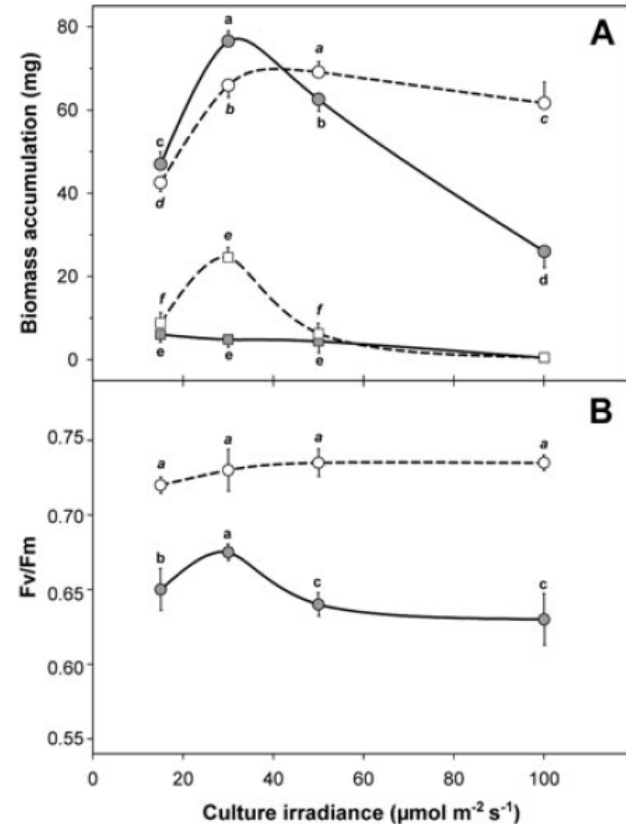
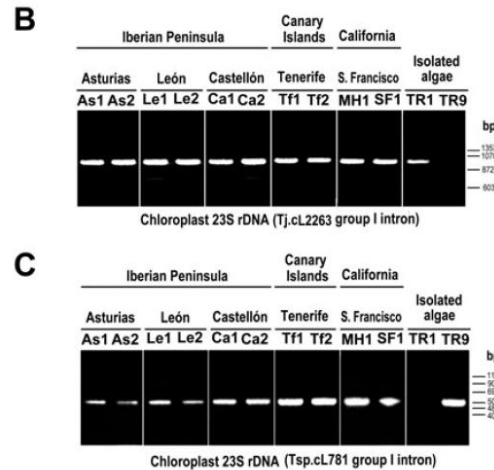
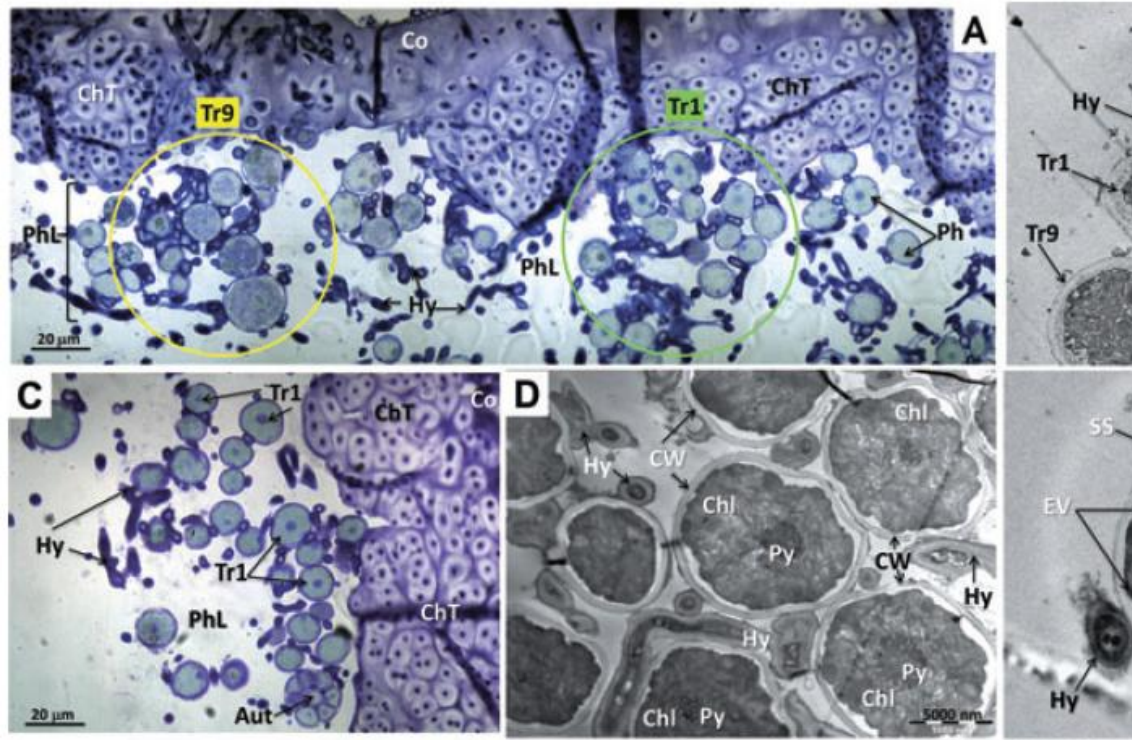


Fig. 4. Effects of temperature and irradiance during culture on growth and photosynthesis in isolated TR1 and TR9 phycobionts. A. TR9 and TR1 biomass accumulation after 30 days of culture at 17°C or 20°C and the indicated irradiances. Grey and white circles represent TR1 and TR9 phycobionts cultured 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 ($\pm$ 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 ($\pm$ 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

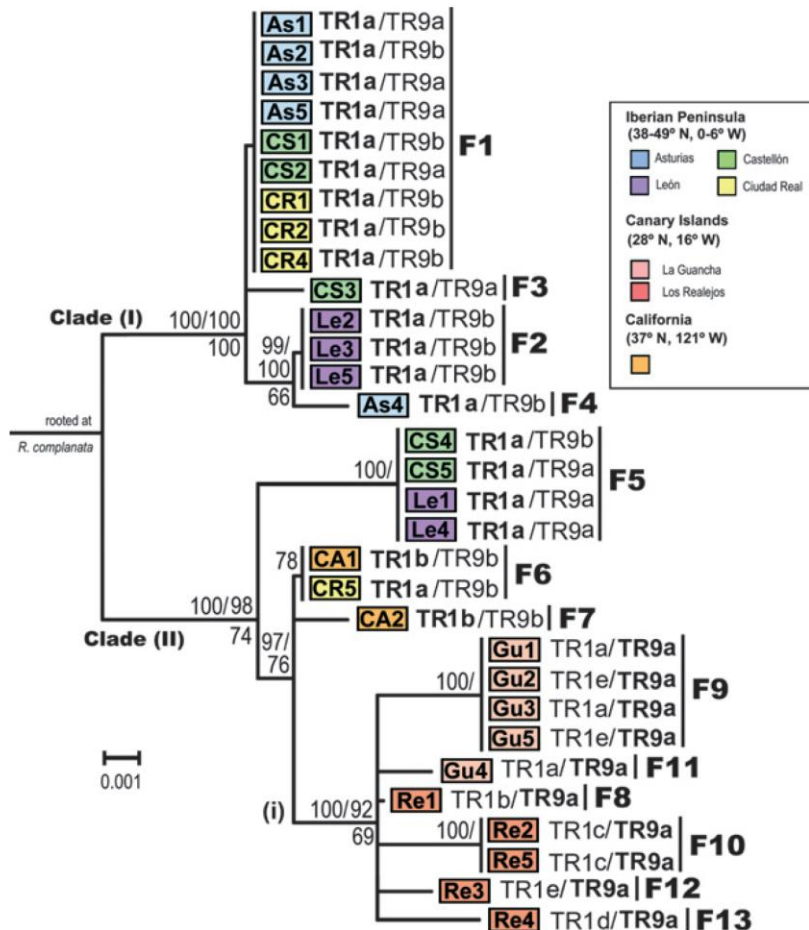
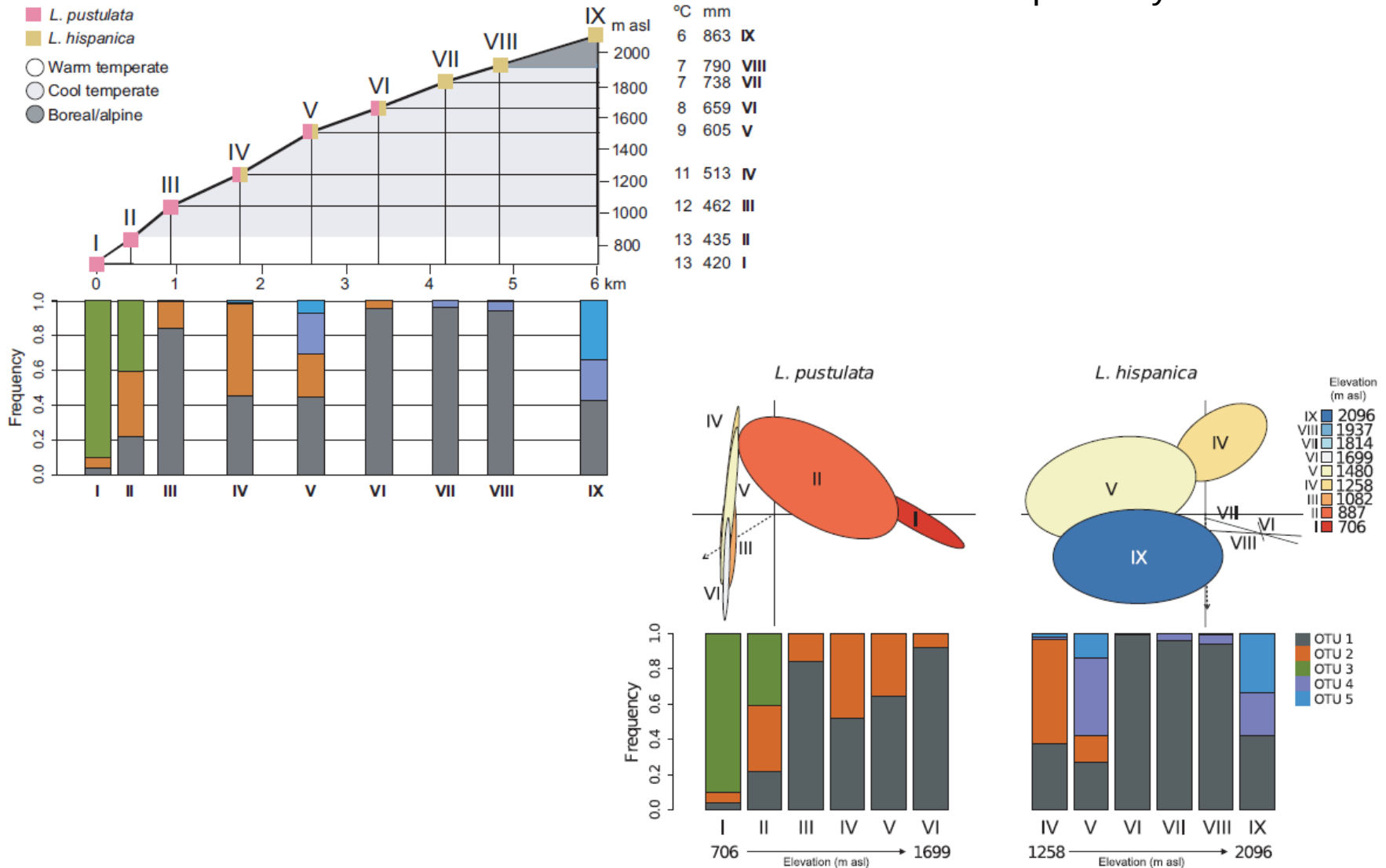


Fig. 1. Phylogram based on the analysis of fungal nrITS and *rpb2* gene sequences in specimens of *Ramalina farinacea*, with *Ramalina complanata* as out-group (accession numbers FJ356152 and DQ883762 for nrITS and *rpb2*, respectively). Vertical bars on the right indicate different fungal haplotypes 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.

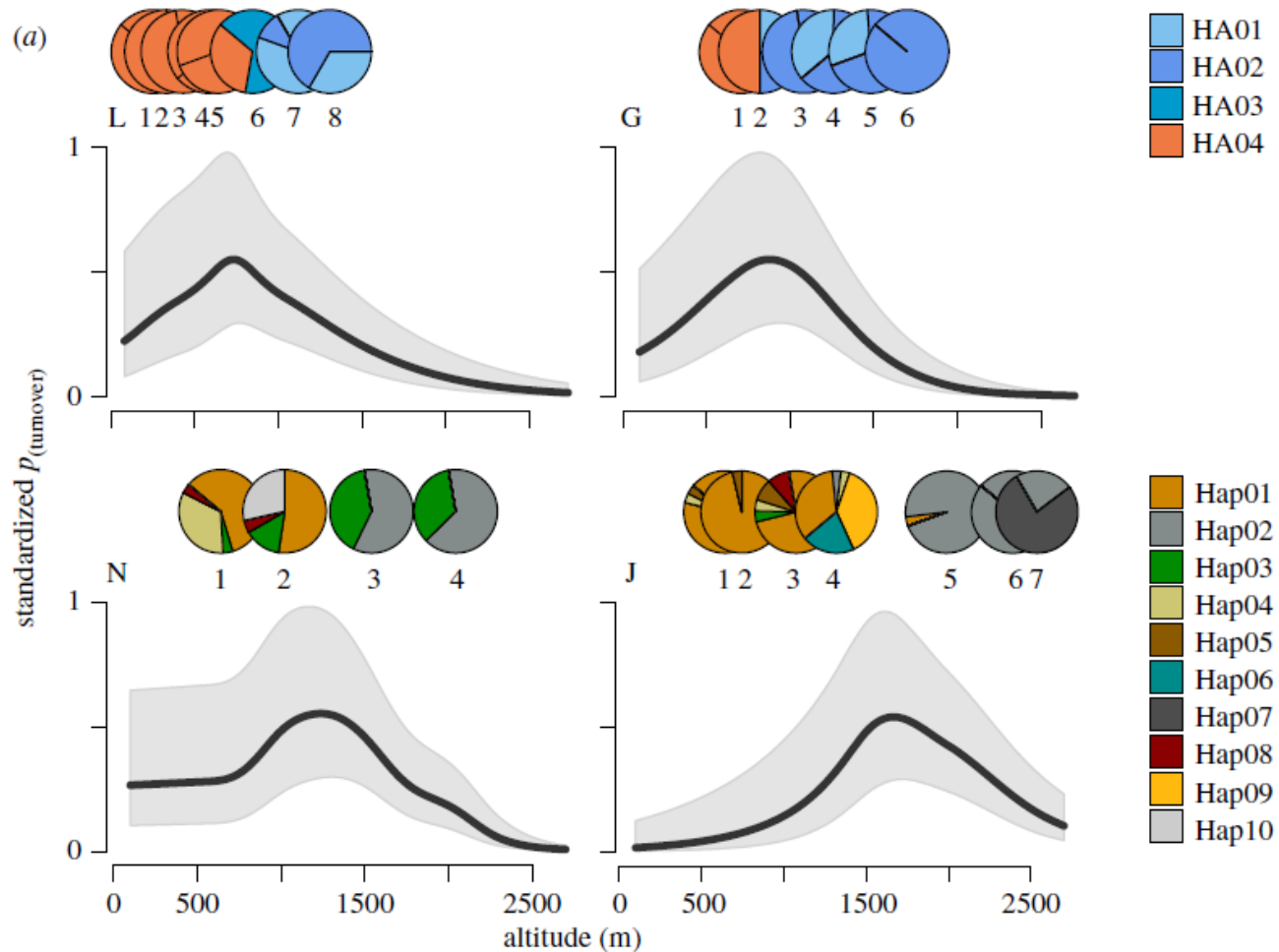
Trebouxiales, *Trebouxia*

Del Grande et al (2017) – *Lasallia* photobionts – ecological differentiation, host specificity



Trebouxiales, *Trebouxia*

Rolshusen et al (2020) – symbiont turnover zones



Trebouxiales, Asterochloris



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journal homepage: www.elsevier.com/locate/ympev



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

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^aDepartment of Botany, Faculty of Science, Charles University in Prague, Benátská 2, CZ-12801 Praha 2, Czech Republic

^bThe West Bohemian Museum in Pilsen, Kopeckého sady 2, CZ-30100 Plzeň, Czech Republic

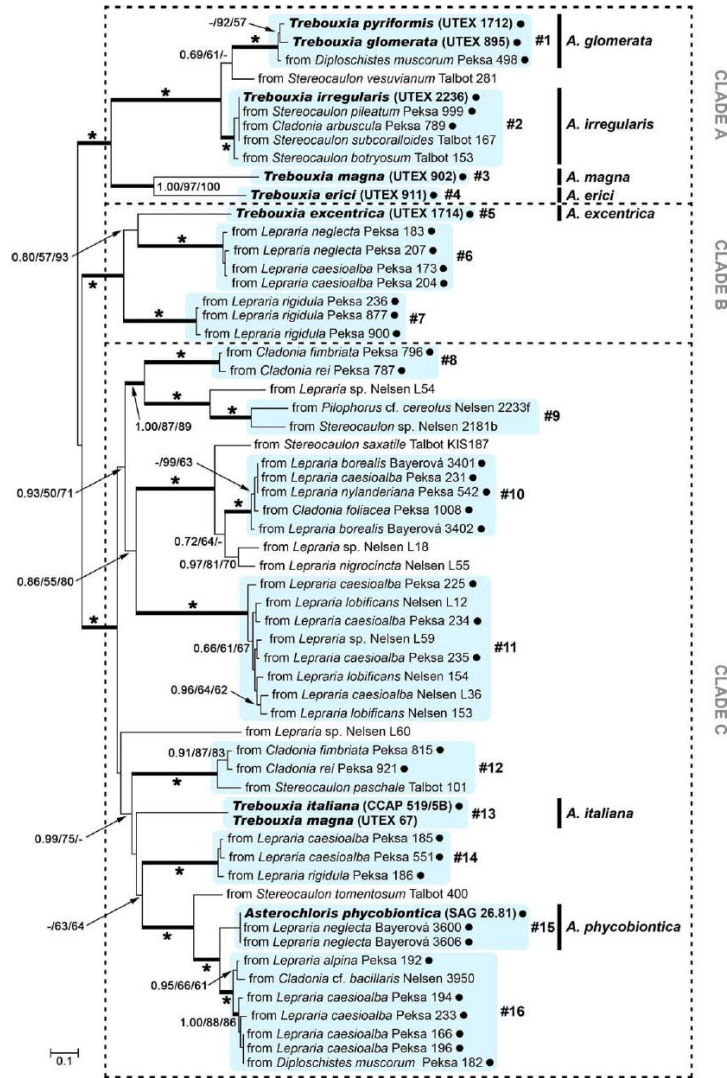
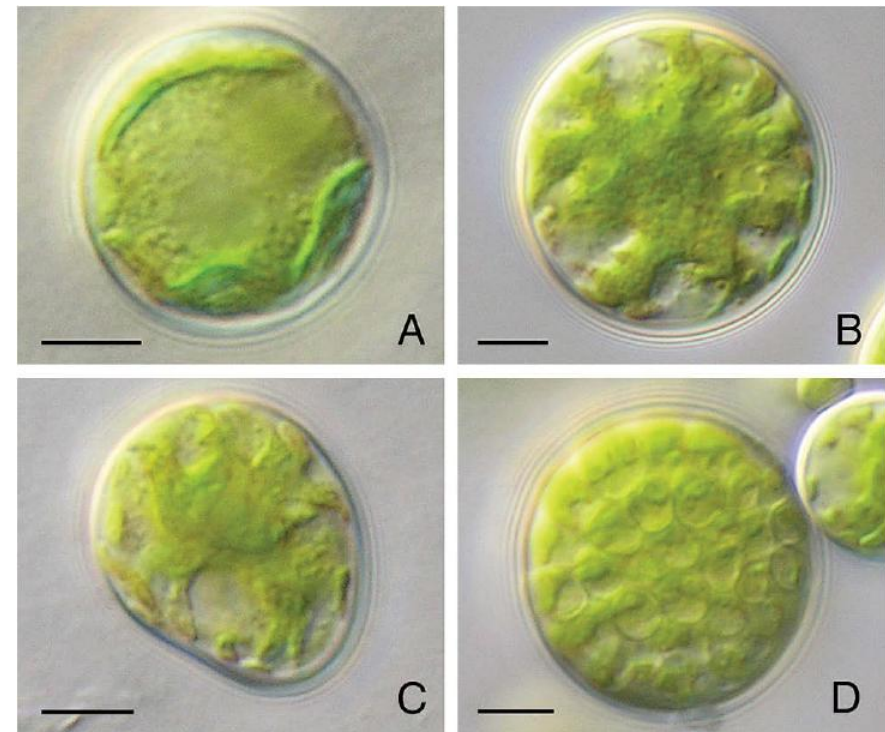


Fig. 3. Unrooted BI analysis based on the combined ITS + actin dataset using a GTR+I model for ITS1, K80+I+I model for ITS2, and JC model for 5.8 rRNA partition; and HKY+I model for the actin-intron 206, HKY+I model for the actin-intron 248, and K80+CP₂₃₊₁ model for the actin-exon partition. The doublet model is applied for the star regions in all ITS rDNA partitions. Values at the nodes indicate statistical support estimated by three methods – MrBayes posterior node probability (left), maximum likelihood bootstrap (in the middle) and maximum parsimony bootstrap (right). Full statistical support (1.00/100/100) is marked with an asterisk. Thick branches represent nodes receiving the highest PP support (1.00). Sequences determined in this study are marked by full circles. Authentic strains of *Asterochloris phycobiontica* and several 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.

Trebouxiales, *Asterochloris*



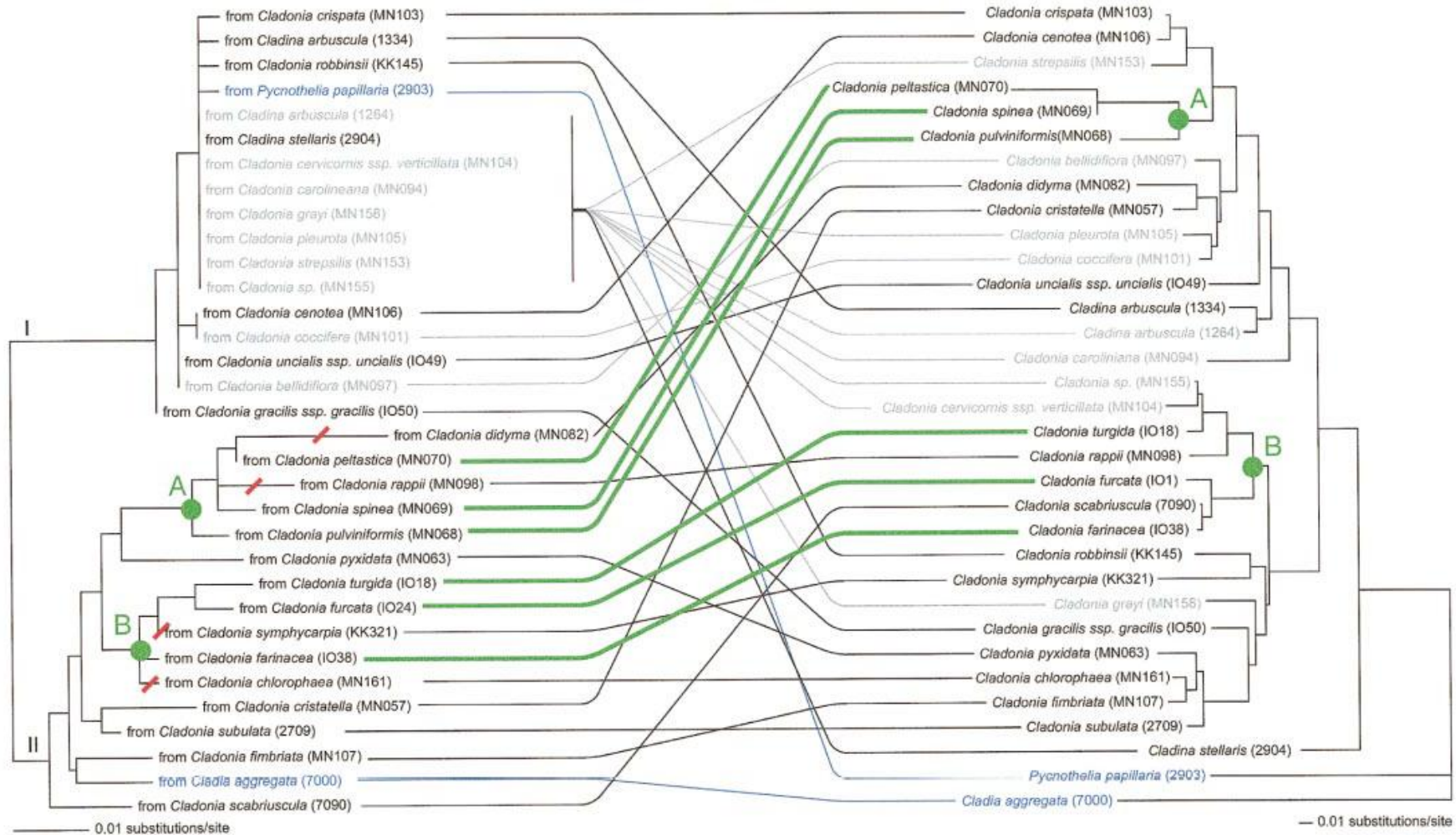
Trebouxiales, *Asterochloris*

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

ALGAL SWITCHING AMONG LICHEN SYMBIOSES¹

MICHELE D. PIERCEY-NORMORE² AND PAULA T. DEPRIEST

- incongruent evolution of algae and fungi
- algal domestication



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)

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*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

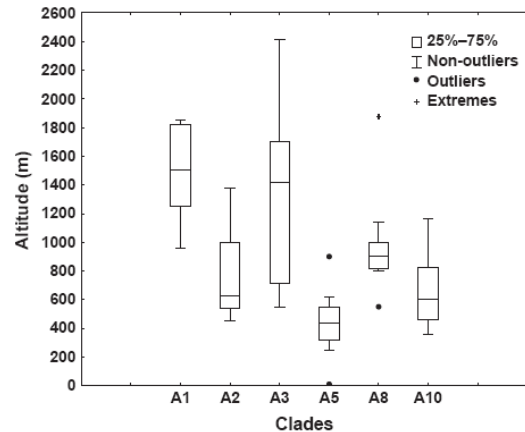


Fig. 3 Differences in the distribution of selected *Asterochloris* clades along the altitudinal gradient. Box and whisker plots are based on altitudinal data from six clades (only those represented by at least eight samples). All samples were collected in similar latitudes in Europe (43–58°N, i.e. somewhere 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.

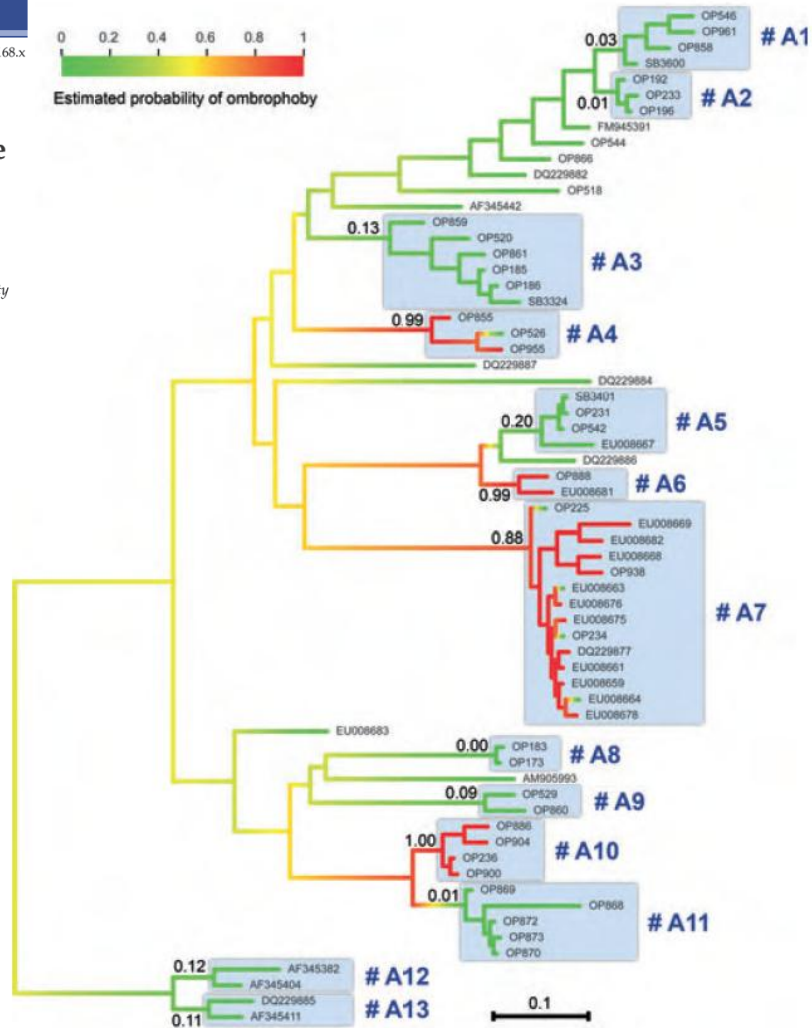
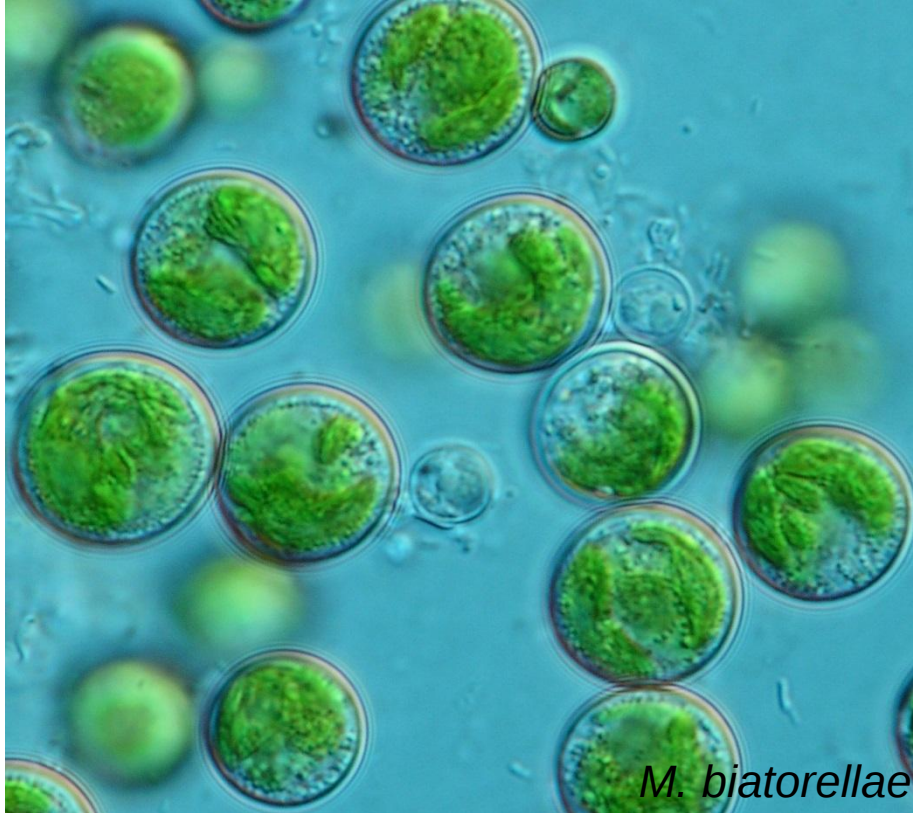


Fig. 2 The evolution of the selected ecological character—the ombrophoby (ombrophily) of lichens—mapped onto the photobiont phylogenetic tree. Colours are used to visualize estimated probabilities of the presence of ombrophoby along the phylogenetic tree. Red indicates a high probability of ombrophoby, 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.

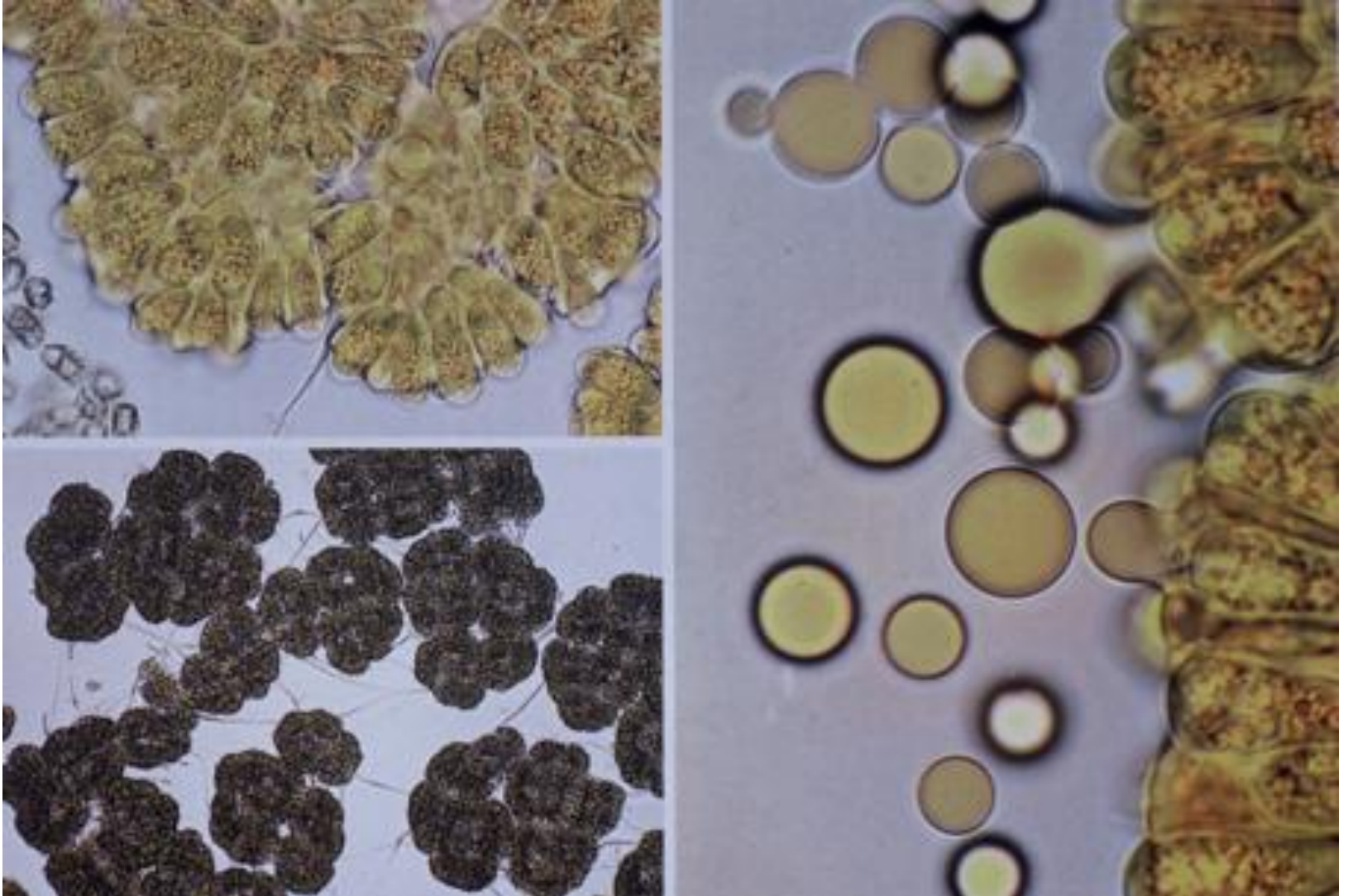
Trebouxiales, *Myrmecia*

- terrestrial, aerophytic
- lichen symbiont



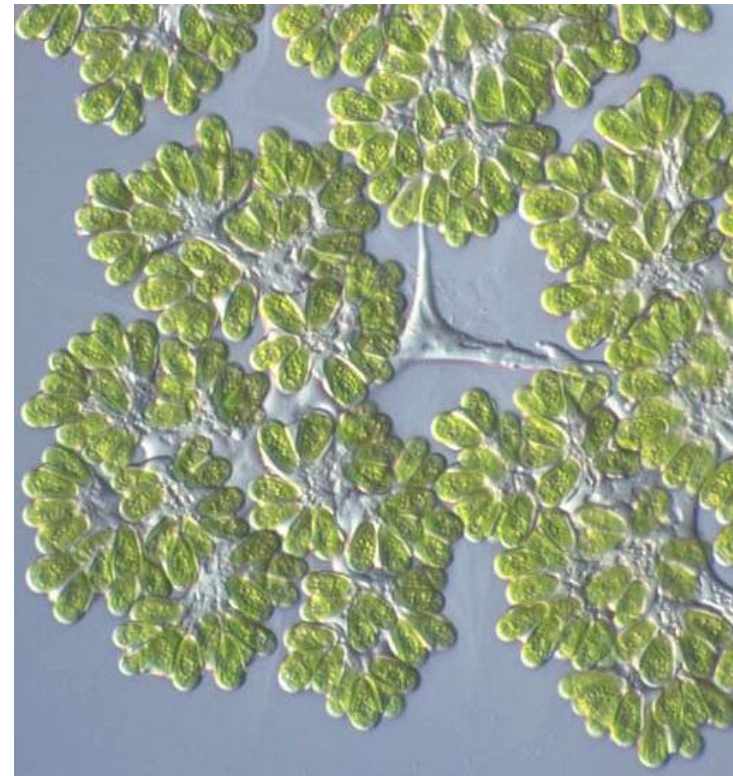
Botryococcus-clade, *Botryococcus*

- *Botryococcus braunii* – colonial green alga



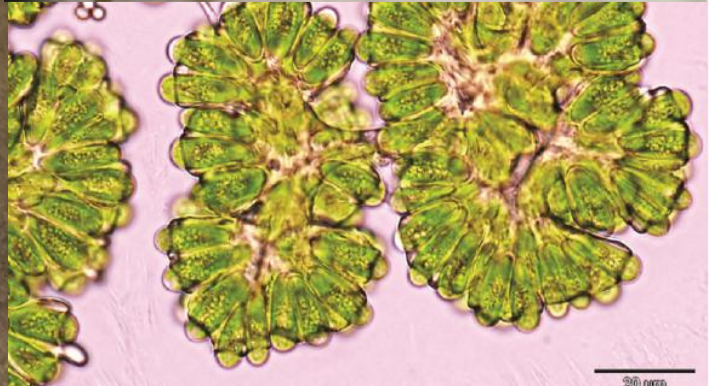
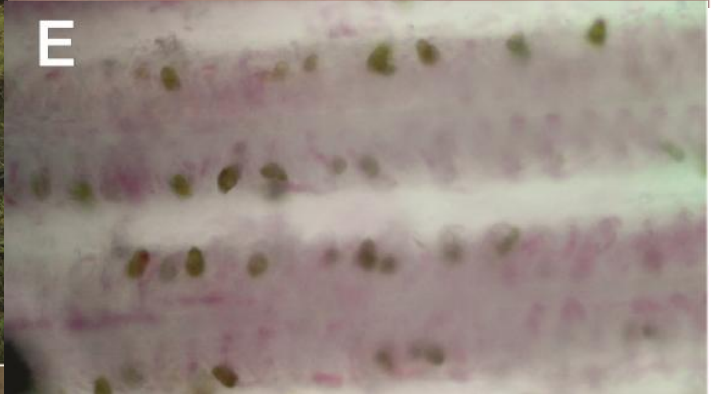
Botryococcus-clade, Botryococcus

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





- fish mortality
- oily droplets in the fish gills



Botryococcus-clade, Botryococcus

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

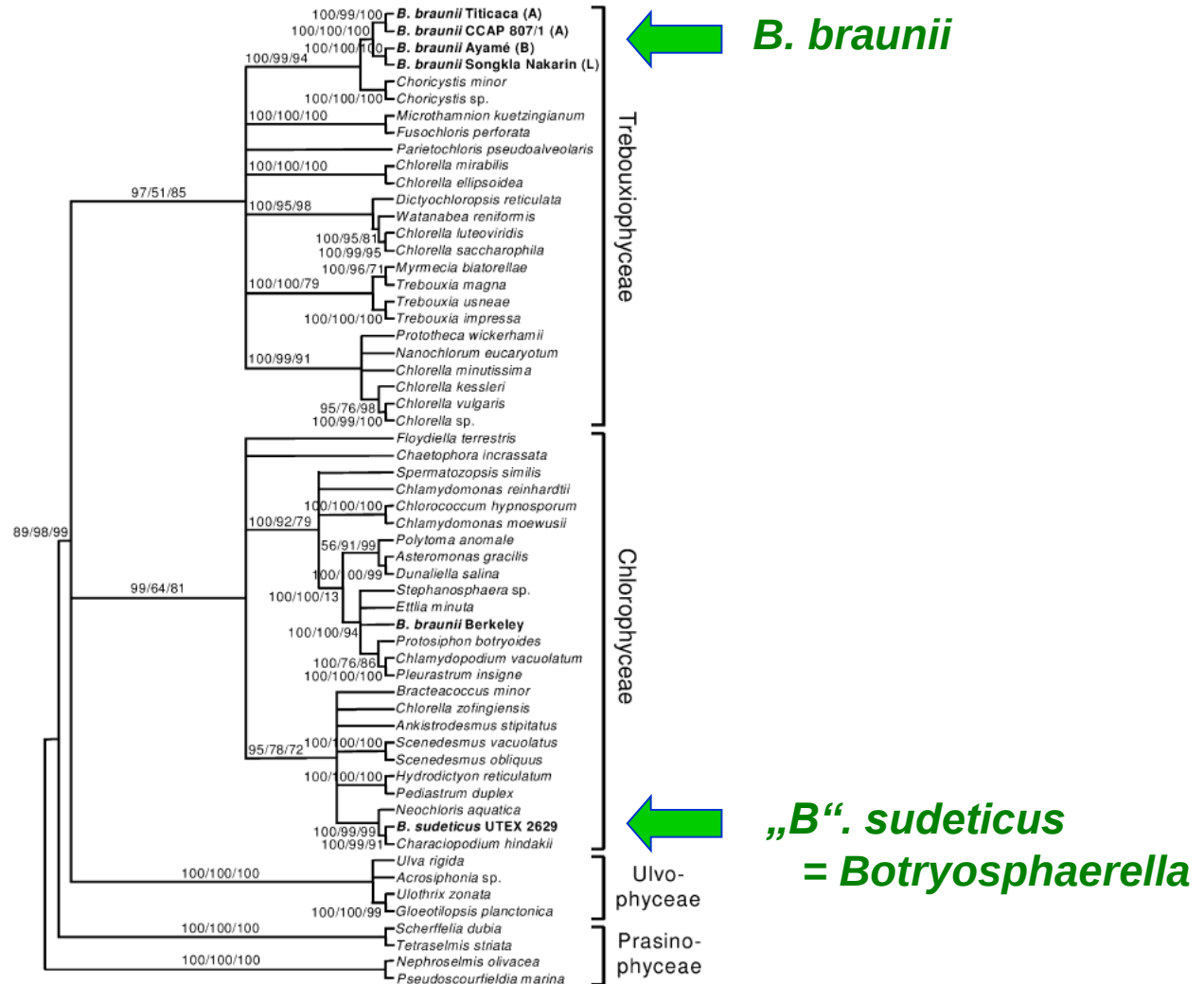
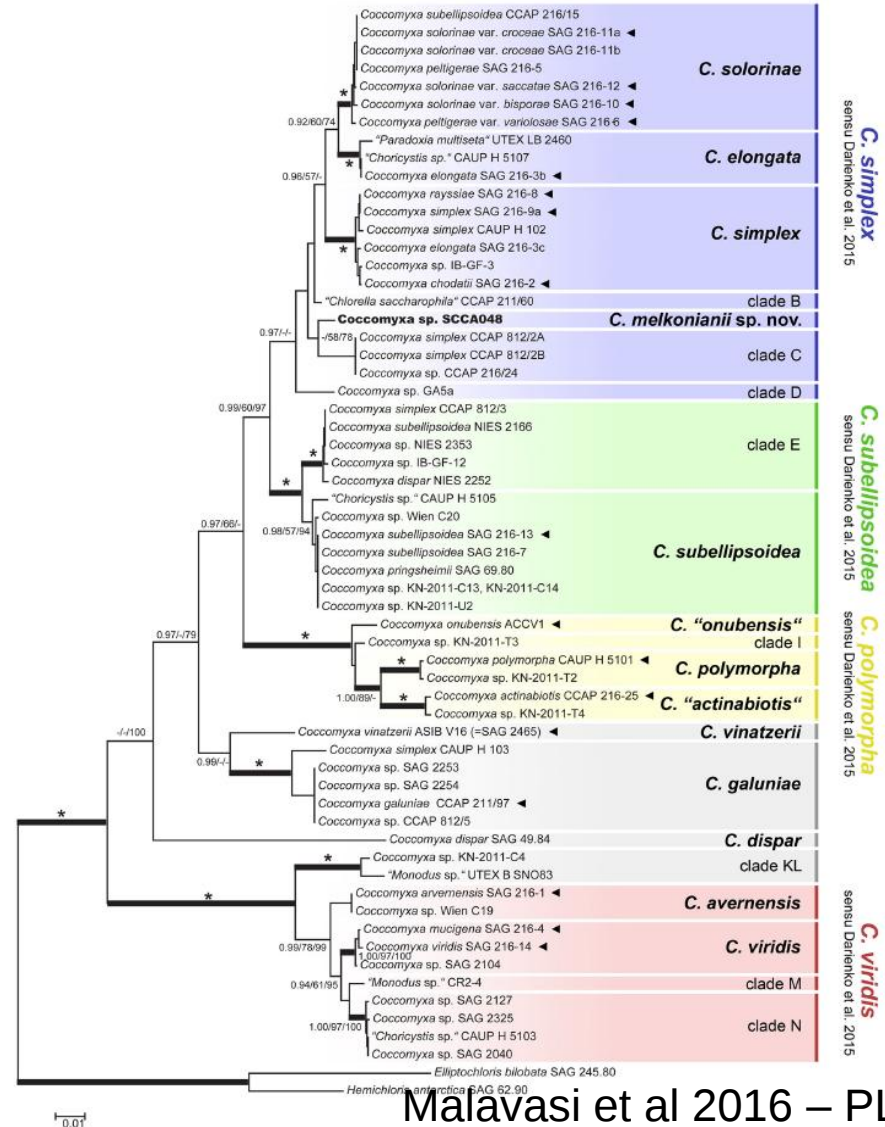
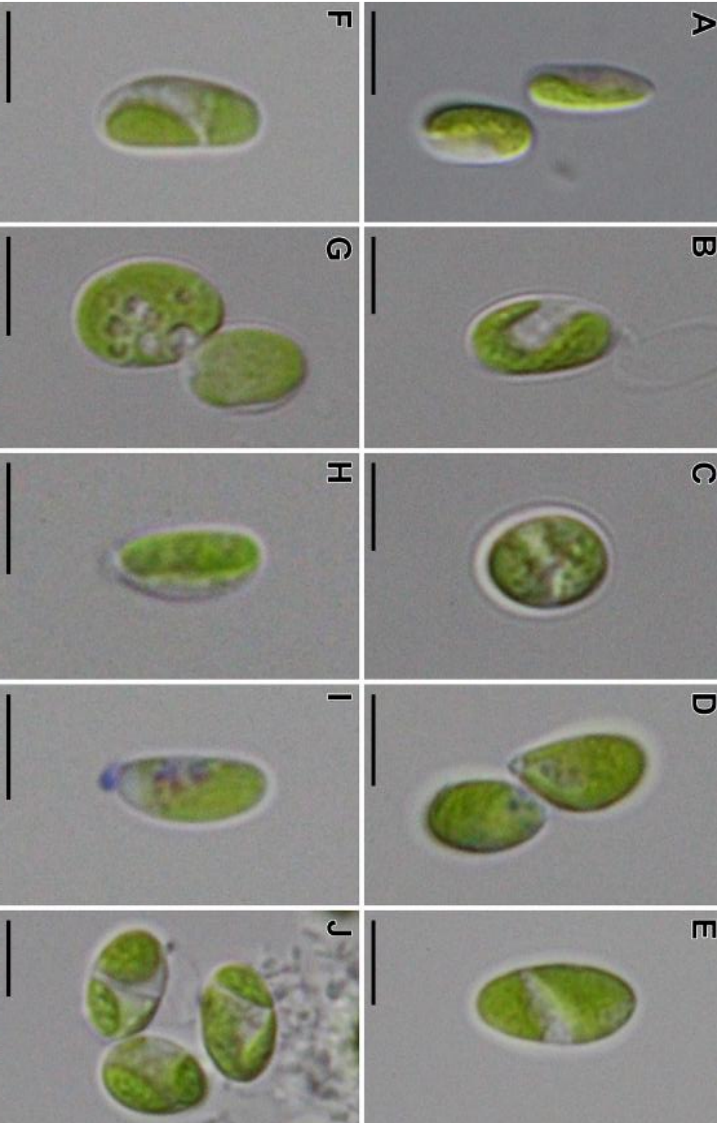


FIG. 5. Consensus tree from trees inferred with different methods of analysis. The numbers shown at the branches are credibility percentages determined using Bayesian inference (left) and bootstrap values determined using weighted parsimony (middle) and minimum evolution (right). Taxa shown in bold letters are the isolates whose 18S rRNA sequences were determined in this study.

Botryococcus-clade, Coccomyxa

- ellipsoid cells, frequent in aerophytic substrate



Botryococcus-clade, Coccomyxa

- lichen photobionts

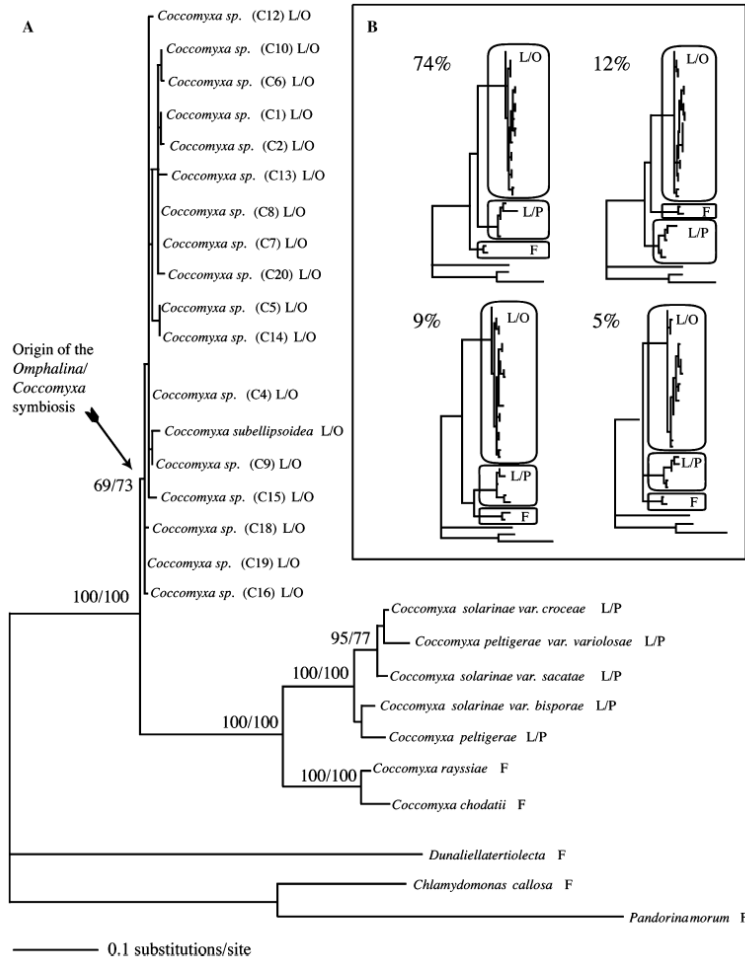


Fig. 3. Phylogenetic relationships among lichenized and non-lichenized *Coccomyxa* algae (dataset AC) as revealed by an ML search using ITS (ITS1-5.8S-ITS2) sequences. *Coccomyxa* isolated from members of the Peltilgerales (Ascomycota) are denoted by a bold L/O after the name. *Coccomyxa* isolated from members of the Peltilgerales (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

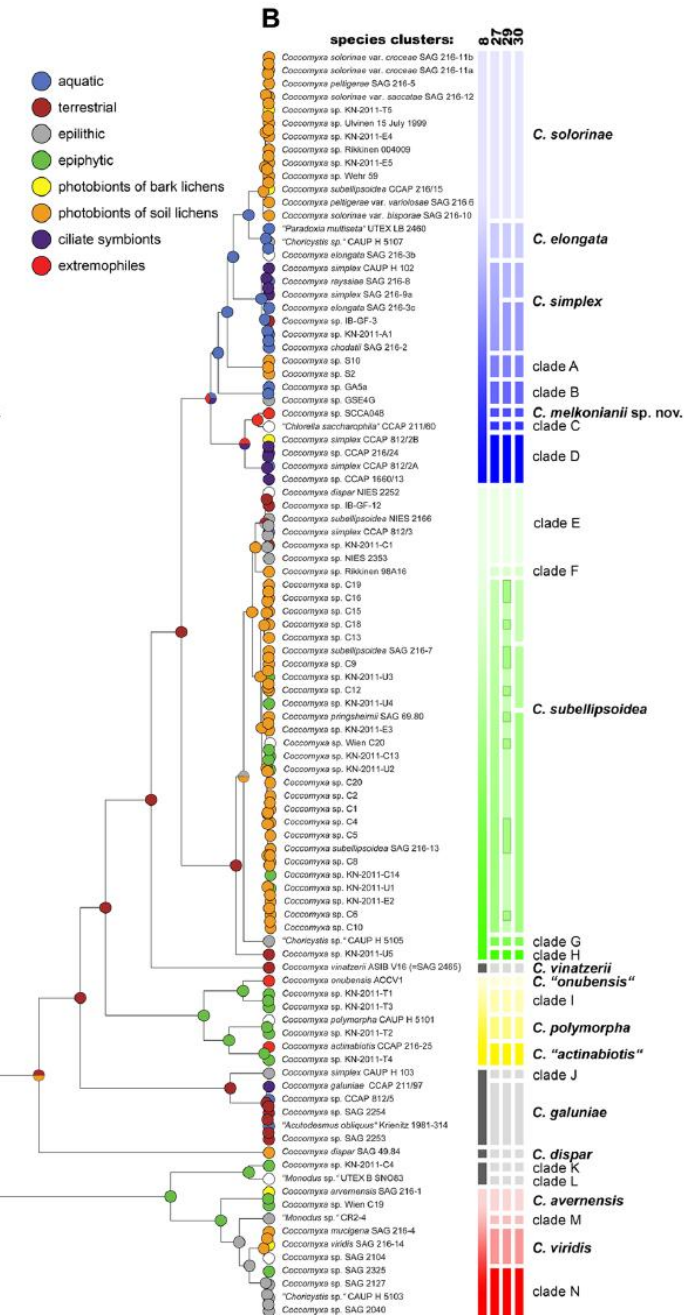
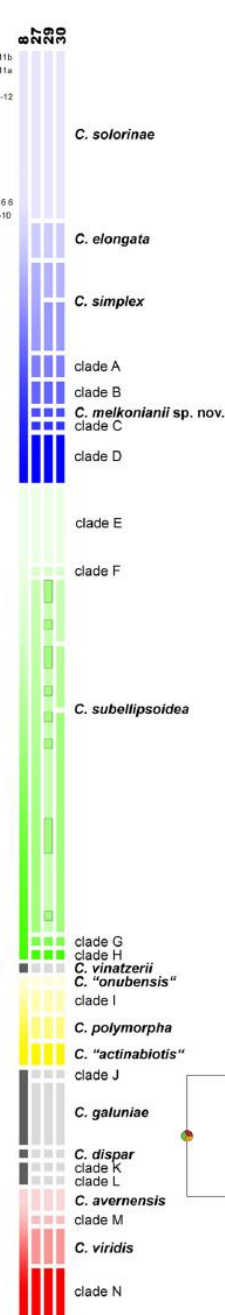
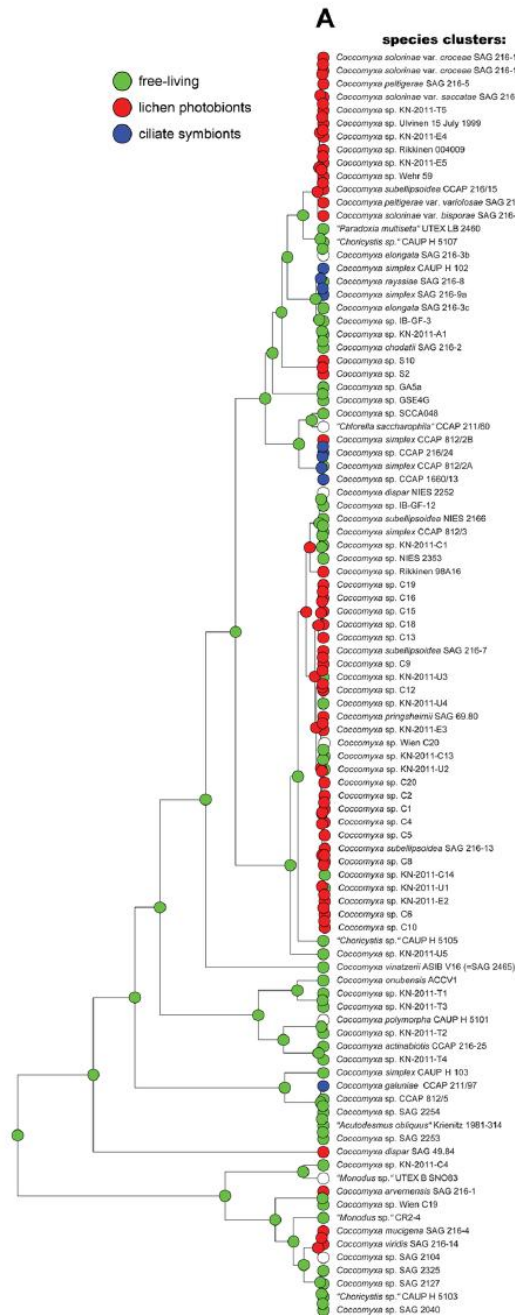
MOLECULAR
PHYLOGENETICS
AND
EVOLUTION

www.elsevier.com/locate/ympev

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, Coccomyxa

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

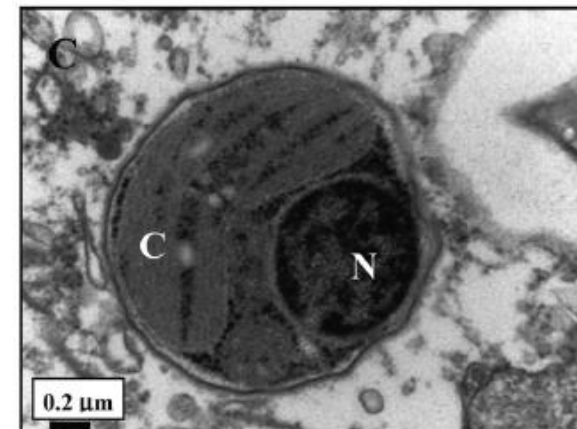
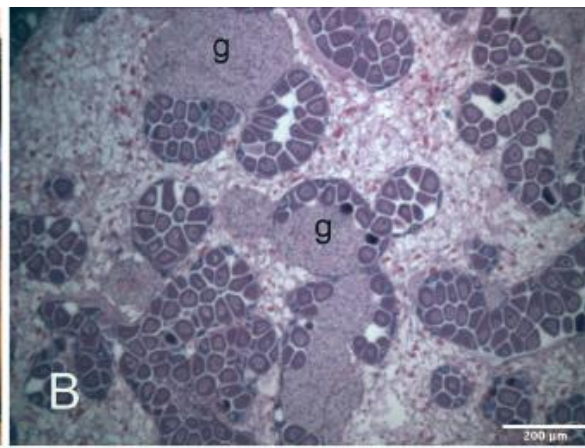
DISEASES OF AQUATIC ORGANISMS
Dis Aquat Org

Published September 24



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. Feist², Laure Guillou¹, Lisbeth S. Harkestad³, Kelly Bateman², Tristan Renault⁴, Stein Mortensen^{3,*}



Botryococcus-clade, Coccomyxa

- *C. actinabiotis*

An extremely radioresistant green eukaryote for radionuclide bio-decontamination in the nuclear industry

Corinne Rivasseau,^{*abcd} Emmanuel Farhi,^{*e} Ariane Atteia,^f Alain Couté,^g
Marina Gromova,^h Diane de Gouvion Saint Cyr,^{abcde} Anne-Marie Boisson,^{abcd}
Anne-Sophie Féret,^{abcd} Estelle Compagnon^e and Richard Bligny^{abcd}

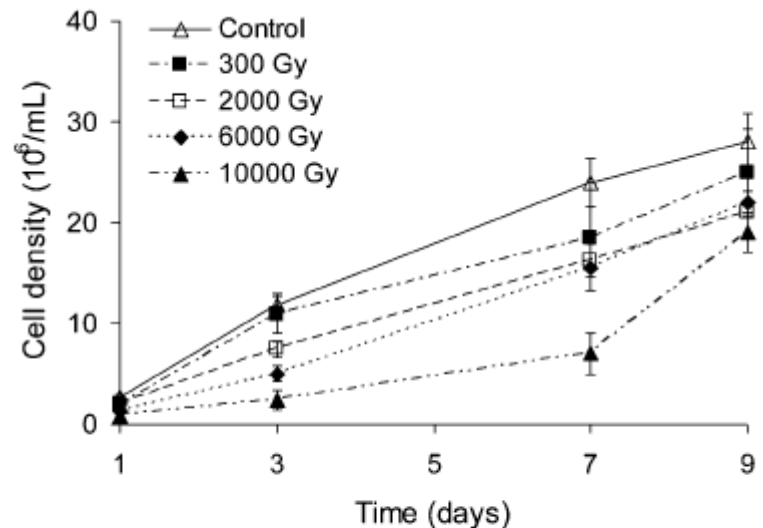
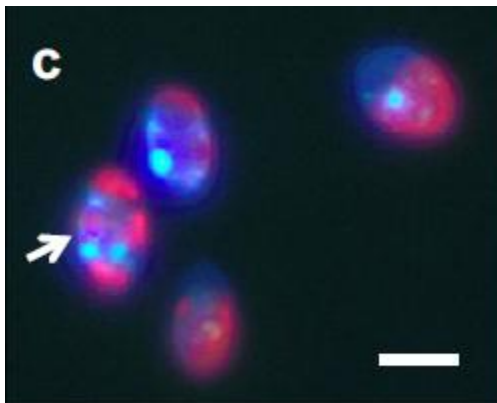
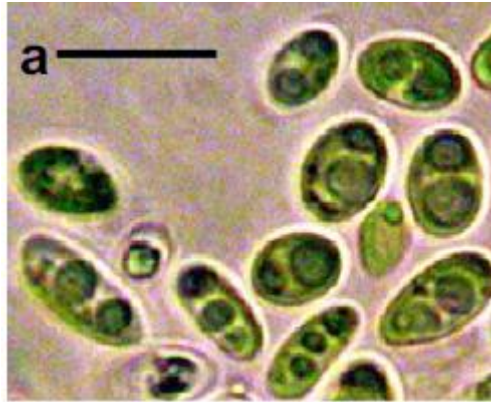
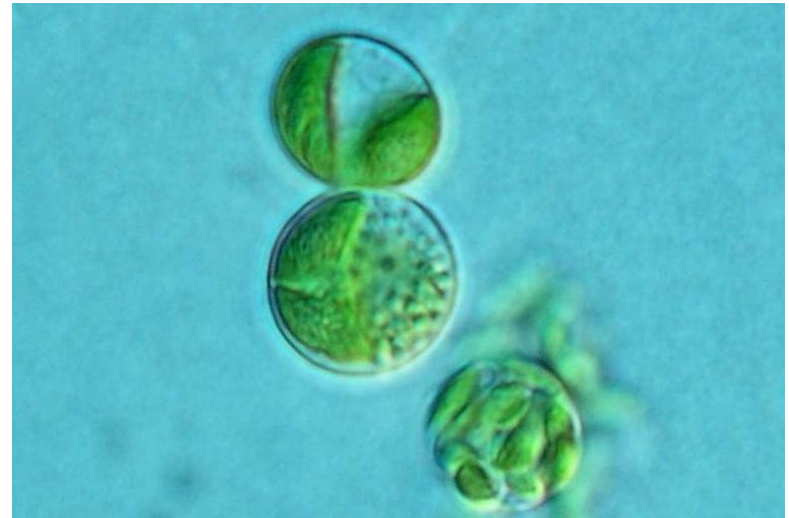
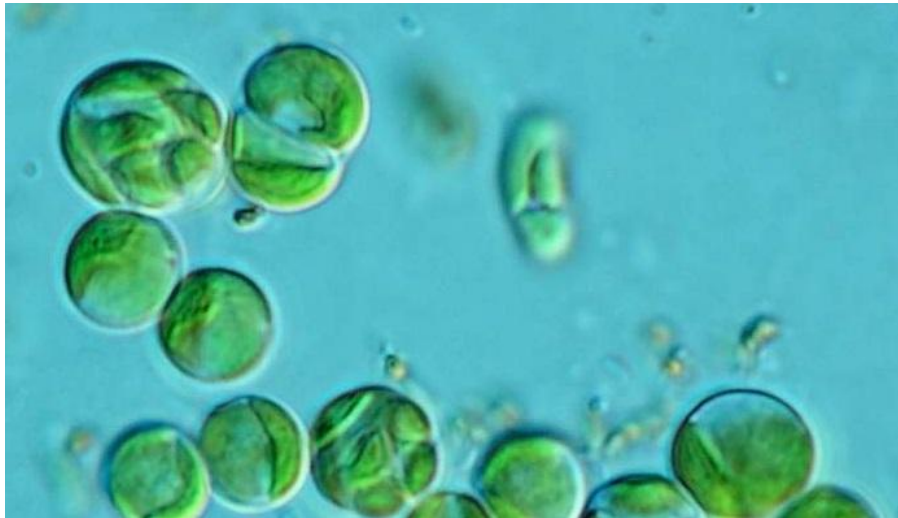
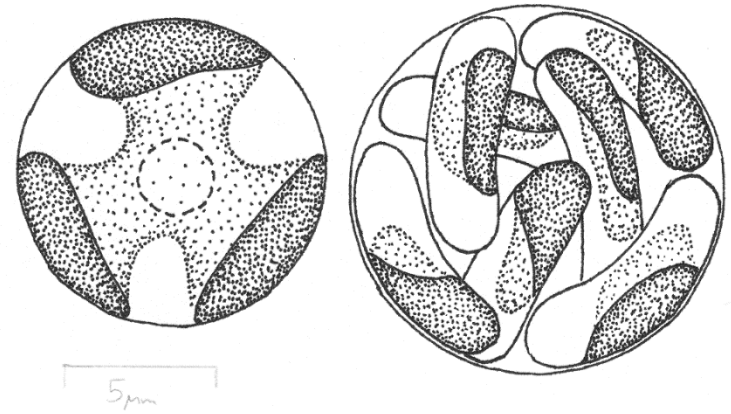
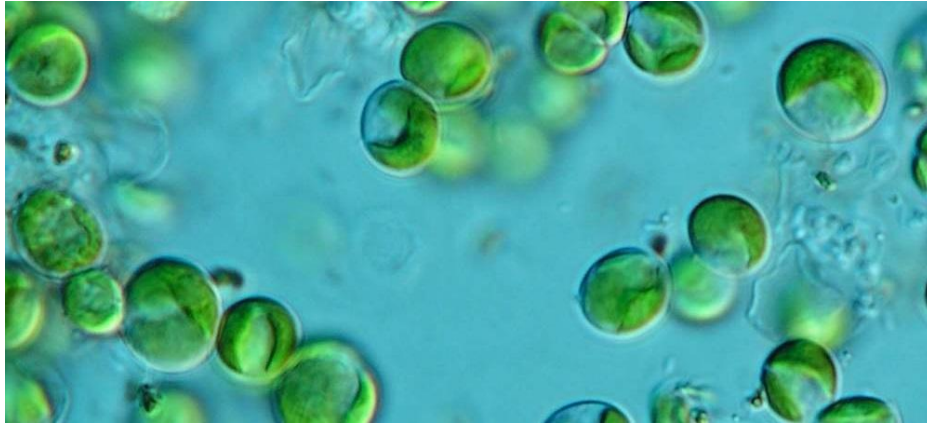


Fig. 3 Growth of *C. actinabiotis* after acute γ -irradiation at 300, 2000, 6000, and 10 000 Gy. Values are average of triplicate experiments $\pm$ standard deviation.

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. Letsch²

Department of Ecology and Evolutionary Biology, University of Connecticut, Storrs, Connecticut 06269, USA

Gisele Muller-Parker

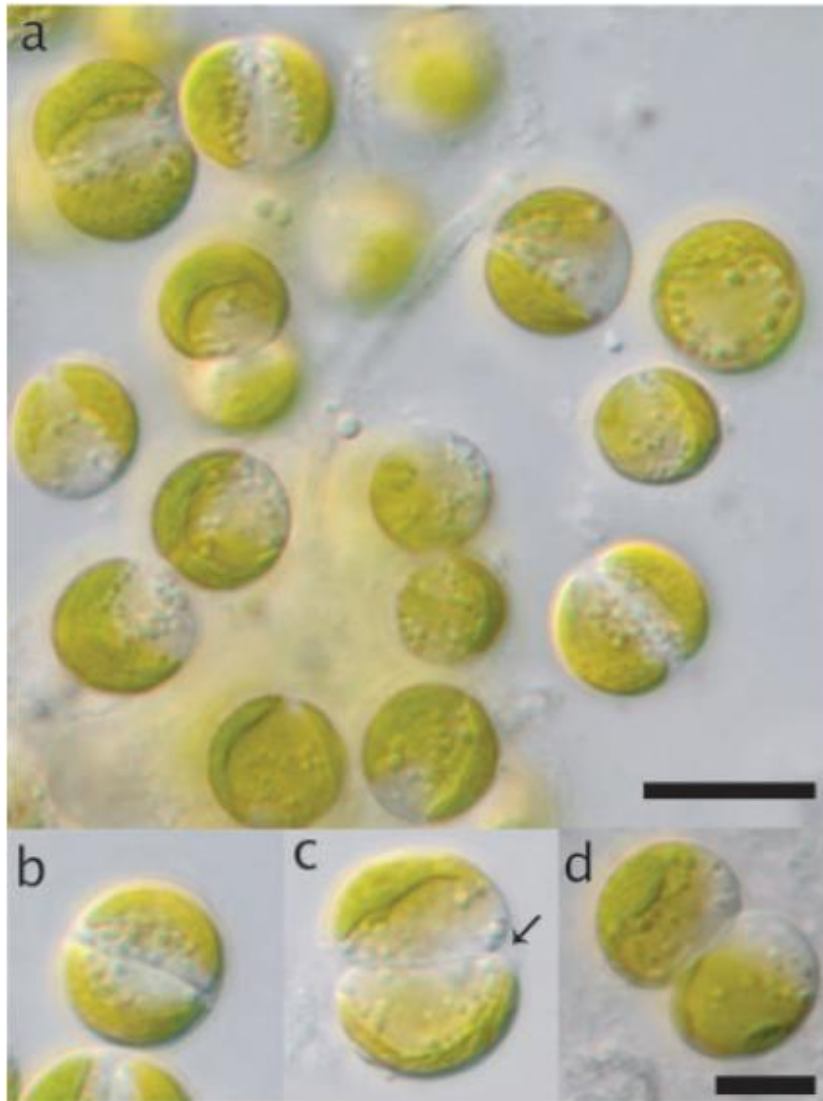
Department of Biology and Shannon Point Marine Center, Western Washington University, Bellingham,
Washington 98225-9160, USA

Thomas Friedl

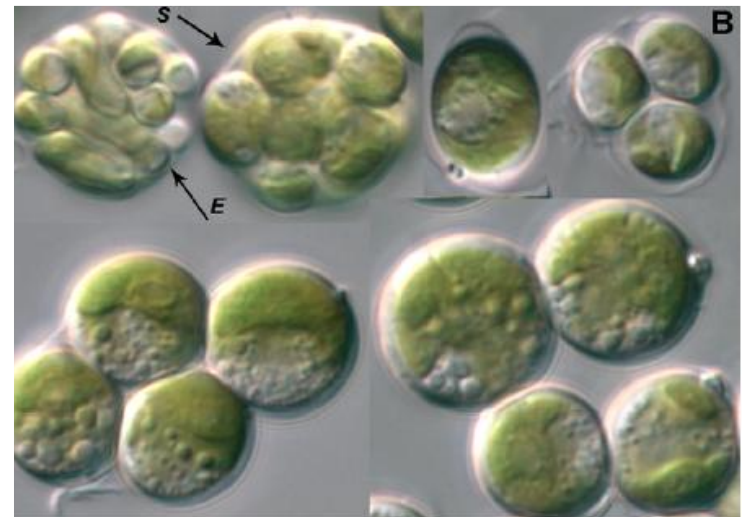
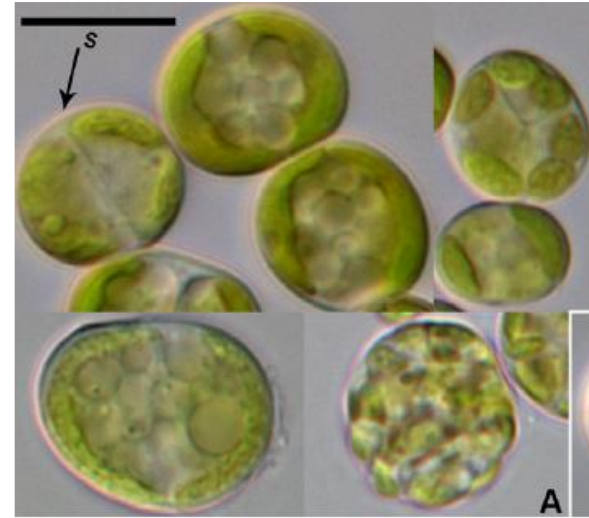
Experimental Phycology and Culture Collection of Algae, Georg-August University Göttingen, Untere Karspüle 2,
37073 Göttingen, Germany

and Louise A. Lewis

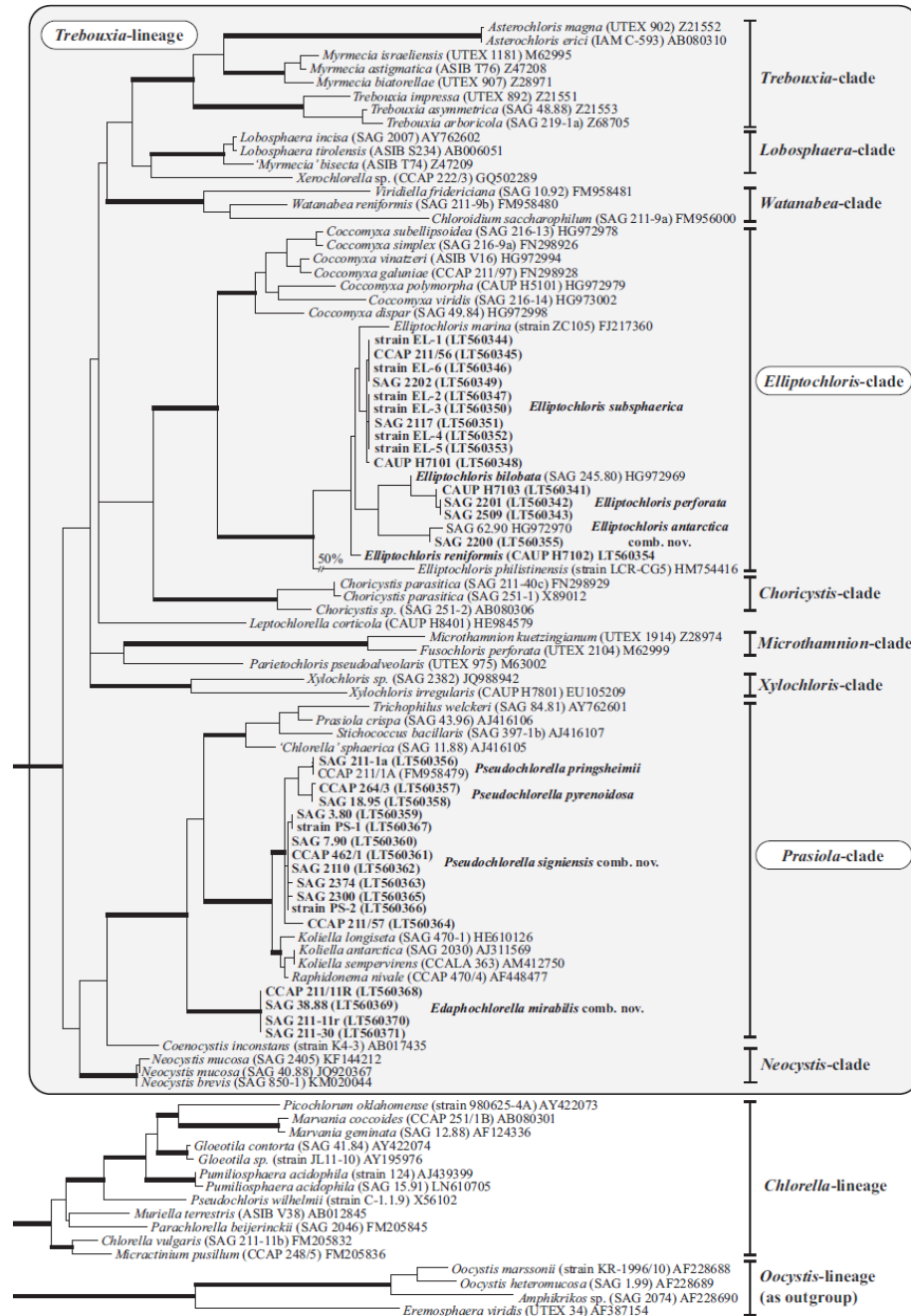
Department of Ecology and Evolutionary Biology, University of Connecticut, Storrs, Connecticut 06269, USA



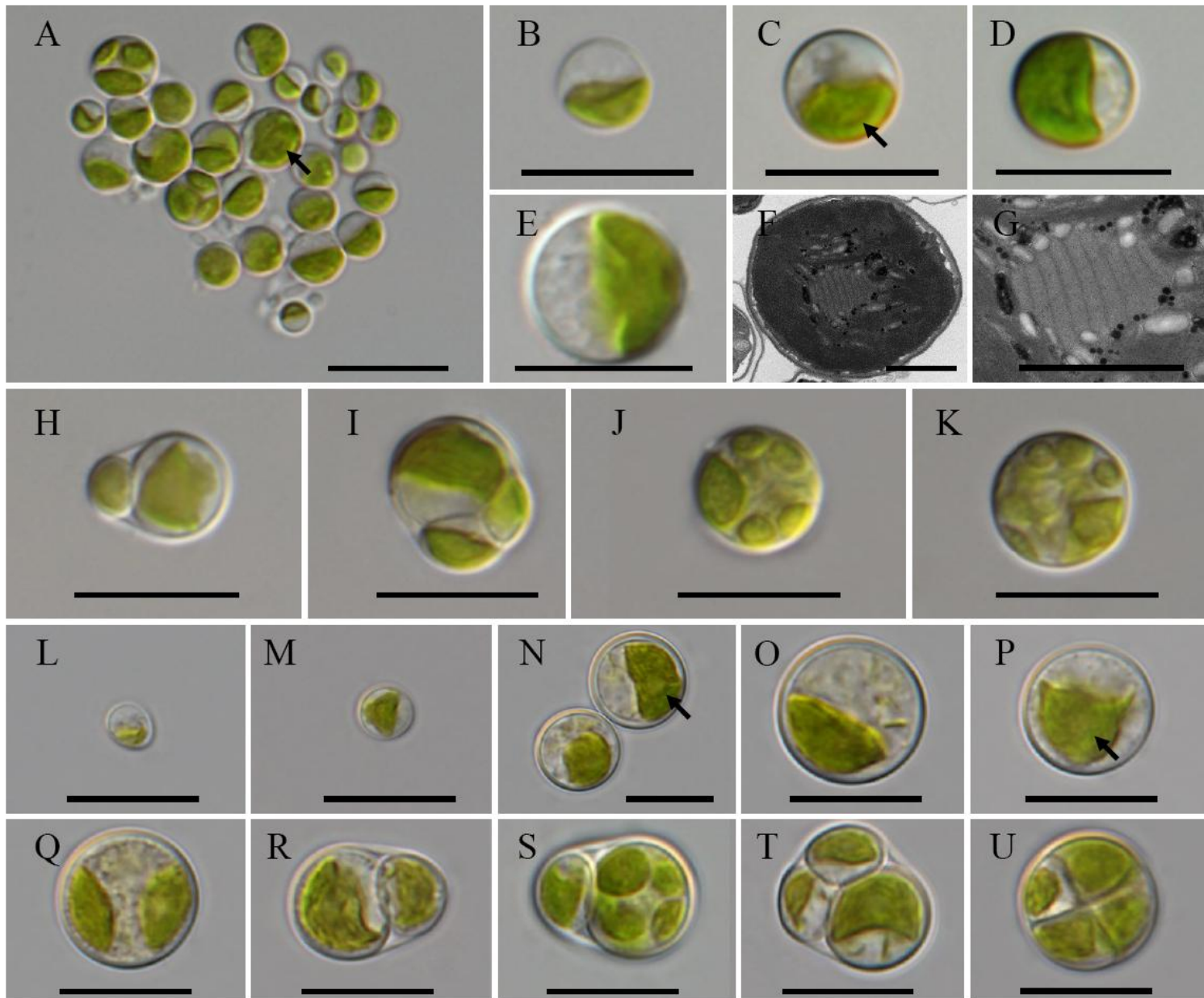
Elliptochloris, Pseudochlorella

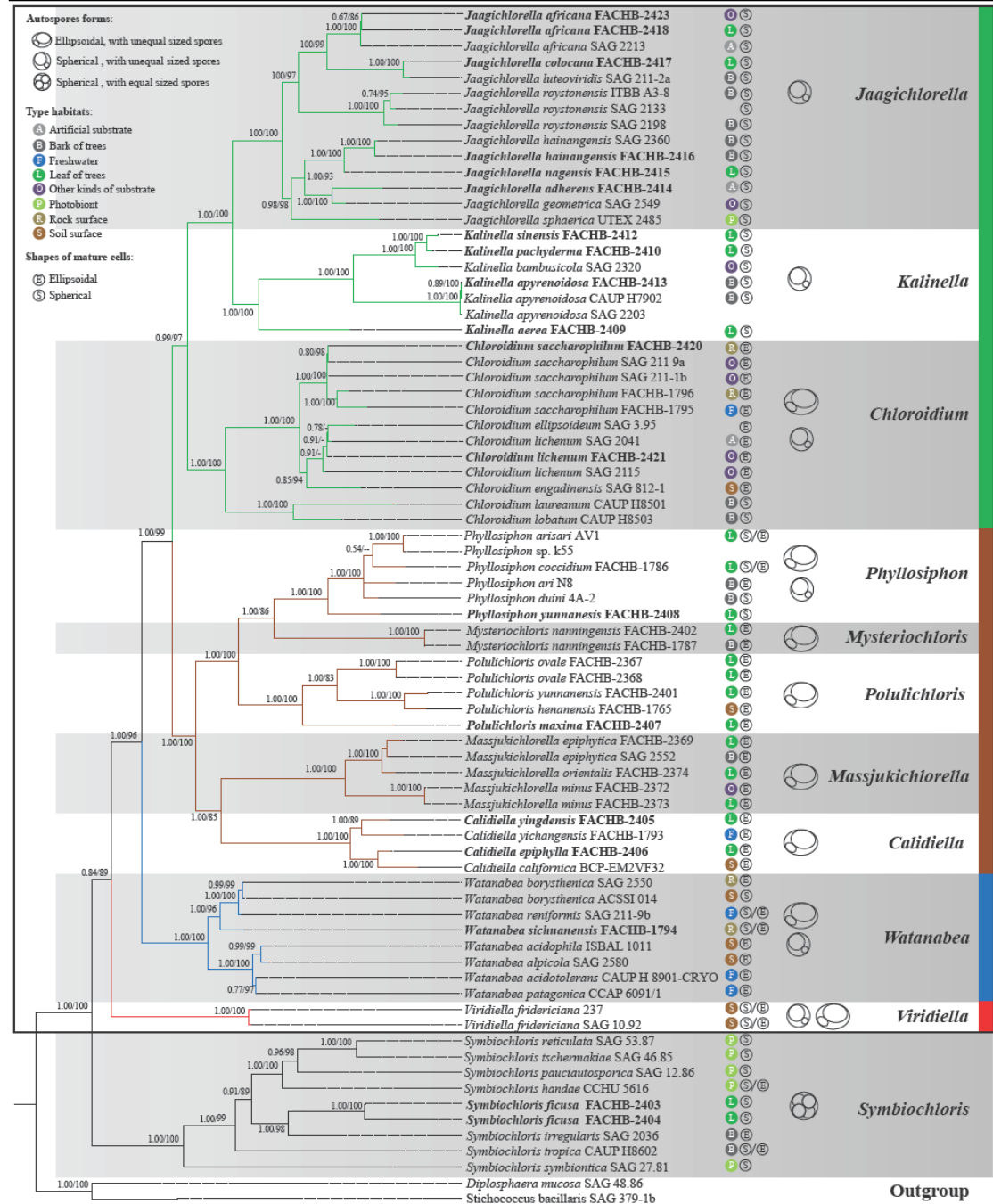


Darienko et al. (2016): J Phycol 52, 1125-1145



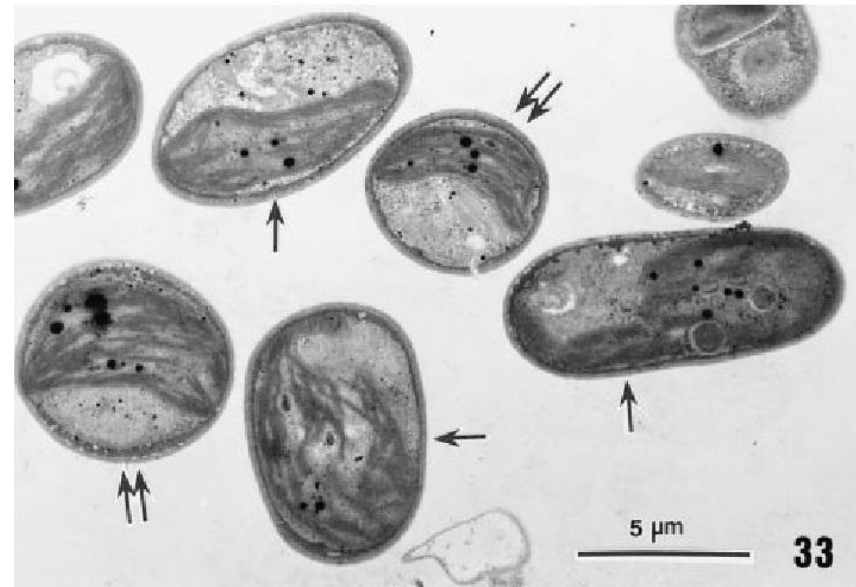
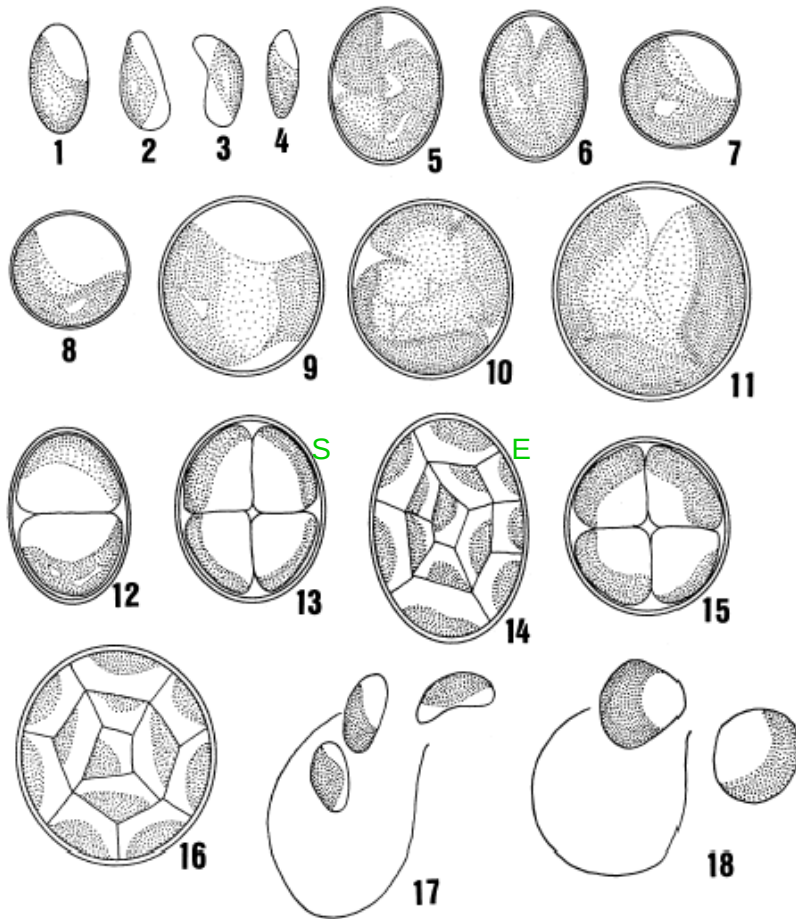
Watanabeales





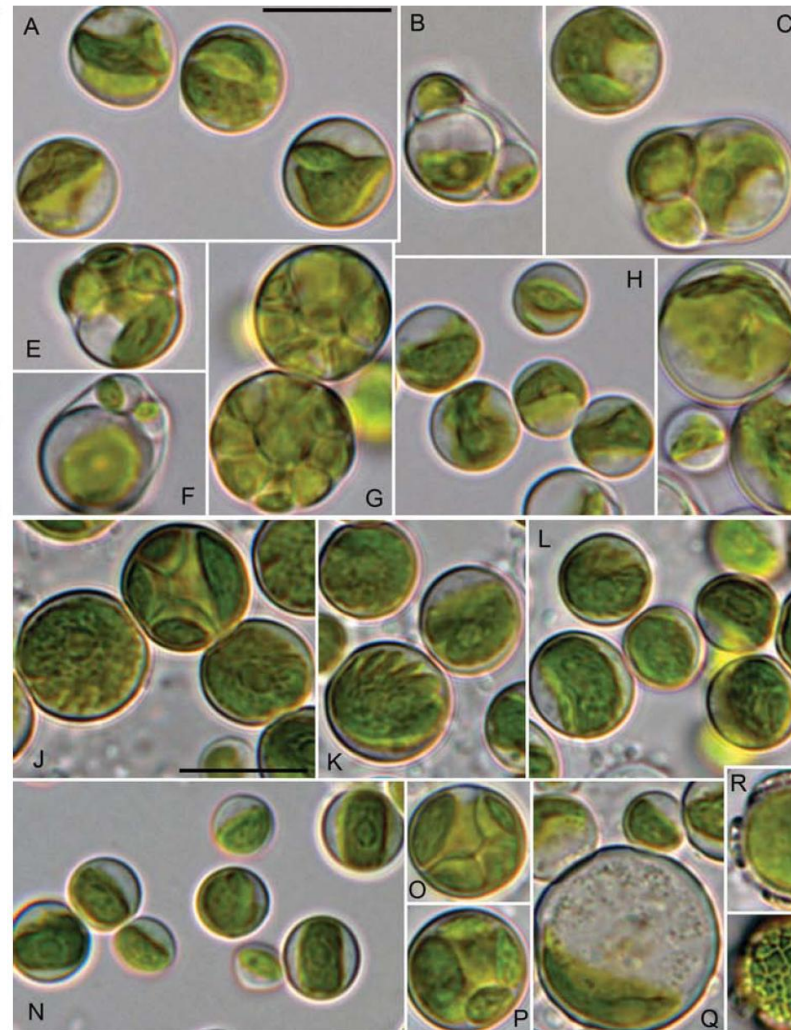
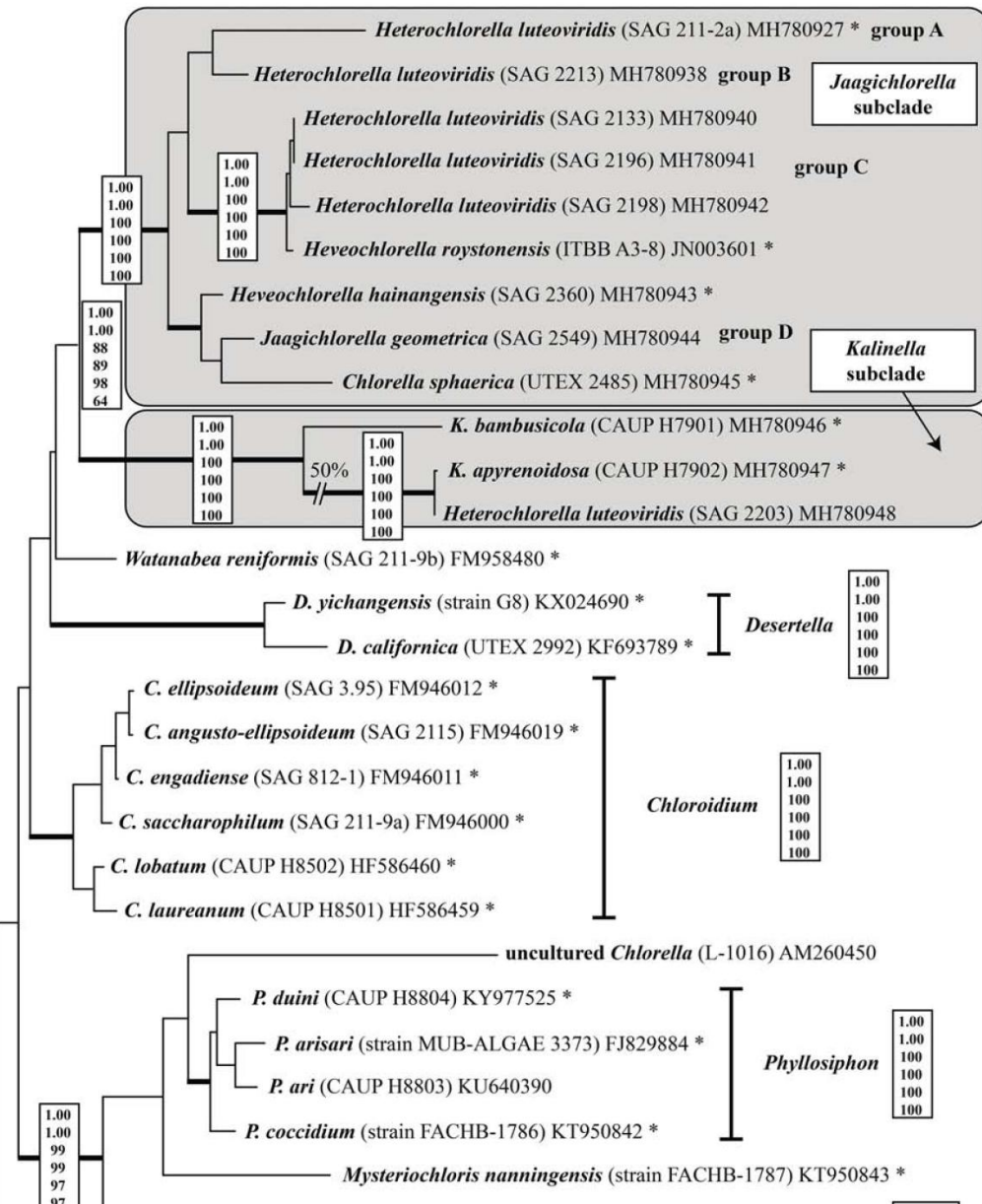
Watanabeales, *Watanabea*

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



- unilayered CW (*Elliptochloris* – trilaminar CW)

Watanabeales, *Jaagichlorella*



Darienko & Pröschold 2019

Watanabeales, *Chloroidium*

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 DARIENKO¹, LYDIA GUSTAVS², OPAYI MUDIMU^{3,5}, CECILIA RAD MENENDEZ⁴, RHENA SCHUMANN², ULF KARSTEN², THOMAS FRIEDL³ AND THOMAS PRÖSCHOLD⁴

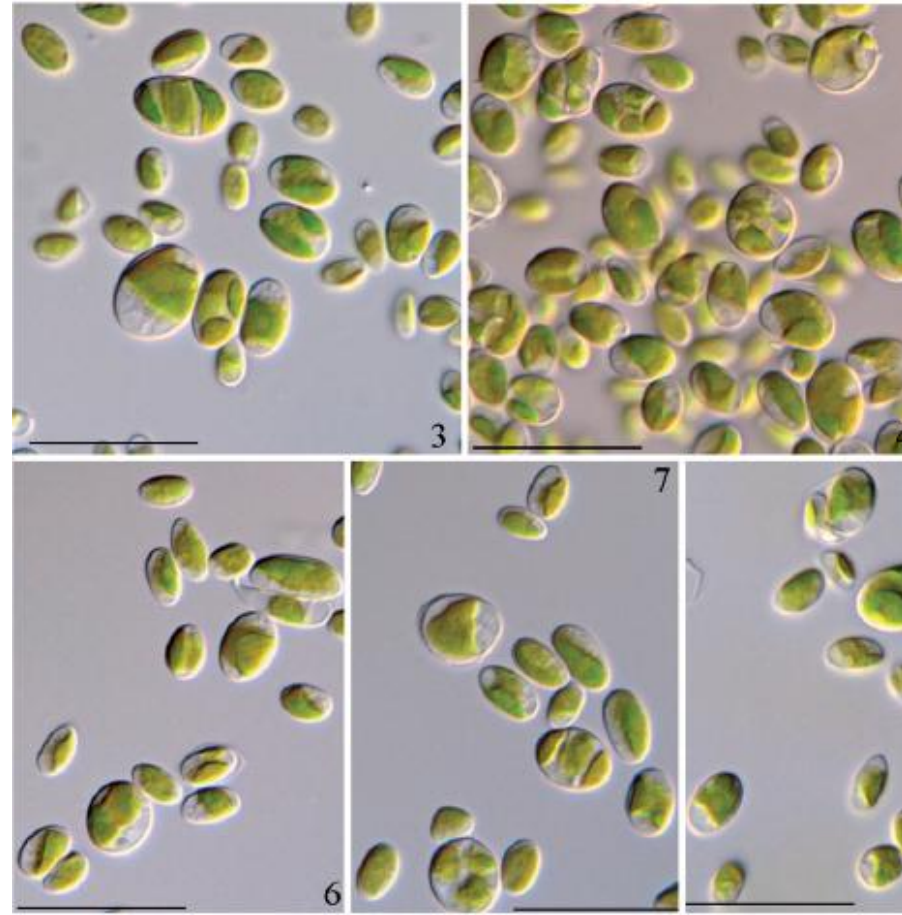
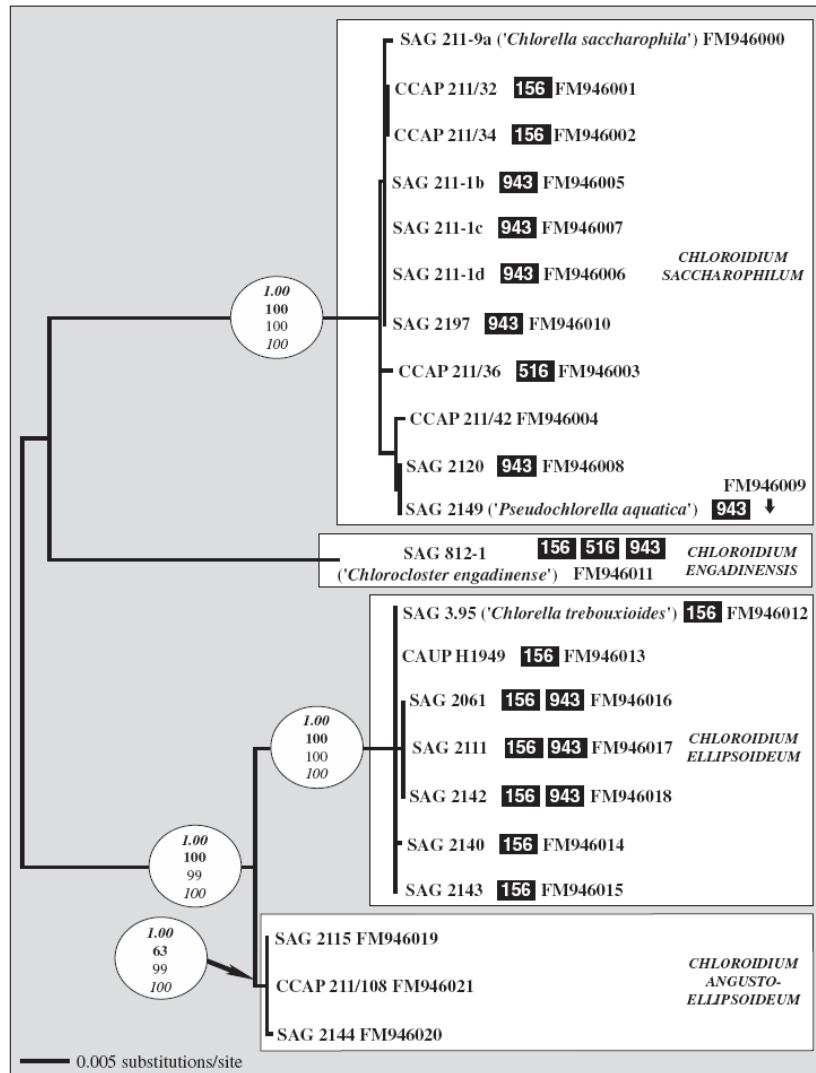
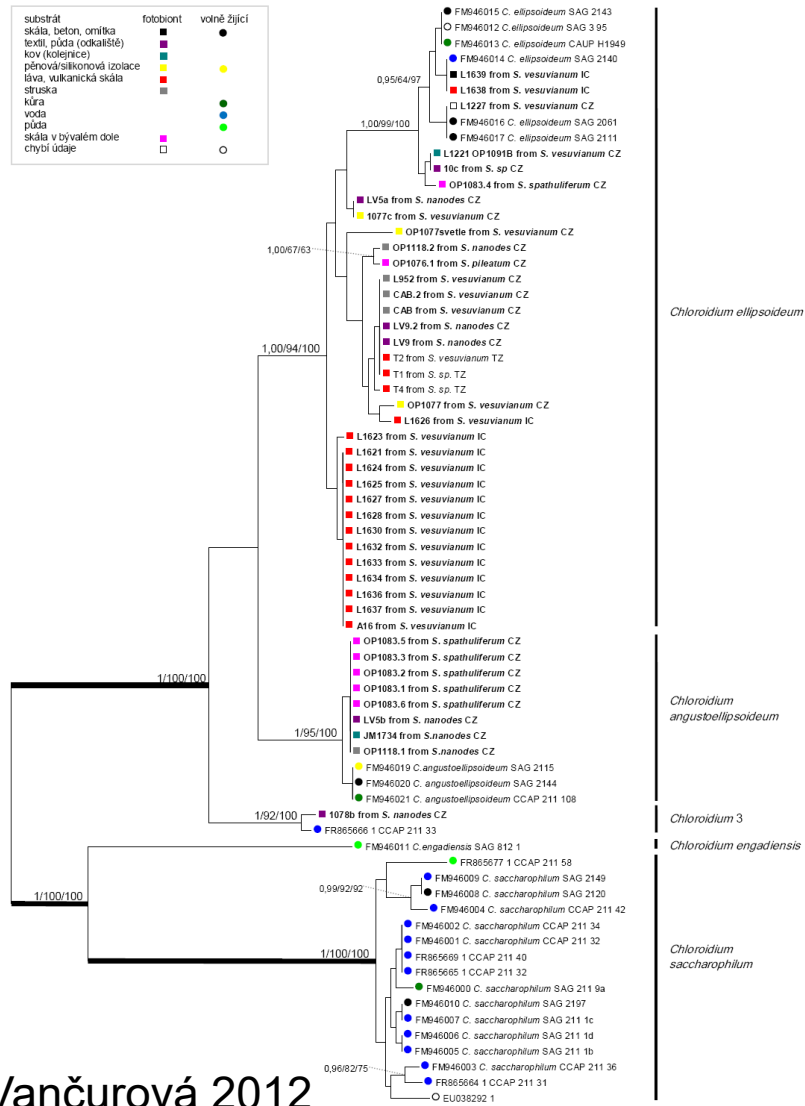


Fig. 2. Molecular phylogeny of *Chloroidium* based on SSU and ITS rDNA sequences, inferred by maximum likelihood (ML) based on a data set of 2500 aligned positions of 22 taxa using PAUP 4.0b10, using GTR model, with proportion of invariable sites $I = 0.86$. Bayesian values (>0.95 ; bold italic) using 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.

Watanabeales, *Chloroidium*



Vančurová 2012

Obrázek 15: Nezakoreněný BI fylogenetický strom založený úseku ITS rDNA. Hodnoty v uzlech vyjadřují statistickou podporu určenou třemi metodami: MrBayes posteriorní pravděpodobnost/maximium likelihood bootstrap/maximium parsimony bootstrap. Zobrazeny jsou pouze hodnoty >0.89 pro BI a >49 pro ML/MP. Popisky sekvencí fotobiotů obsahují označení DNA, druh mykobakteria a geografický původ (CZ – Česká republika, IC – Kanárské ostrovy, TZ – Tanzánie). Popisky sekvencí volně žijících zástupců obsahují číslo sekvence v GenBanku, druh dřel (Darieneko et al., 2010) a číslo sbírkového kmeně.

Watanabeales, *Phyllosiphon*

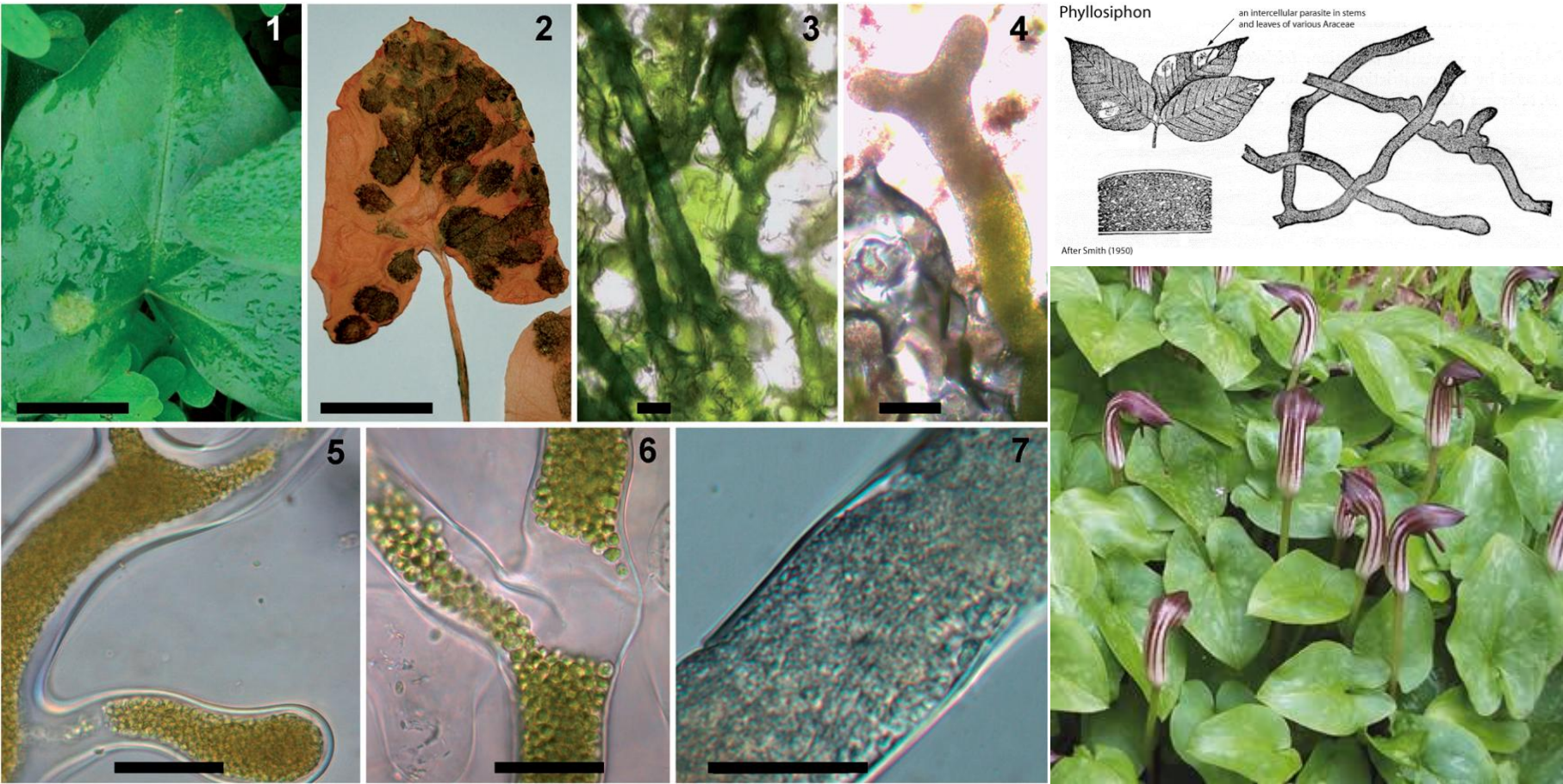
- sifonal parasitic alga
- leaves of *Arisarum*

Eur. J. Phycol. (2011) 46(3): 181–192

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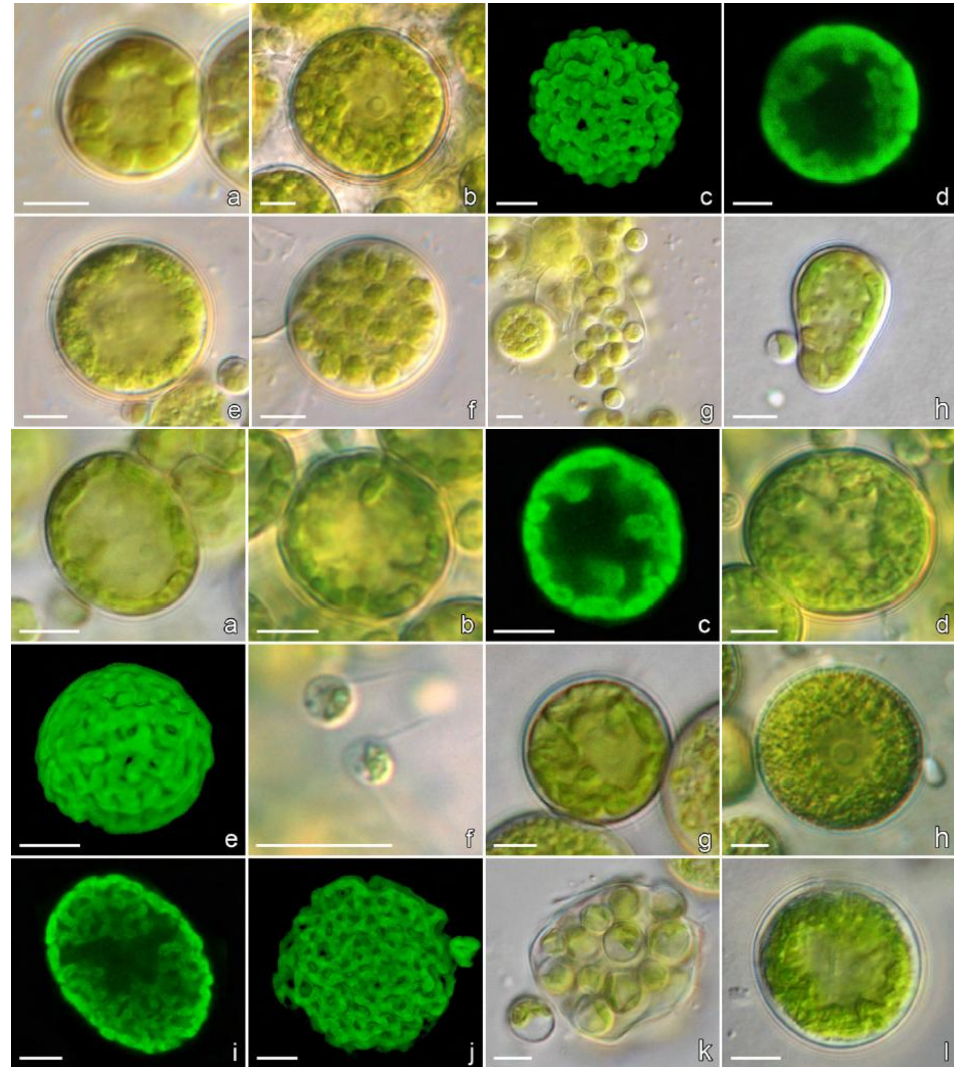
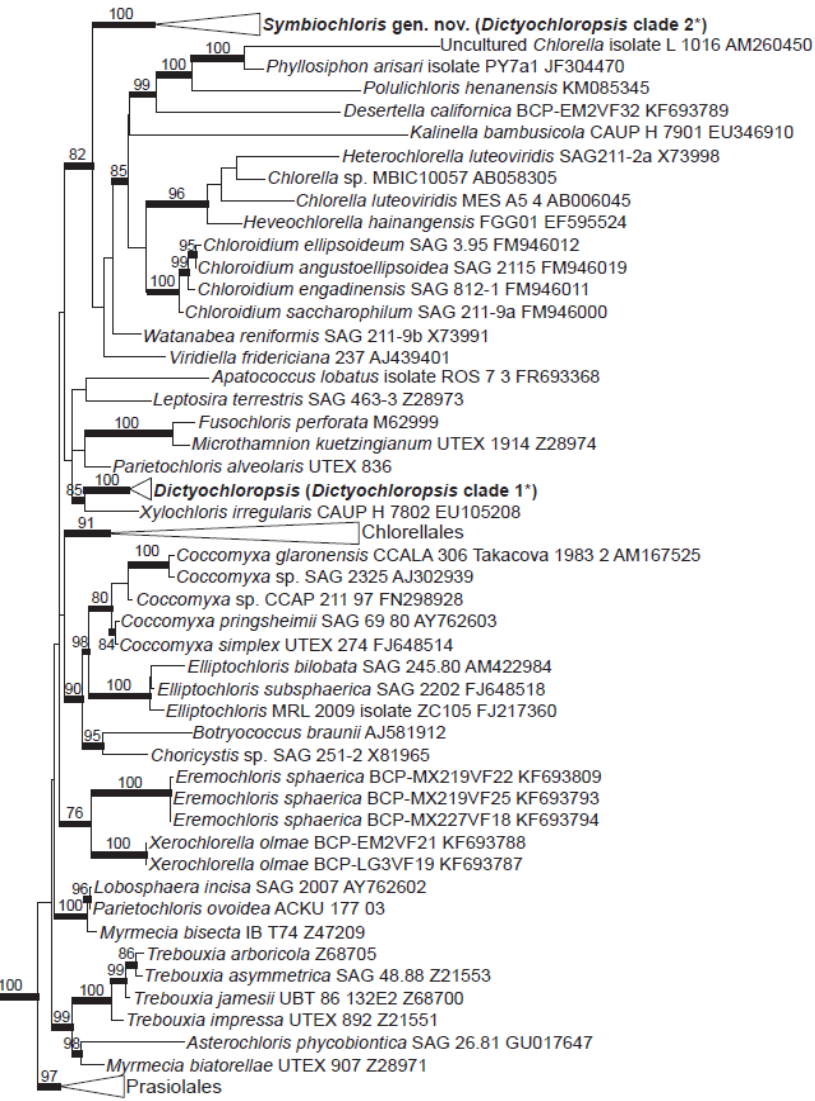
Morphology, fine structure, life cycle and phylogenetic analysis
of *Phyllosiphon arisari*, a siphonous parasitic green alga

MARINA ABOAL¹ AND OLAF WERNER²



Watanabeales, *Symbiochloris*

- aerophytic alga, lichen symbiont



Watanabeales

Zhu et al. BMC Plant Biology (2018) 18:365
https://doi.org/10.1186/s12870-018-1588-7

BMC Plant Biology

RESEARCH ARTICLE

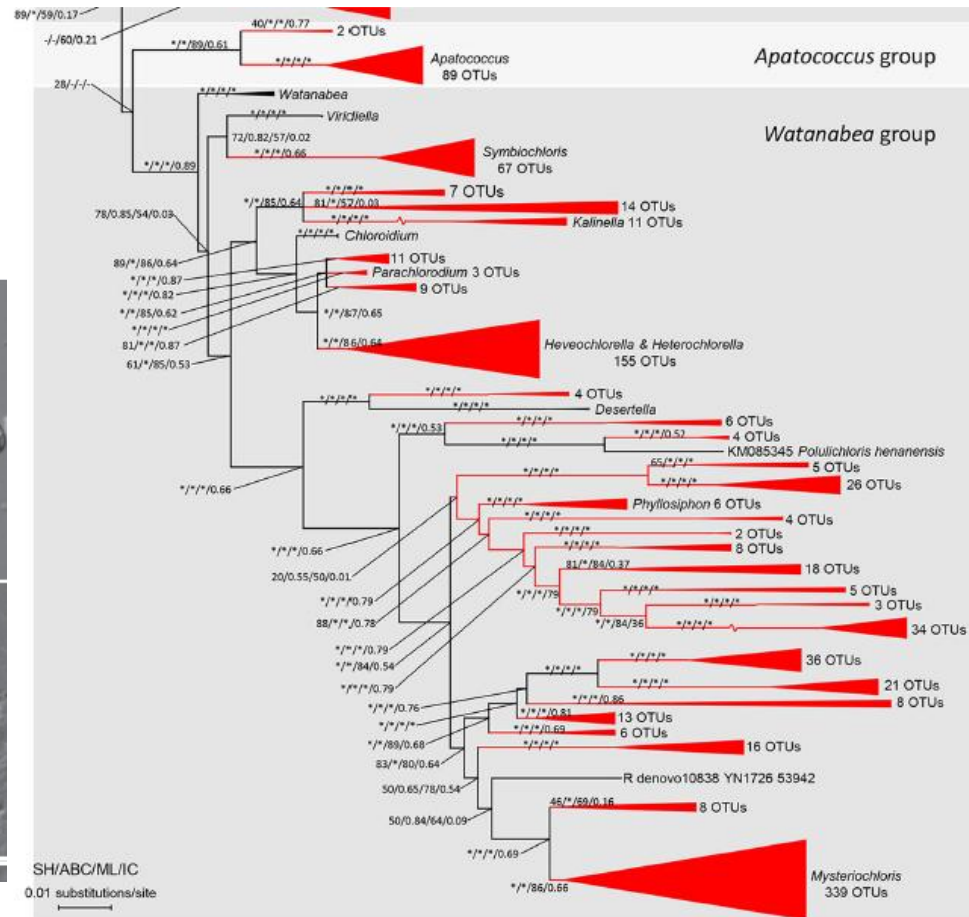
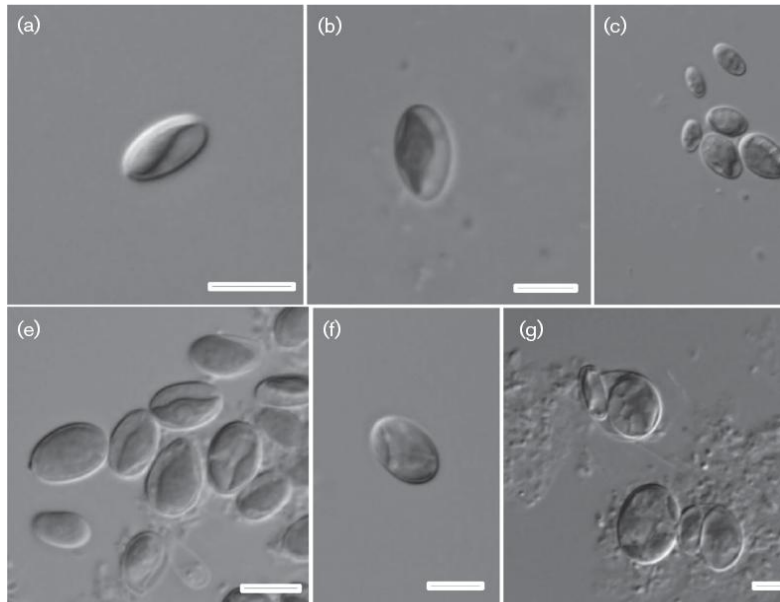
Open Access



Molecular characterization of eukaryotic algal communities in the tropical phyllosphere based on real-time sequencing of the 18S rDNA gene

Huan Zhu¹, Shuyin Li¹, Zhengyu Hu² and Guoxiang Liu^{1*}

- a number of novel lineages
- Mysteriochloris* as the most abundant lineage



Apatococcus



Apatococcus

- building facades, painted iron substrates

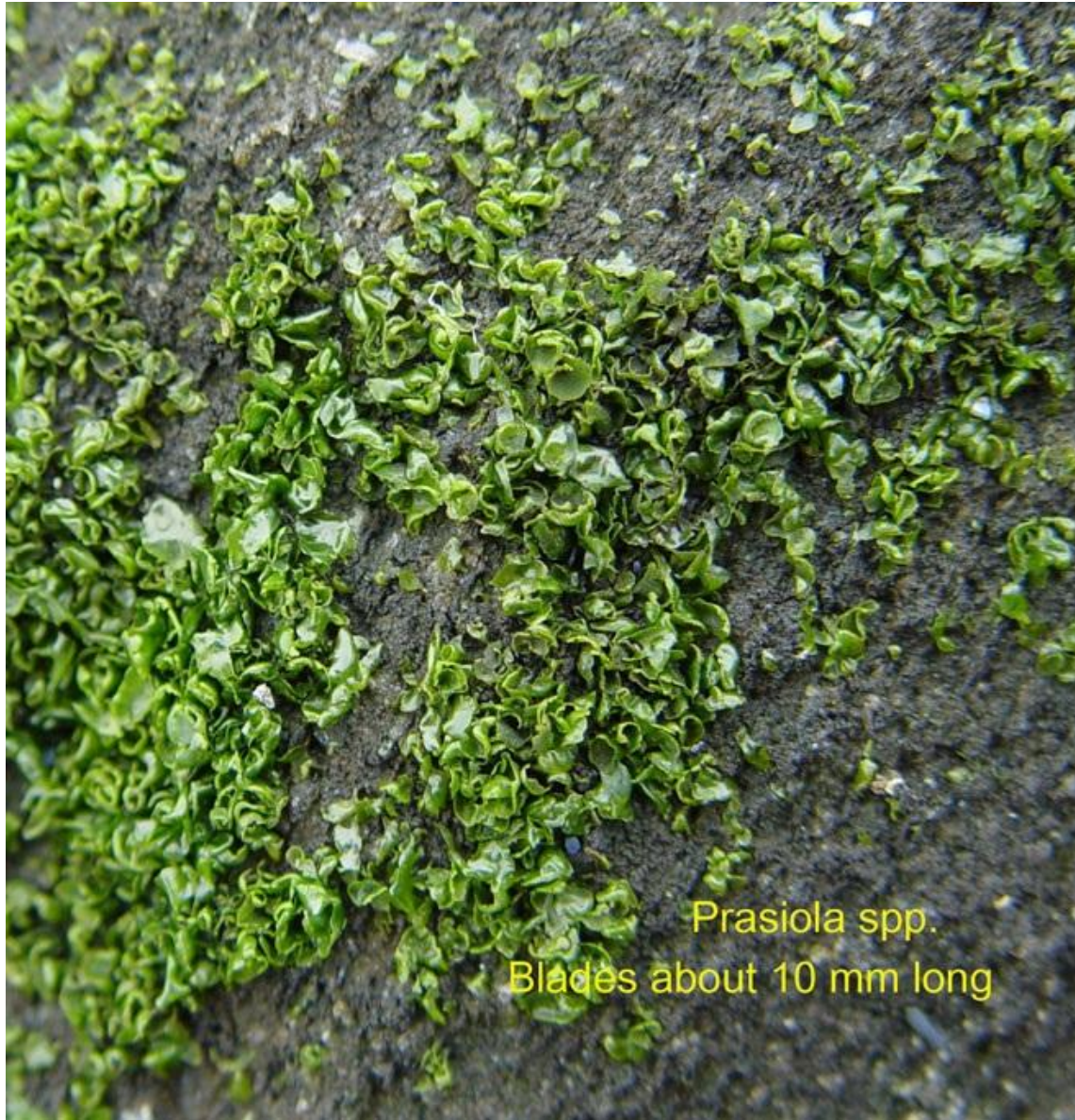


Microthamniales, *Microthamnion*

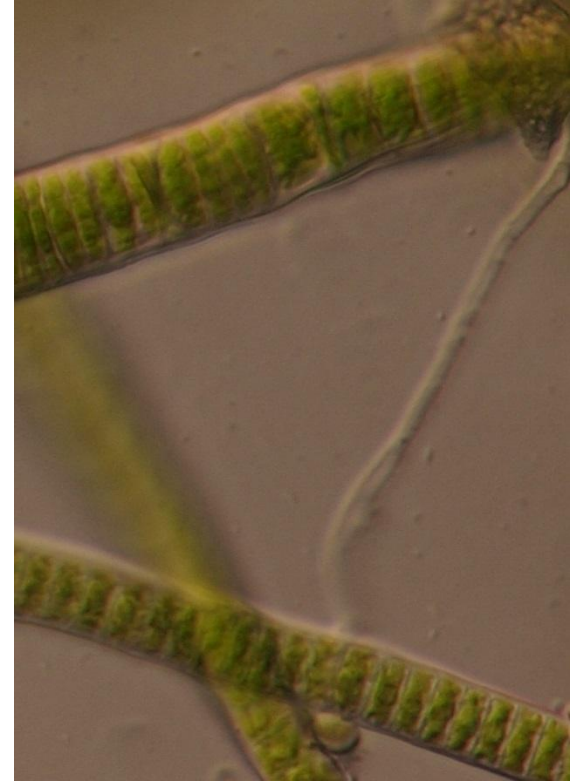


M. kuetzingianum

Prasiolales, *Prasiola*

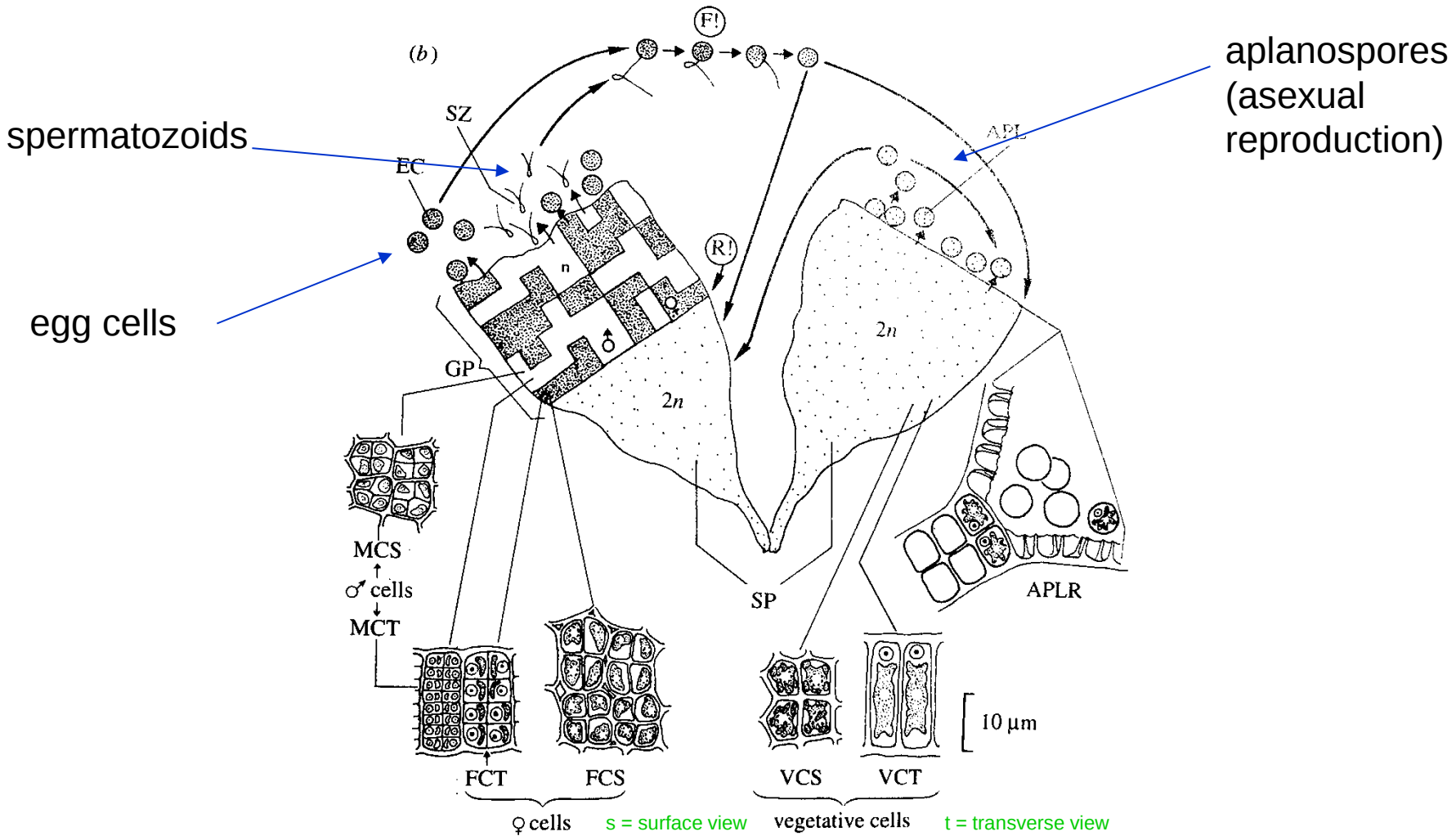


Prasiola spp.
Blades about 10 mm long



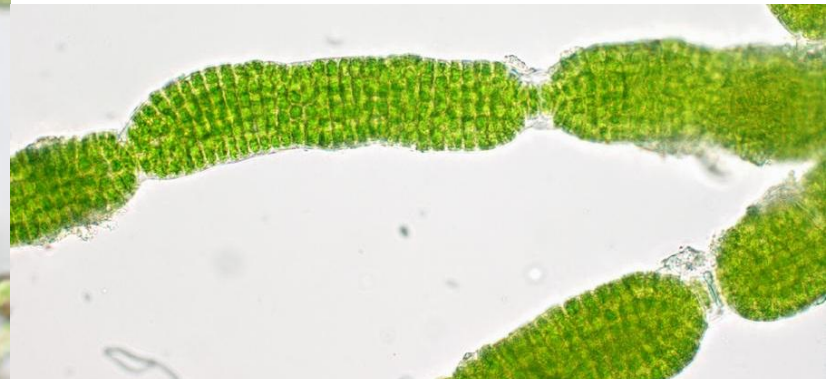
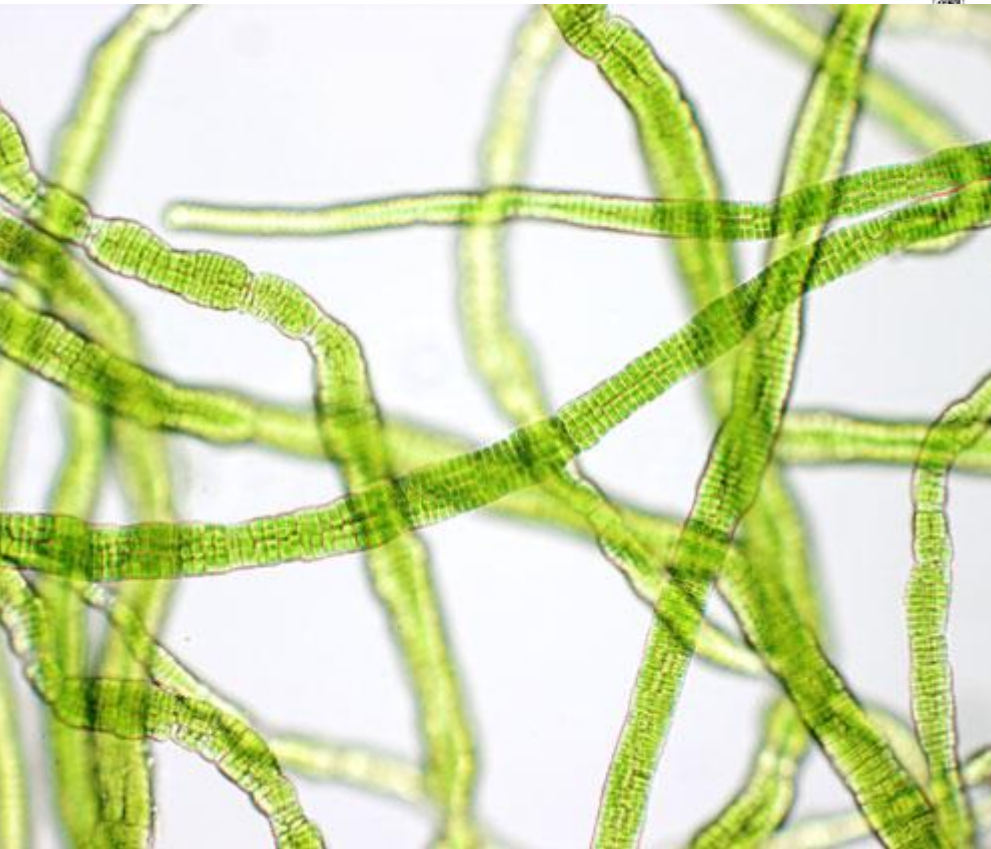
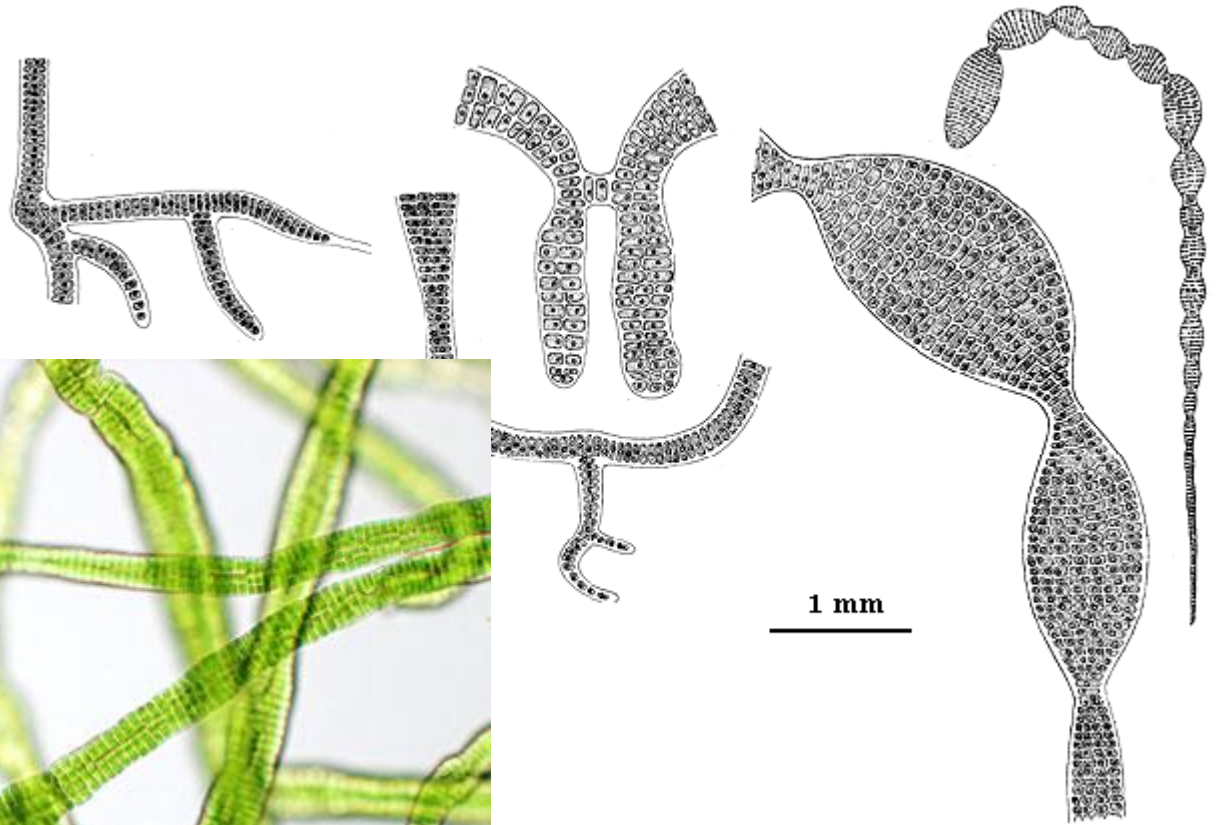
Prasiolales, *Prasiola*

- mosaic sexual reproduction



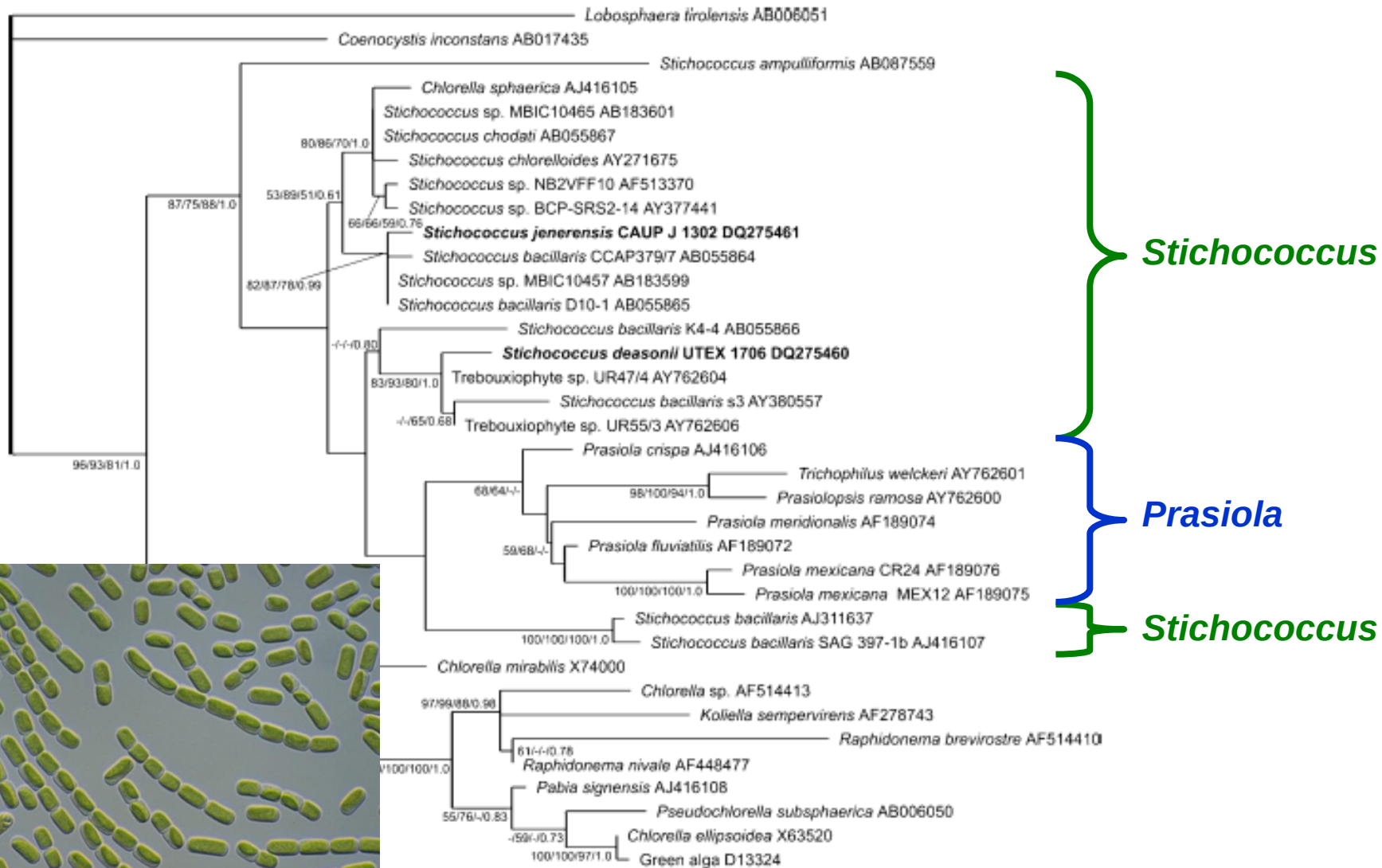
Prasiolales, *Rosenvingiella*

haploid thallus,
zygotic meiosis

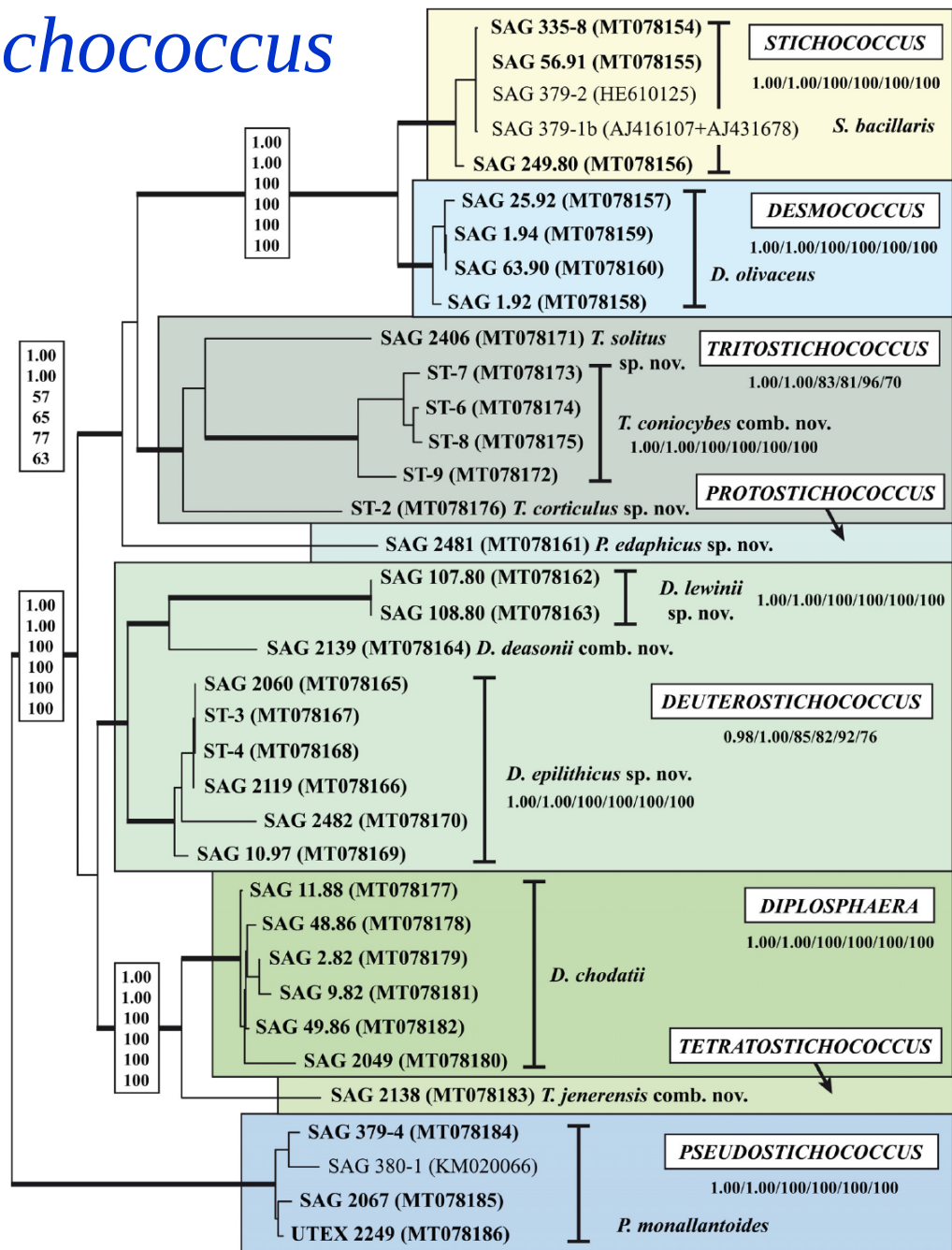
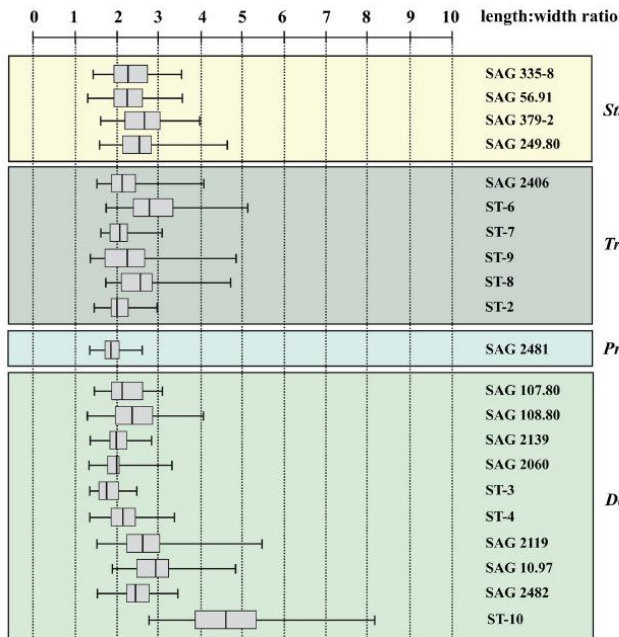
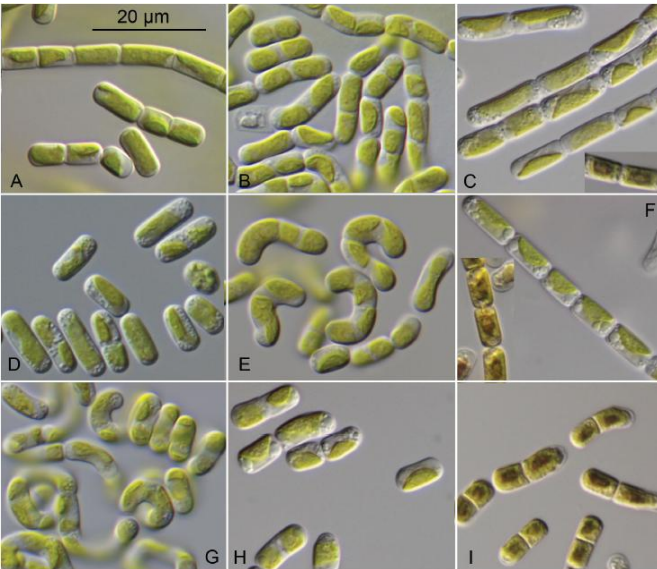


Prasiolales, *Stichococcus*

- Prasiola* – crown group in *Stichococcus* lineage



Prasiolales, *Stichococcus*



Prasiolales, *Diplosphaera*

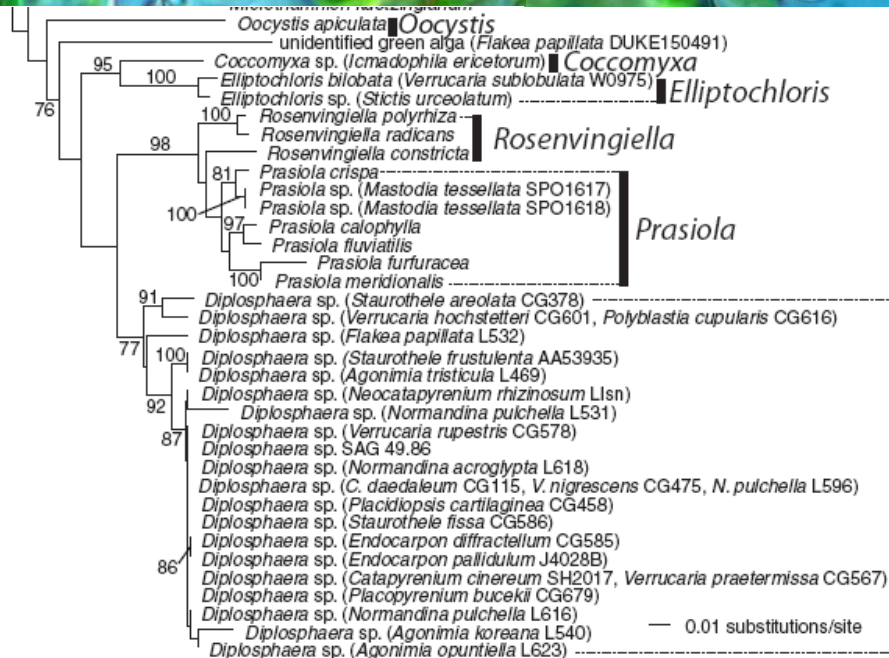
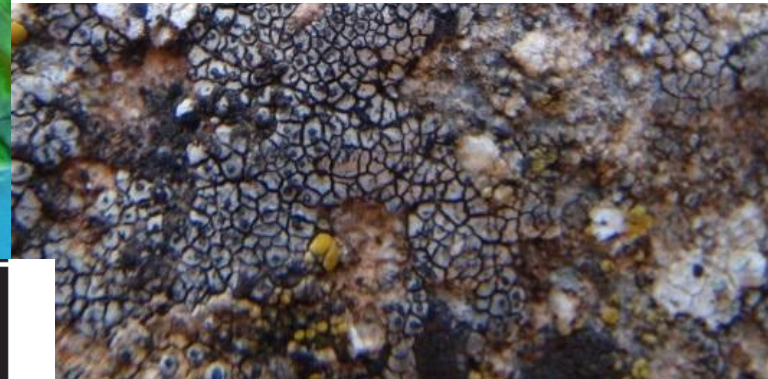
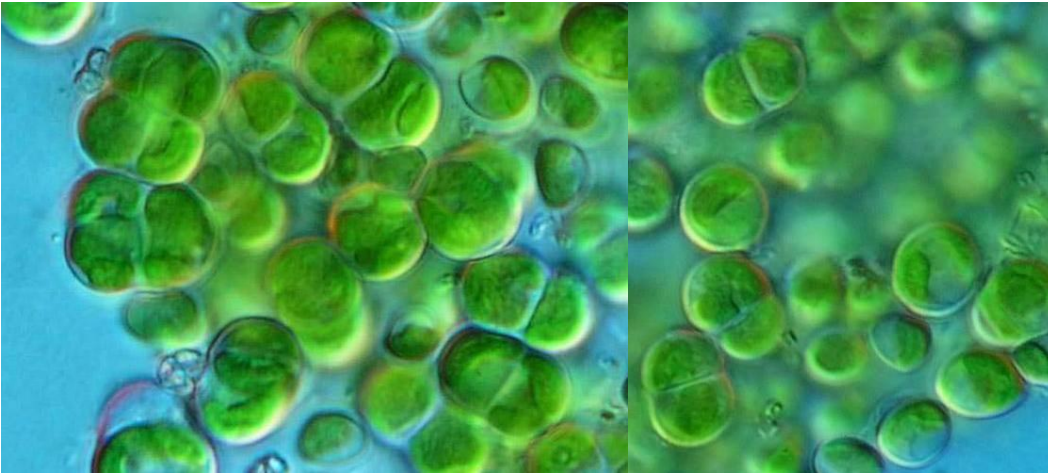
- free living, lichen photobiont

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



Revisiting photobiont diversity in the lichen family Verrucariaceae (Ascomycota)

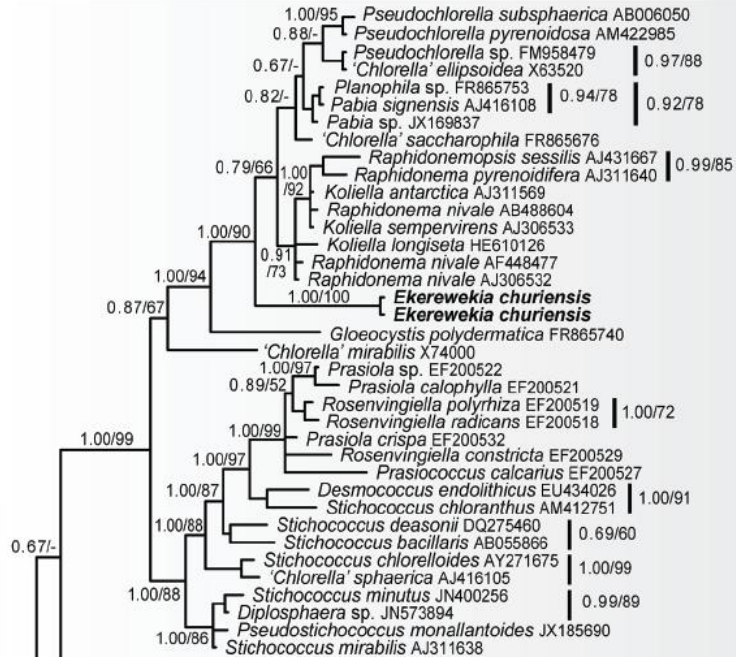
HOLGER THÜS¹, LUCIA MUGLIA², SERGIO PÉREZ-ORTEGA³, SERGIO E. FAVERO-LONGO⁴, SUZANNE JONES⁵, HEATH O'BRIEN⁶, MATTHEW P. NELSEN^{7,8}, RHINAIXA DUQUE-THÜS¹, MARTIN GRUBE², THOMAS FRIEDL⁹, JULIET BRODIE¹, CARRIE J. ANDREW^{2,10}, ROBERT LÜCKING⁷, FRANÇOIS LUTZONI¹¹ AND CÉCILE GUEIDAN¹



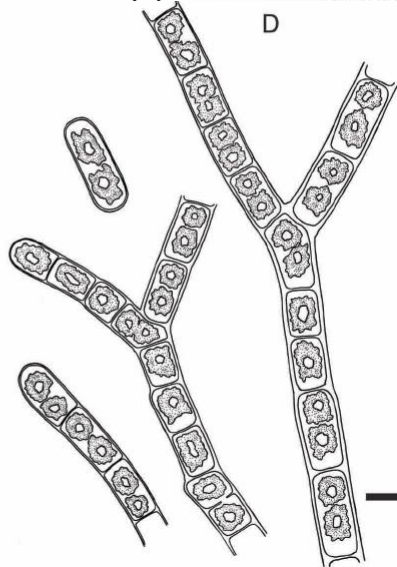
Diplosphaera

Prasiola-group

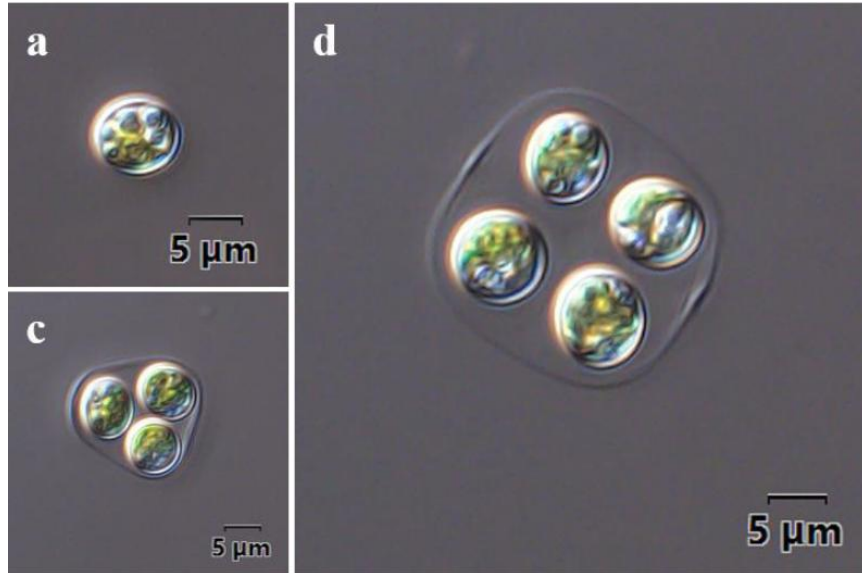
Prasiolales, *Ekerewekia*



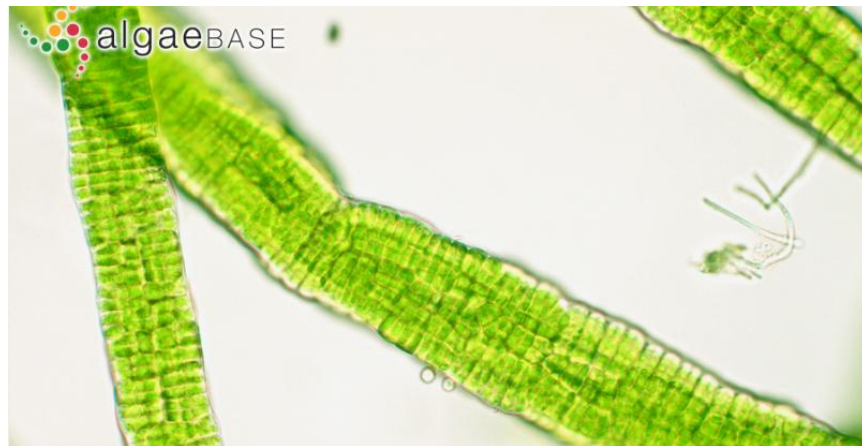
Prasiola clade



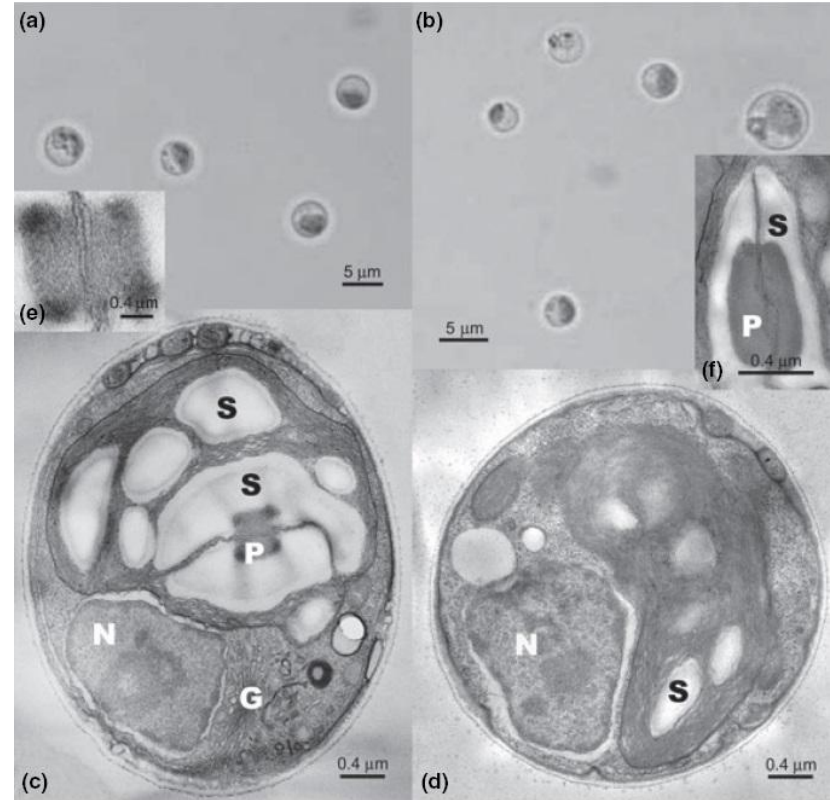
Marine Trebouxiophyceae



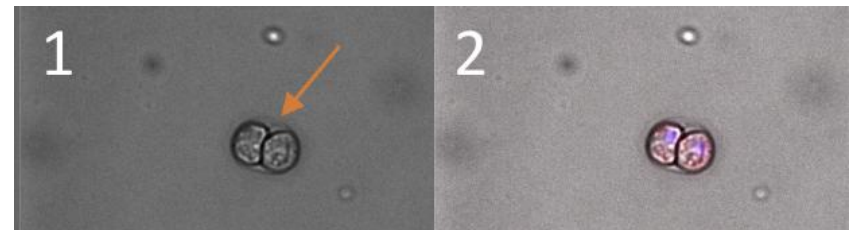
Euchlorocystis marina (2022)



Rosenvingiella



Marinichlorella kaistiae (2017)



Nannochloris desiccata (2022)

C

Marine Trebouxioophyceae

environmental
microbiology

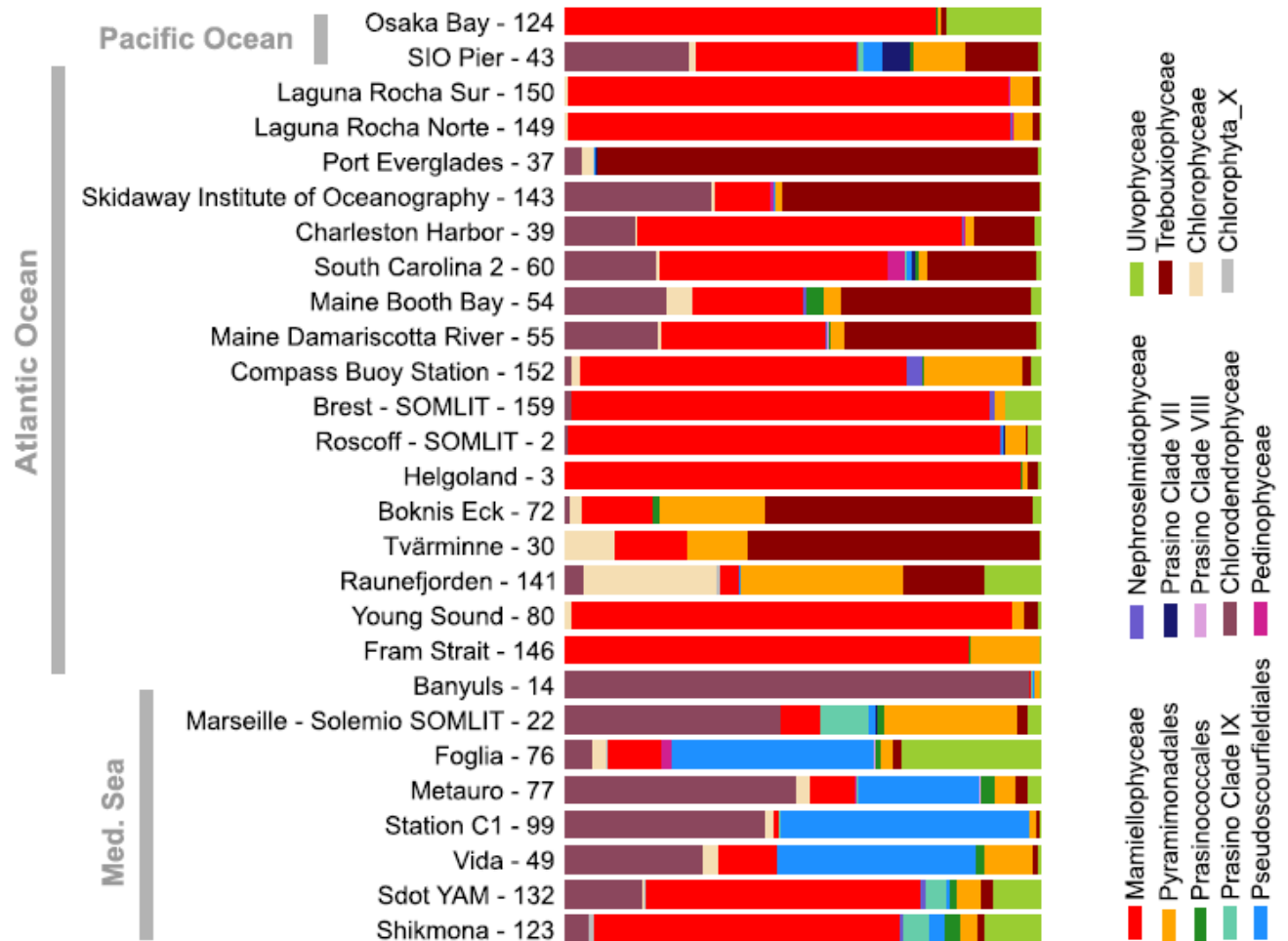
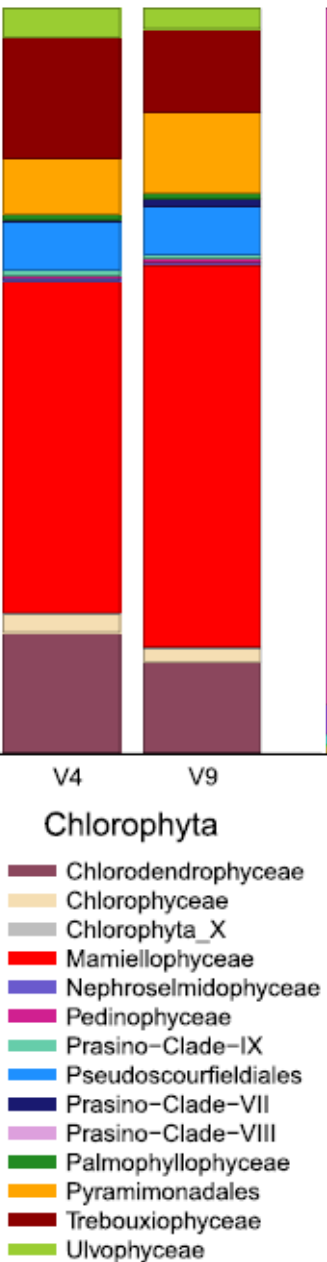


Environmental Microbiology (2018) 20(2), 506–520

doi:10.1111/1462-2920.13952

Comparison of coastal phytoplankton composition estimated from the V4 and V9 regions of the 18S rRNA gene with a focus on photosynthetic groups and especially Chlorophyta

Margot Tragin,¹ Adriana Zingone² and Daniel Vault^{1*}



Marine Trebouxiophyceae

environmental
microbiology

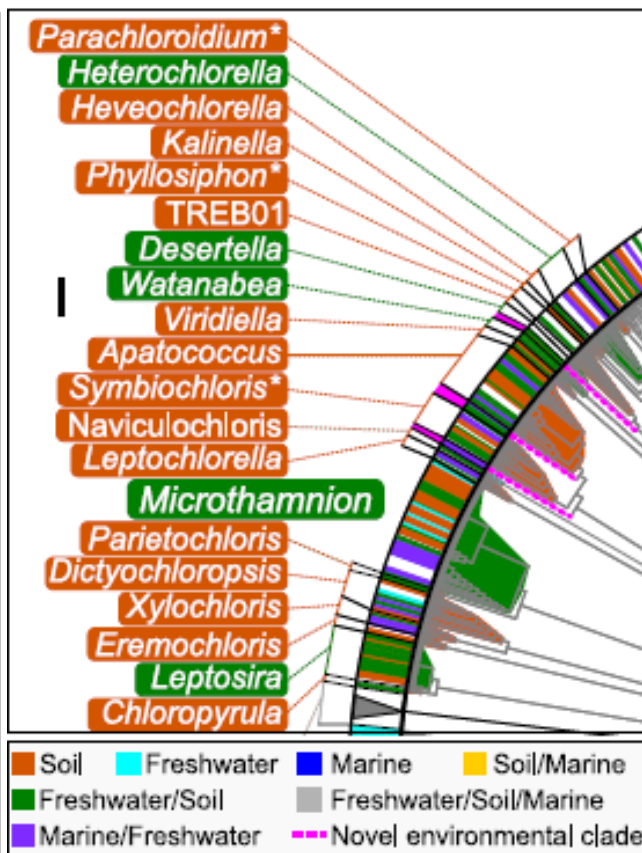
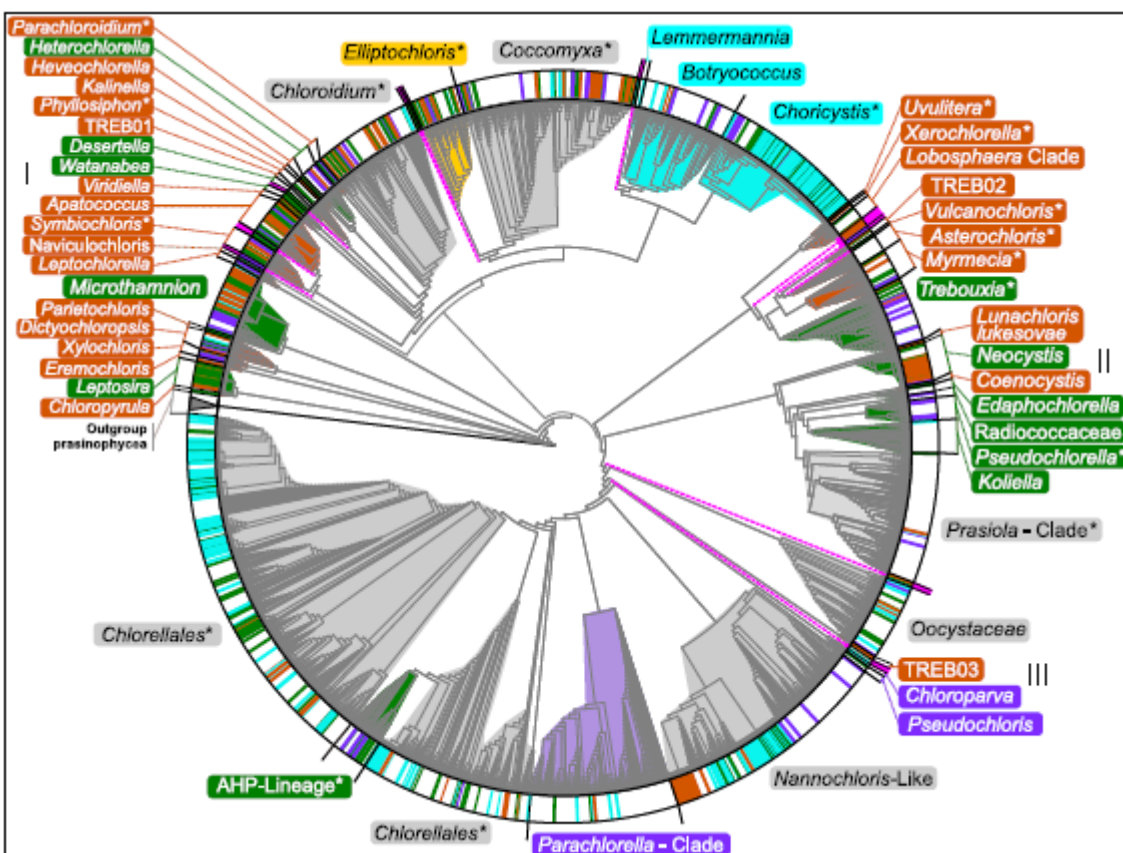


Environmental Microbiology (2019) 21(10), 3885–3895

doi:10.1111/1462-2920.14738

Global distribution of Trebouxiophyceae diversity explored by high-throughput sequencing and phylogenetic approaches

Sebastian Metz ¹, David Singer ^{2,3},
Isabelle Domaizon ⁴, Fernando Unrein ¹ and
Enrique Lara ^{1,5*}



Soil Freshwater Marine Soil/Marine
Freshwater/Soil Freshwater/Soil/Marine
Marine/Freshwater Novel environmental clade

Monophyly of Trebouxioophyceae



New phylogenetic hypotheses for the core Chlorophyta based on chloroplast sequence data

Karolina Fučíková¹, Frederik Leliaert^{2,3}, Endymion D. Cooper⁴, Pavel Škaloud⁵, Sofie D'Hondt², Olivier De Clerck², Carlos F. D. Gurgel⁶, Louise A. Lewis¹, Paul O. Lewis¹, Juan M. Lopez-Bautista³, Charles F. Delwiche⁴ and Heroen Verbruggen^{7*}

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² Phycology Research Group, Biology Department, Ghent University, Ghent, Belgium

³ Department of Biological Sciences, The University of Alabama, Tuscaloosa, AL, USA

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⁵ Department of Botany, Faculty of Science, Charles University in Prague, Prague, Czech Republic

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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, Trebouxioophyceae, 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 Trebouxioophyceae and Ulvophyceae are likely not monophyletic as currently defined. Our results also support relationships among several trebouxioophycean 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 Trebouxioophyceae, 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

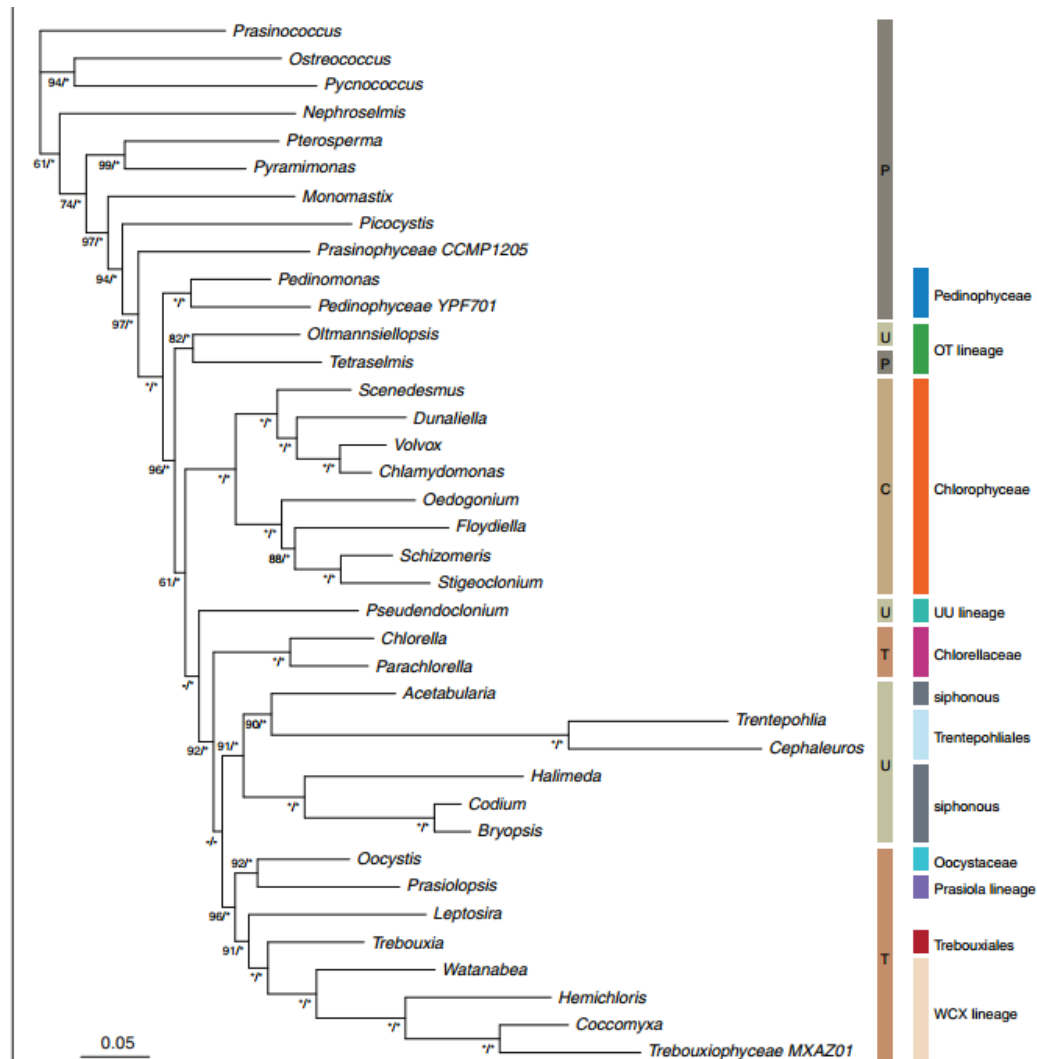


FIGURE 3 | Maximum likelihood phylogeny inferred from the genome-scale alignment (80% slowest sites). Bootstrap percentages and Bayesian posterior probabilities (MrBayes) are indicated along branches. The classical classification into Prasinophyceae (P), Chlorophyceae (C),

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 *.



Neoproterozoic origin and multiple transitions to macroscopic growth in green seaweeds

Andrea Del Cortona^{a,b,c,d,1}, Christopher J. Jackson^e, François Buchini^{b,c}, Michiel Van Bel^{b,c}, Sofie D'hondt^a, Pavel Škaloud^f, Charles F. Delwiche^g, Andrew H. Knoll^h, John A. Raven^{i,j,k}, Heroen Verbruggen^e, Klaas Vandepoel^{b,c,d,1,2}, Olivier De Clerck^{h,1,2}, and Frederik Leliaert^{a,i,1,2}

