

Species delimitation in protists

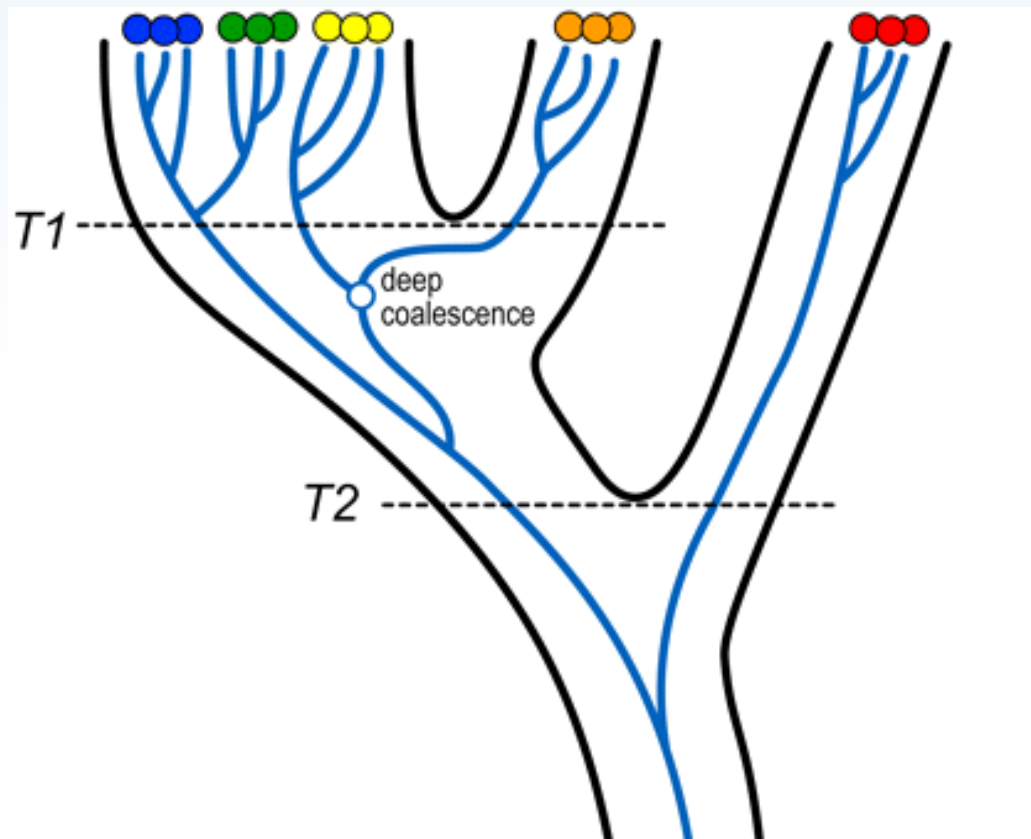


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Species delimitation

- Importance of taxa delimitation
- Species concepts in protists
- Species delimitation in *Asterochloris*



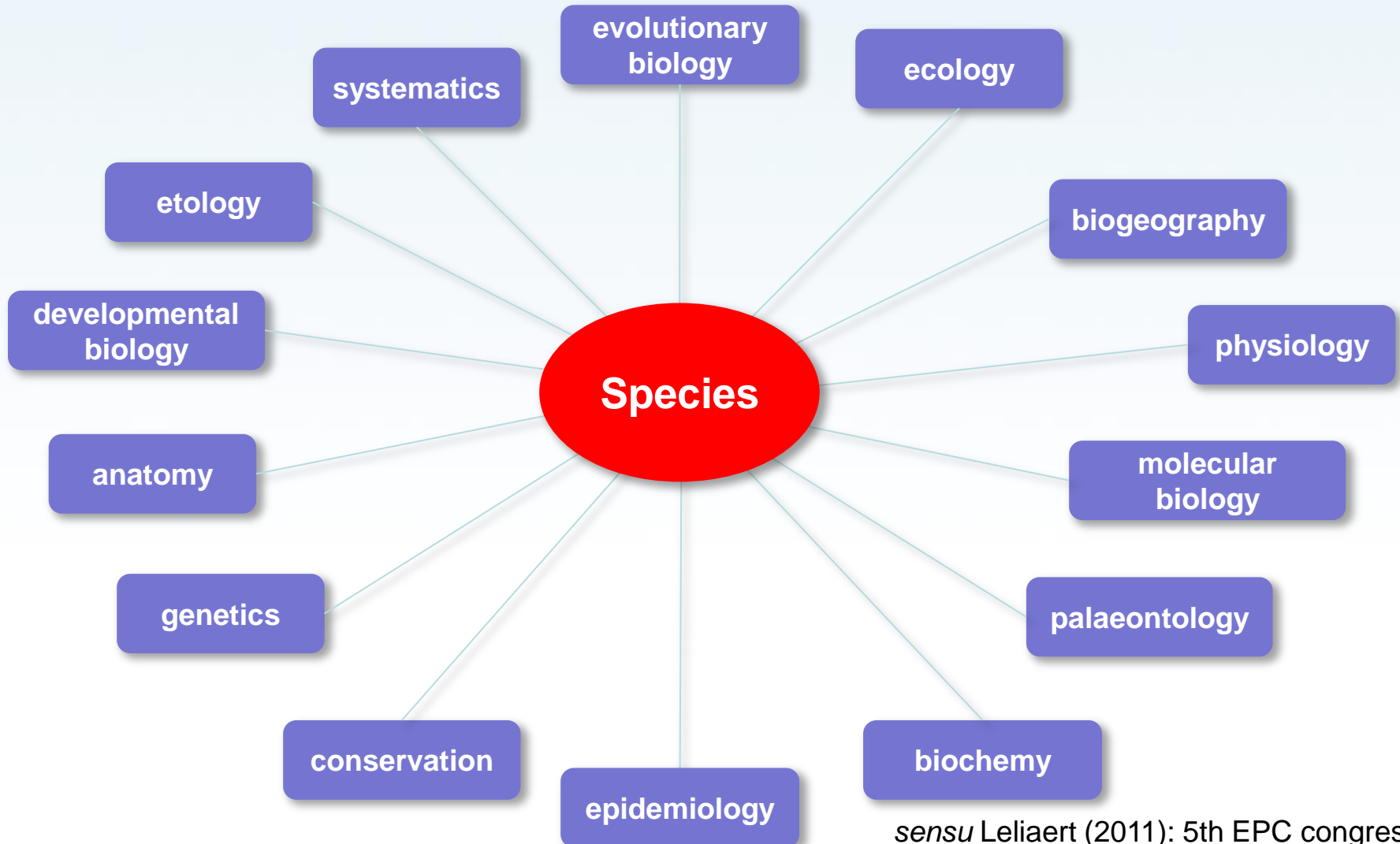
Species

- Fundamental units of the systematics
 - Organisation of biodiversity to the well arranged system



Species

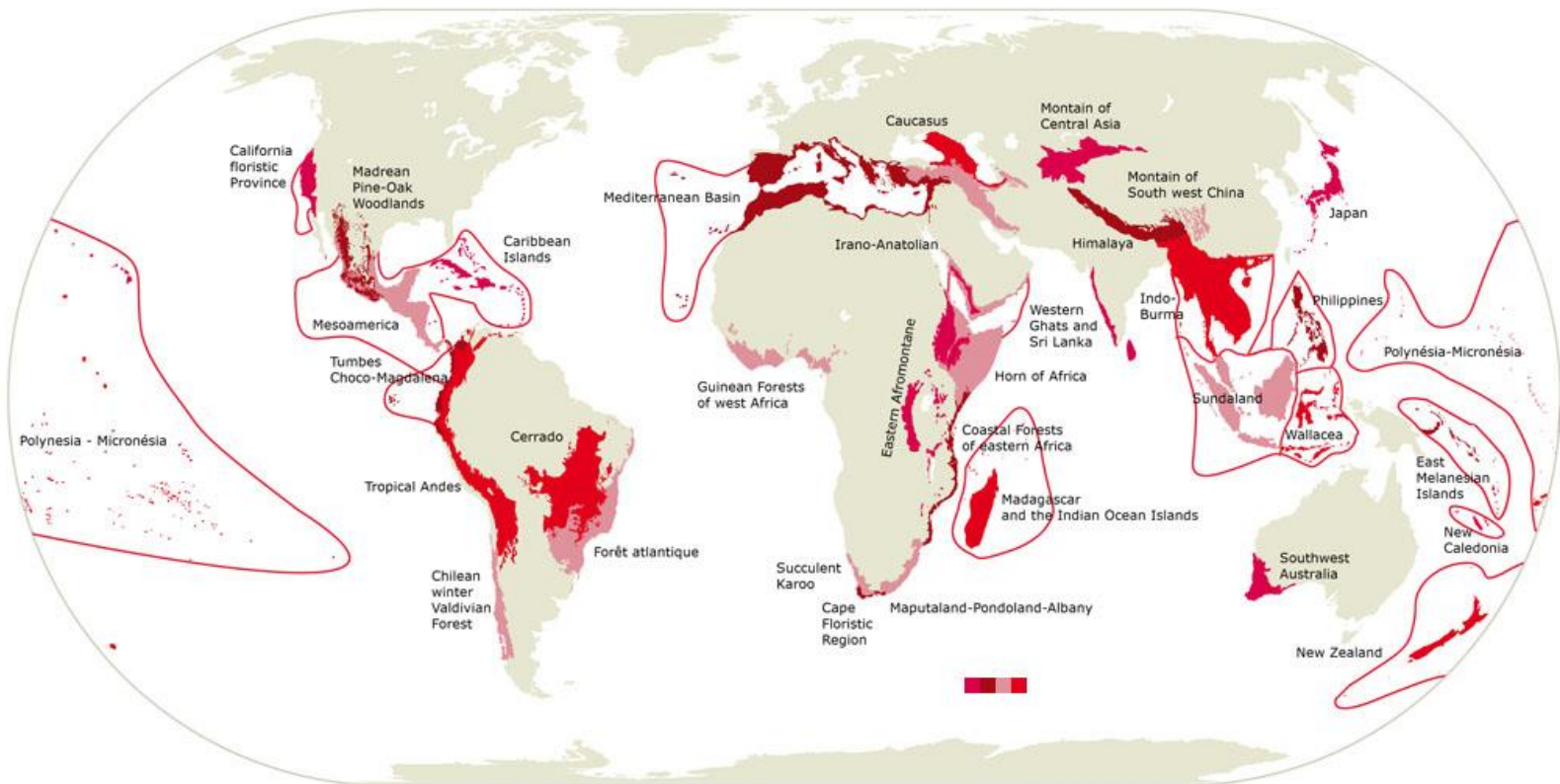
- Fundamental units in all biological disciplines
- It is of a great importance to delimit the species correctly



Species delimitation consequences

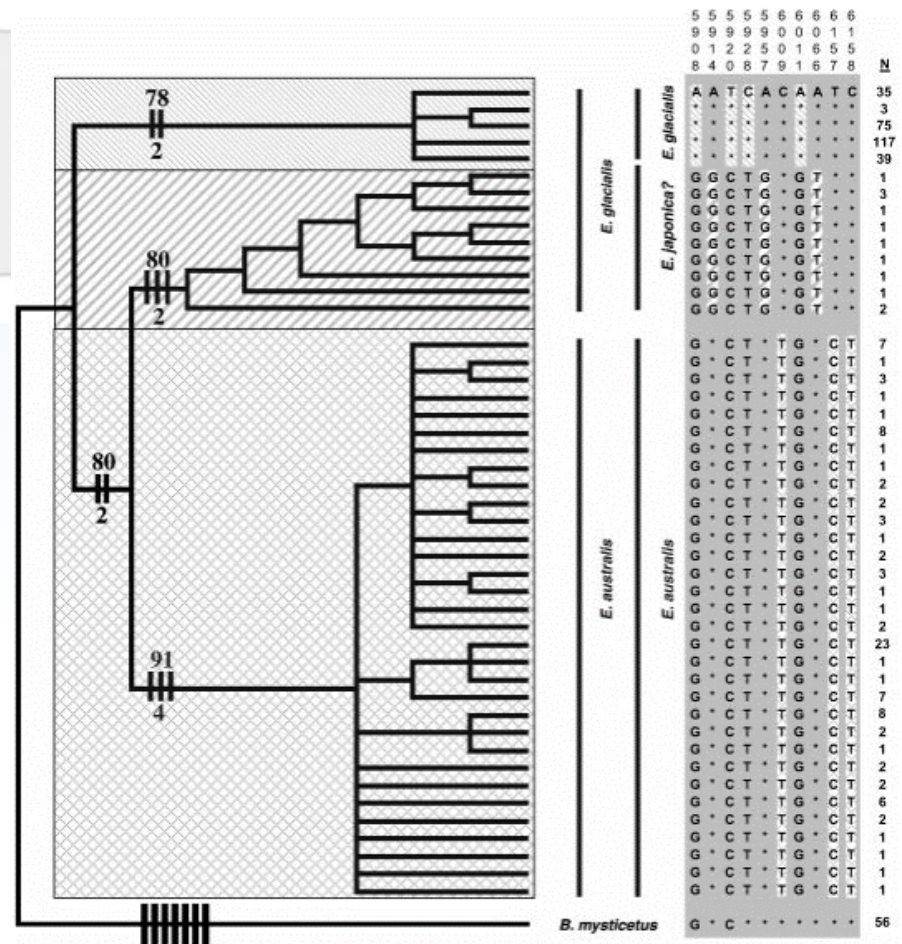
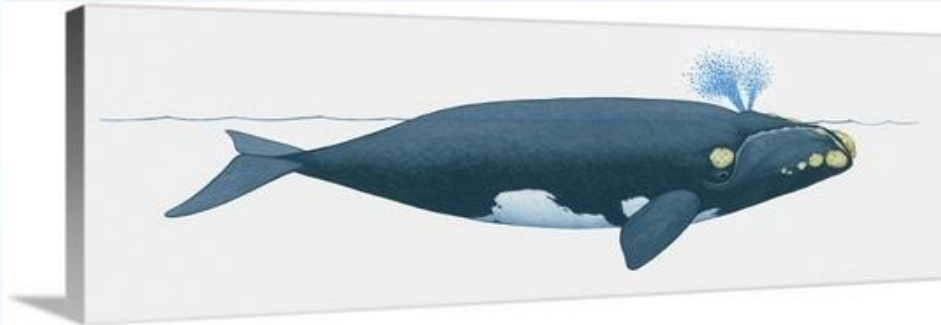
- Species as biodiversity indicators
 - Conservation management (biodiversity hotspots)

HOTSPOTS MAP OF CONSERVATION INTERNATIONAL (NGO)



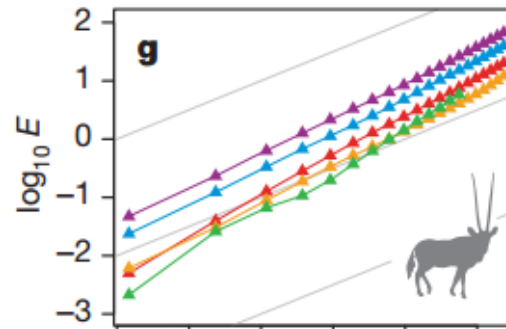
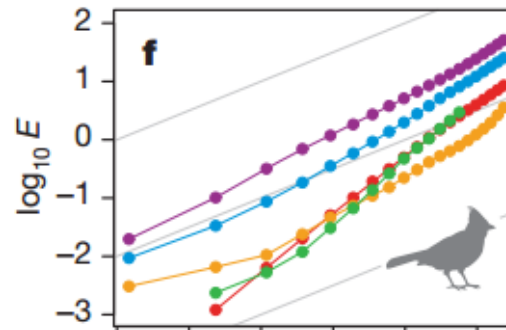
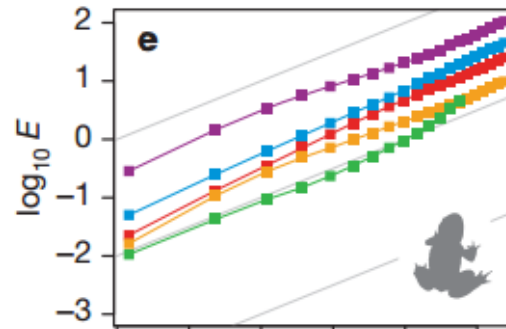
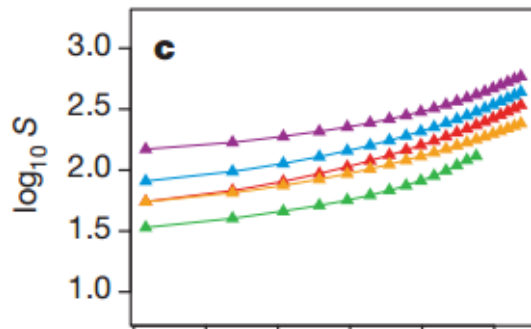
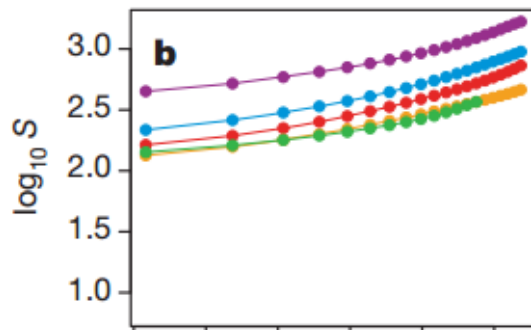
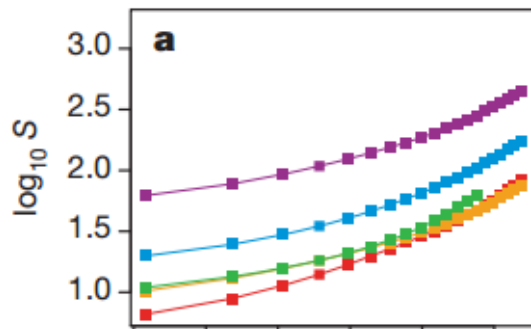
Species delimitation consequences

- Conservation
 - Japanese whale (*Eubalena japonica*): described in 2000, since 2008 registered as an endangered species



Species delimitation consequences

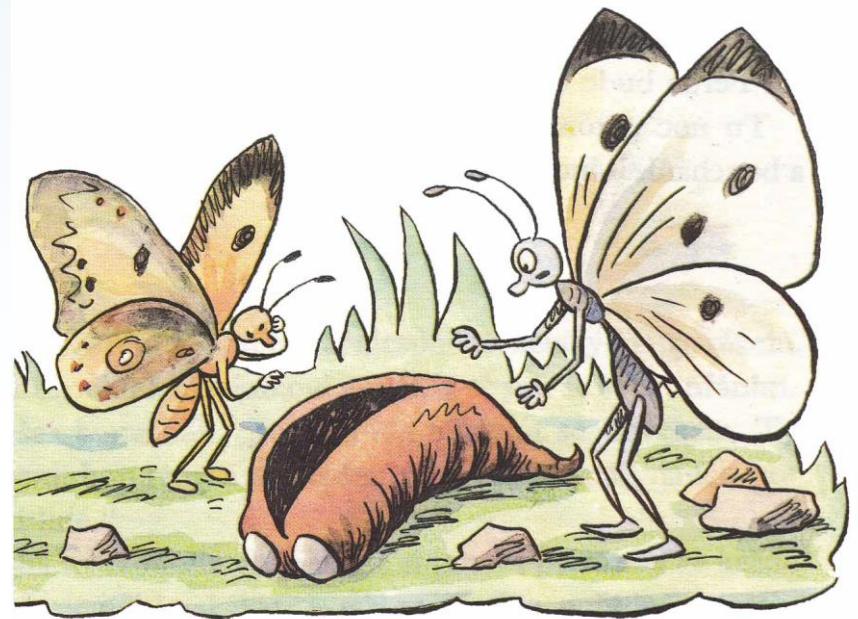
□ Amphibians, ○ Birds, △ Mammals
Africa, Eurasia, North America, South America, Australia



- Macroecology
 - Species as fundamental units for testing general ecological hypotheses

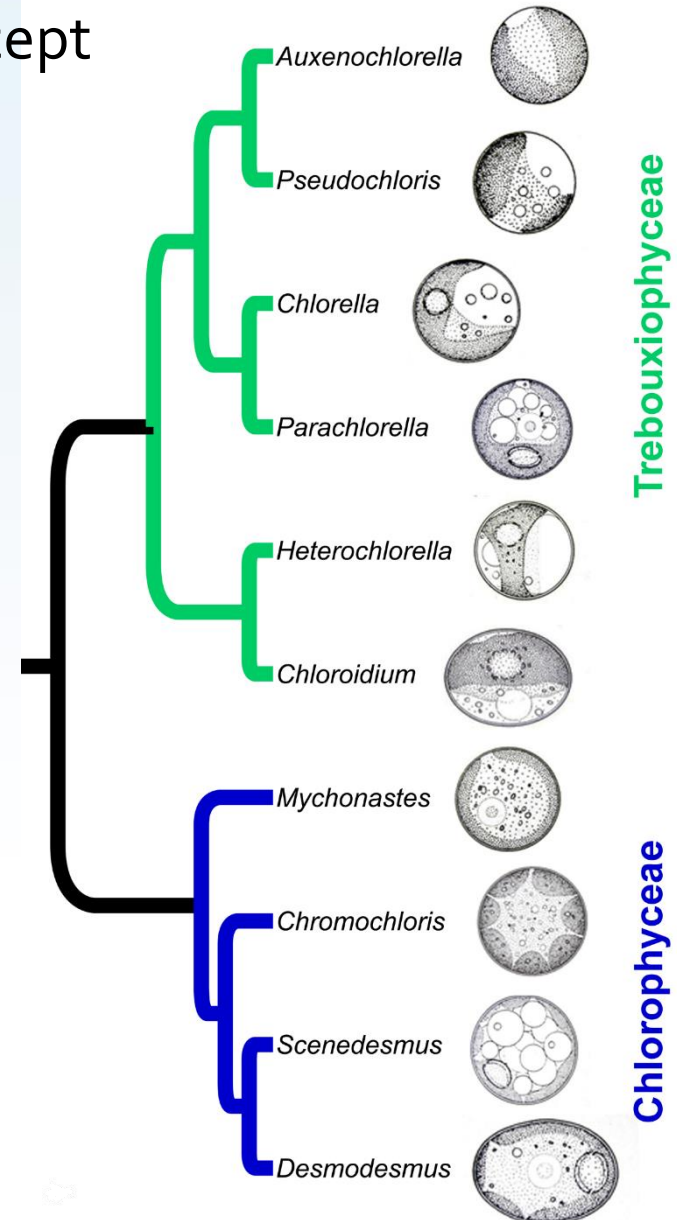
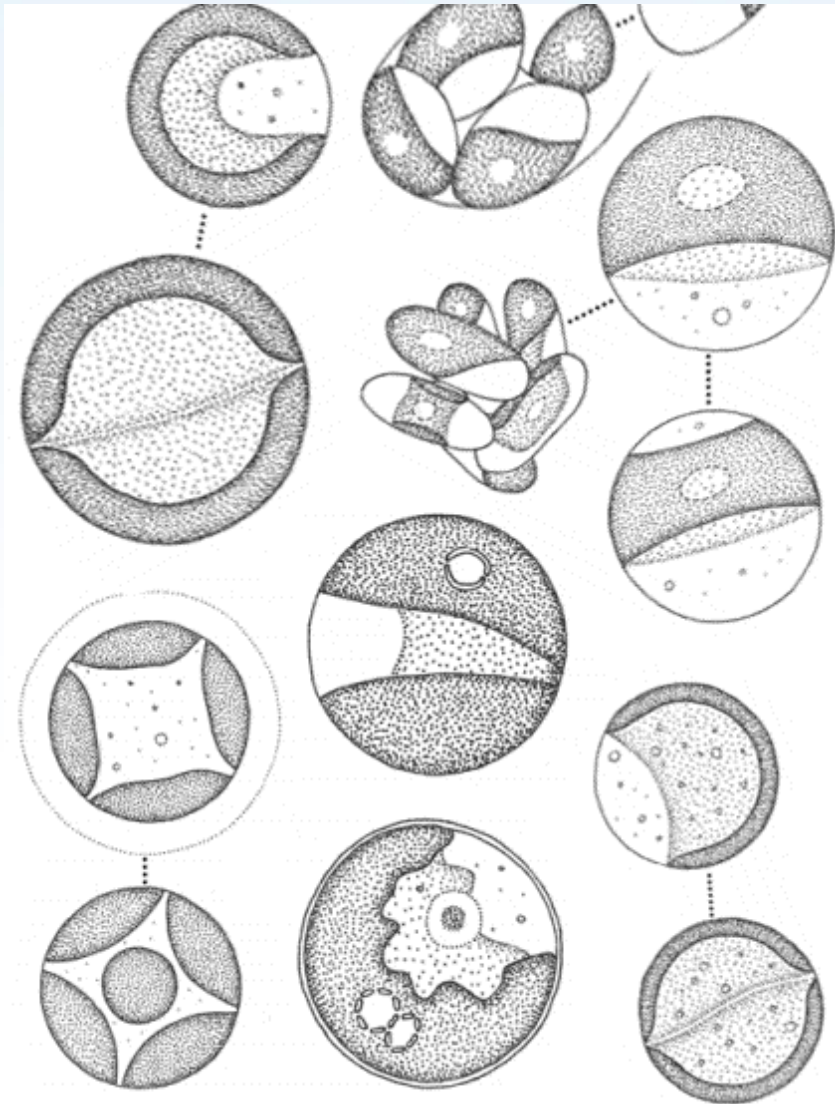
Species delimitation consequences

- Species numbers can be highly biased by species concepts employed
- Macroecology
 - Species as fundamental units for testing general ecological hypotheses



Species delimitation consequences

- *Chlorella* = morphological species concept



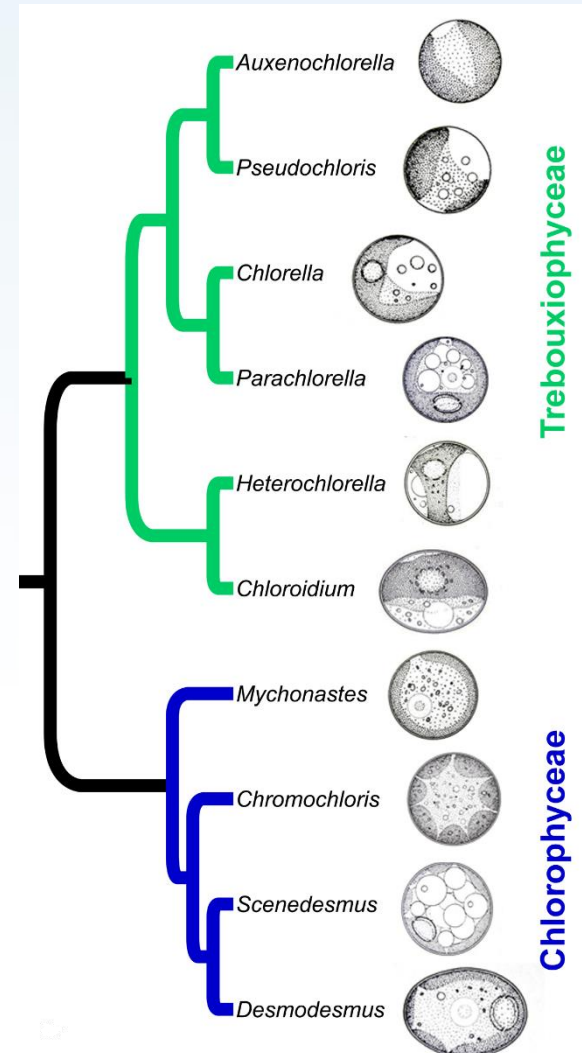
Species delimitation consequences

- *Chlorella* = broadly used in industry
 - sales of more than US\$ 38 billion annually worldwide
 - strain selection based on lipid content and fatty acid profiles

		EPA (omega-3)	18:1(9Z)	18:2(9Z,12Z)	18:3 (9Z,12Z,15Z)	9-Octadecanamid
<i>Chlorella</i> sp.	SAG 1.80	0	6	18	16	14
<i>Chlorella</i> sp.	SAG 3.83	0	10	14	15	14
<i>Chlorella</i> sp.	SAG 9.95	0	2	20	9	19
<i>Chlorella</i> sp.	SAG 15.93	0	2	20	17	20
<i>Chlorella</i> sp.	SAG 211-18	0	1	16	17	21
<i>Chlorella</i> sp.	SAG 211-6	0	1	11	20	23
<i>Chlorella</i> sp.	SAG 211-80	0	19	41	7	9
<i>Chlorella</i> sp.	SAG 241-80	0	1	11	22	17
<i>Chlorella</i> sp.	SAG 242.80	24	7	10	3	9
<i>Chlorella</i> sp.	SAG 69.94	9	19	12	28	0

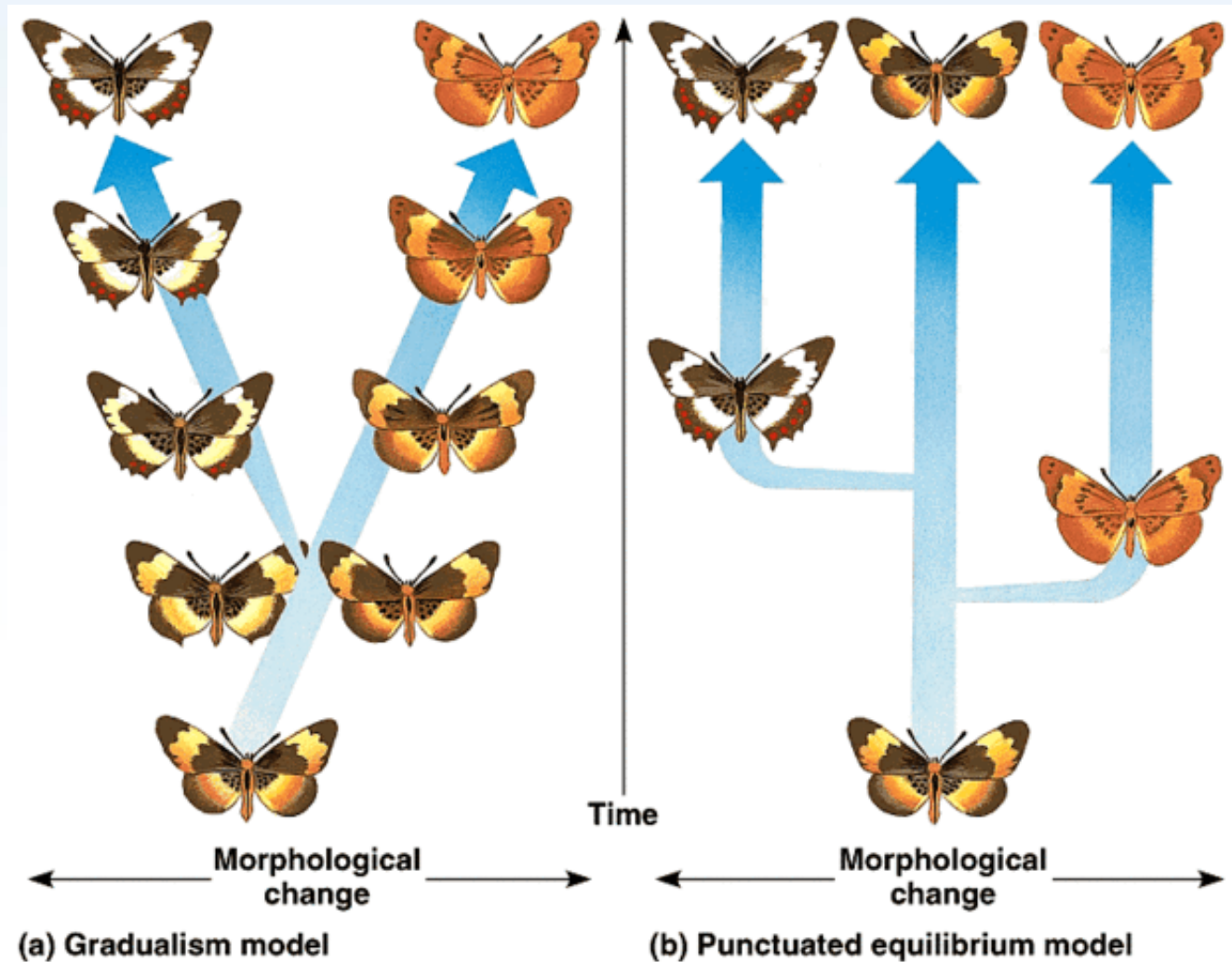
Species delimitation consequences

- *Chlorella* = registration as food products
 - list of permitted organisms (*Chlorella vulgaris*, *Ch. pyrenoidosa*)



Species delimitation

- Difficulty of simple species definitions
 - Species are not rigid, but evolving entities

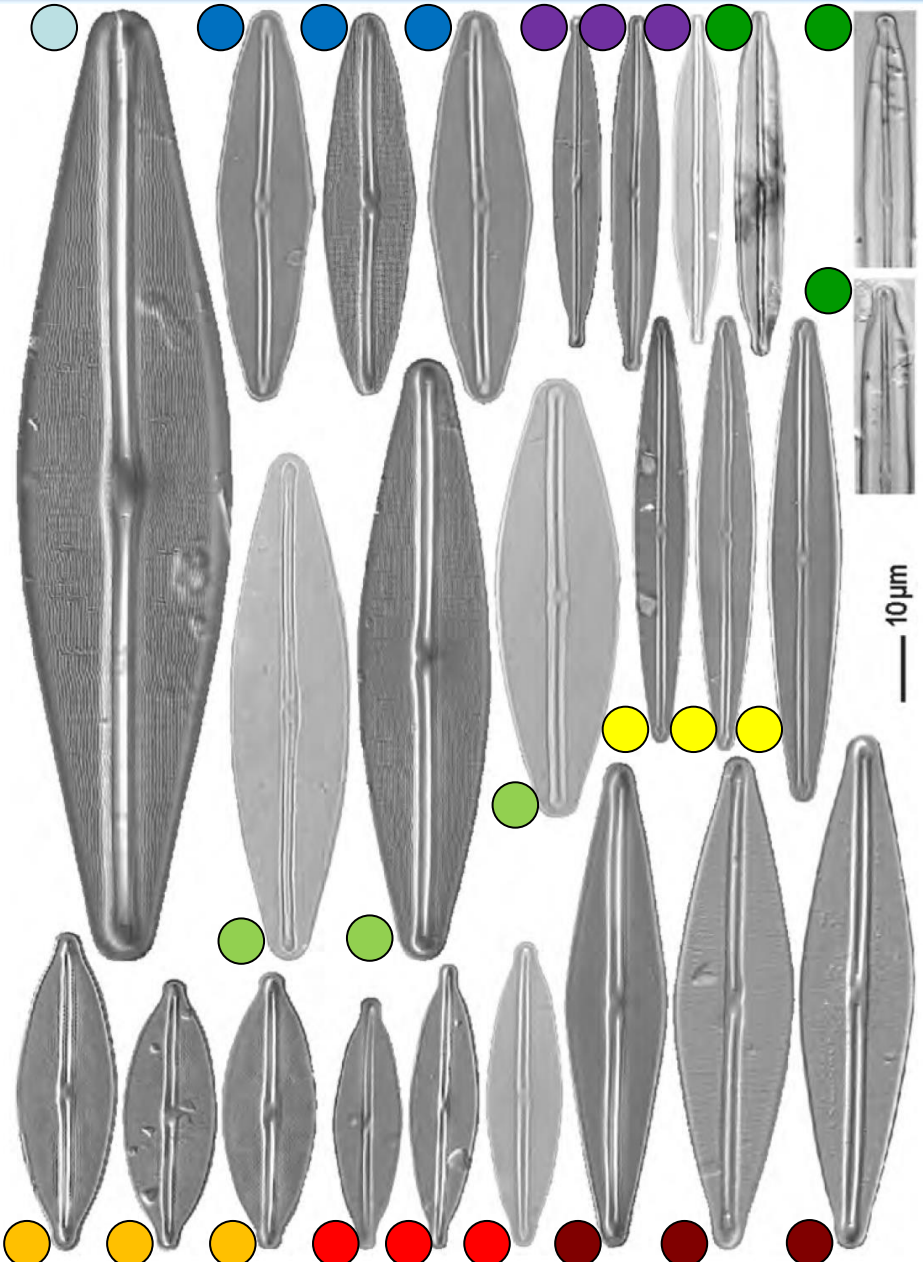
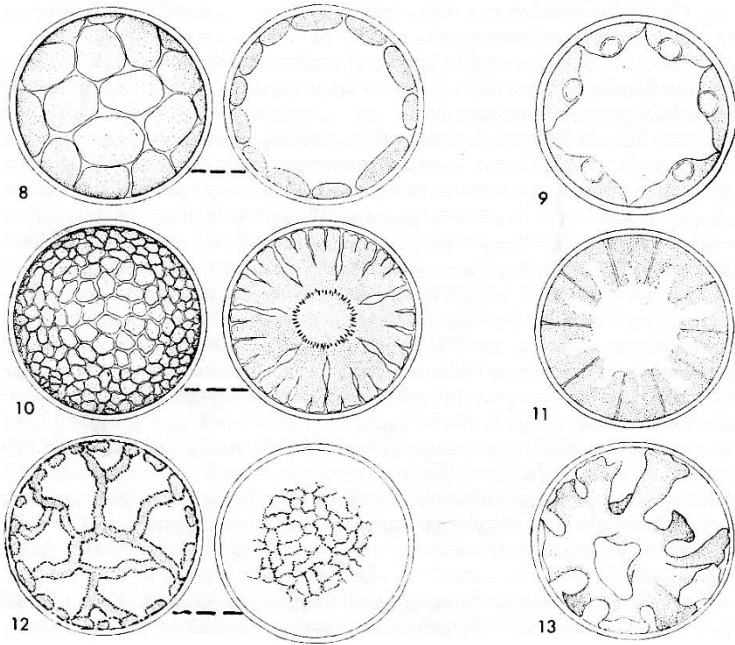


Species concepts in protists

Cohesion species concept	Biological species concept	Evolutionary significant unit
	Phylogenetic species concept	Polythetic species concept
Cladistic species concept		Recognition species concept
	Genealogical concordance concept	
Internodal species concept		Reproductive competition concept
	Hennigian Species concept	
Composite species concepts		Genetic species concept
	Evolutionary species concept	
Ecological species concept		Palaeospecies concept
	Morphological species concept	Successional species concept
Non-dimensional species concept		Taxonomic species concept
	Linnean species concept	
Phenetic species concept		Genotypic cluster definition
	Agamospecies concept	

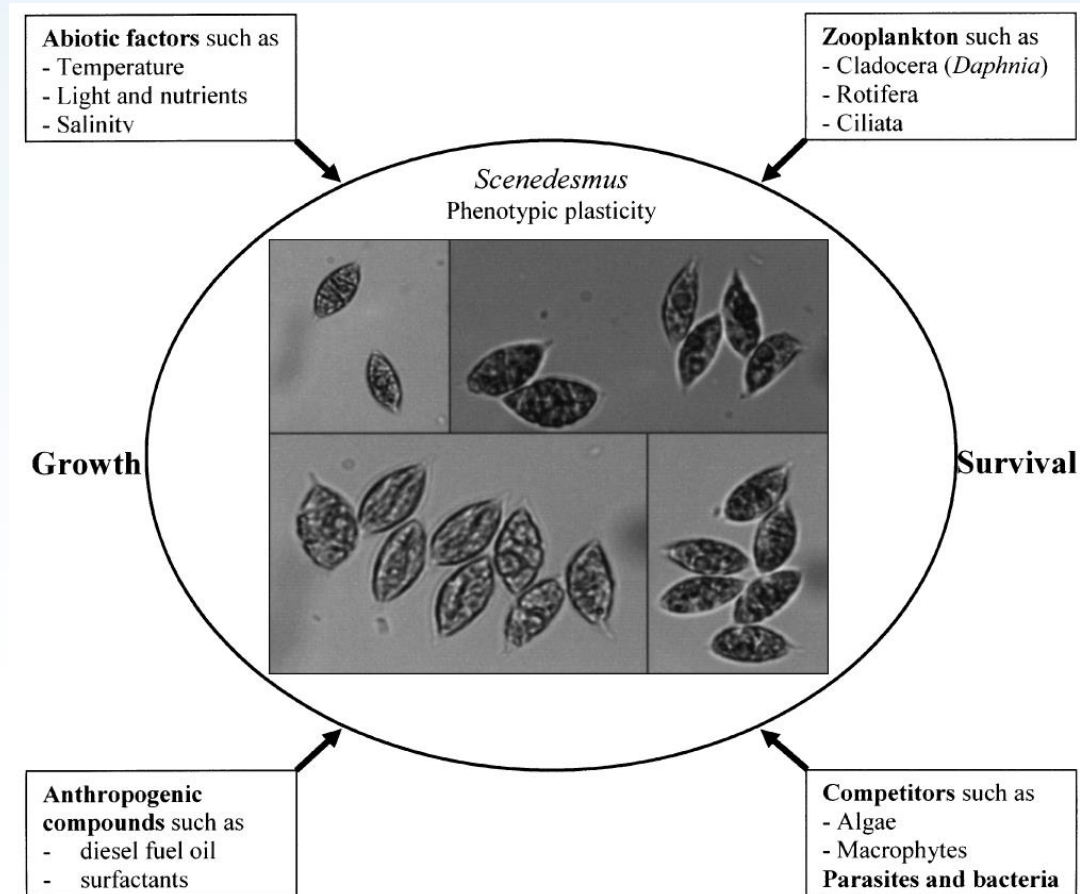
Morphological species concept

- A tradition!
 - Still employed in some groups of algae



Morphological species concept

- Species delimited based on investigation of natural samples
 - No data on phenotypic plasticity (*Scenedesmus*)



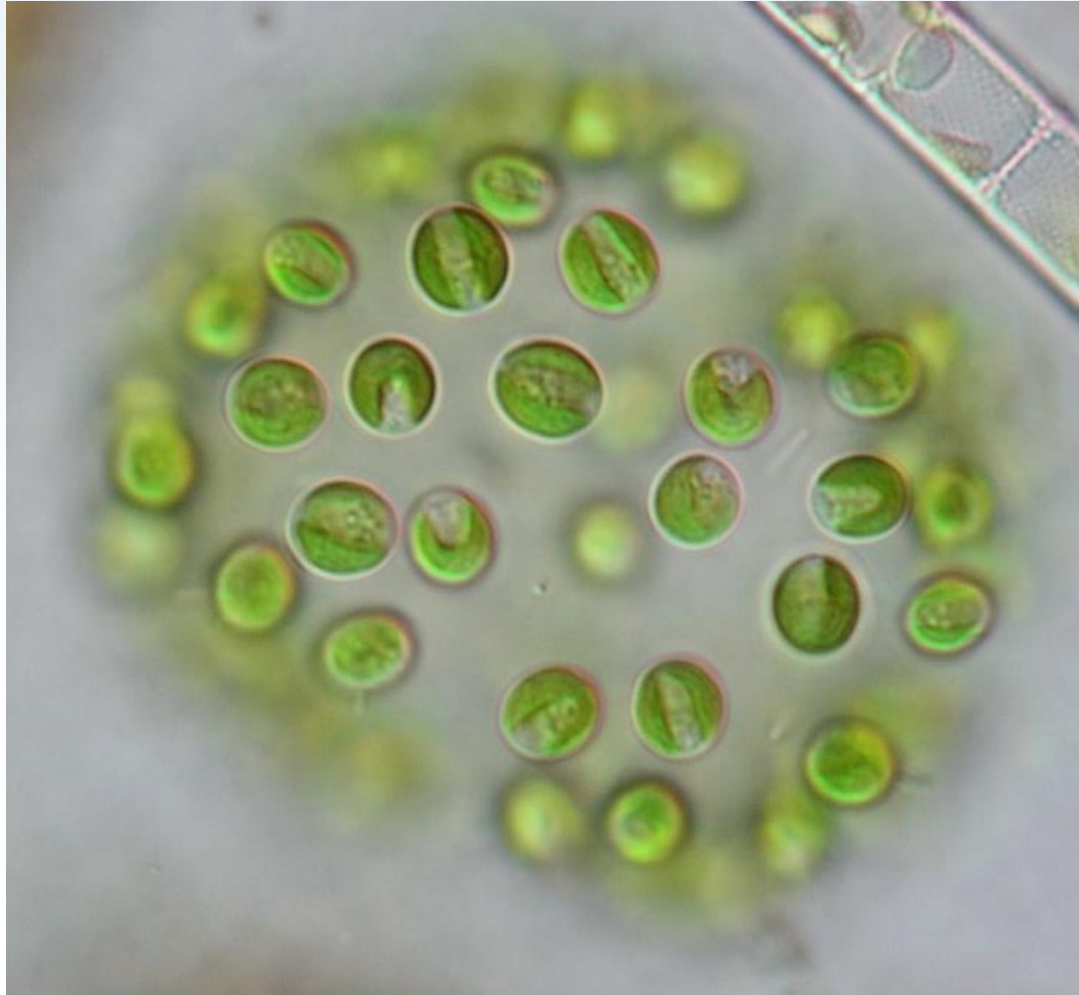
Morphological species concept

- Species delimited based on investigation of cultured strains
 - Absence of traits manifested only in nature (*Micractinium*)



Morphological species concept

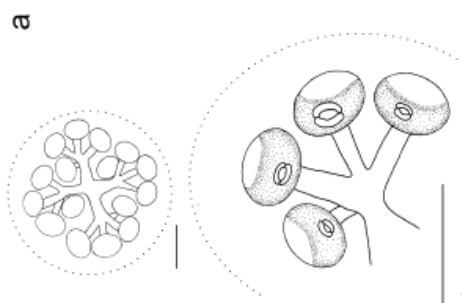
- Convergent morphological evolution
 - *Dictyosphaerium*



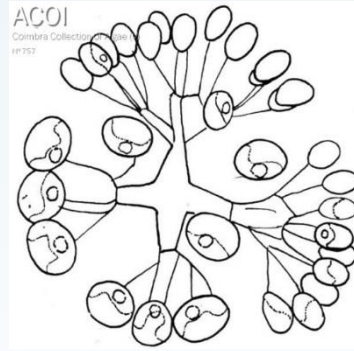
Morphological species concept

- Convergent morphological evolution
 - *Dictyosphaerium* (9 cryptic genera)

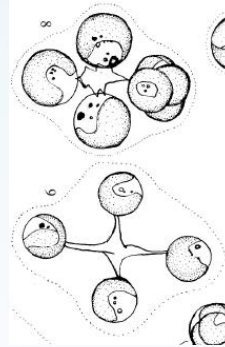
Dictyosphaerium



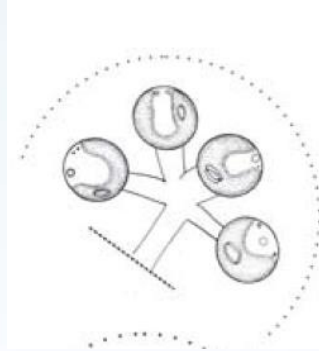
Hindakia



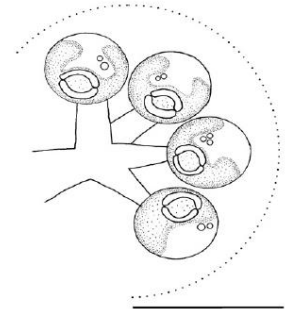
Mychonastes



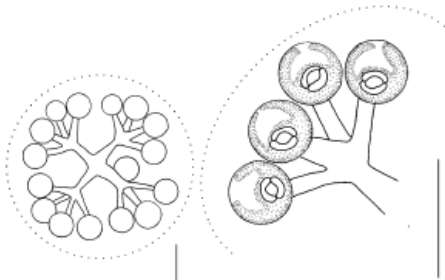
Chlorella



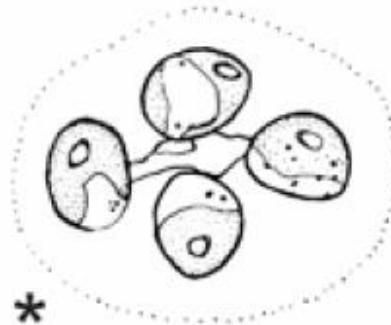
Heynigia



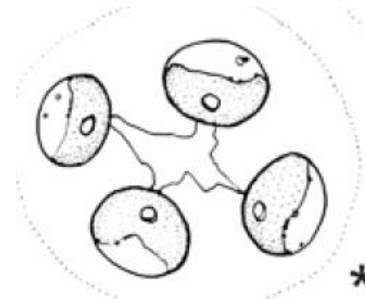
Mucidosphaerium



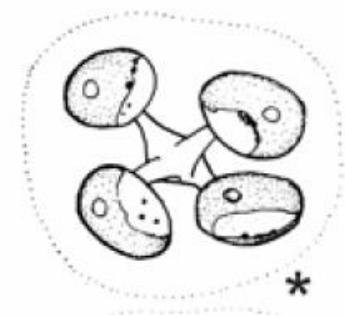
Compactochlorella



Kalenjinia

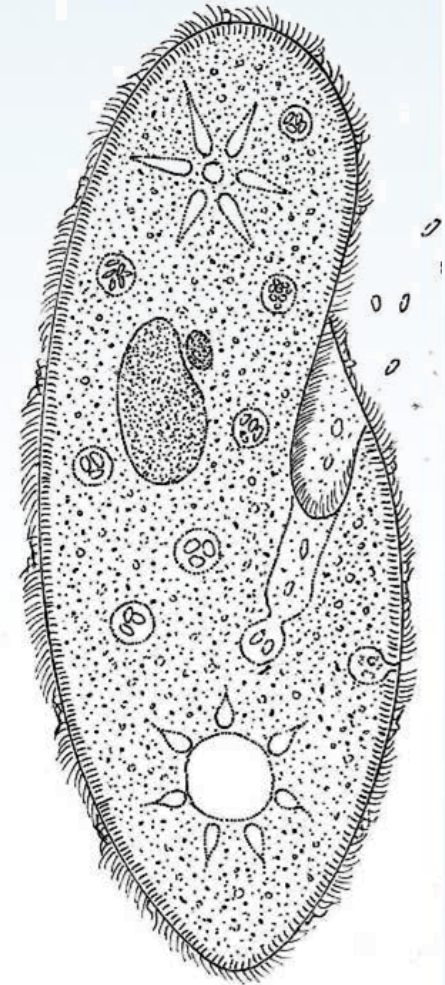
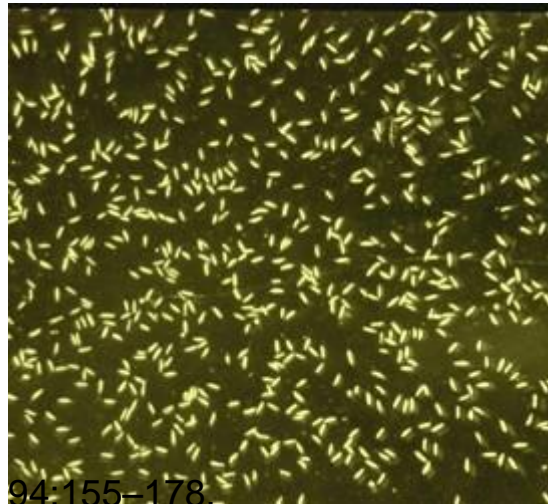
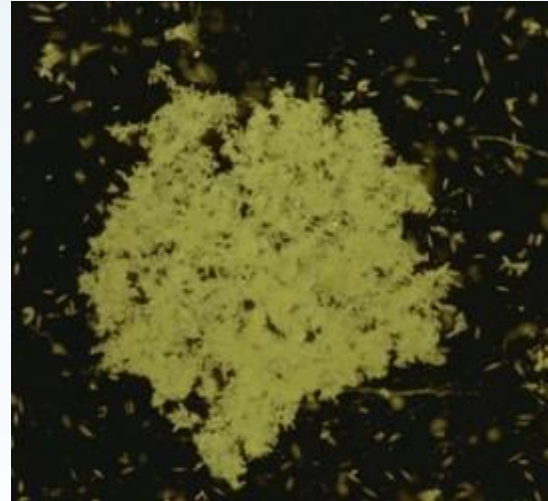
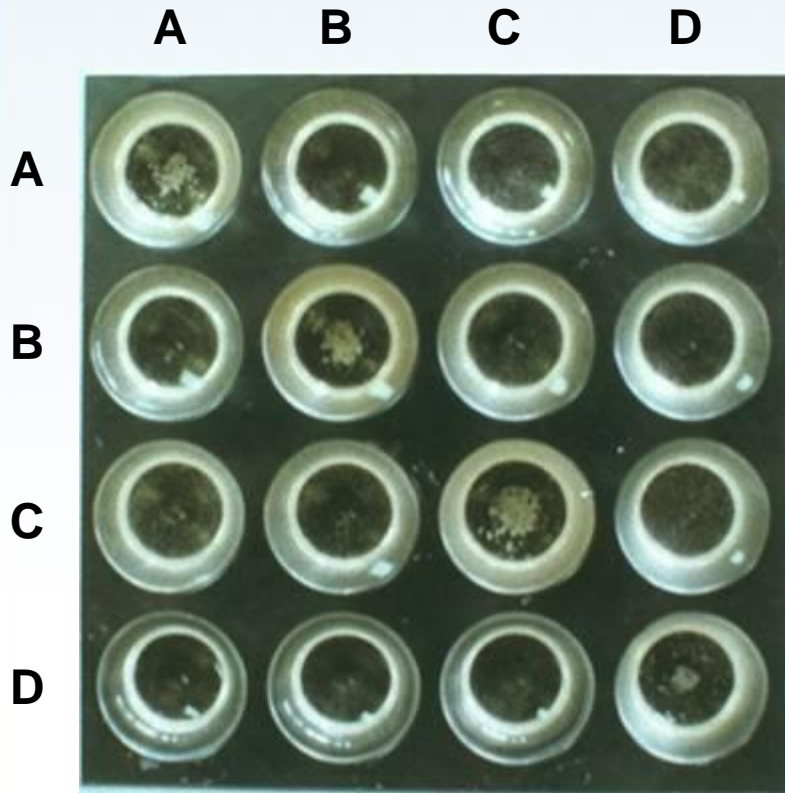


Masaia



Biological species concept

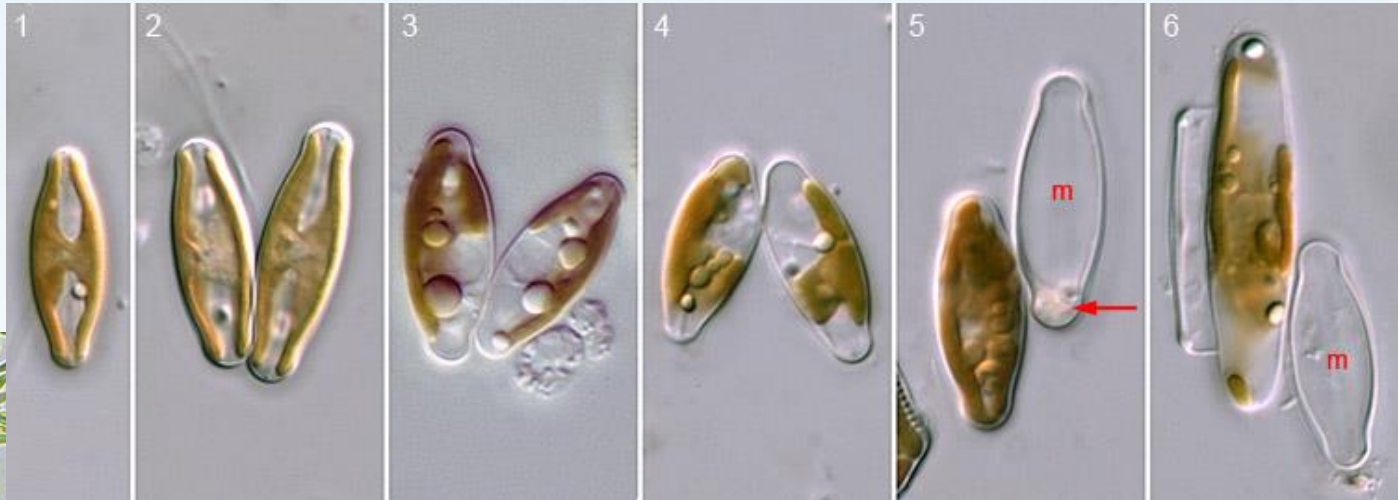
- Applicable only on sexually reproducing organisms
 - ciliates (syngens in *Paramecium aurelia*)



Biological species concept

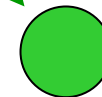
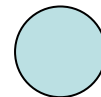
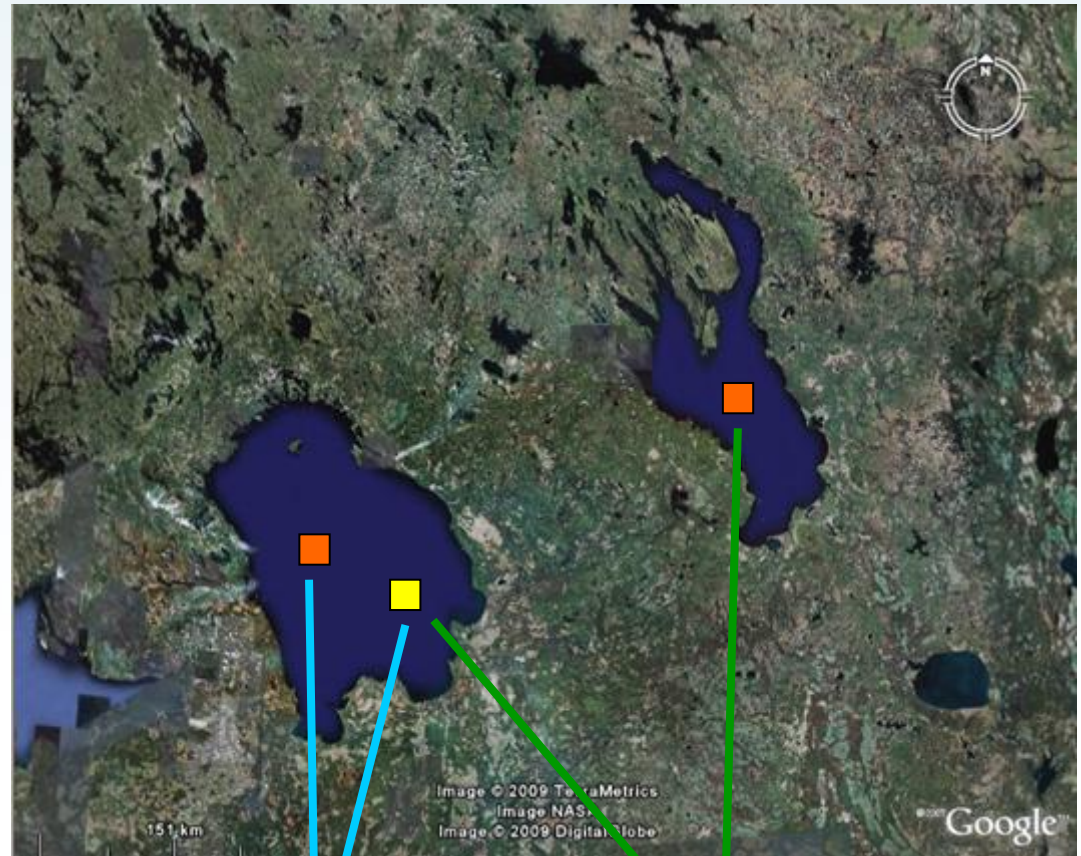
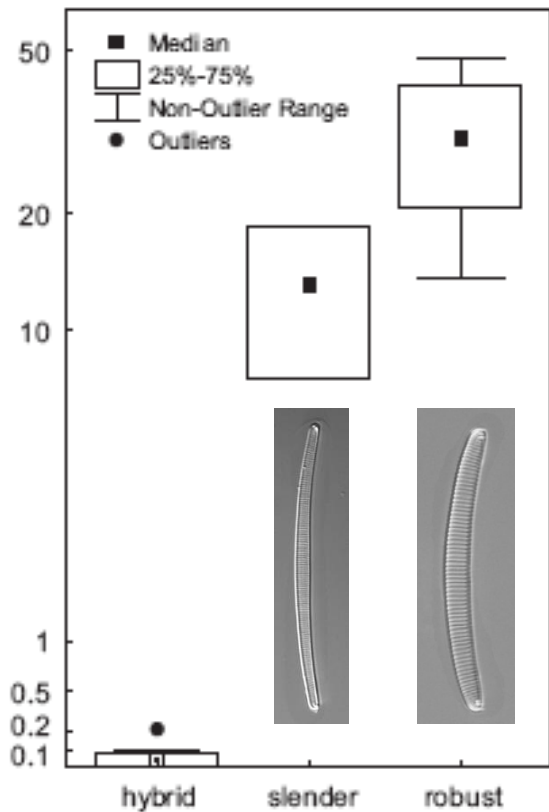
- Applicable only on sexually reproducing organisms

➤ diatoms



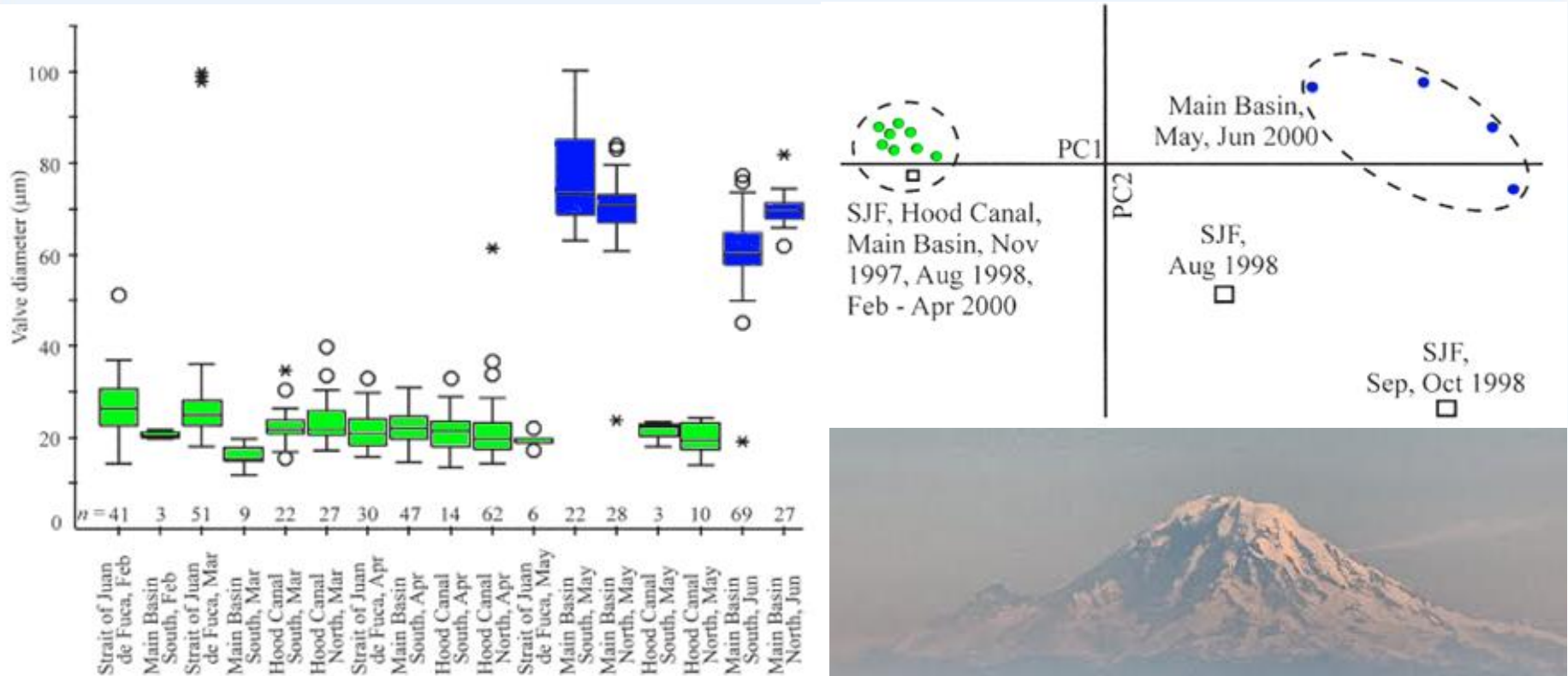
Biological species concept

- Often incomplete reproduction barriers
 - A problem of allopatric populations (*Eunotia*)



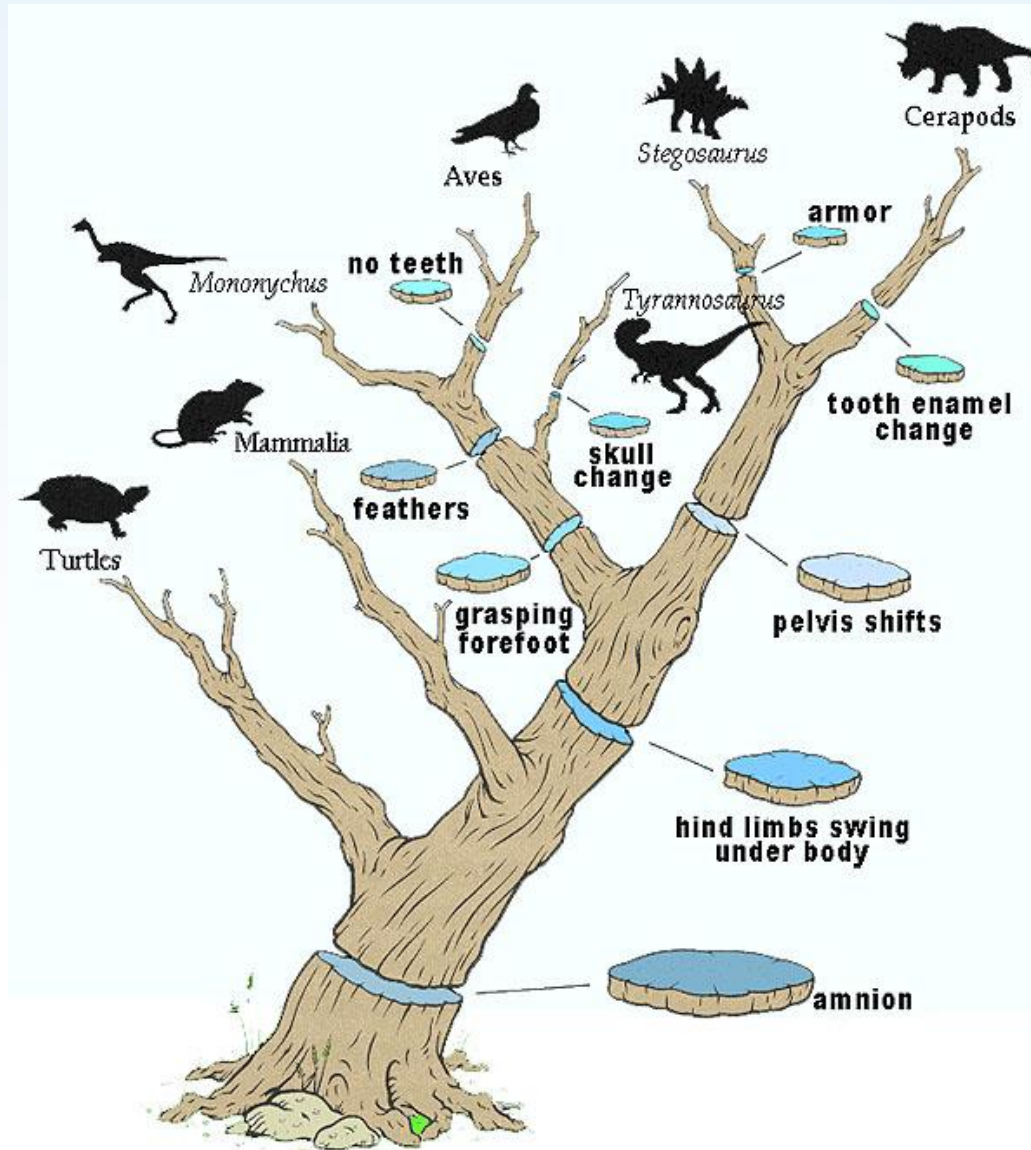
Biological species concept

- Laboratory crossing experiments test the incompatibility
 - a problem of temporal isolation (*Ditylum*)



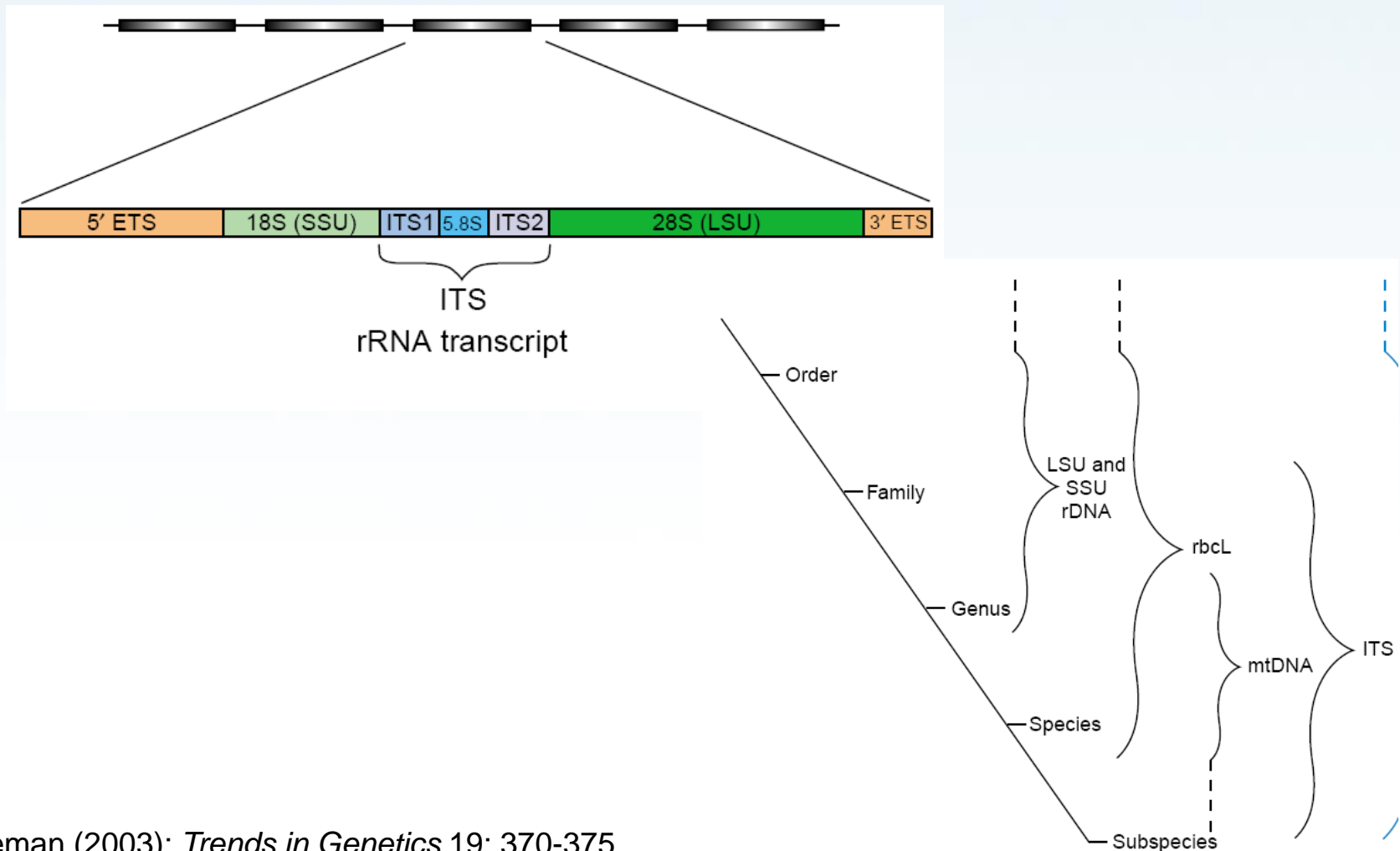
Phylogenetic species concept

- Based on tree topology (monophyly, branch lengths, supports)



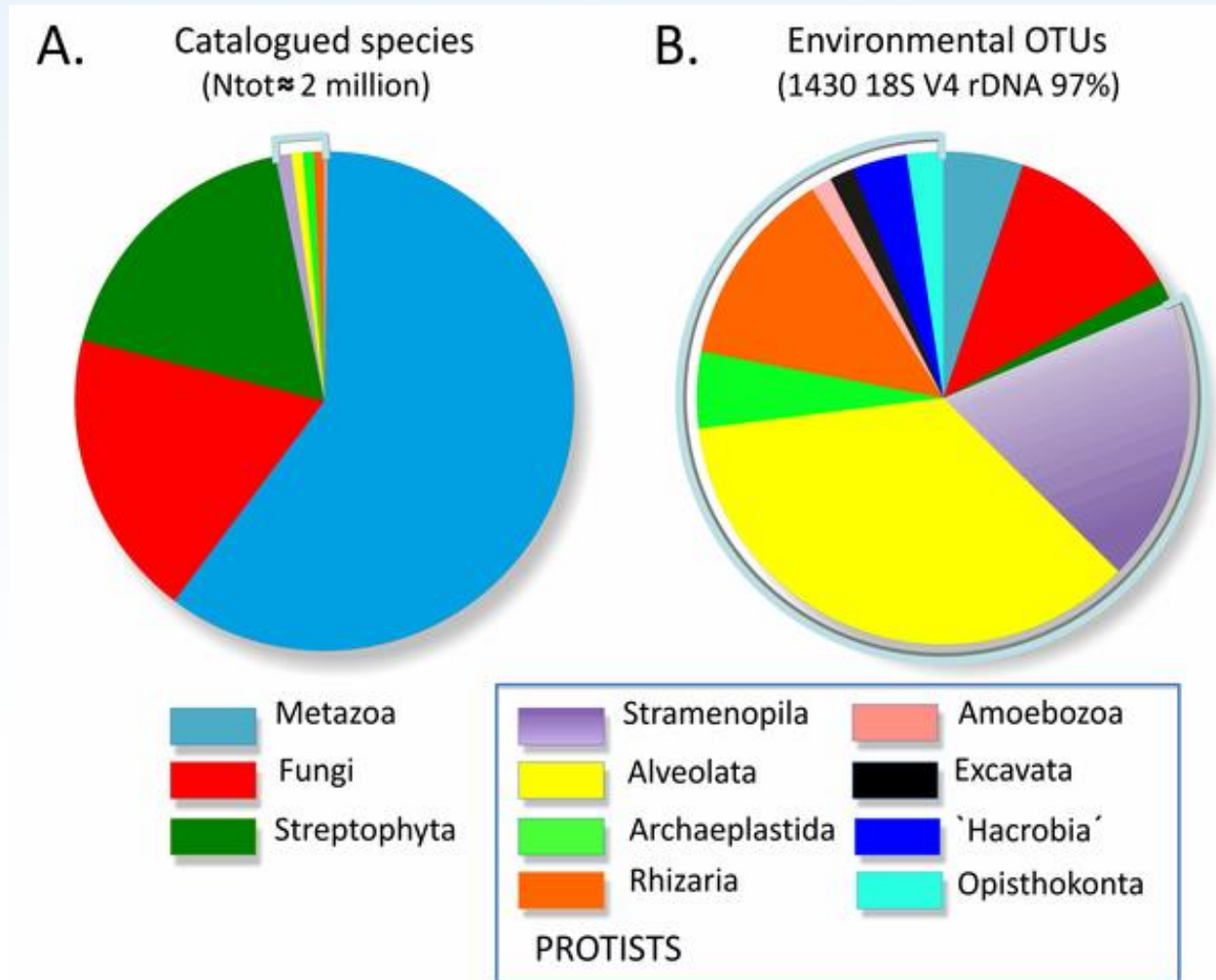
Phylogenetic species concept

- Ribosomal operon as the frequently used marker



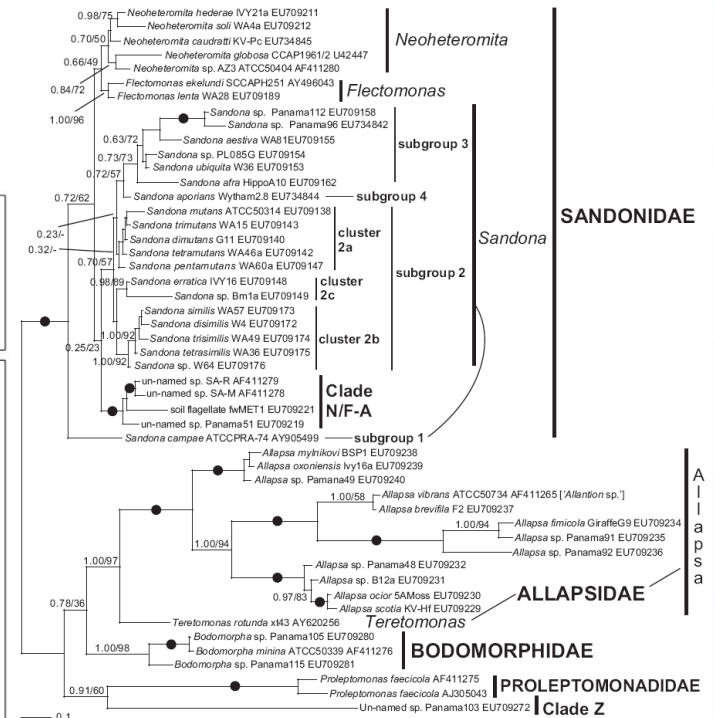
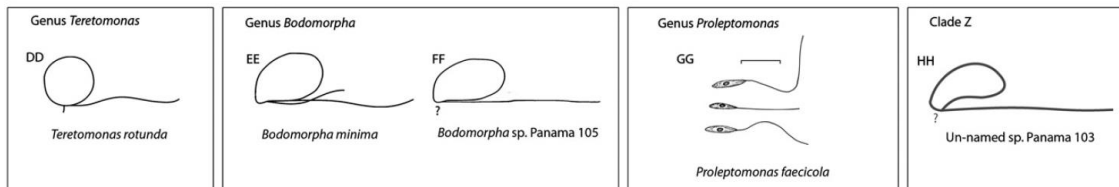
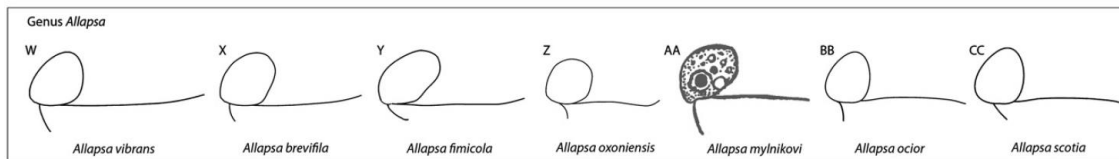
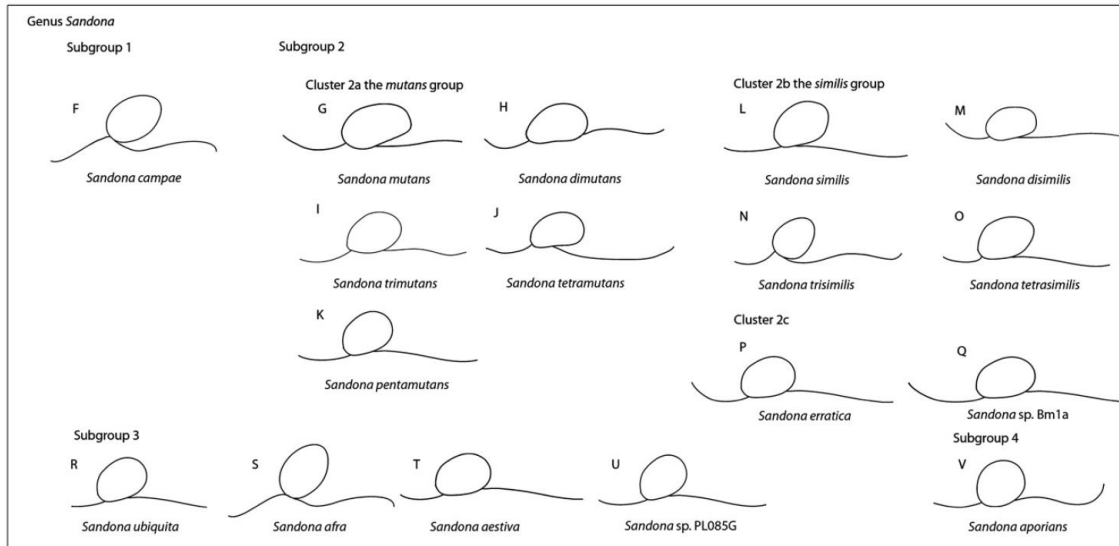
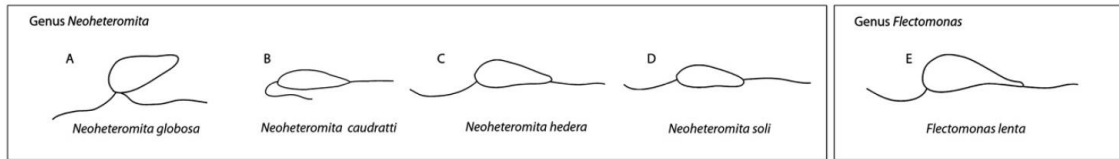
Phylogenetic species concept

- Cryptic diversity of protists




Phylogenetic species concept

- Cryptic diversity of protists
 - glissomoads



Phylogenetic species concept

- Cryptic diversity of protists
 - mere accumulation of neutral mutations?
 - the extent of genetic polymorphism is dependent on mutation rate (μ) and effective population size (N_e)


$$\theta = 4 N_e \mu$$

Marine plankton – 10^{25} cells

Phylogenetic species concept

- Cryptic diversity of protists (*Pentapharsodinium*)
 - population size: $\approx 2.9 \times 10^{14}$
 - $N_e \approx 178-1183$

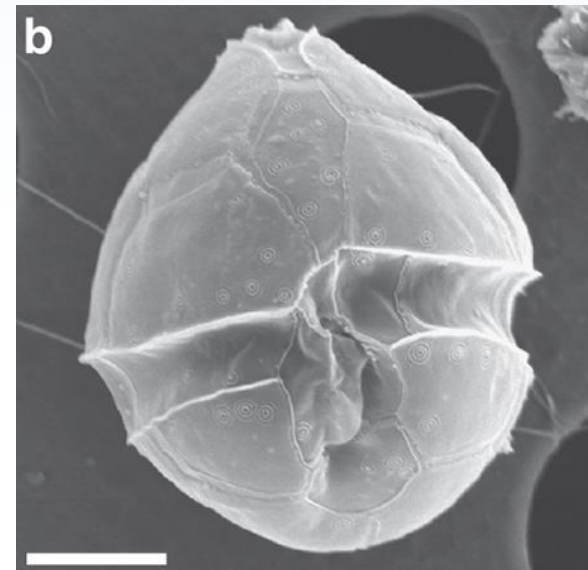
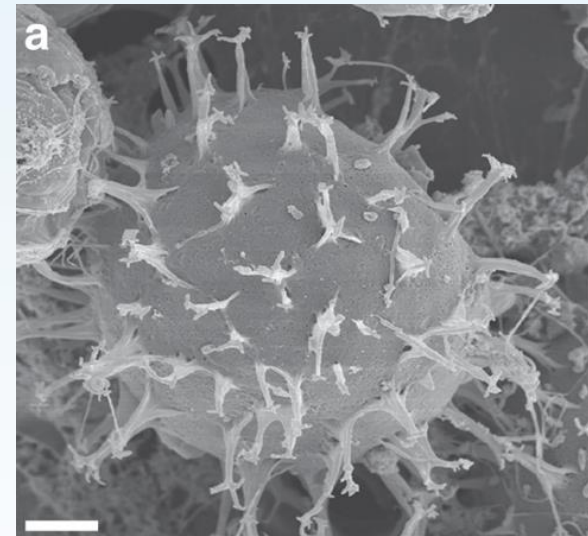


Table 1. Estimates of contemporary effective population size (N_e) for samples of the marine dinoflagellate *P. dalei* revived from sediment cores (dated to 1922, 1960, 1985 and 2006) from Koljö Fjord, Sweden. Mean N_e (\pm 95% confidence intervals) was estimated for pairs of samples using ML [8] and moment estimators [6].

sample comparison	contemporary effective population size (N_e)	
	ML (95% CI)	moment (95% CI)
2006–1985	270 (161–544)	178 (98–343)
2006–1960	439 (252–924)	375 (195–793)
2006–1922	815 (401–2489)	1183 (476–5545)
1985–1960	264 (148–592)	342 (166–905)
1985–1922	305 (187–538)	652 (325–1528)
1960–1922	179 (109–320)	266 (134–570)

Phylogenetic species concept

- Based on tree topology (monophyly, branch lengths, supports)

➤ Where to set species boundaries?

➤ **Objective criteria?**

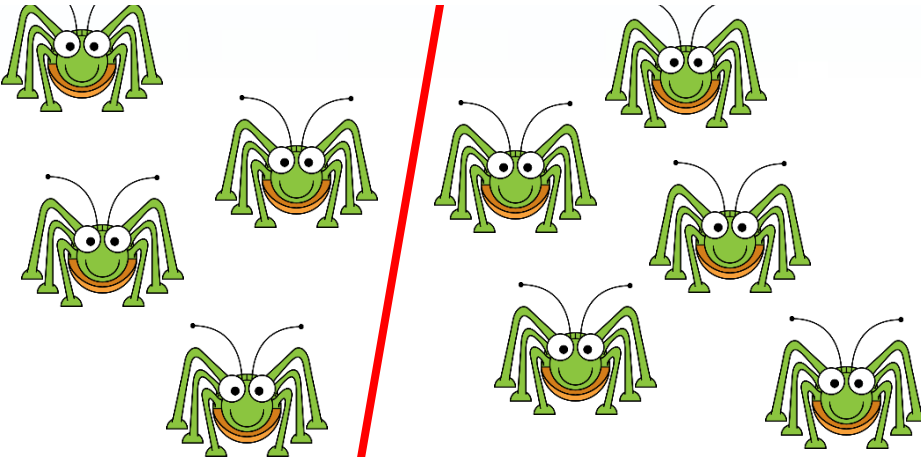
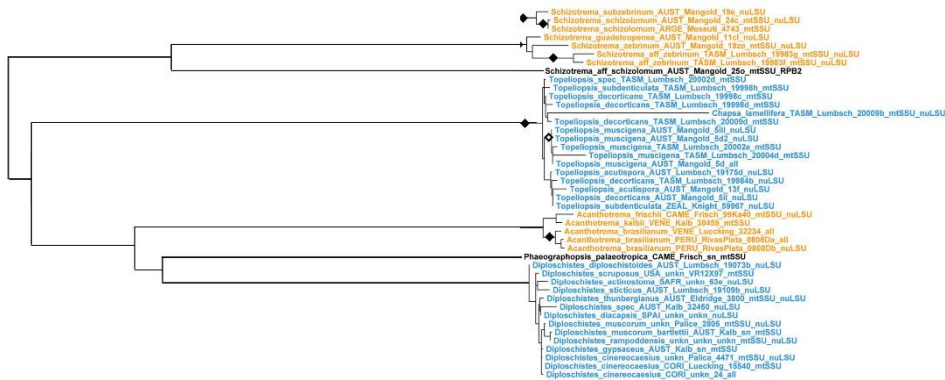
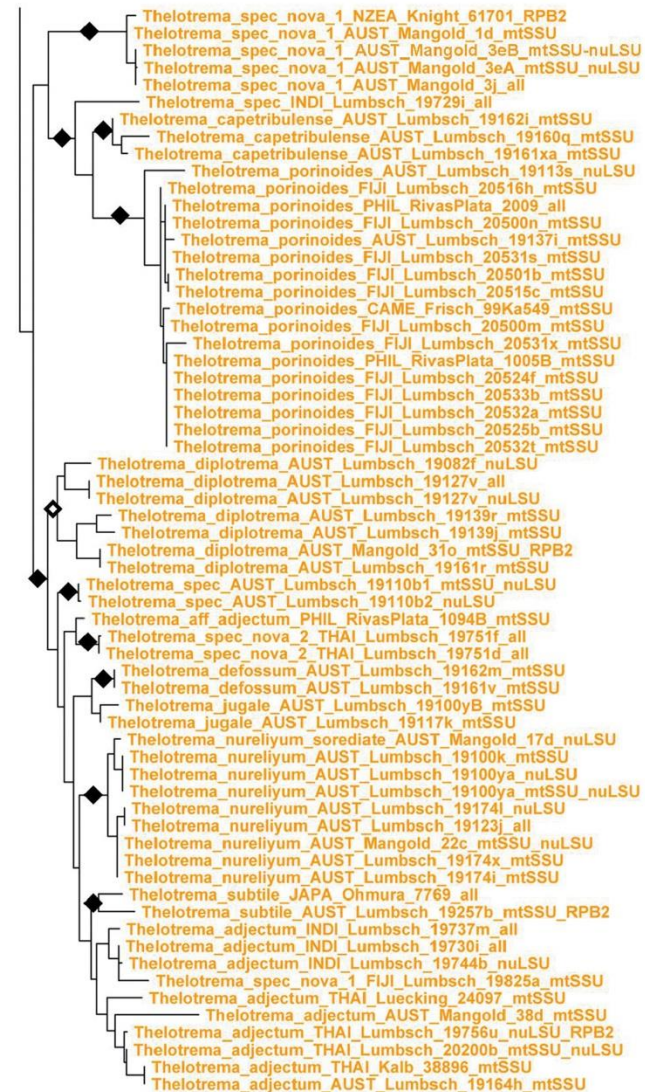
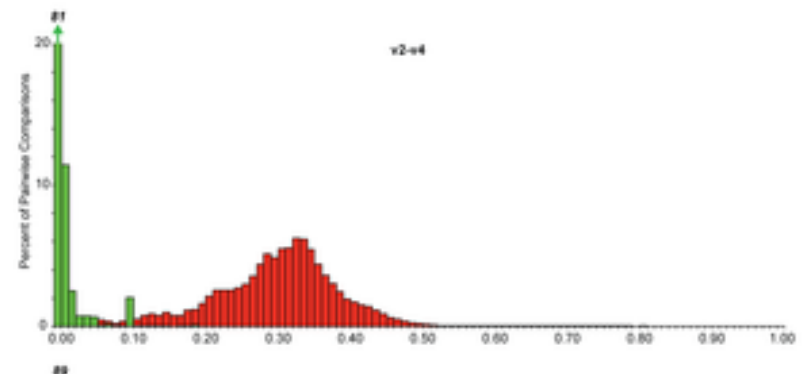
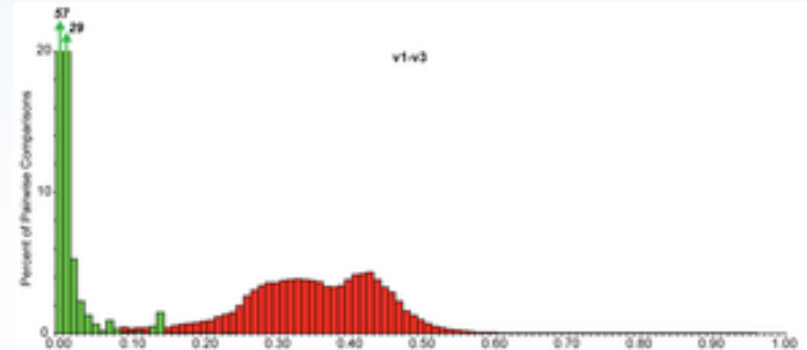
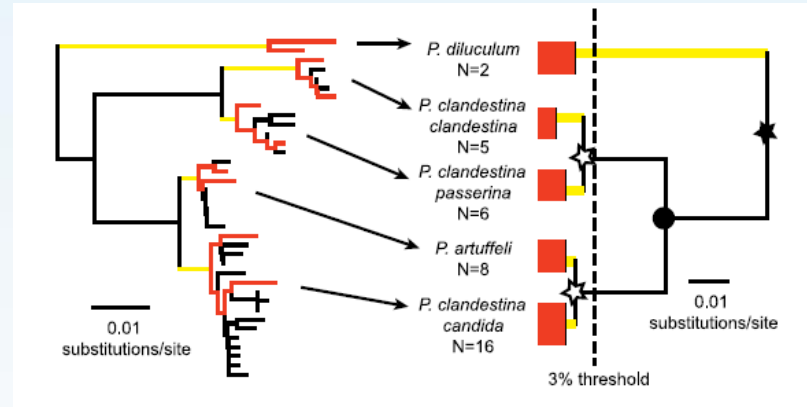
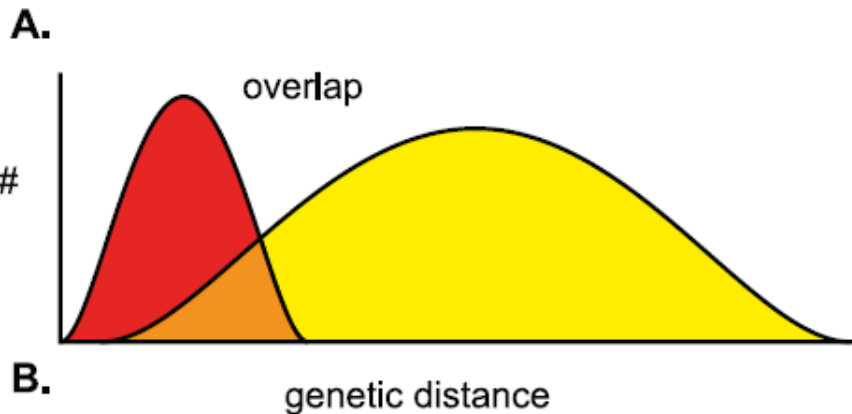
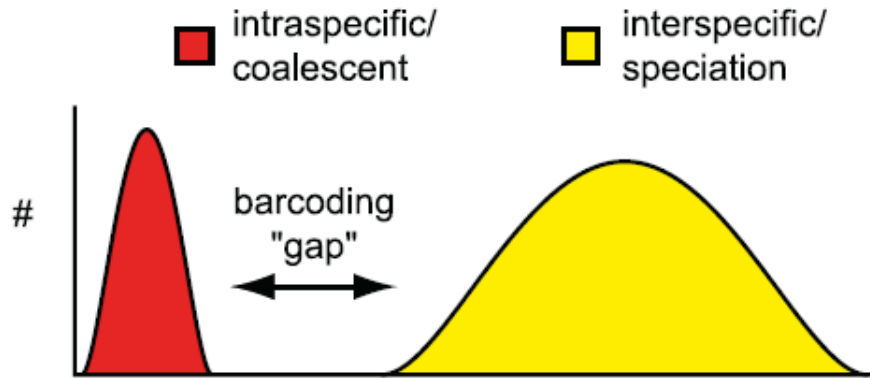


Fig. 8



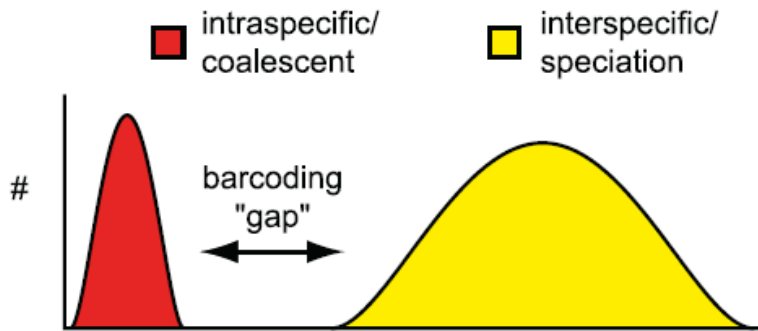
DNA barcoding

- „barcoding gap“

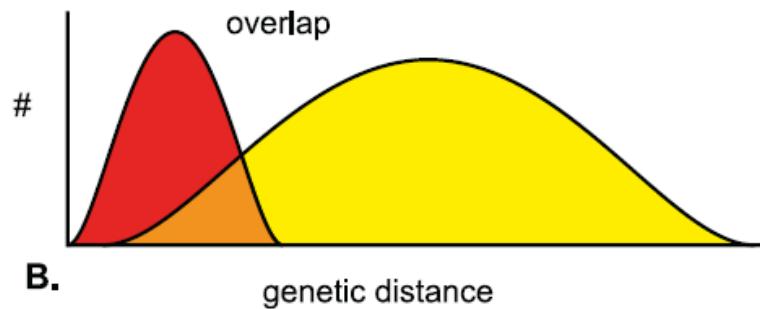


DNA barcoding

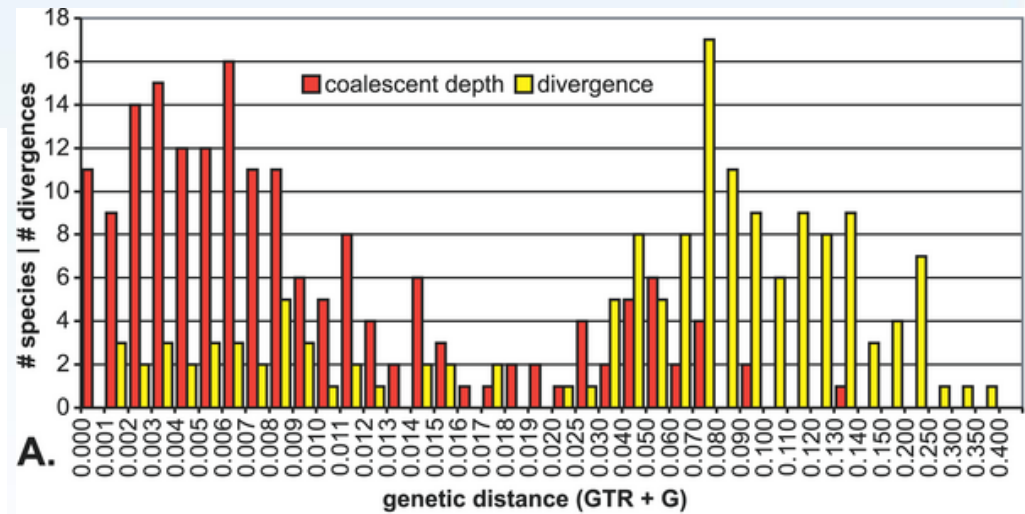
- More sampling – less obvious barcoding gap



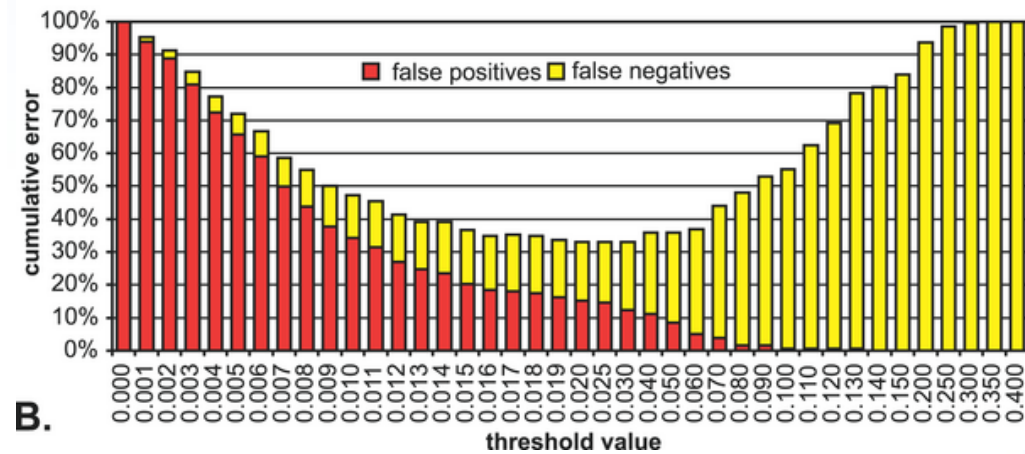
A.



B.



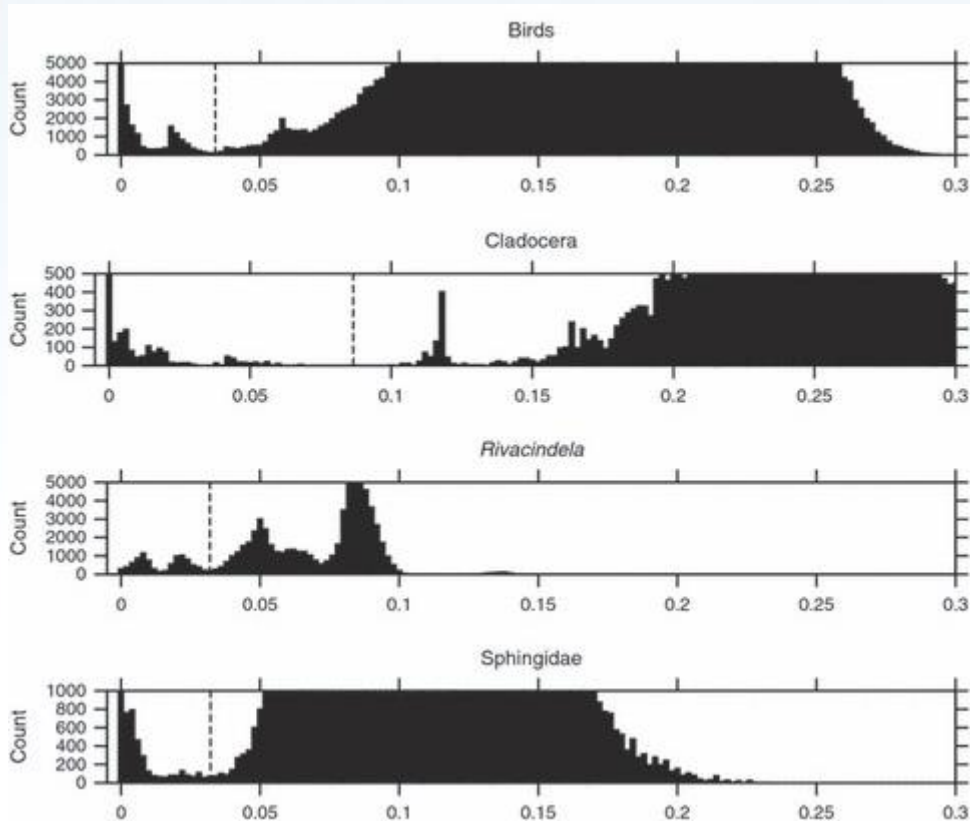
A.



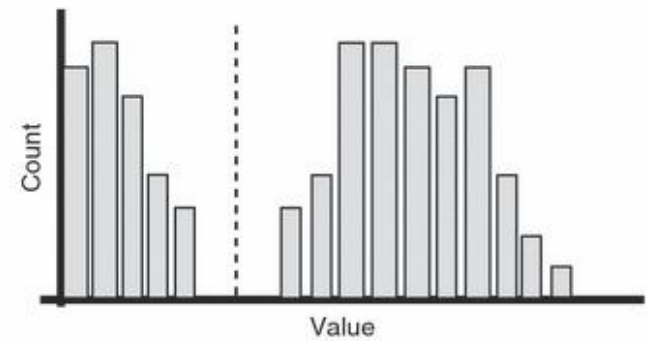
B.

ABGD

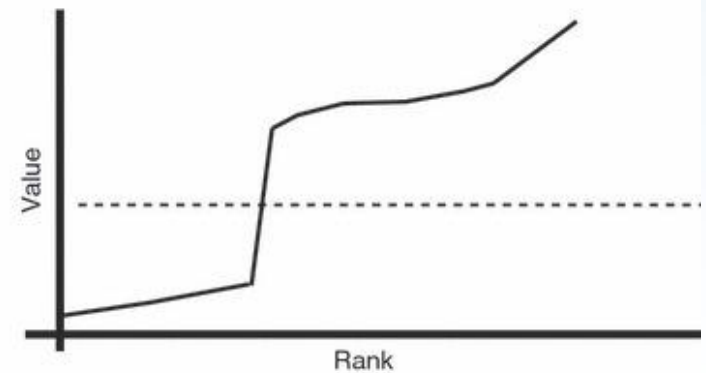
- Automatic Barcode Gap Discovery
 - Alignment as an input file
 - Scanning a range of intraspecific divergence to find the barcode gap



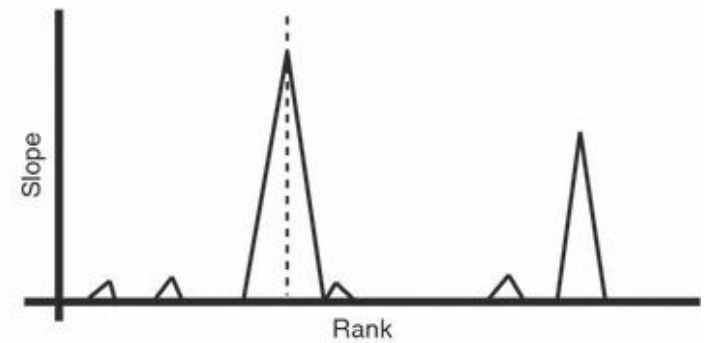
(a) Distribution of pairwise differences



(b) Ranked pairwise differences

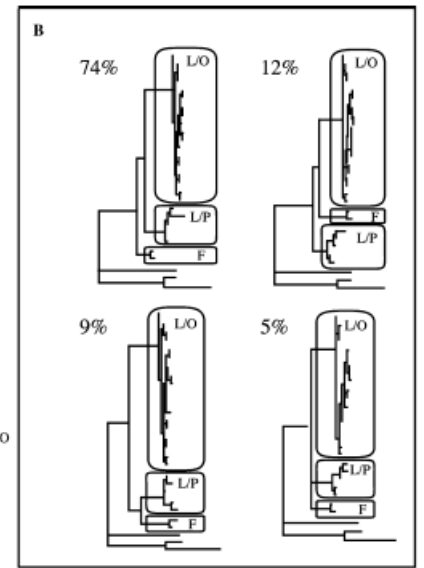
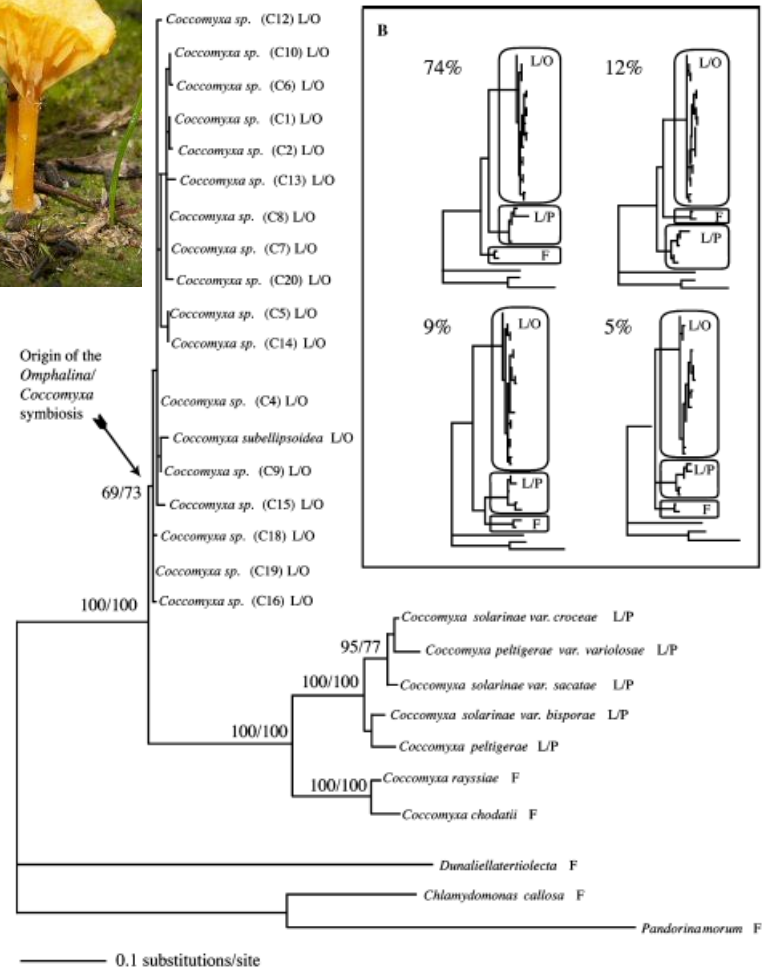
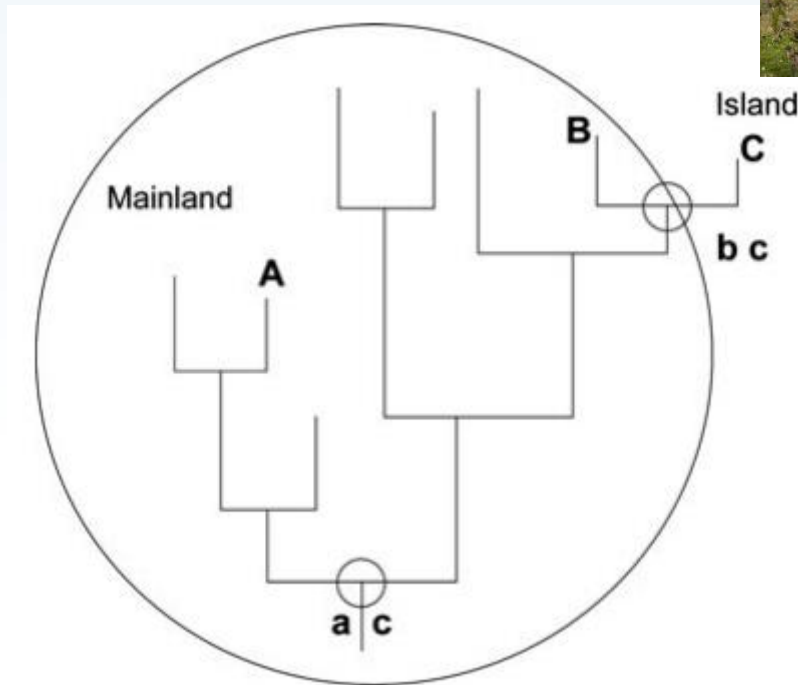


(c) Slope of ranked pairwise differences



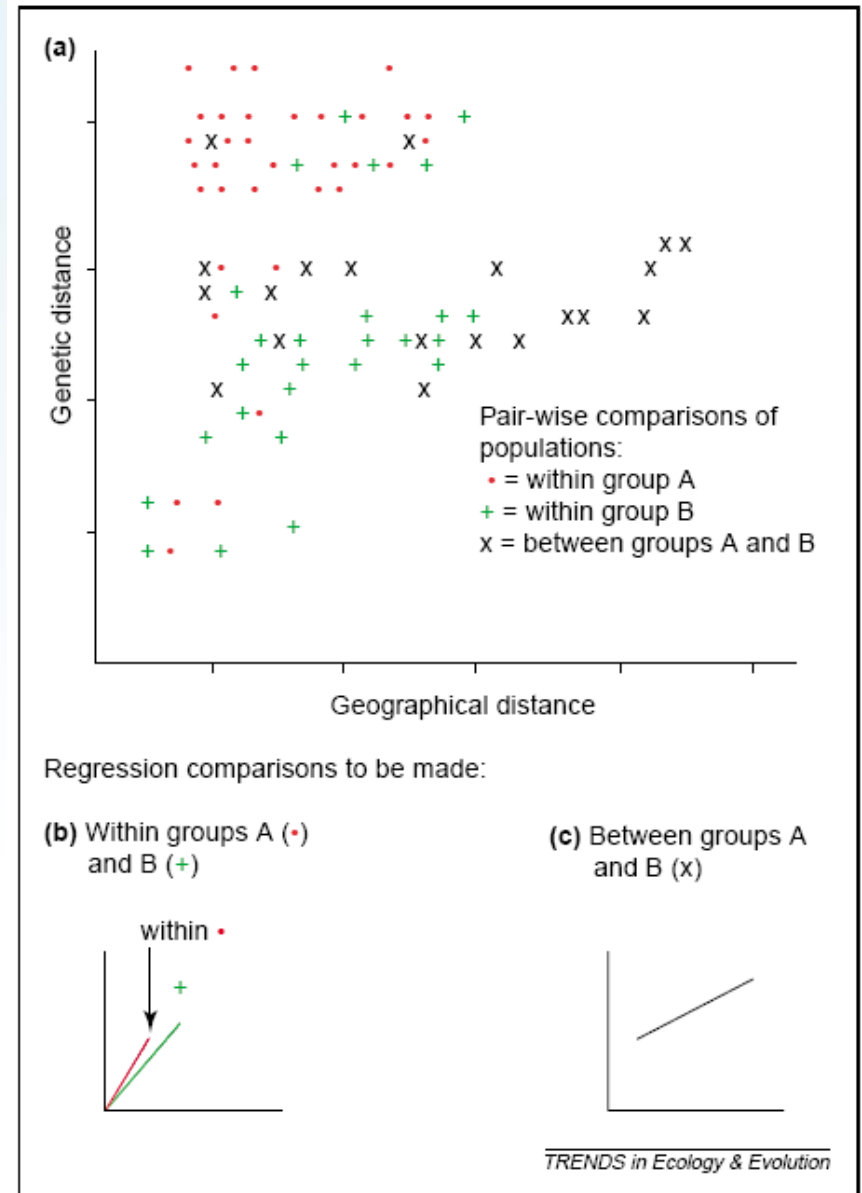
DNA barcoding

- Uneven mutation rates
 - tropics ~ temperate
 - islands ~ continents
 - free-living ~ symbionts



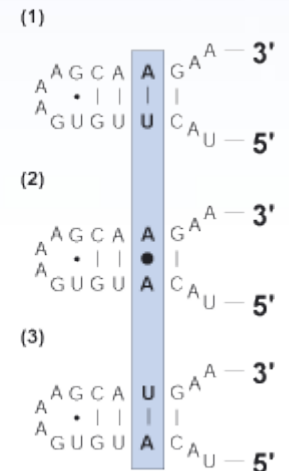
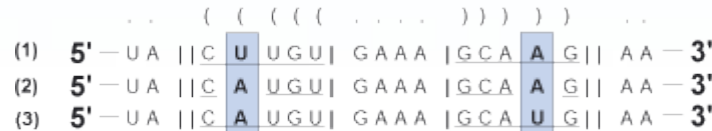
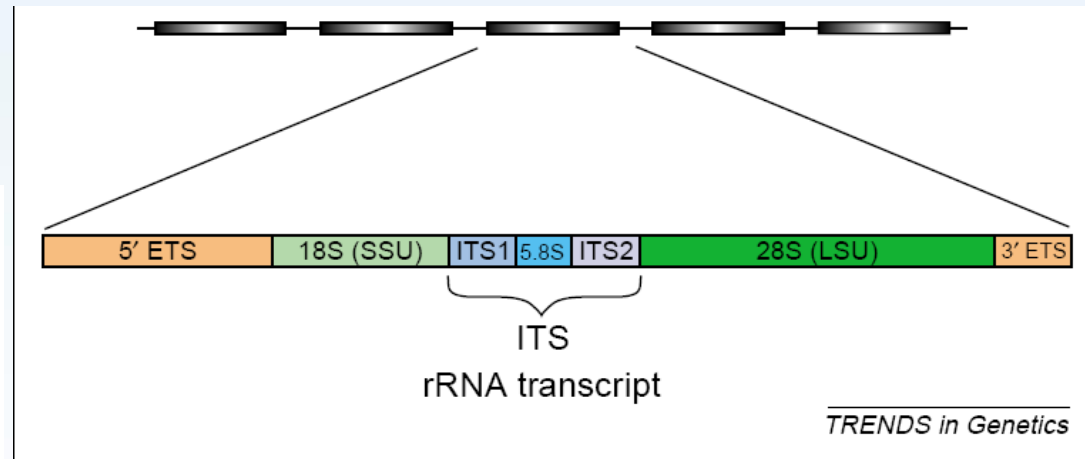
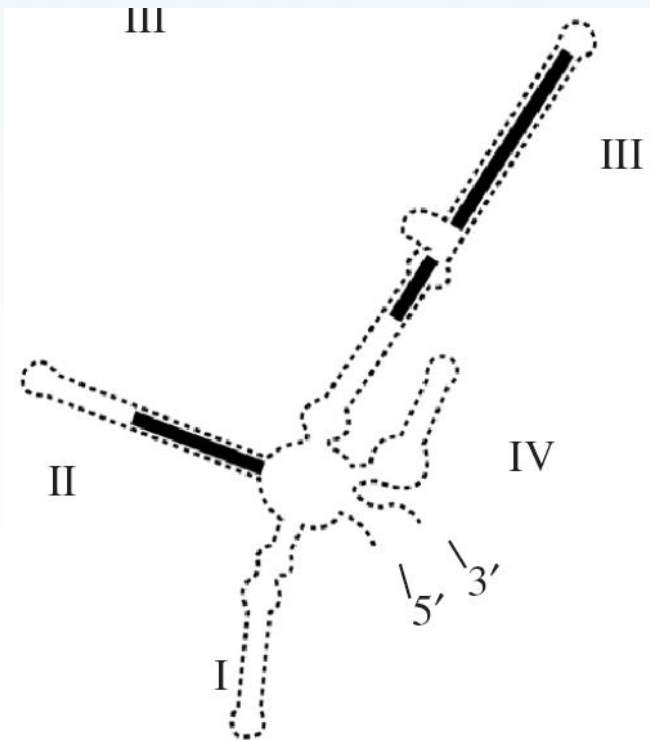
Good & Wake method

- test of *a priori* defined species
- linear regression of genetic and geographic distances should in single species go through the graph origin (gene flow with isolation-by-distance)
- Different regression indicates the presence of two distinct, genetically isolated species



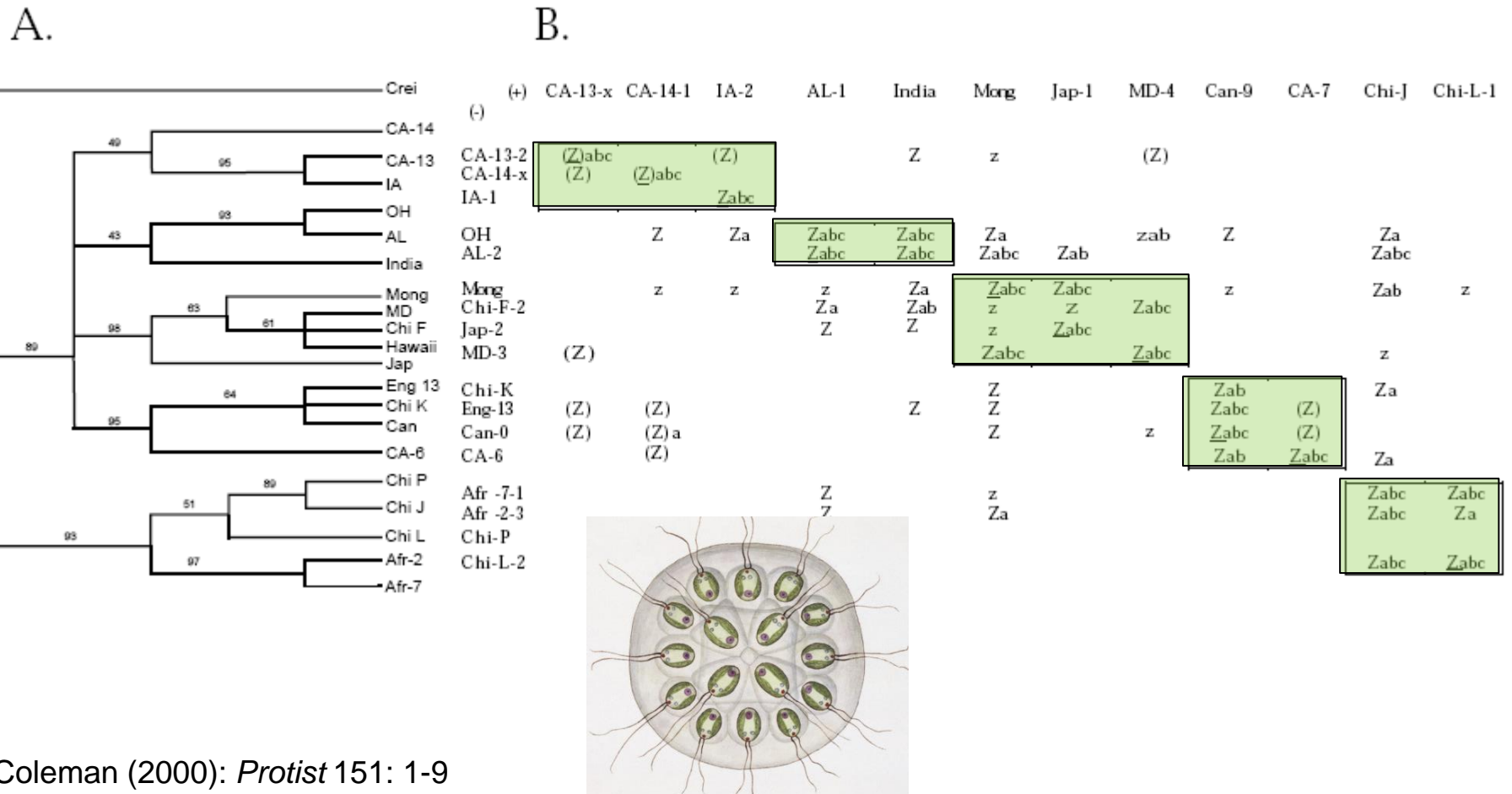
CBC concept

- Species delimited based on differences in conservative regions of the ITS2 molecule



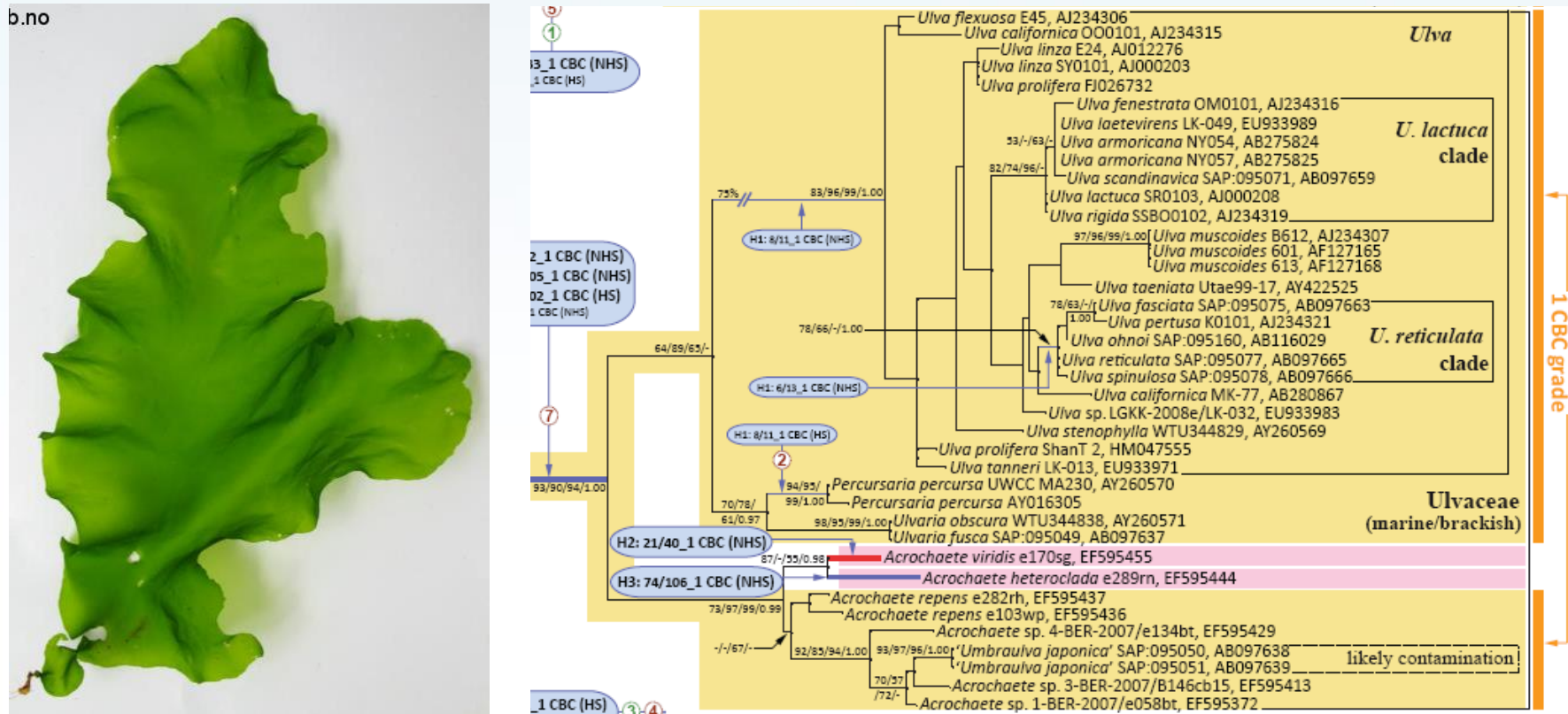
CBC concept

- Species delimited based on differences in conservative regions of the ITS2 molecule
 - correlation between CBC and sexual compatibility (*Gonium*)



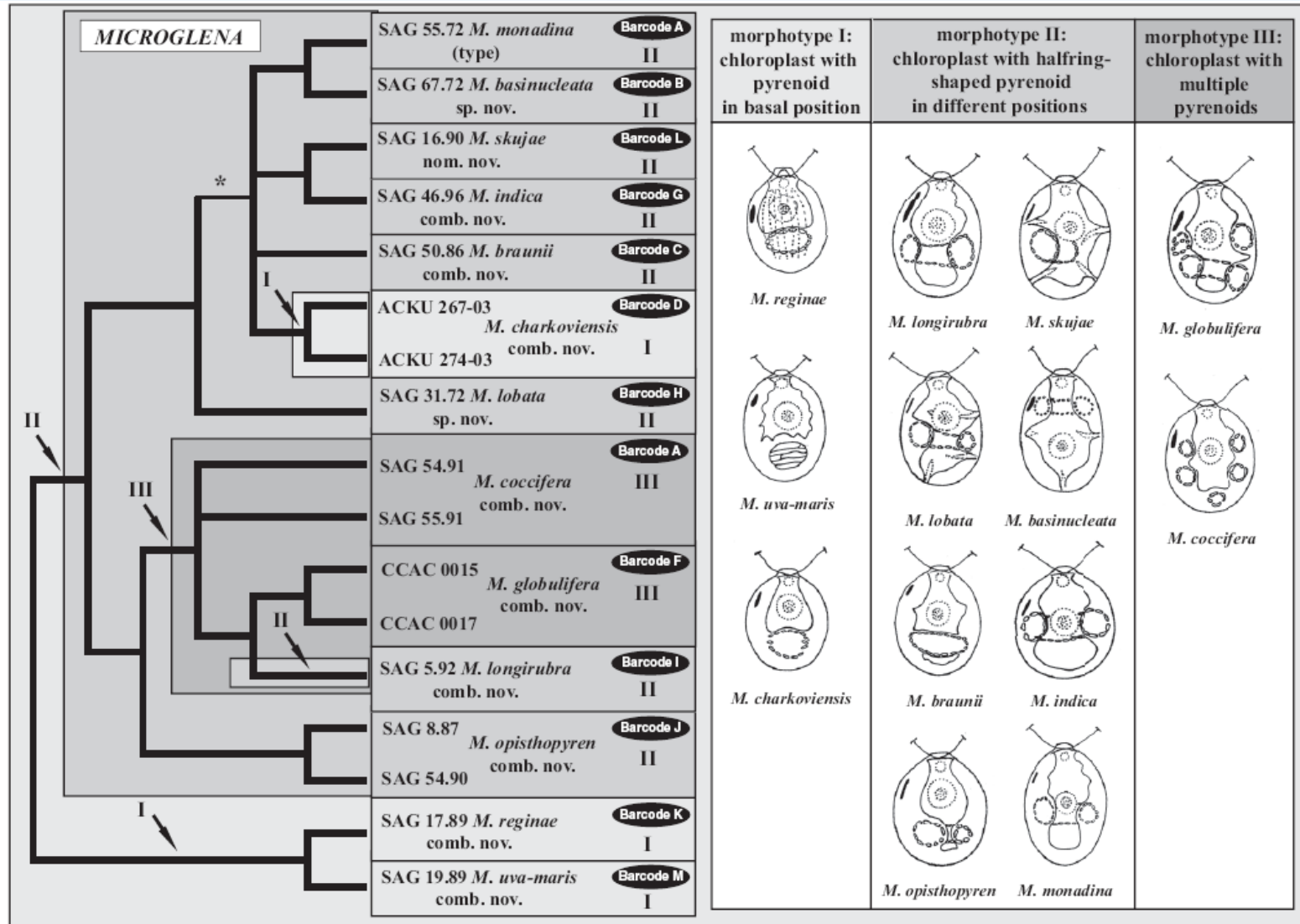
CBC concept

- Species delimited based on differences in conservative regions of the ITS2 molecule
 - not a universal concept
 - CBCs as a measure of genetic relation, not species marker



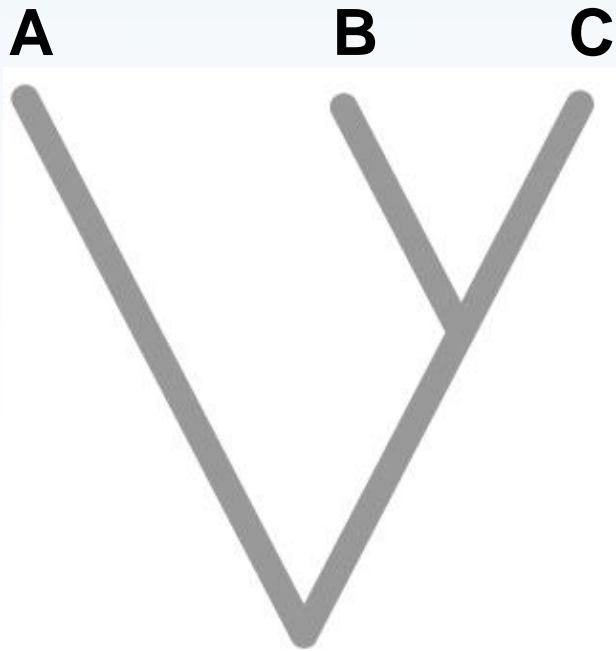
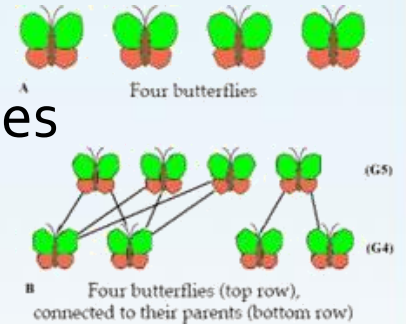
ITS2-barcode concept

- Again, CBCs is a measure of genetic relation, not species marker

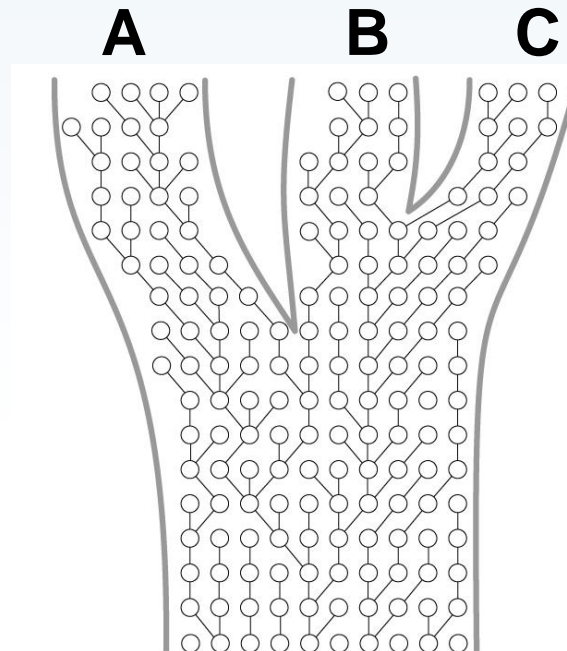


Coalescent theory

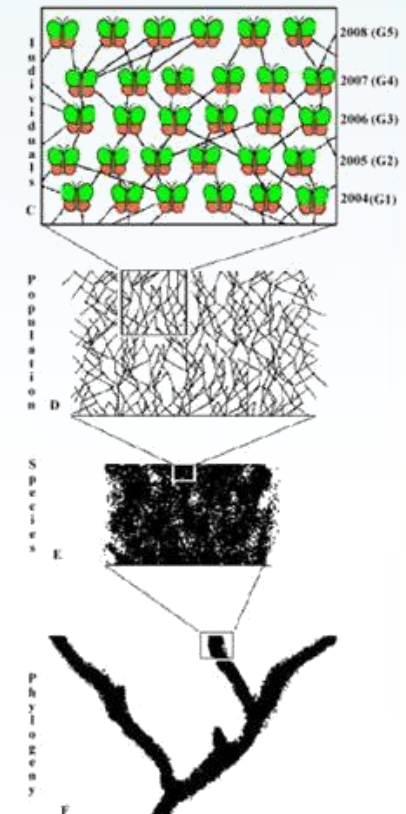
- Linking phylogenetics and population genetics
 - Identification of independently evolving lineages
 - GMYC, bPTP, ABGD, BP&P,



Phylogenetics

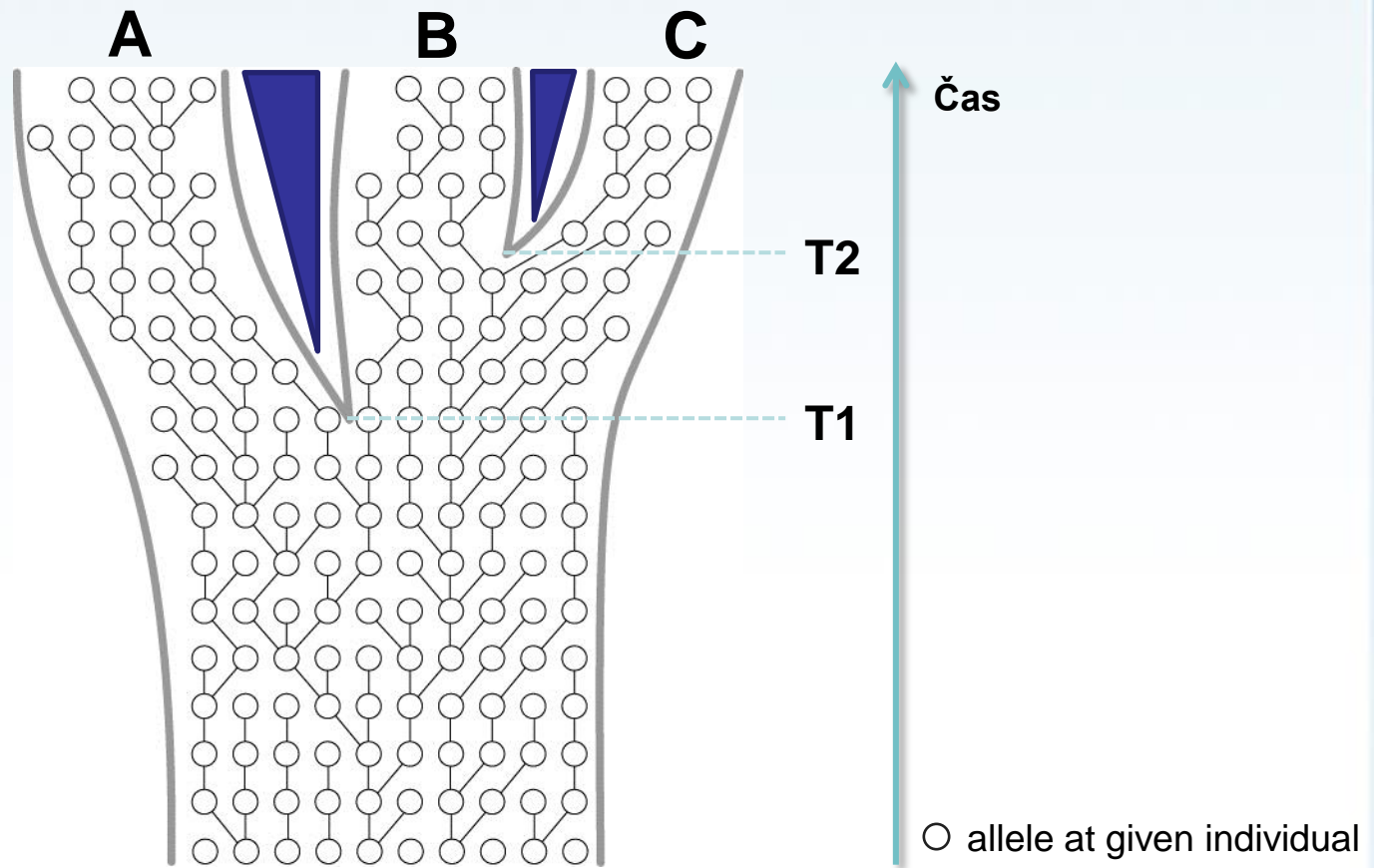


Population genetics



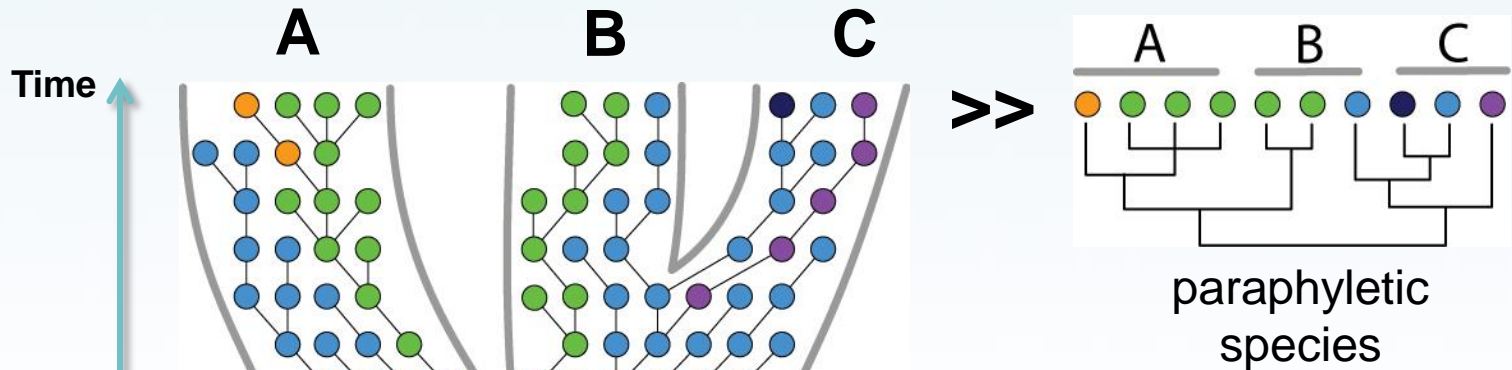
Coalescent theory

- Coalescence processes (Wright-Fisher)
 - allelic transfer to next generations
 - allelic frequencies vary across generations



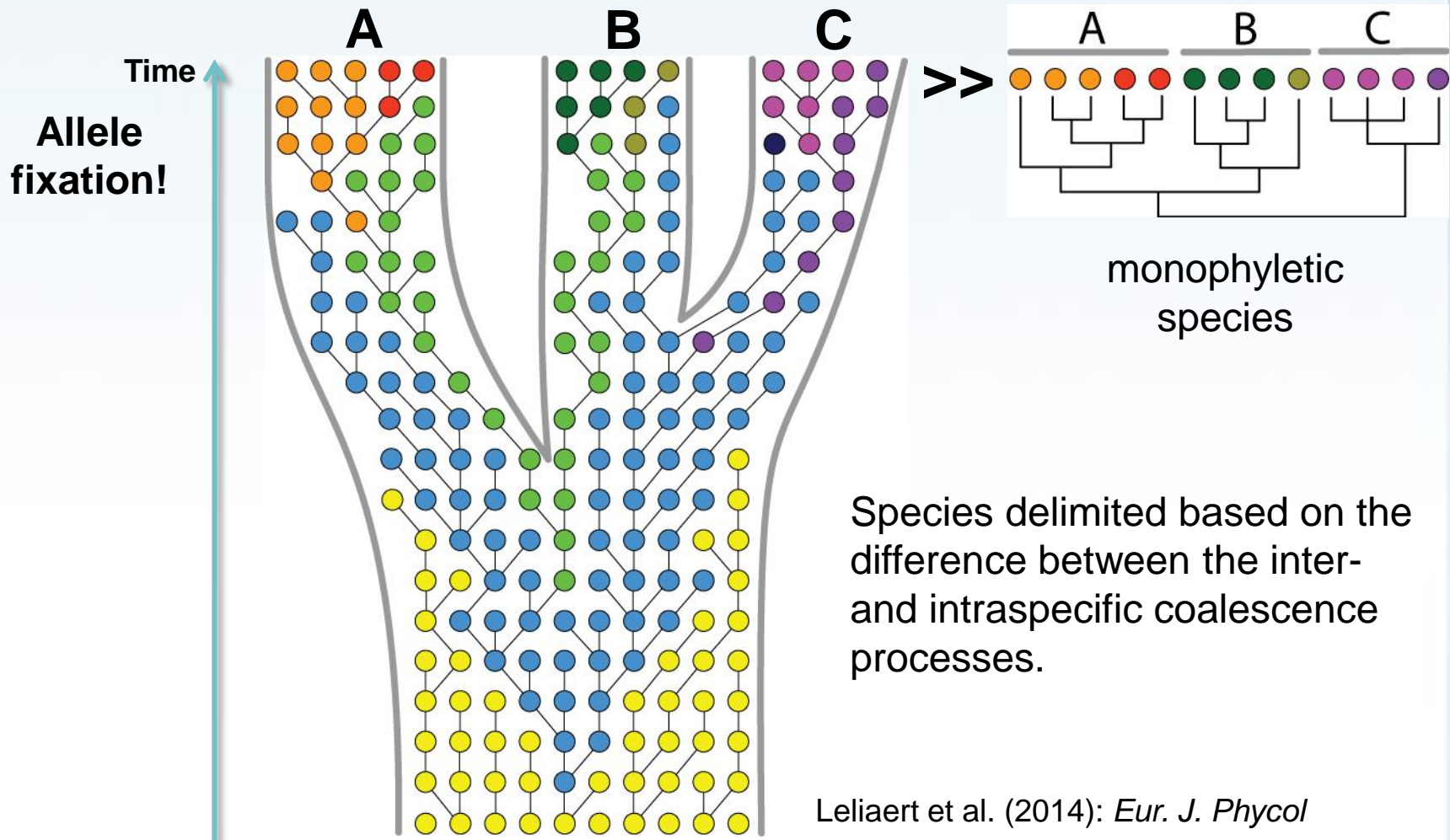
Coalescent theory

- Coalescence processes (Wright-Fisher)
 - during the coalescence, gene tree topologies resolve the species as polyphyletic, paraphyletic, and monophyletic



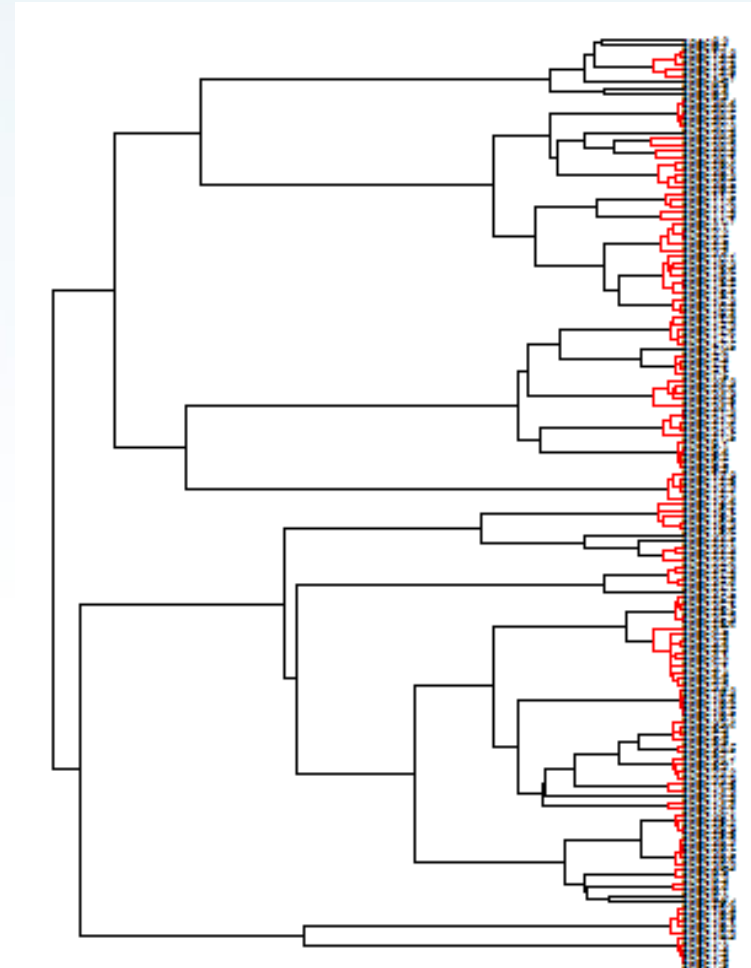
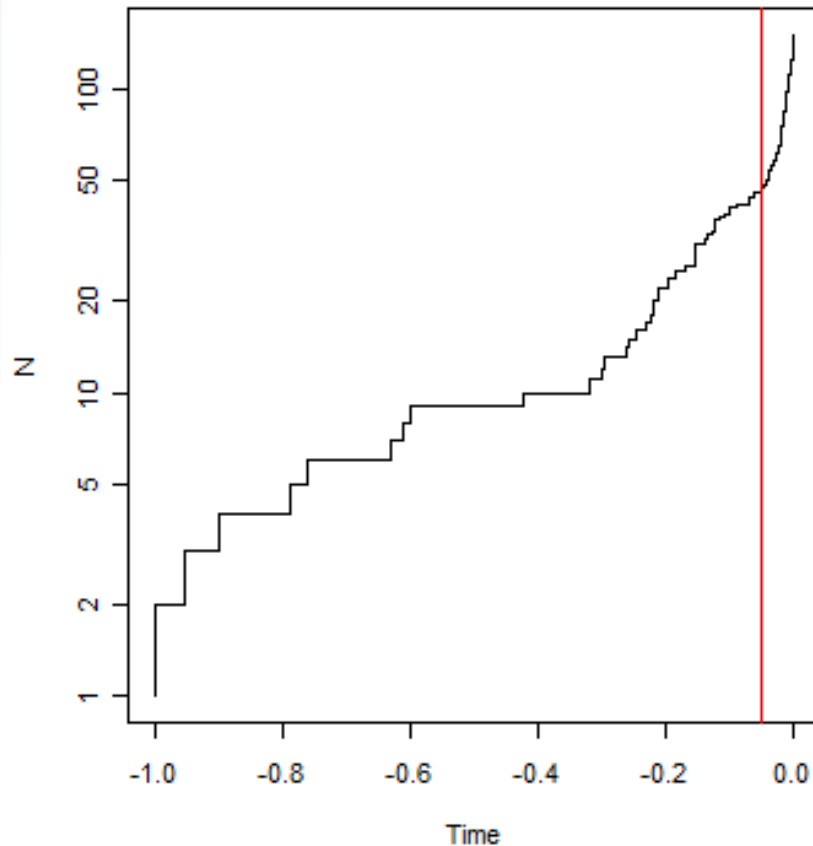
Coalescent theory

- Coalescence processes(Wright-Fisher)
 - during the coalescence, gene tree topologies resolve the species as polyphyletic, paraphyletic, and monophyletic



GMYC method

- Different branching patterns within and among species
 - A combination of species diversification (Yule model) and intraspecific coalescence models



GMYC method

- Different branching patterns within and among species
 - statistical test, confidence interval

```
>summary(result)
```

```
Result of GMYC species delimitation
```

```
method: single
```

```
likelihood of null model: 858.9326
```

```
maximum likelihood of GMYC model: 872.3755
```

```
likelihood ratio: 26.88581
```

```
result of LR test: 6.220952e-06***
```

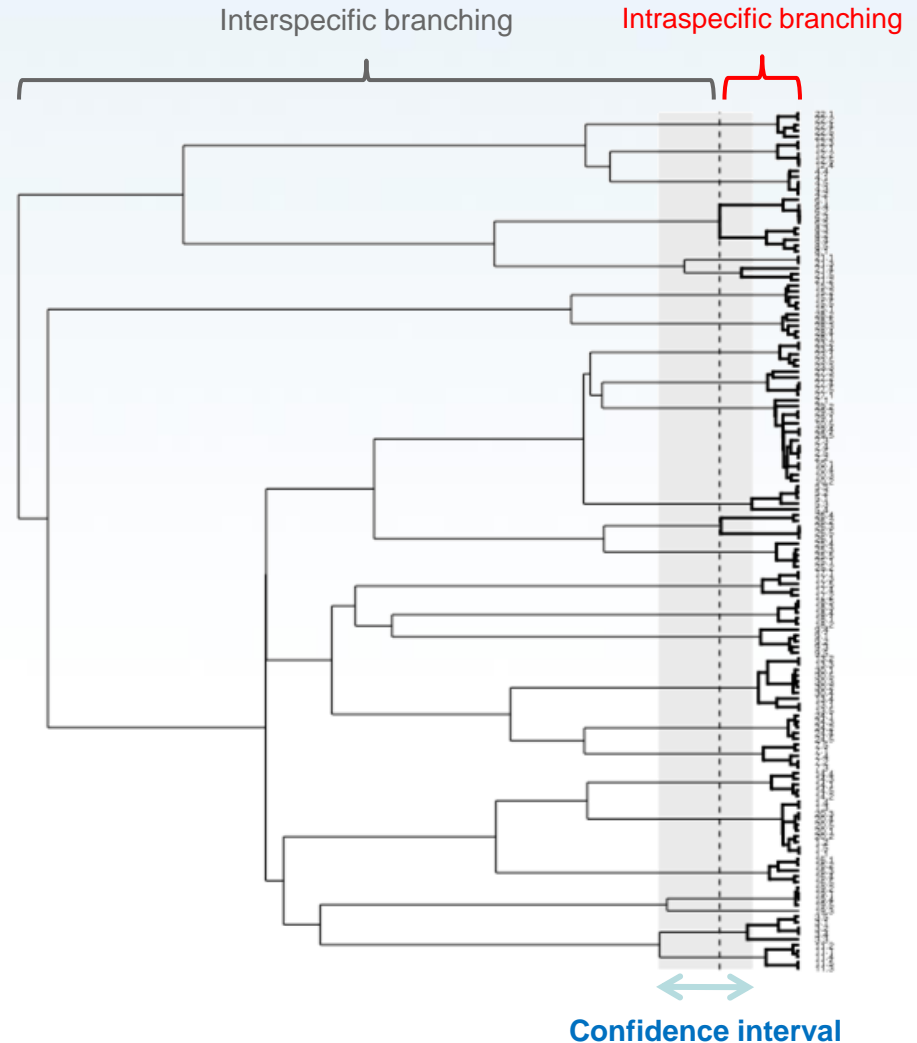
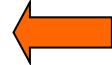
```
number of ML clusters: 33
```

```
confidence interval: 31-34
```

```
number of ML entities: 46
```

```
confidence interval: 42-56
```

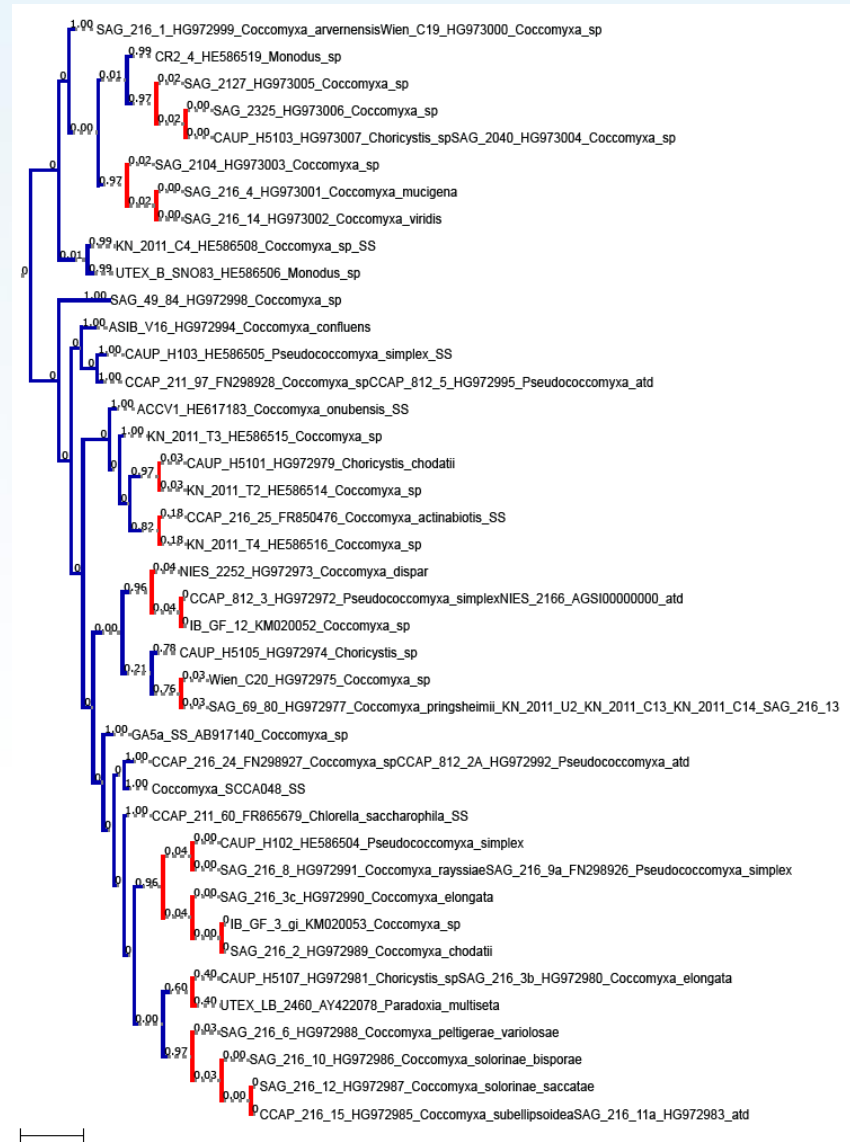
```
threshold time: -0.05174417
```



bPTP

- Bayesian Poisson tree processes method

- Similar to GMYC
- No need of ultrametric tree
- Using directly the number of substitutions (instead of time) to simulate speciation and coalescent events

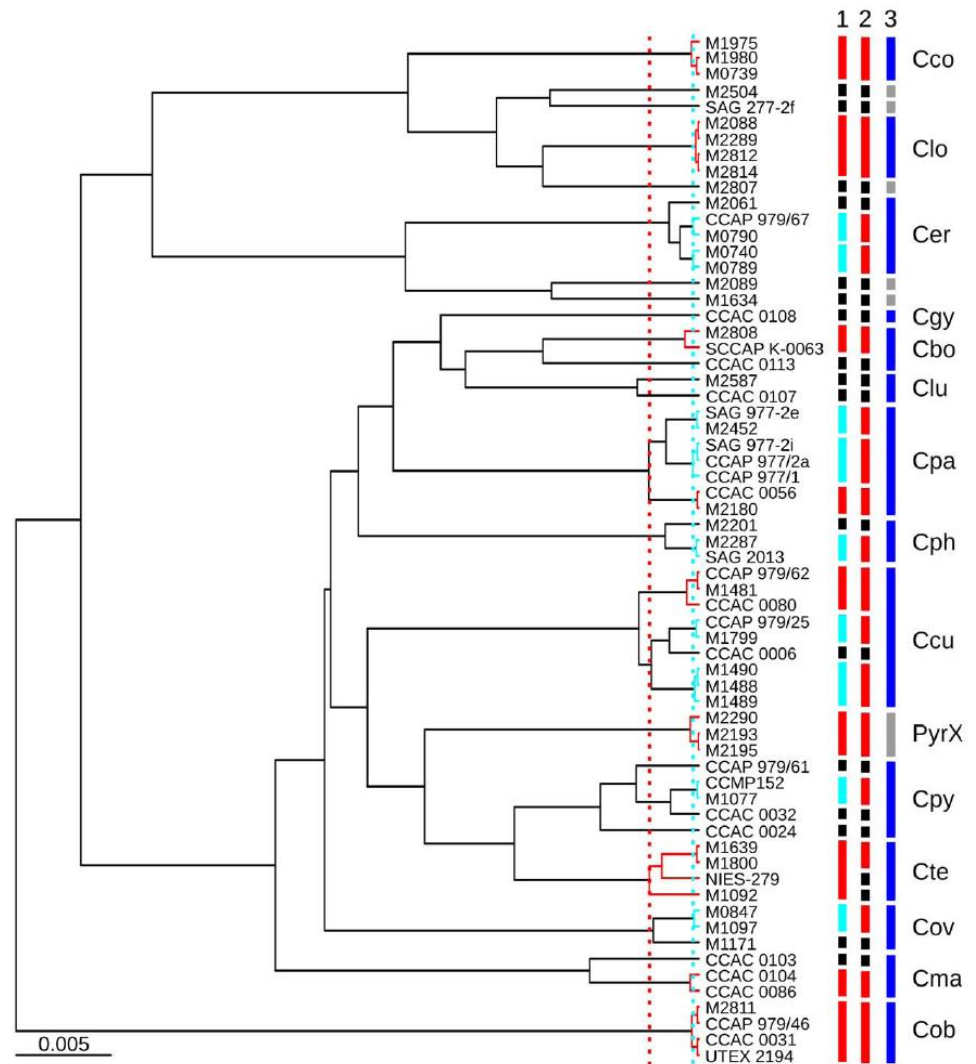


DNA-based species delimitation methods

Reference	Existing species	Species after delimitation	No. of samples	No. of loci	Discovery approaches	Validation approaches
Avila <i>et al.</i> (2006)	6	>12	293	1	Statistical parsimony (NCA)	None
Barrett & Freudenstein (2011)	3	3	162	5	Morphological cluster analysis, PCA	BPP
Burbrink <i>et al.</i> (2011)	1	1	45	3	Structurama	BPP
Camargo <i>et al.</i> (2012)	3	1	505	4	None	spedeSTEM, BPP, ABC
Carstens & Dewey (2010)	3	7	42	6	None	spedeSTEM, Bayes Factors
Carstens & Satler (2013)	1	2	82	21	Structurama, Gaussian Clustering	spedeSTEM, BPP
Duminil <i>et al.</i> (2012)	Unknown	Unstated	103	7	Morphometric clustering; structure	None
Esselstyn <i>et al.</i> (2012)	13	18–19	413	1	GMYC	None
Florio <i>et al.</i> (2012);	1	2	111	1	Canonical variates analysis	None
Flot <i>et al.</i> (2010)	1		74	3	Haplowebs	None
Hamilton <i>et al.</i> (2011)	4	3	147	1	Combo WP and barcoding gap, monophyly, GMYC	
Kelly <i>et al.</i> (2008)	39	1	114	1	WP	None
Leaché & Fujita (2010)	1	3	51	6	Structure	BPP
Leavitt <i>et al.</i> (2012)	19	2	414	6	Structure	BPP, mean genetic distance
Leliart <i>et al.</i> (2009)	19	13	175	1	GMYC, statistical parsimony (NCA)—clades that exceed 95% cut off	None
Niemiller <i>et al.</i> (2012)	1	19	135	9	O'Meara clustering	BPP
Pons <i>et al.</i> (2006)	24	54	468	1	Parsimony network, PAA, CHA, WP, GMYC	None
Puillandre <i>et al.</i> (2009)	1	4	44	2	Elliptic Fourier analysis on shape to the mollusc shell; qualitative phylogenetic evidence	None
Puillandre <i>et al.</i> (2012)	43	27	1000	2	GMYC, ABGD	None

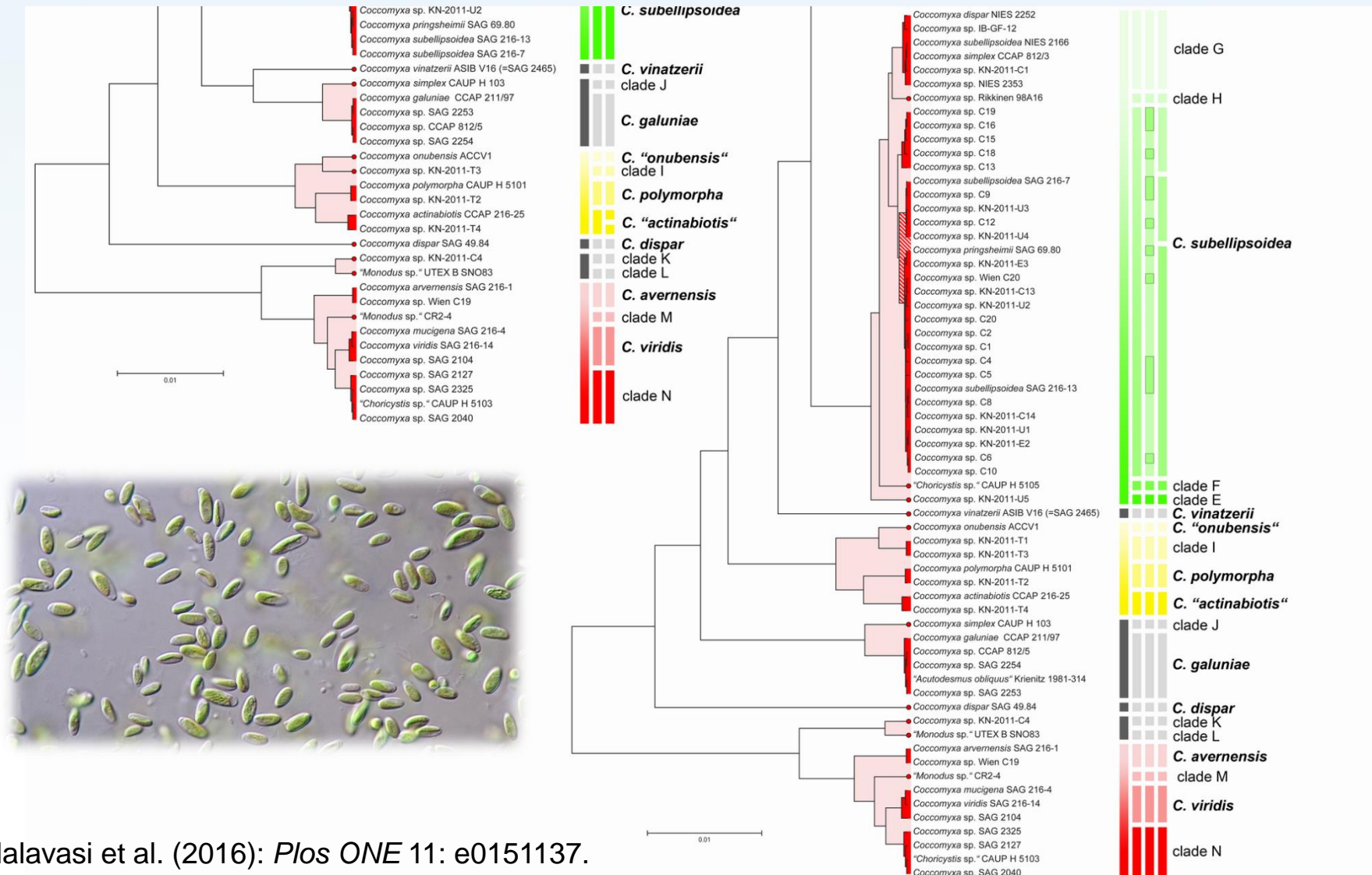
Pitfalls of DNA-based species delimitation

- Incongruence between species delimited by GMYC and by those delimited by a combined molecular and morphological approach



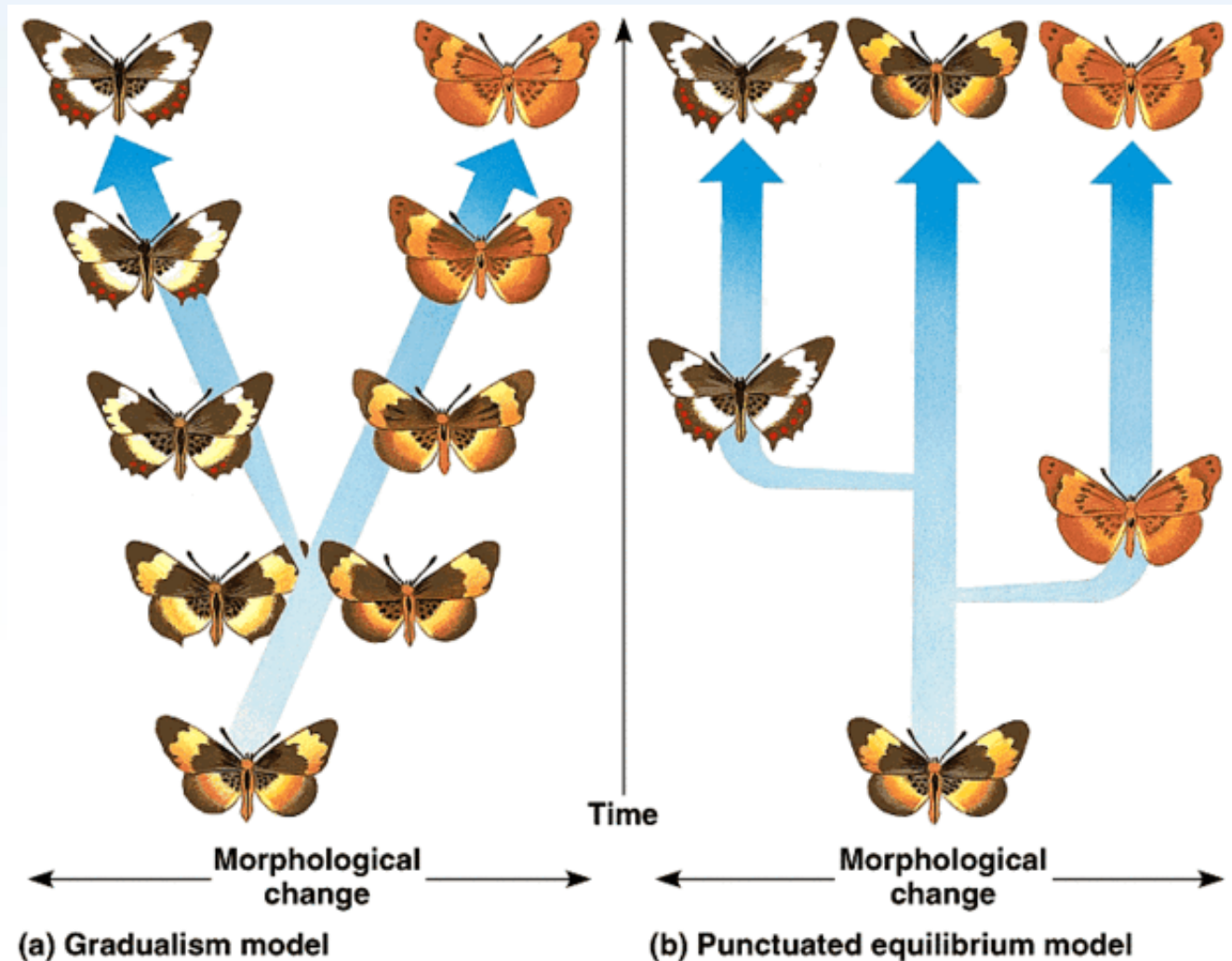
Pitfalls of DNA-based species delimitation

- Problems with taxon sampling, using identical sequences



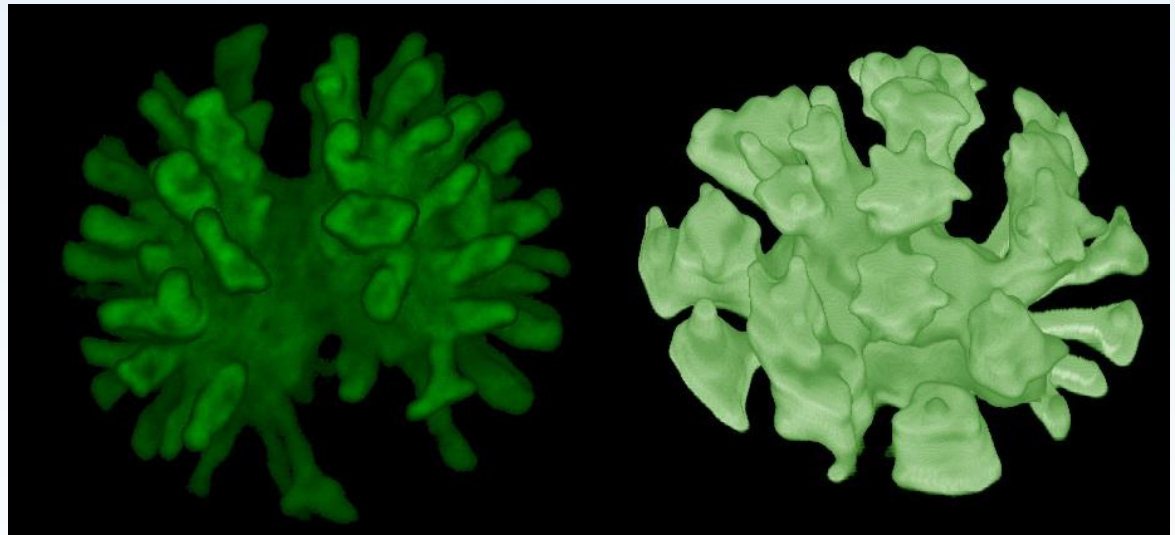
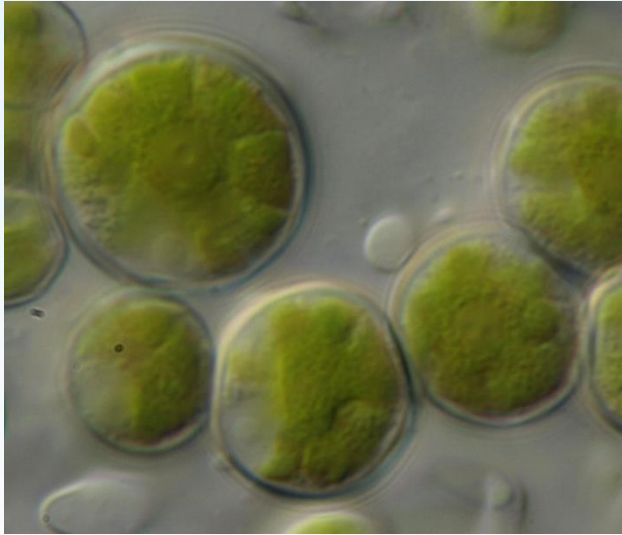
Universal species concept?

- Species are not rigid units, but evolving entities!
- A polyphasic, specific approach



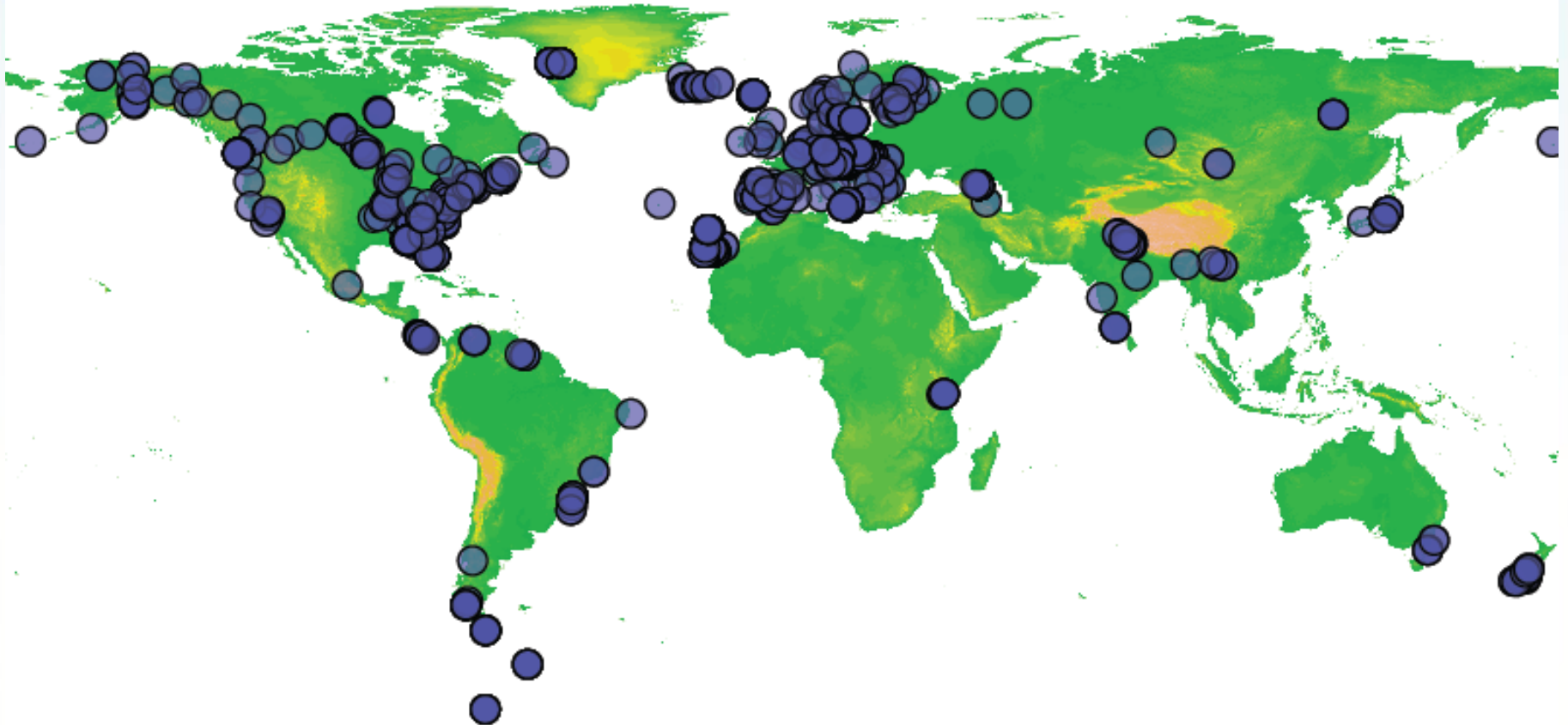
Species delimitation in *Asterochloris*

- *Asterochloris* – one of the most common lichen symbionts



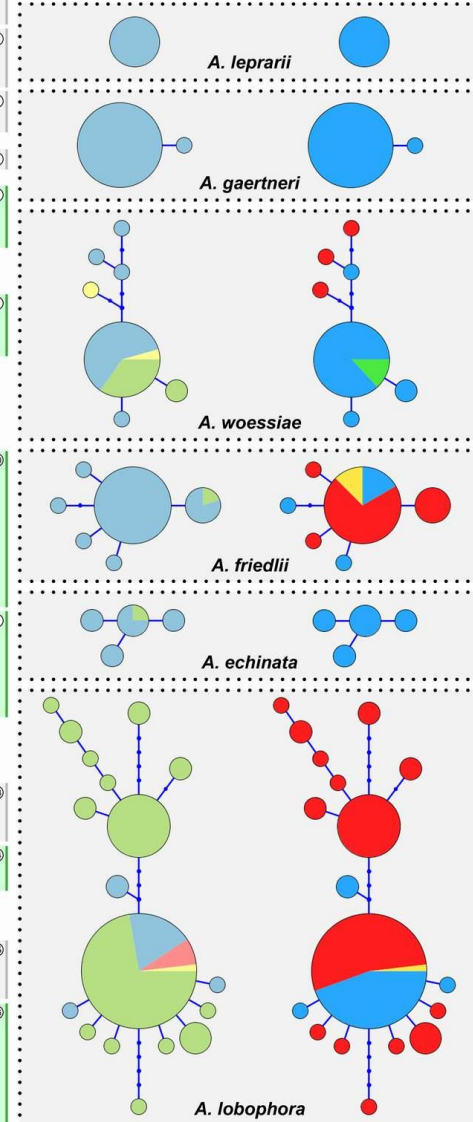
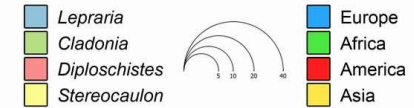
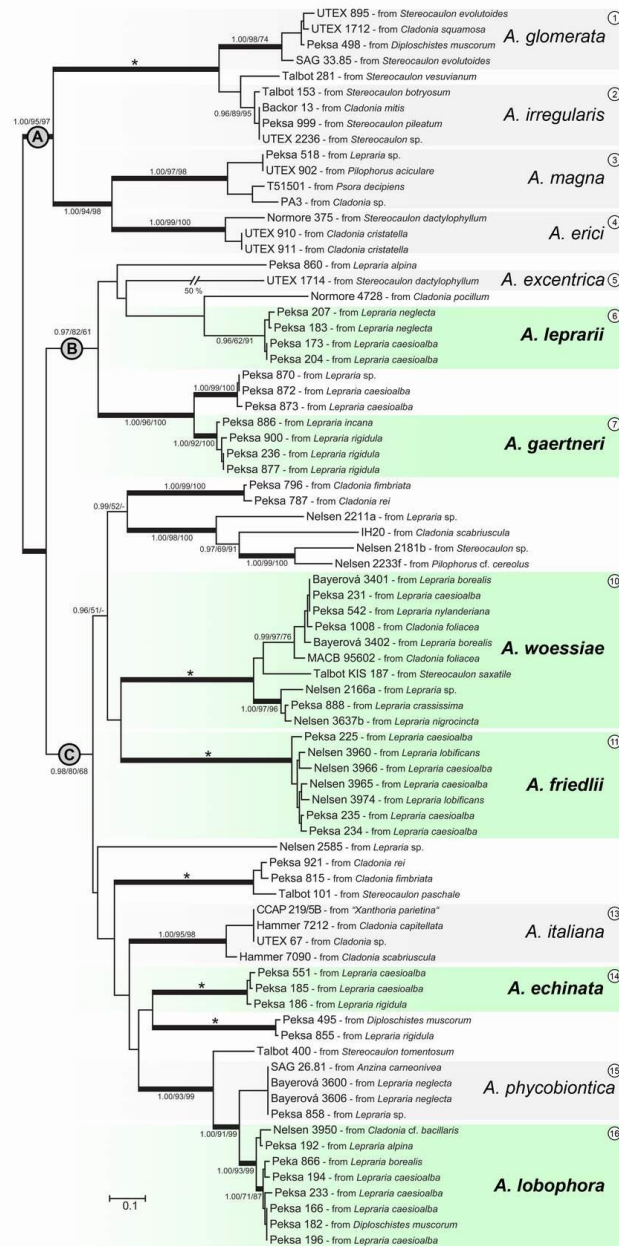
Species delimitation in *Asterochloris*

- A total of 1509 lichen samples
 - Algal ITS rDNA + actin sequences
 - Substrate data, mycobiont identity (ITS rDNA), climatic data
 - Culturing (morphological analyses)



Species delimitation in *Asterochloris*

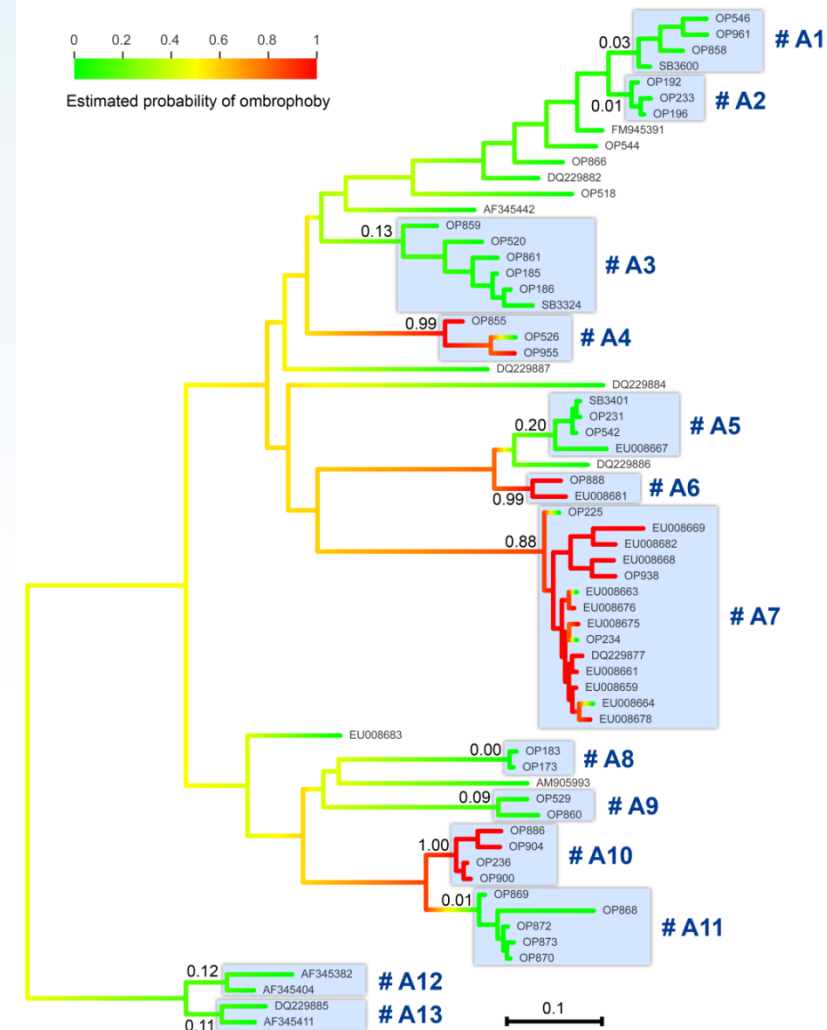
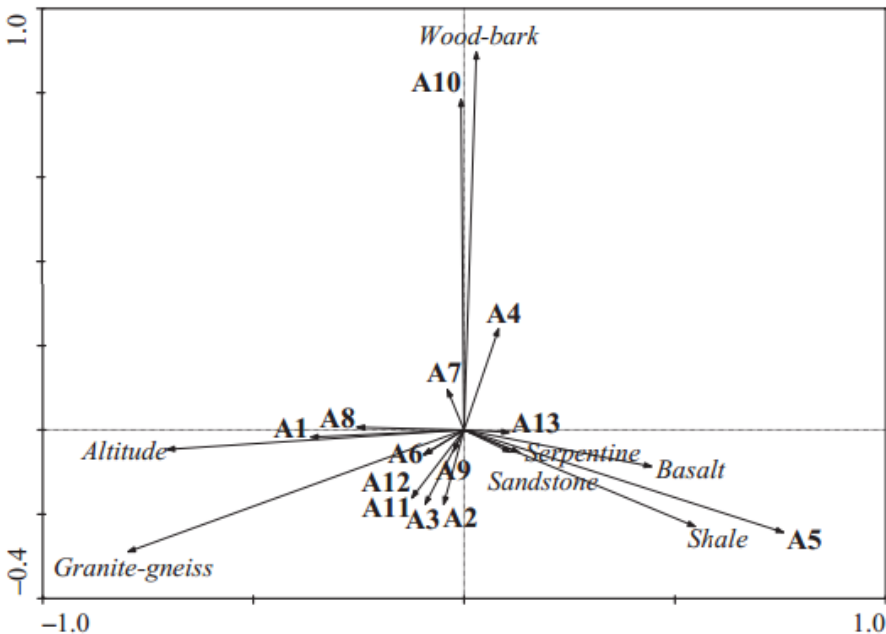
- molecular data
(ITS rDNA + actin)



Species delimitation in *Asterochloris*

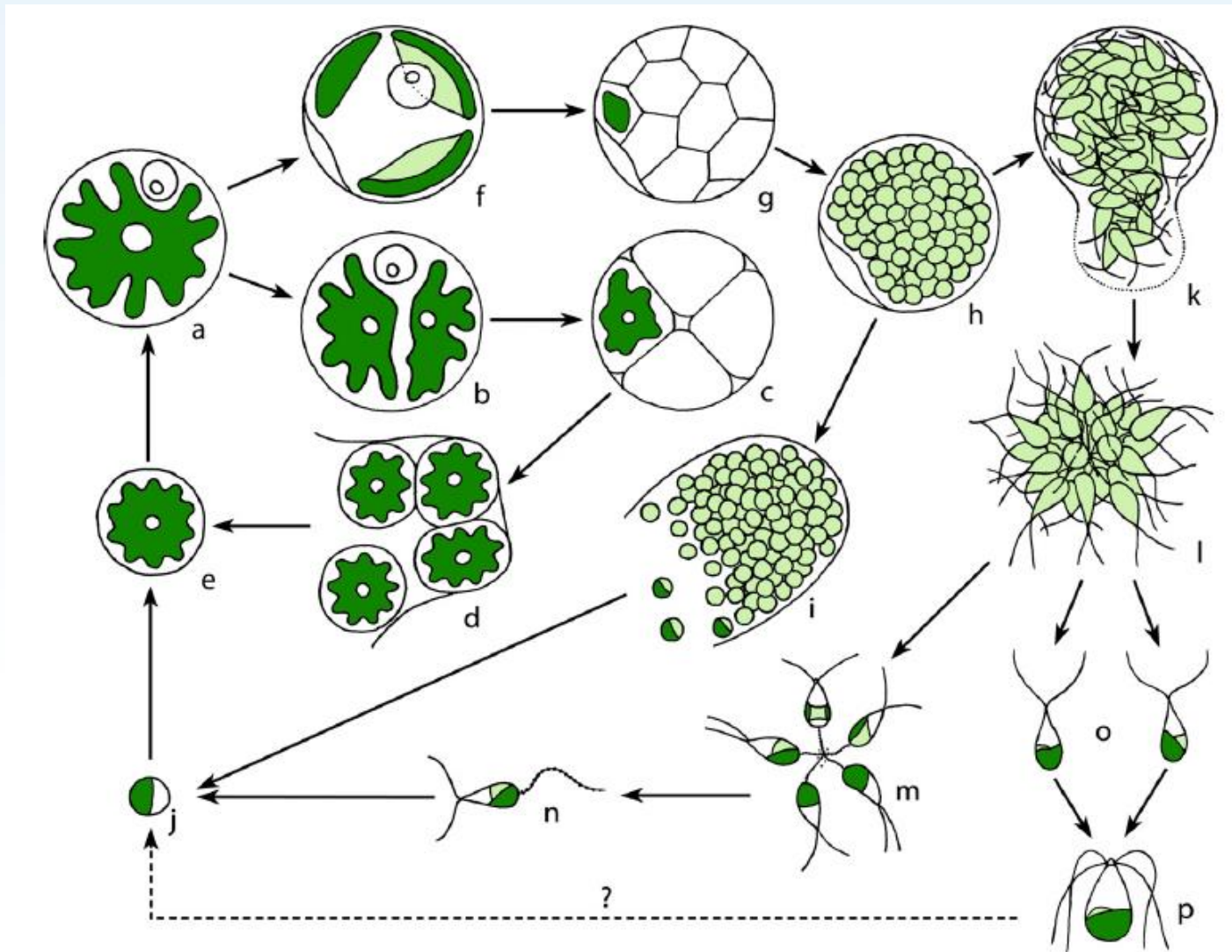
- ecology
 - substrate specificity, altitude, ombrotrophy

Trait	Pagel's λ		
	λ	Likelihood ratio	P-value
Exposure to rain	0.946	1.53	<0.0001
Altitude	0.045	1.01	<0.0001
Substrate type	0.652	1.05	0.0011



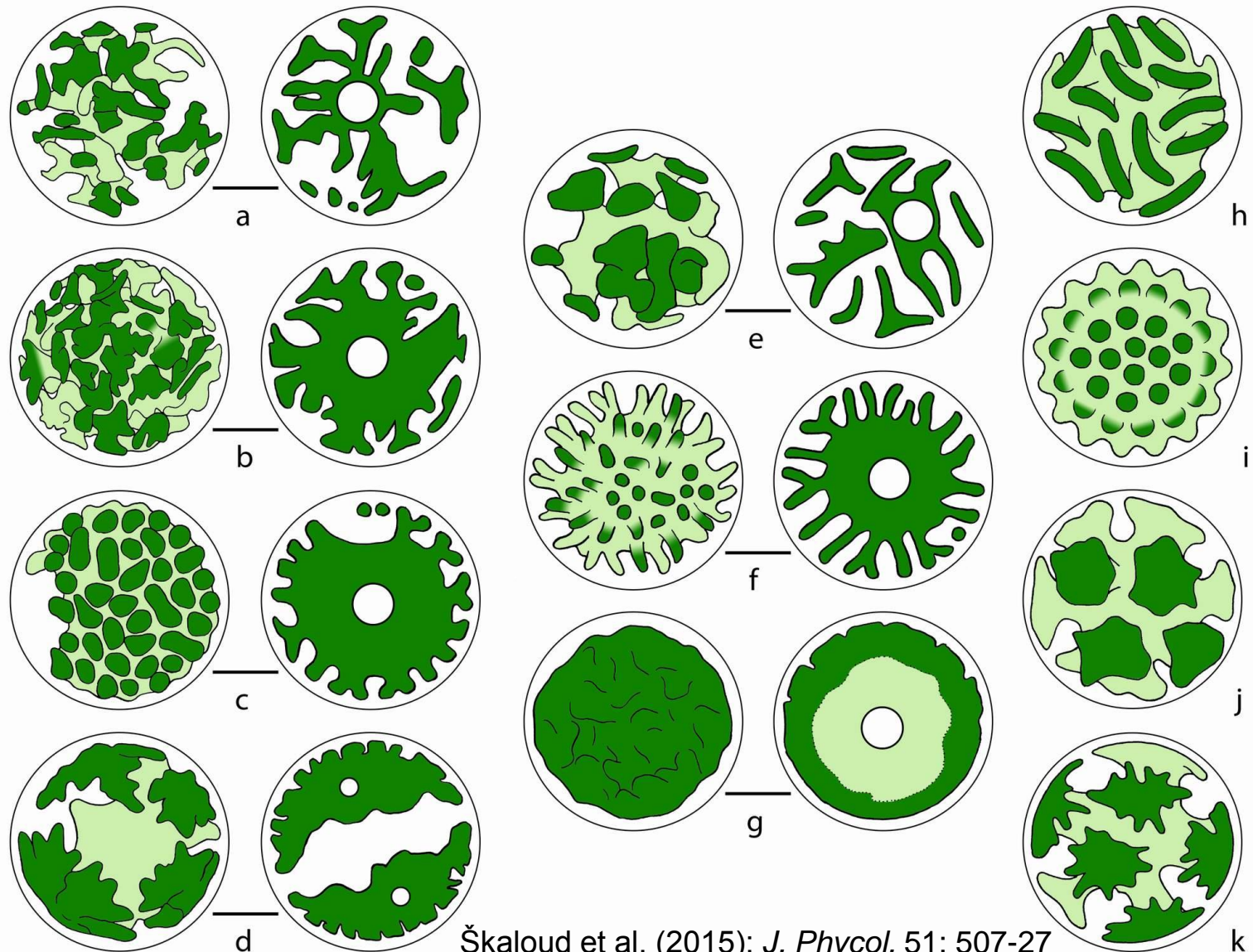
Species delimitation in *Asterochloris*

- Ontogeny



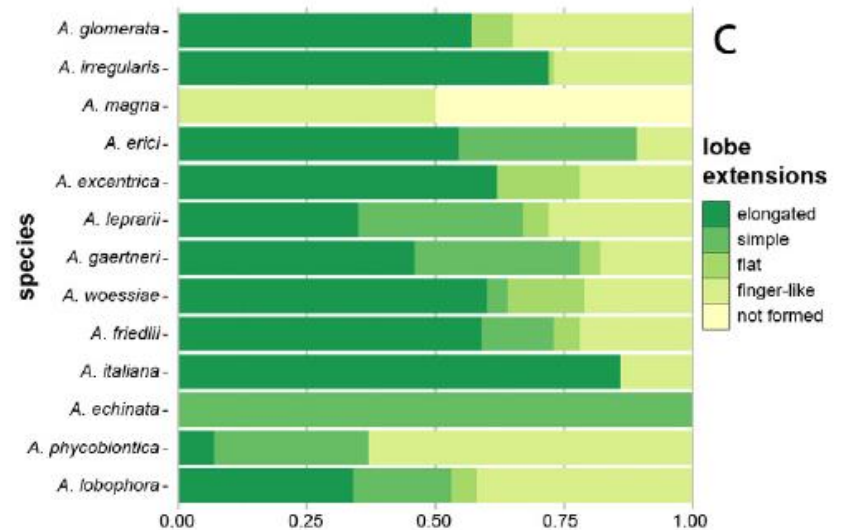
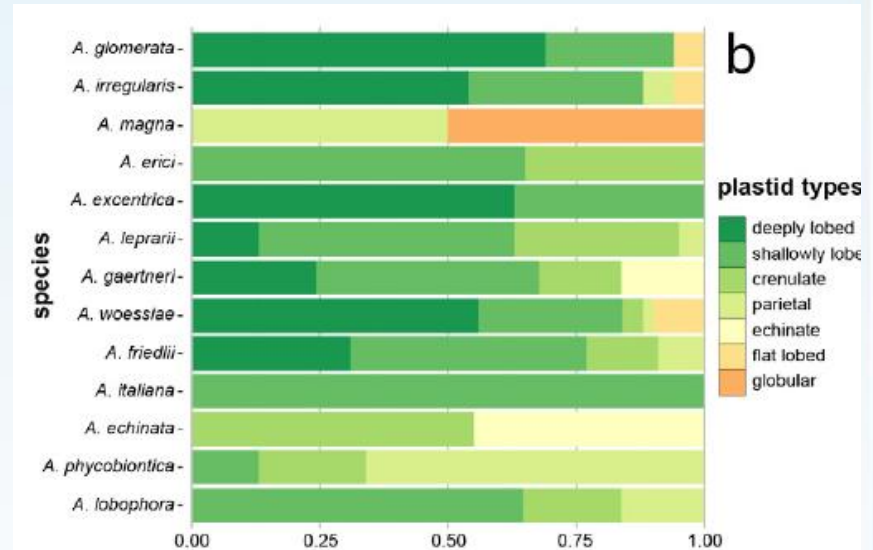
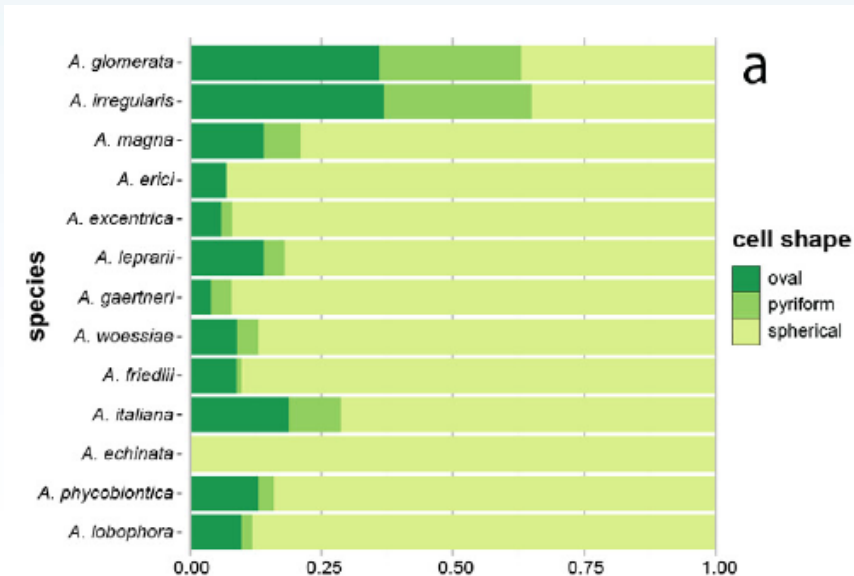
Species delimitation in *Asterochloris*

- Chloroplast morphology



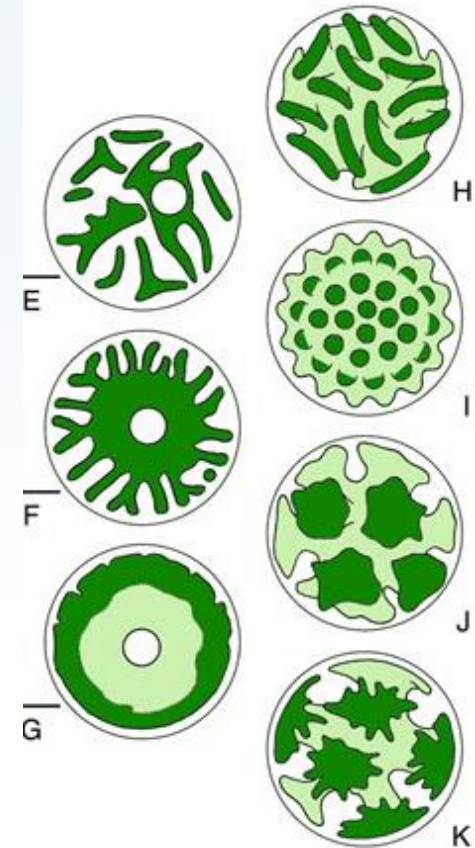
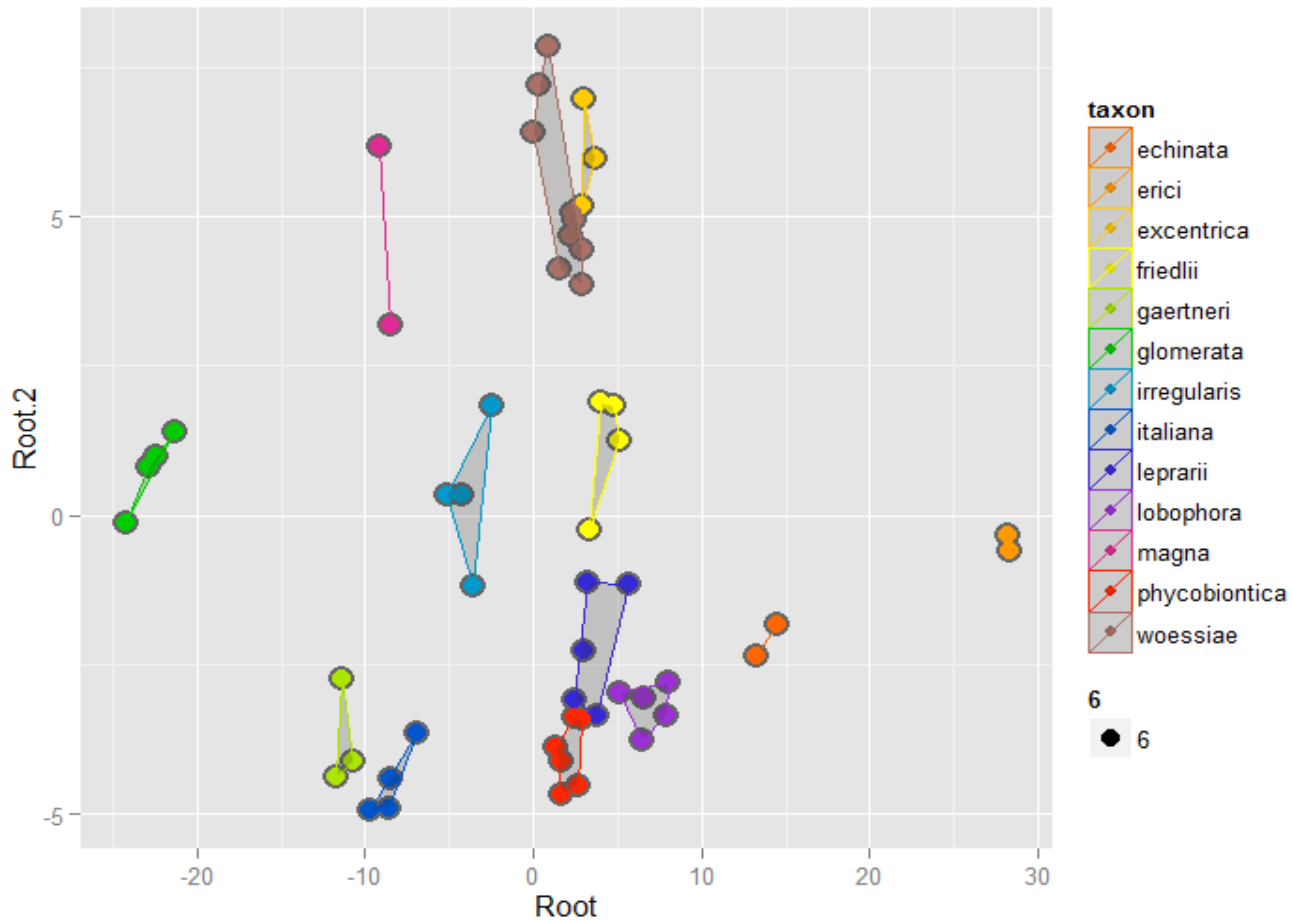
Species delimitation in *Asterochloris*

- Morphology
 - cell shape, cell dimensions, chloroplast shape, number of zoo- and aplanospores



Species delimitation in *Asterochloris*

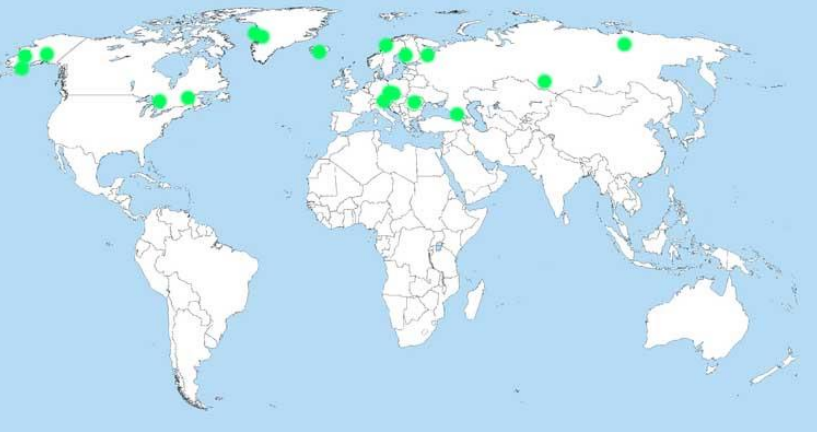
- Morphology – canonical discriminant analysis
 - cell shape, cell dimensions, chloroplast shape, number of zoo- and aplanospores



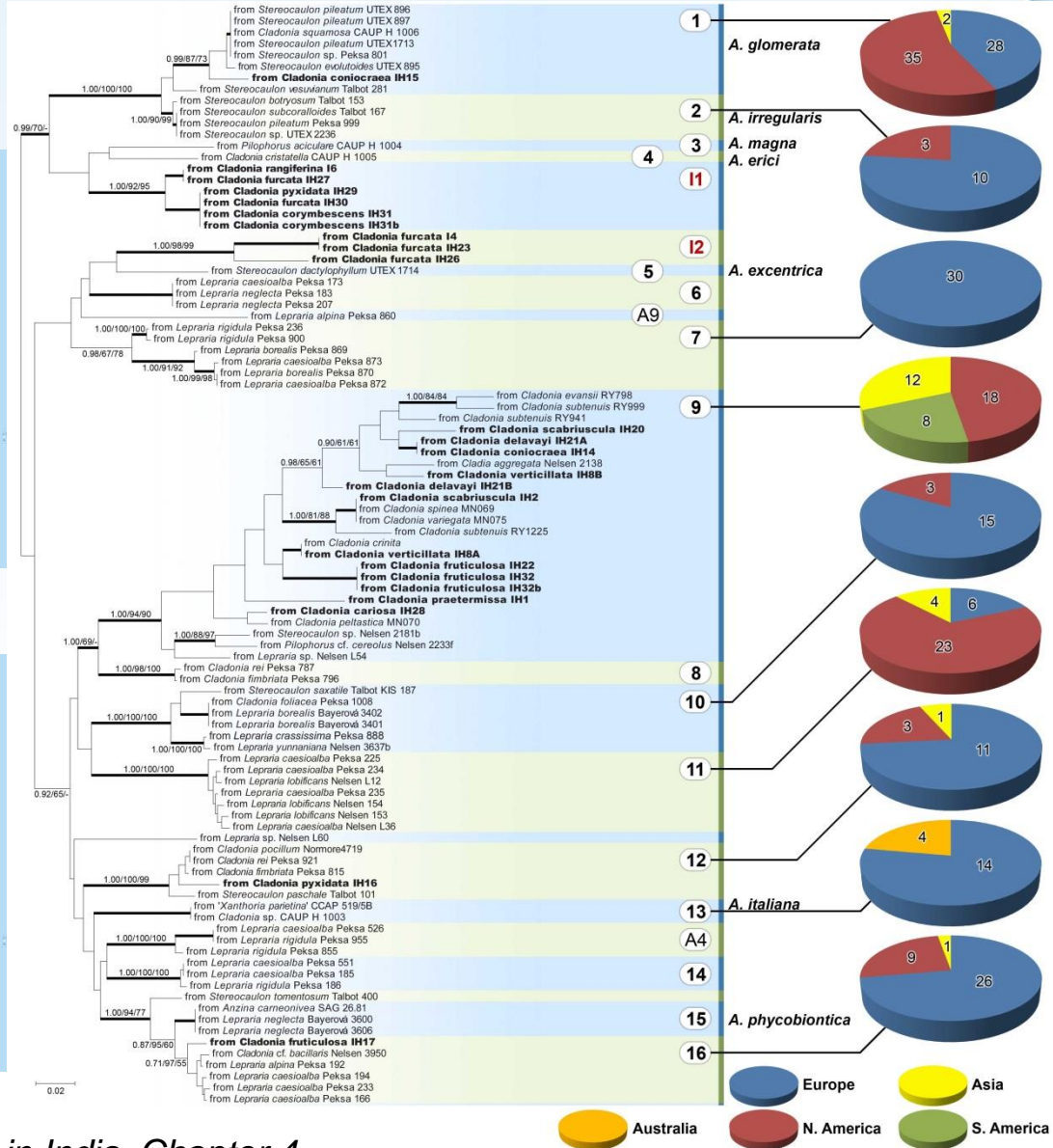
Species delimitation in *Asterochloris*

- Biogeography

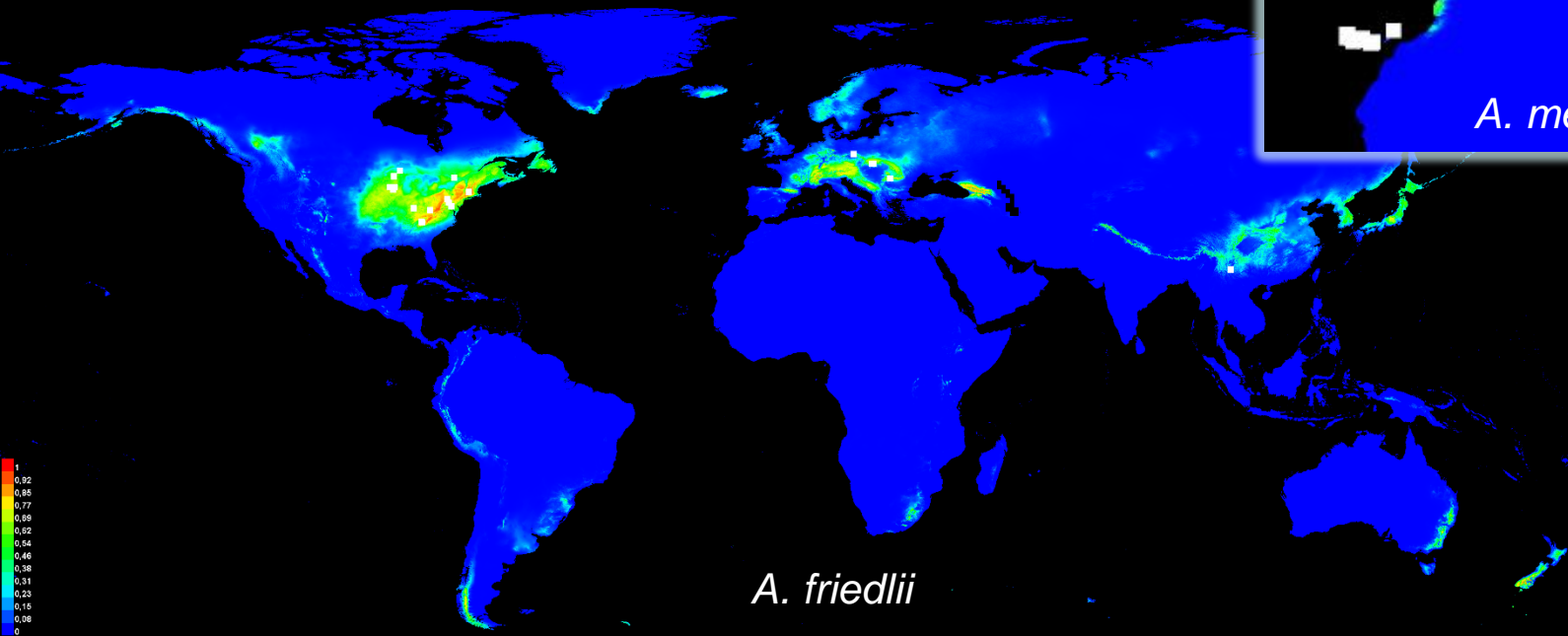
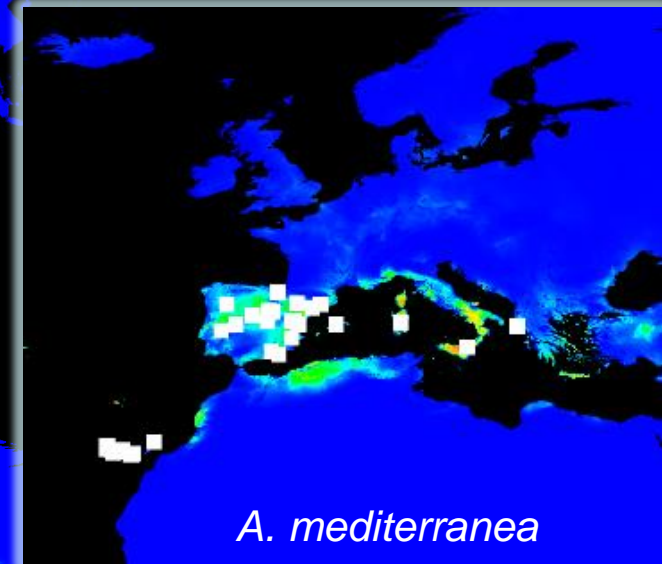
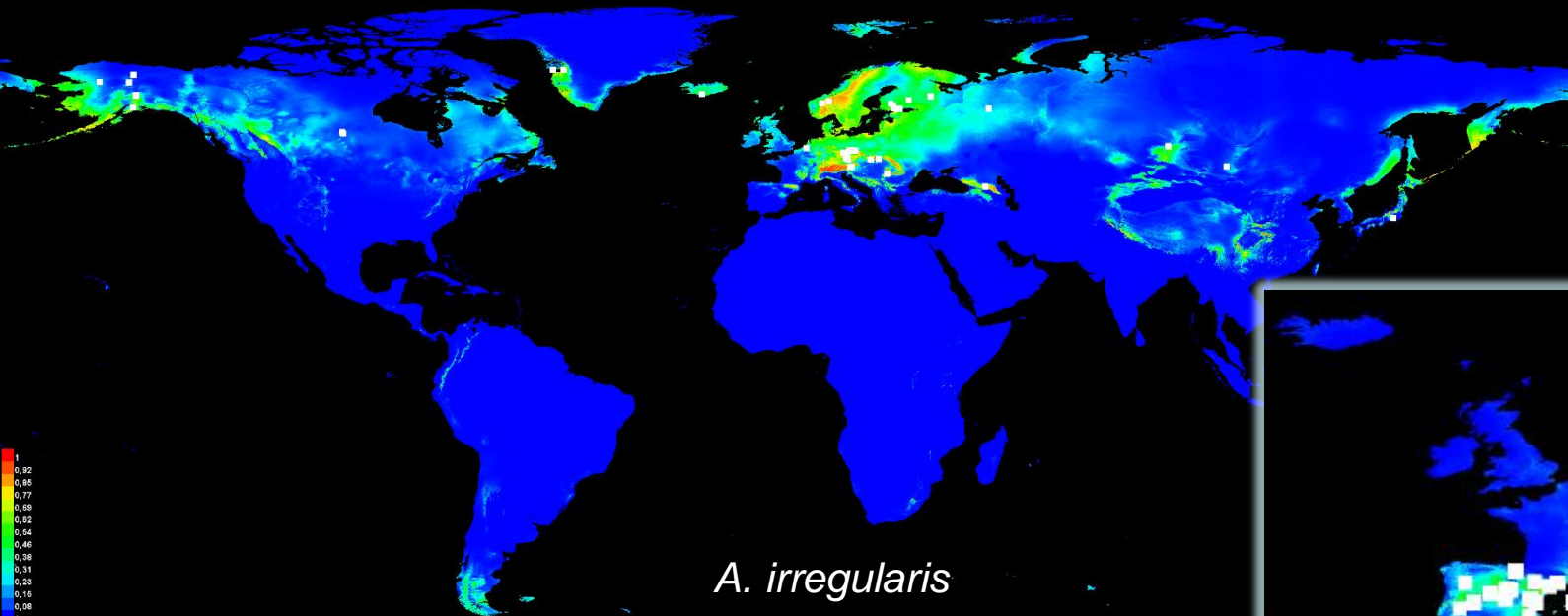
A. irregularis



clade 9

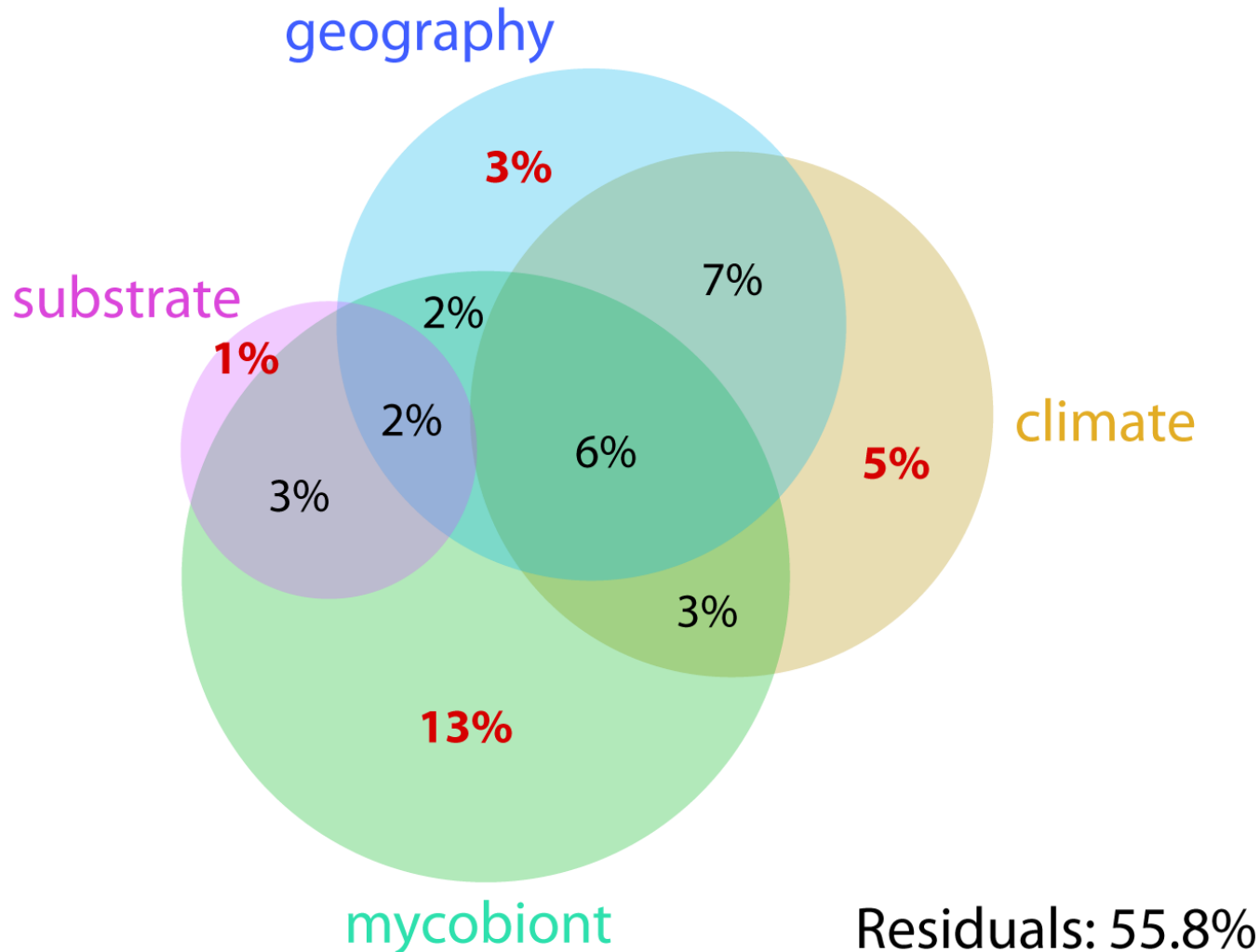


- Biogeography: niche modelling



Species delimitation in *Asterochloris*

- Mycobiont selectivity

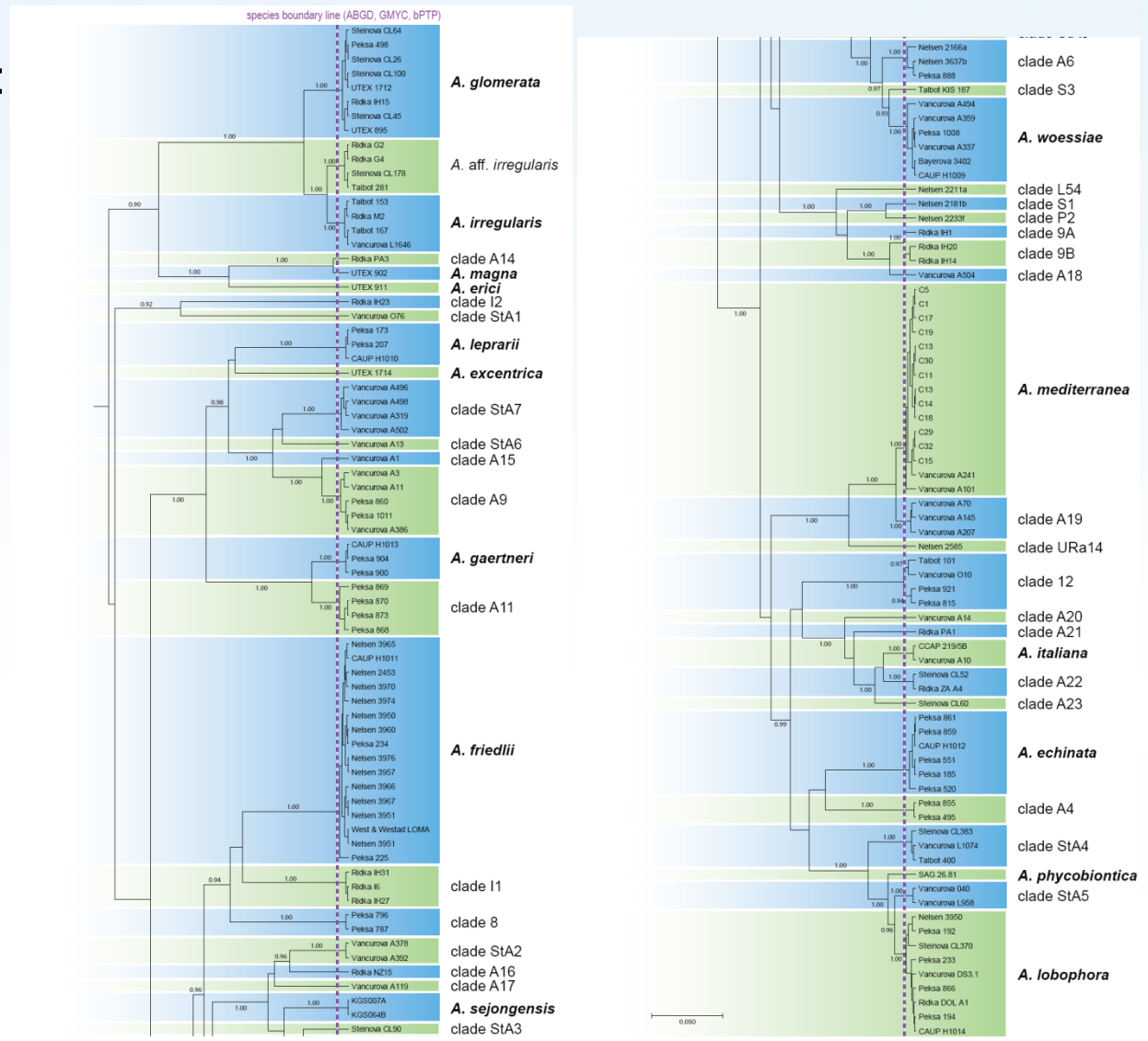


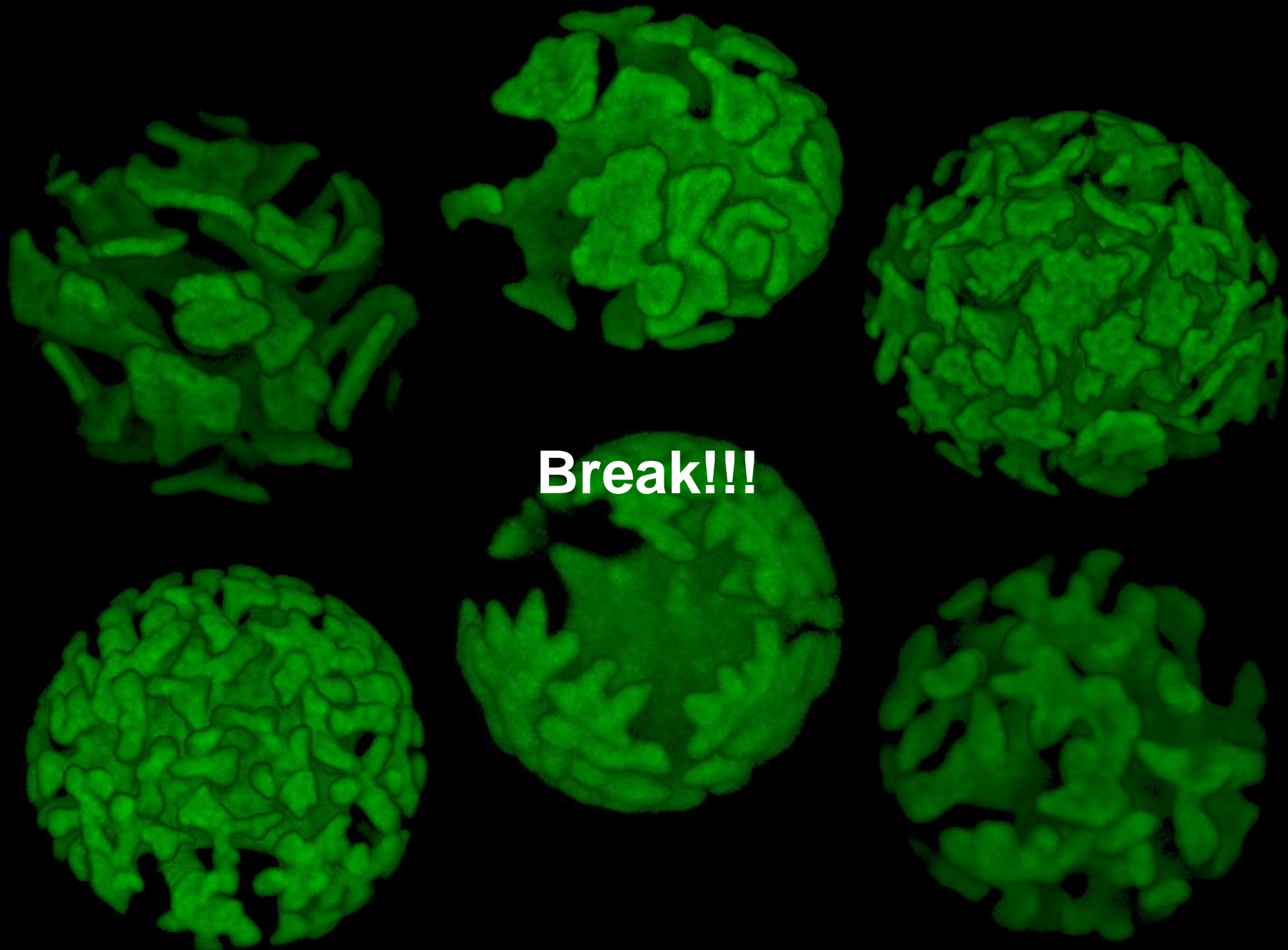
Species delimitation in *Asterochloris*

- At the moment, 48 species lineages recognized

- Species delimitation:

- Morphology
- Ecology
- Distribution
- Mycobiont selectivity





Break!!!