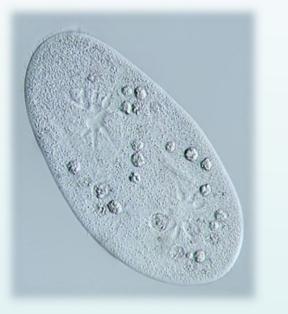
Species delimitation in protists







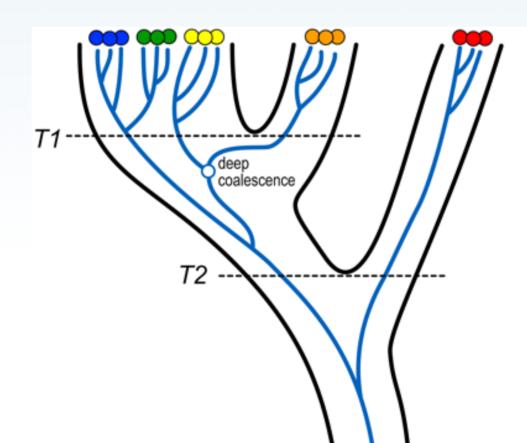


Pavel Škaloud, Algal speciation & evolution lab Charles University, Prague Czech Republic



Species delimitation

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



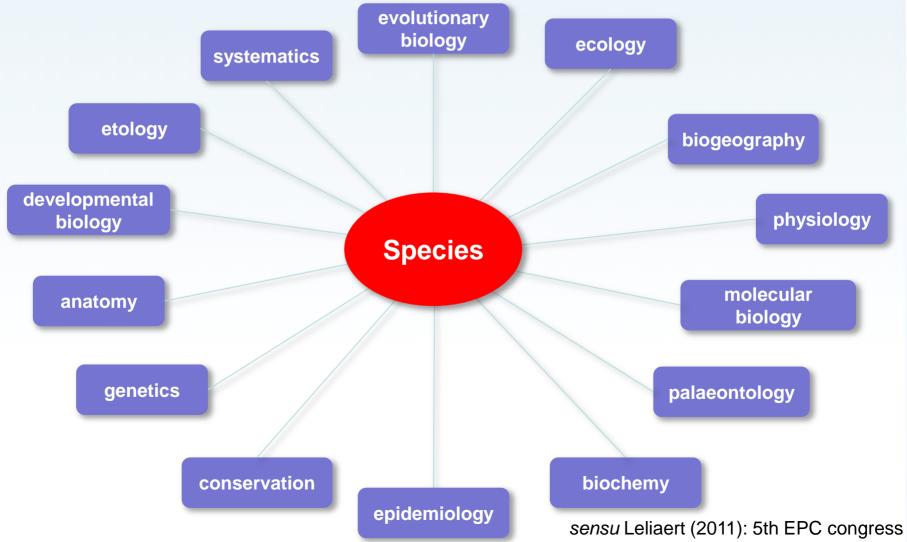
Species

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

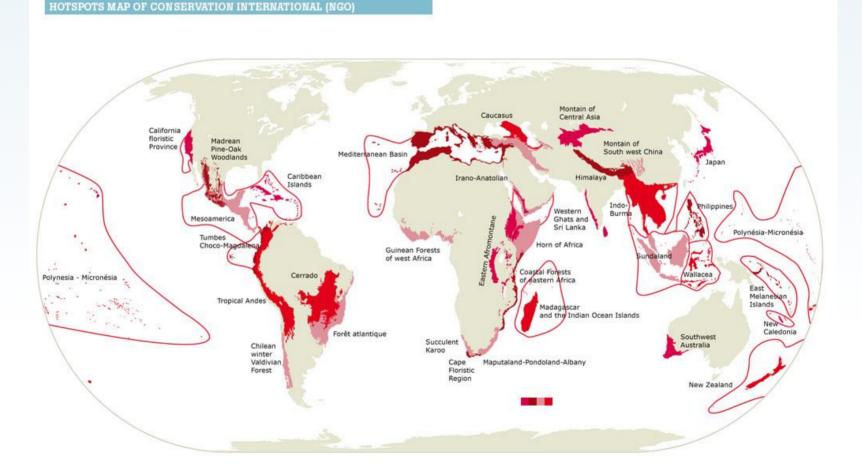


Species

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

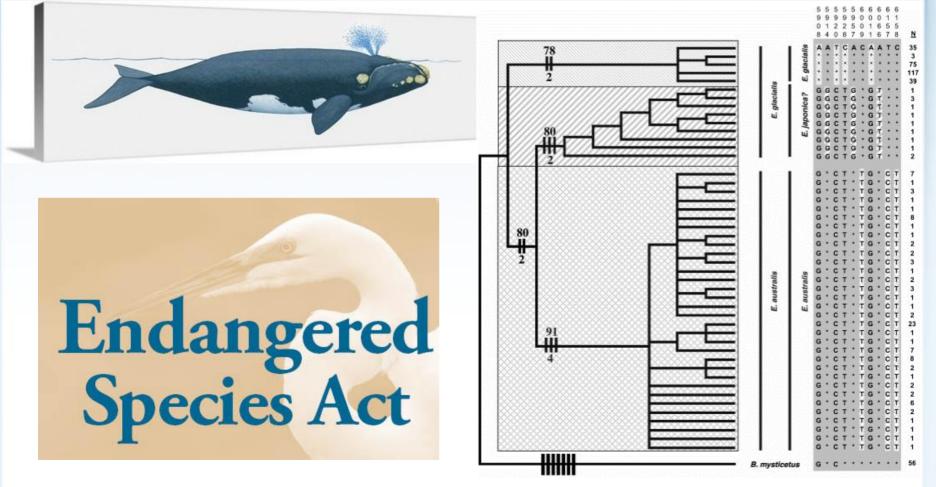


- Species as biodiversity indicators
 - Conservation management (biodiversity hotspots)



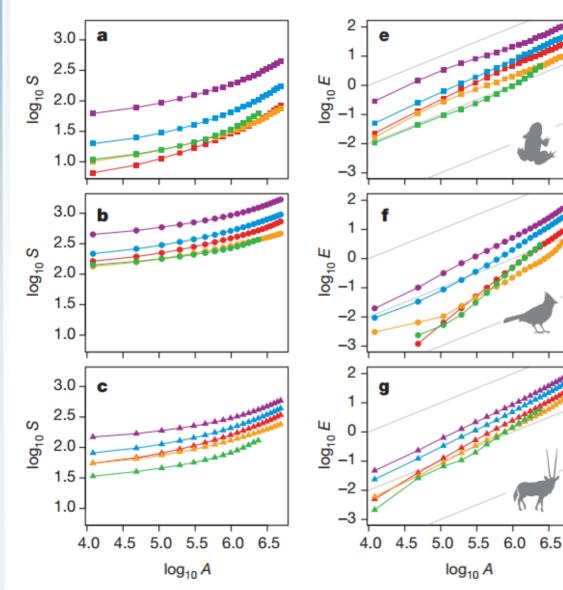
Conservation

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



Rosenbaum et al. (2000): Mol. Ecol. 9: 1793-1802

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



Macroecology

 Species as fundamental units for testing general ecological hypotheses

Storch et al. (2012): Nature 488: 78-81

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



Chlorella = morphological species concept • Auxenochlorella **Frebouxiophyceae** Pseudochloris Chlorella Parachlorella Ő Heterochlorella Chloroidium Mychonastes Chlorophyceae Chromochloris Scenedesmus Desmodesmus

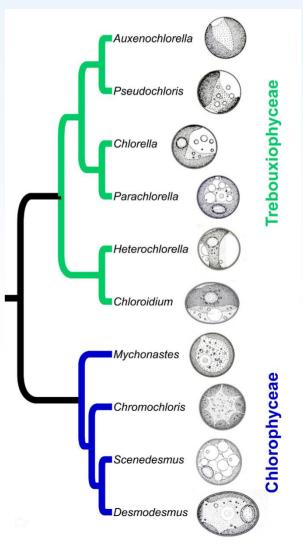
- *Chlorella* = broadly used in industry
 - sales of more than US\$ 38 billion annually worldwide
 - strain selection based on lipid content and fatty acid profiles

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

Lang et al. (2011): NBMC Plant Biol. 11: 124

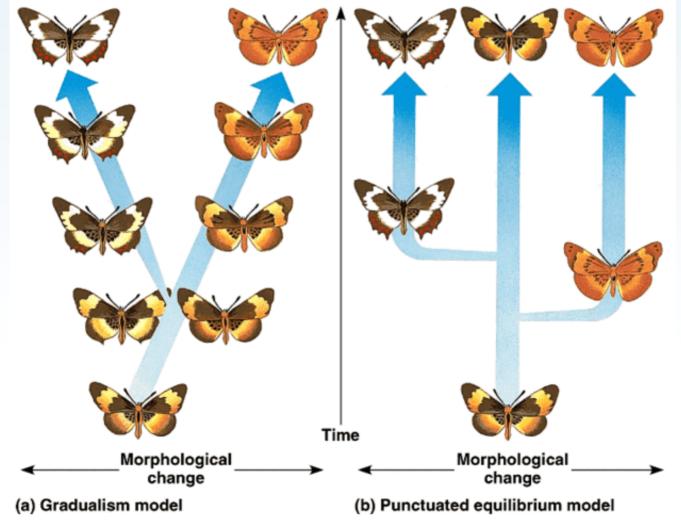
- *Chlorella* = registration as food products
 - Iist of permitted organisms (Chlorella vulgaris, Ch. pyrenoidosa)





Species delimitation

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

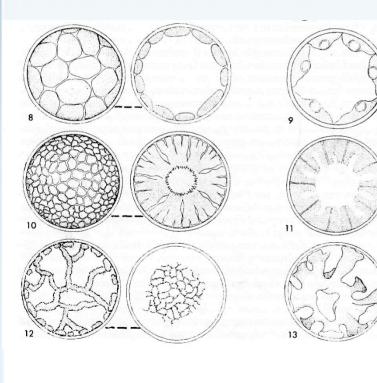


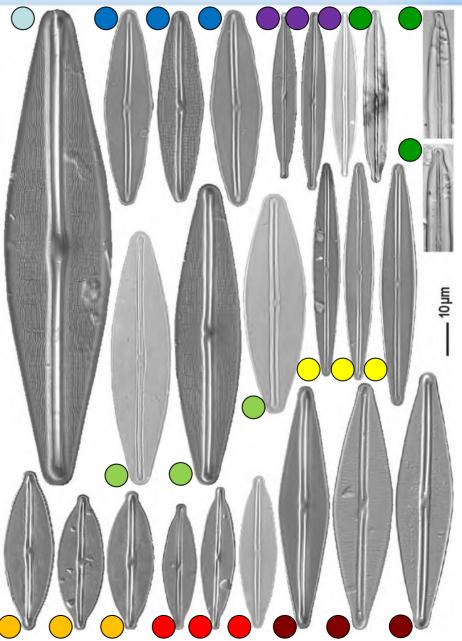
Copyright @ Pearson Education, Inc., publishing as Benjamin Cummings.

Species concepts in protists

	Biological species concept	Evolutionary significant unit		
Cohesion species concept	200 C			
	Phylogenetic species concept	Polythetic species concept		
Cladiatia anagina agregat				
Cladistic species concept		Recognition species concept		
	Genealogical concordance concept	recegnier openee concept		
Internodal species concept	Re	eproductive competition concept		
	Hennigian Species concept			
	Tieningian Opecies concept			
Composite species concepts	Genetic species concept			
	Evolutionary species concept	Palaeospecies concept		
Ecological species concept				
	Morphological species concept	Successional species concept		
Non-dimensional species concept		Taxonomic species concept		
	Linnean species concept			
		Genotypic cluster definition		
Phenetic species concept	Agamaspasias concent	Centrypic cluster demitter		
	Agamospecies concept			
	Mayden (1997)	: In: Species: the Units of Biodiversity		

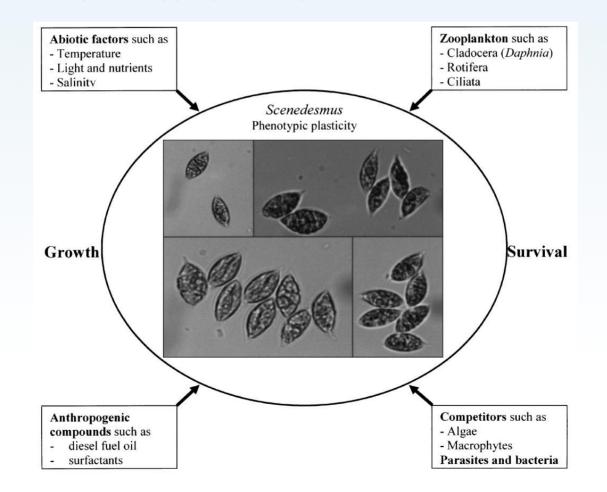
- A tradition!
 - Still employed in some groups of algae





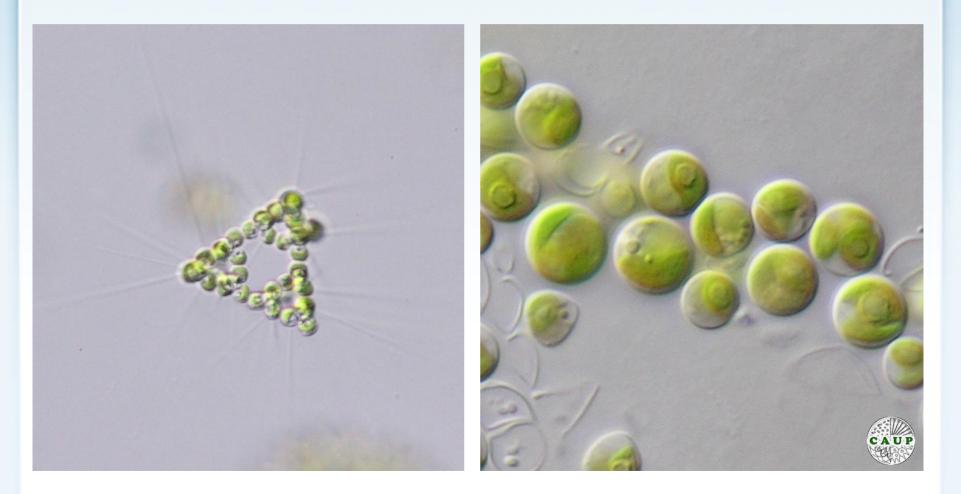
Beier & Lenge-Bertalot (2007): Nova Hedwigia 85: 73-91

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

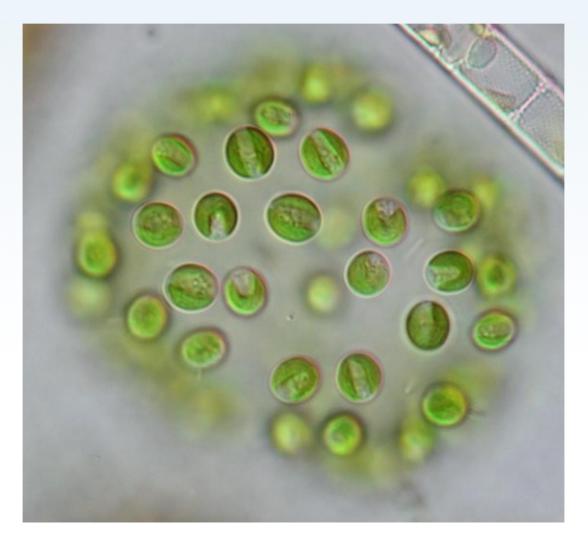


Lürling (2009): Ann. Limnol. - Int. J. Lim. 39: 85-101

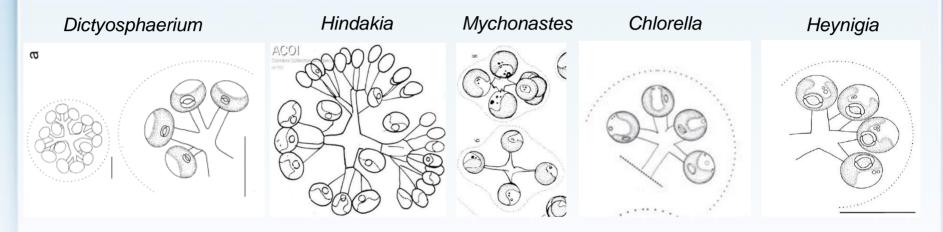
Species delimited based on investigation of cultured strains
 > Absence of traits manifested only in nature (*Micractinium*)



- Convergent morphological evolution
 - > Dictyosphaerium



- Convergent morphological evolution
 - Dictyosphaerium (9 cryptic genera)

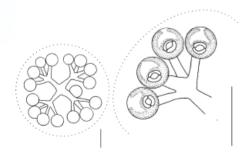


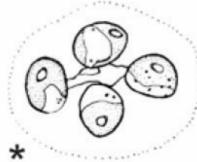
Mucidosphaerium

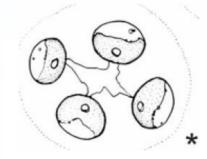
Compactochlorella

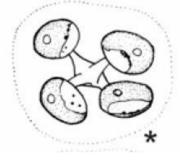
Kalenjinia

Masaia

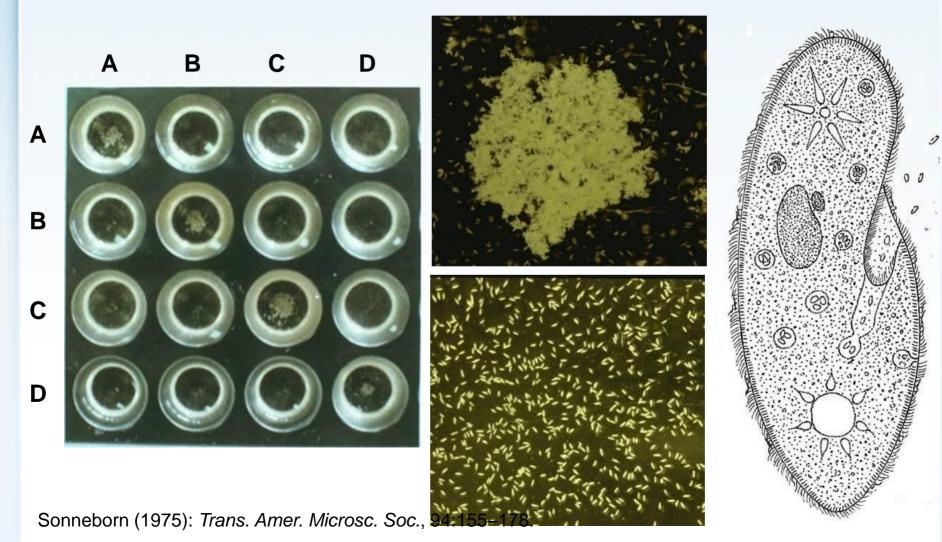








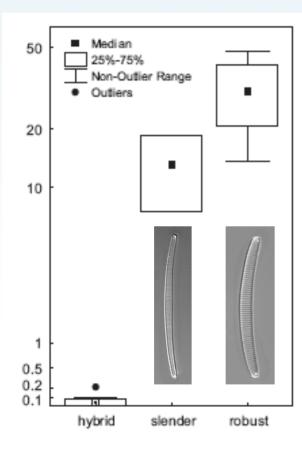
Applicable only on sexually reproducing organisms
 > cilliates (syngens in *Paramecium aurelia*)

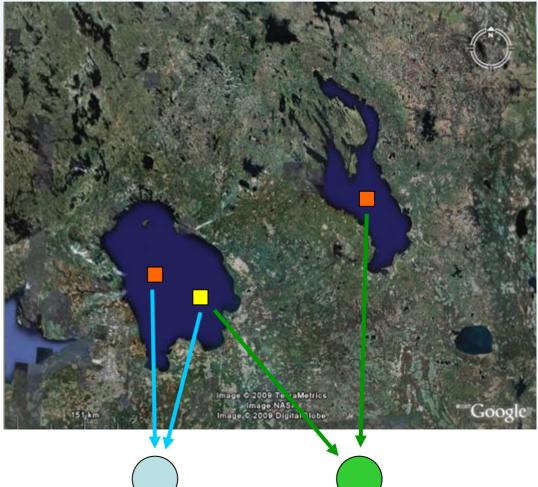


Applicable only on sexually reproducing organisms



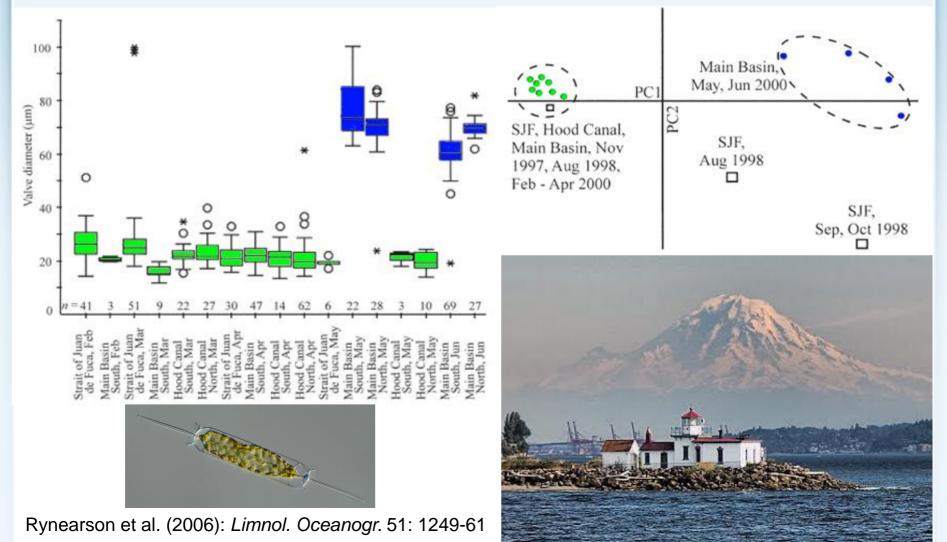
- Often incomplete reproduction barriers
 - > A problem of allopatric populations (*Eunotia*)



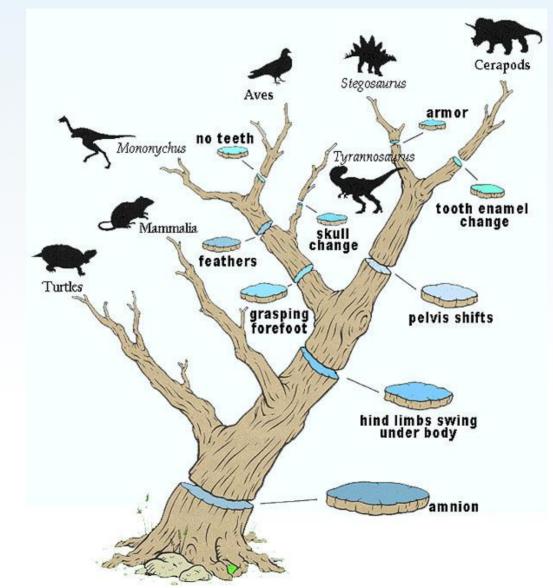


Vanormelingen et al. (2008): Protist 159: 73-90

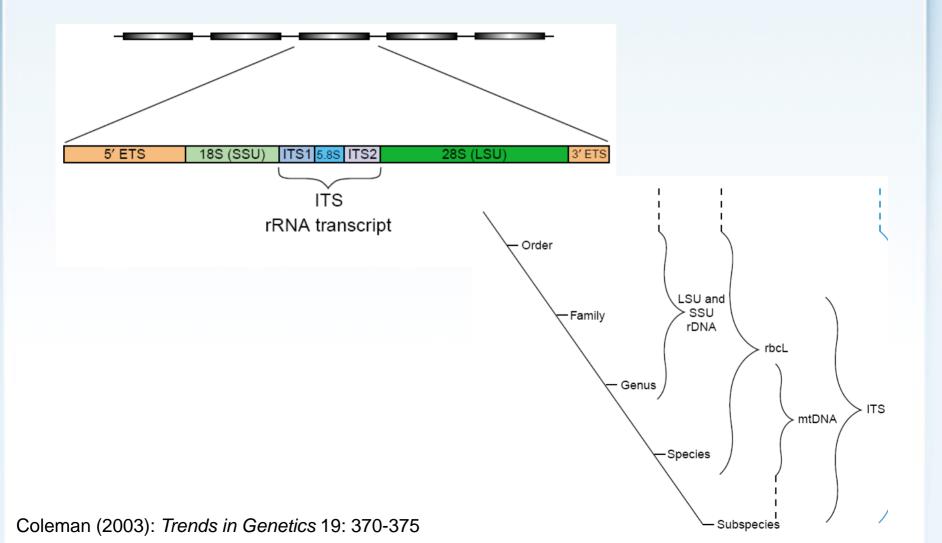
Laboratory crossing experiments test the incompatibility
 > a problem of temporaral isolation (*Ditylum*)



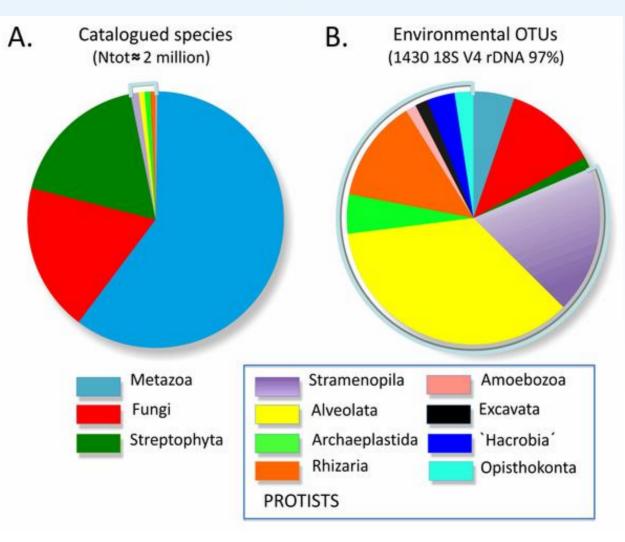
• Based on tree topology (monophyly, branch lengths, supports)



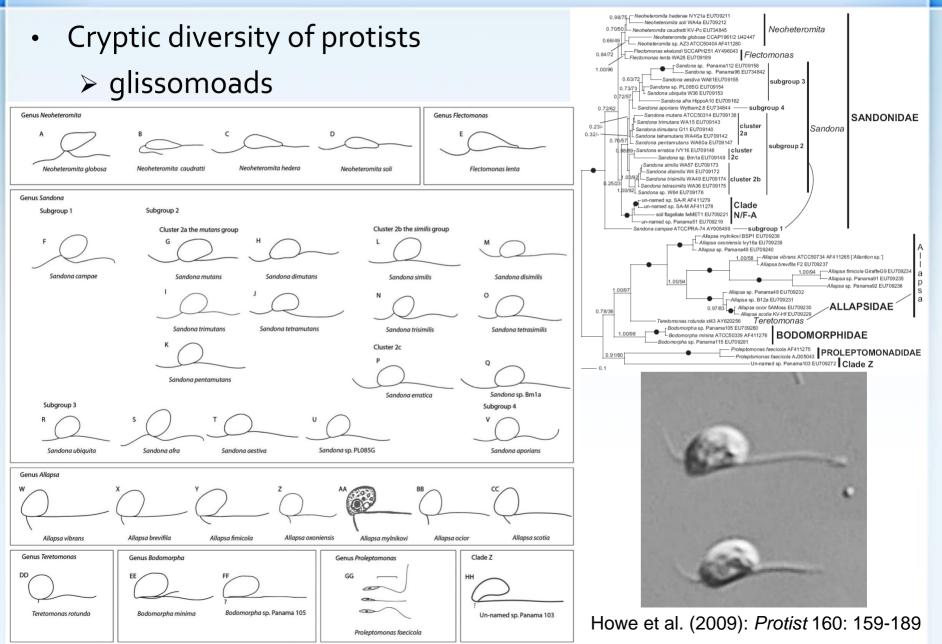
• Ribosomal operon as the frequently used marker



• Cryptic diversity of protists



Pawlowski et al. (2012): PLoS Biol. 10: e1001419



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 – 10²⁵ cells

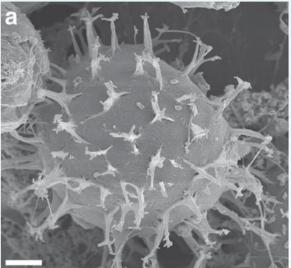
Fenchel & Finlay (2006): Phil. Trans. R. Soc. B 361: 1965-1973

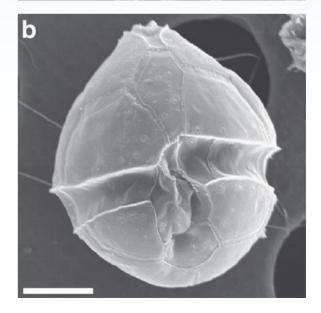
Cryptic diversity of protists (*Pentapharsodinium*)
 > population size: ≈ 2.9 × 10¹⁴
 > N_e ≈ 178-1183

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].

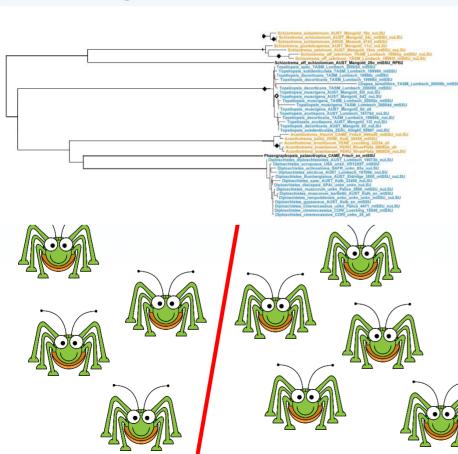
	contemporary effective population size (<i>N</i> _e)			
sample comparison	ML (95% CI)	moment (95% Cl)		
2006 - 1985	270 (161-544)	178 (98-343)		
2006-1960	439 (252–924)	375 (195–793)		
2006-1922	815 (401-2489)	1183 (476–5545)		
1985 - 1960	264 (148-592)	342 (166-905)		
1985 - 1922	305 (187–538)	652 (325–1528)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

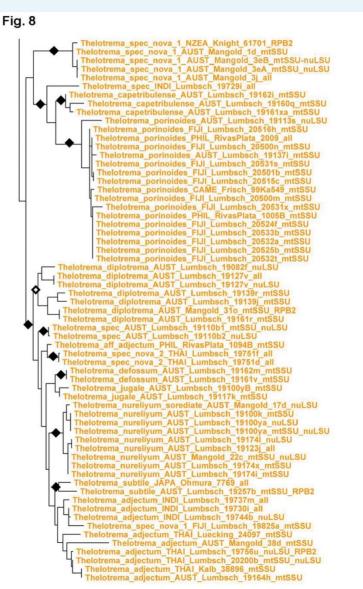
Watts et al. (2013): Biol. Lett. 9: 20130849





- Based on tree topology (monophyly, branch lengths, supports)
 - Where to set species boundaries?
 - > Objective criteria?

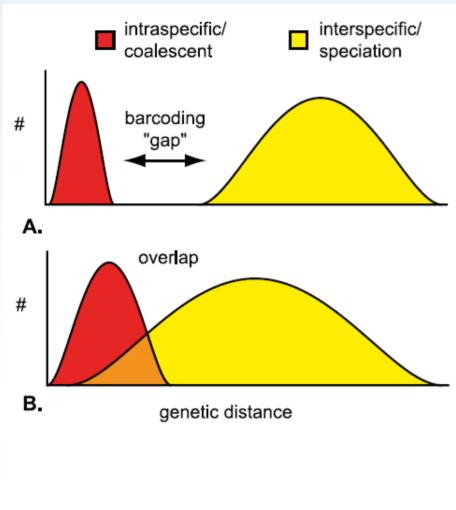




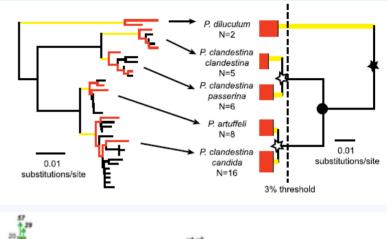
DNA barcoding

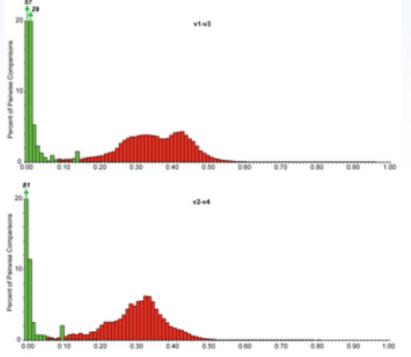
89

"barcoding gap"



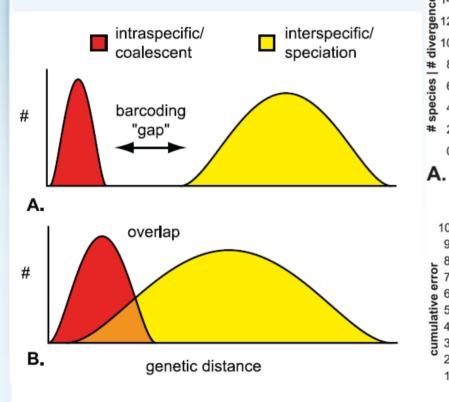
Meyer & Paulay (2005): *PLoS Biol.* 3: e422

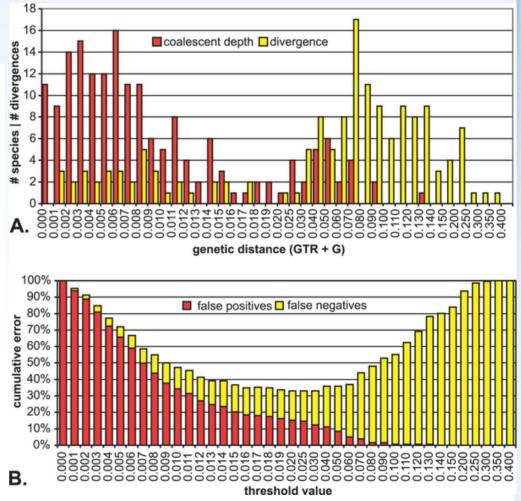




DNA barcoding

More sampling – less obvious barcoding gap

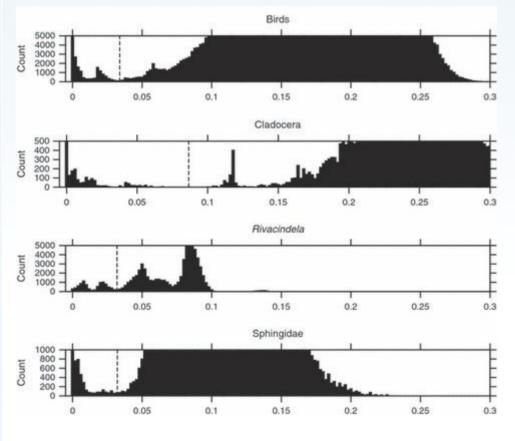




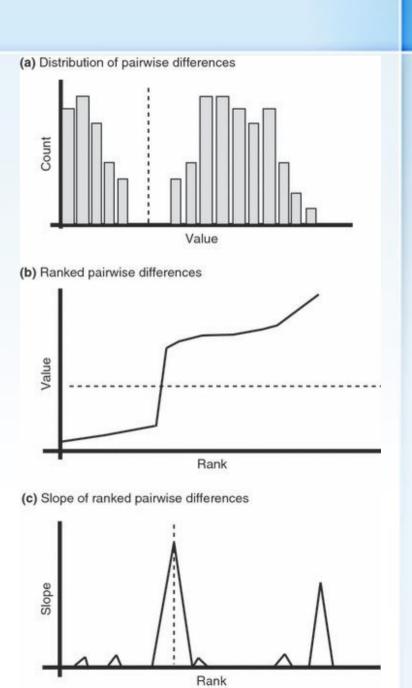
Meyer & Paulay (2005): *PLoS Biol.* 3: e422

ABGD

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

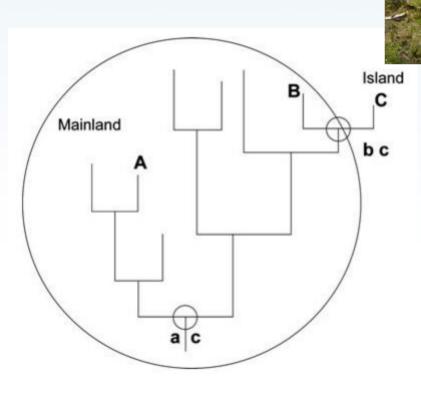


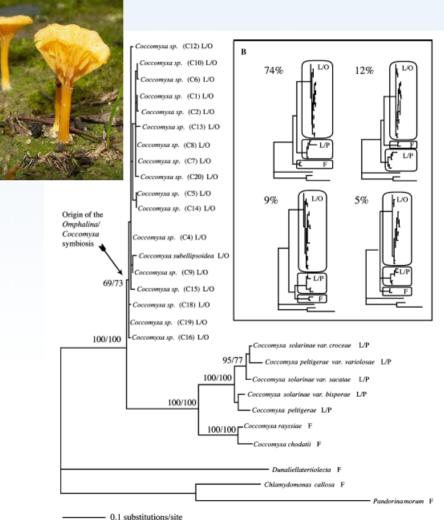
Puillandre et al. (2011): Mol Ecol 21: 1864



DNA barcoding

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

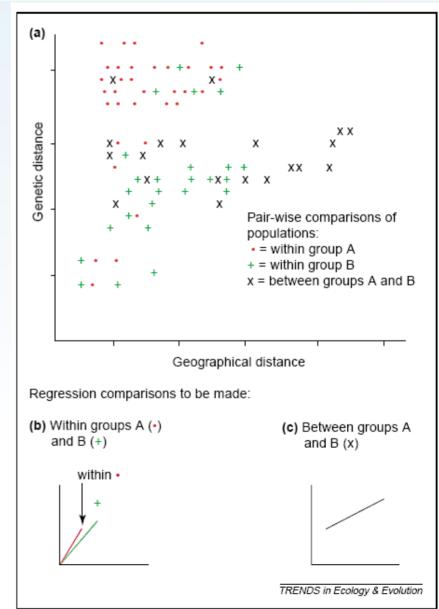




Wright et al. (2009): *Evolution* 63: 2275-2287

Good & Wake method

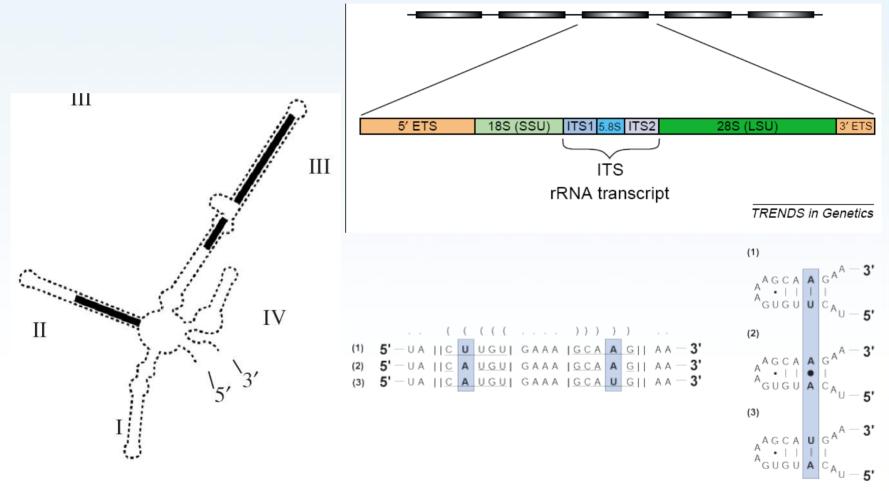
- test of *a priori* defined species
- linear regression of genetic and geographic dostances should in single species go through the graph origin (gene flow with isolation-by-distance)
- Different regression indicates the presence of two distinct, genetically isolated species



Sites & Marshall (2012): Trends Ecol. Evol. 18: 462-470

CBC concept

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

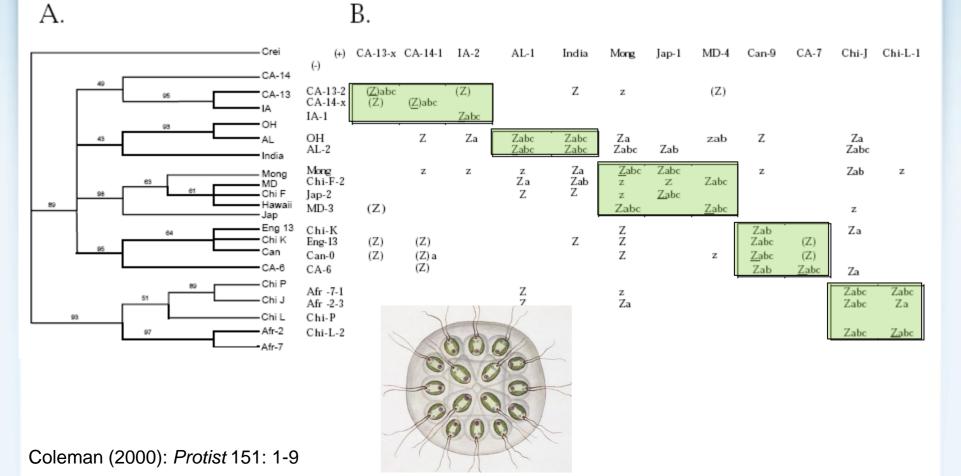


Coleman (2007): Nucleic Acids Res. 2007: 1-8

CBC concept

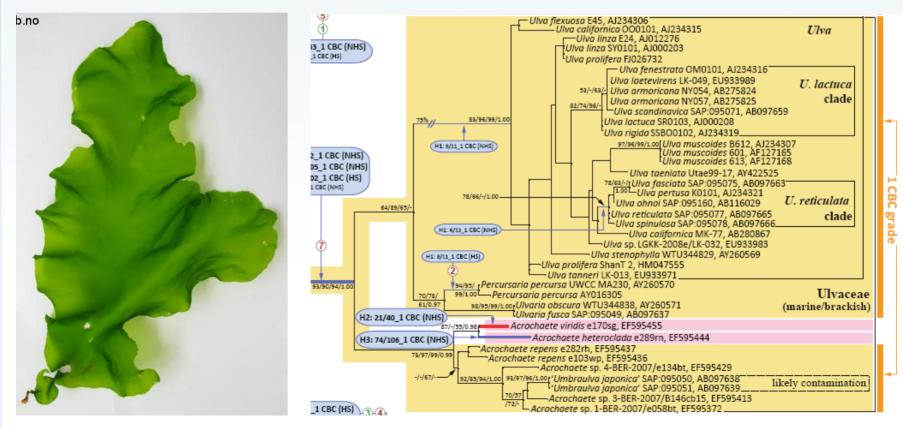
• Species delimited based on differences in conservative regions of the ITS2 molecule

> correlation between CBC and sexual compatibility (*Gonium*)



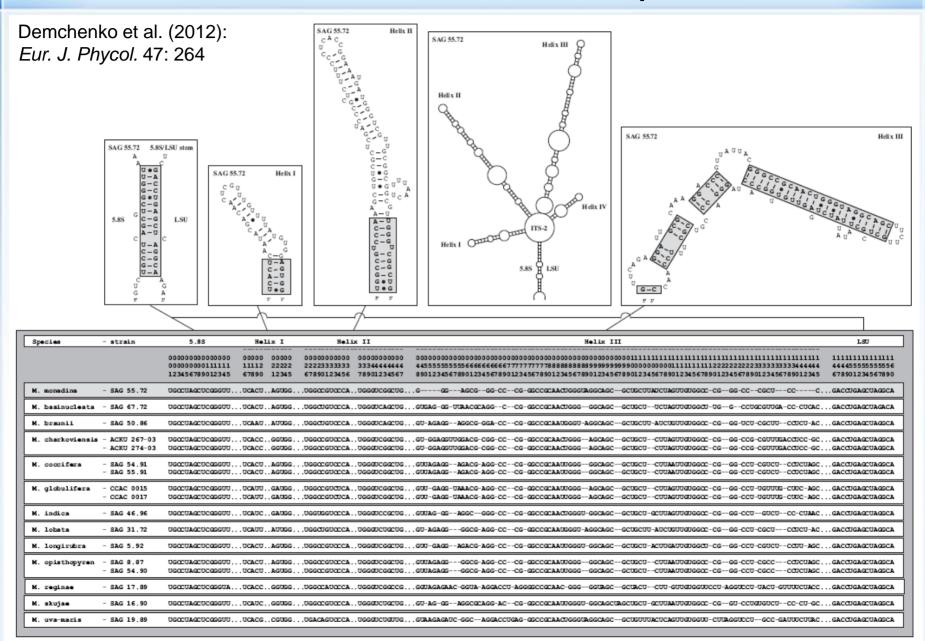
CBC concept

- 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



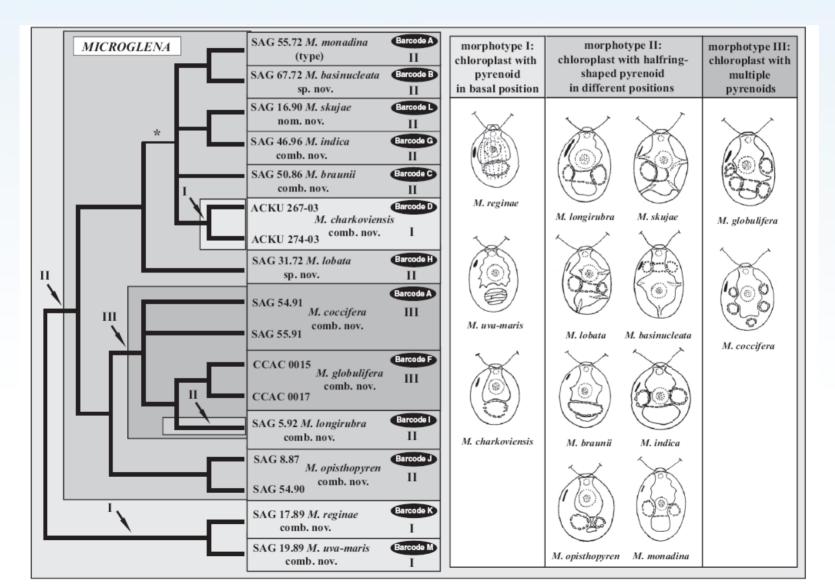
Caisová et al. (2011): *BMC Evol. Biol.* 11: 262

ITS2-barcode concept



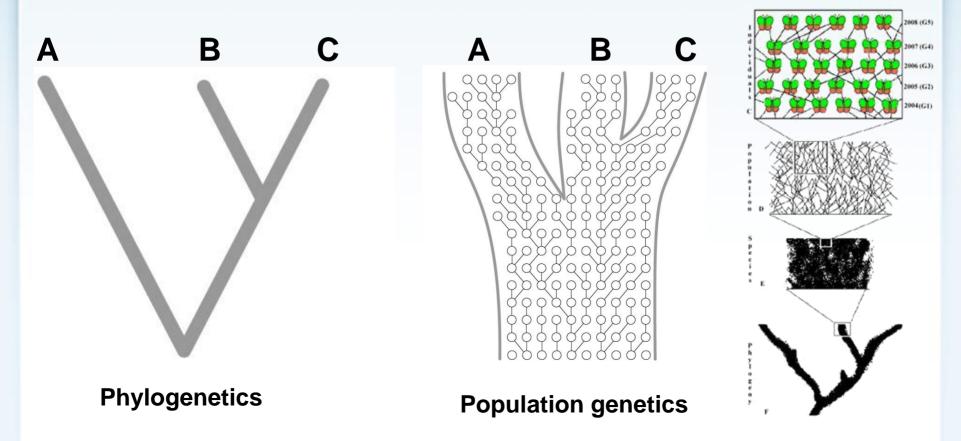
ITS2-barcode concept

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

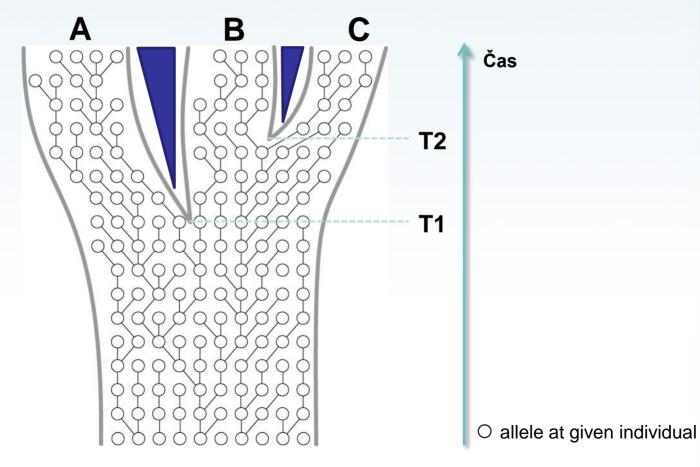


Linking phylogenetics and population genetics
 Identification of independently evolving lineages
 GMYC, bPTP, ABGD, BP&P,

A Four butterflies Ges Four butterflies (G B Four butterflies (top row), connected to their parents (bottom row)

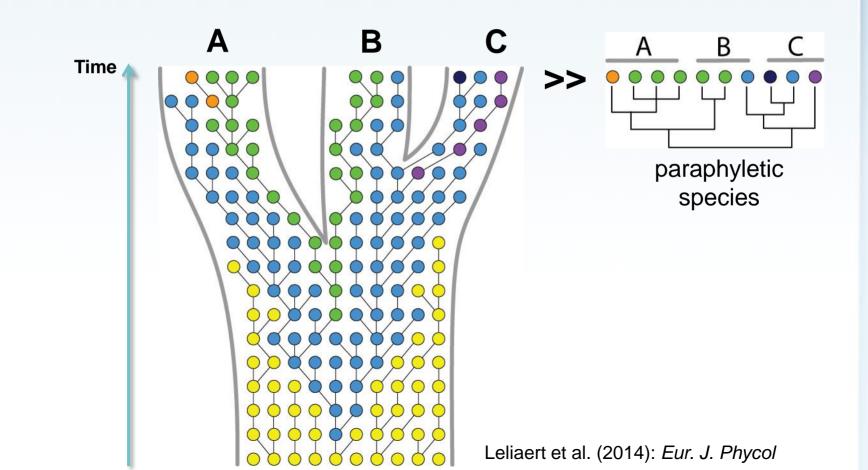


- Coalescence processes (Wright-Fisher)
 > allelic transfer to next generations
 - > allelic frequences vary across generations



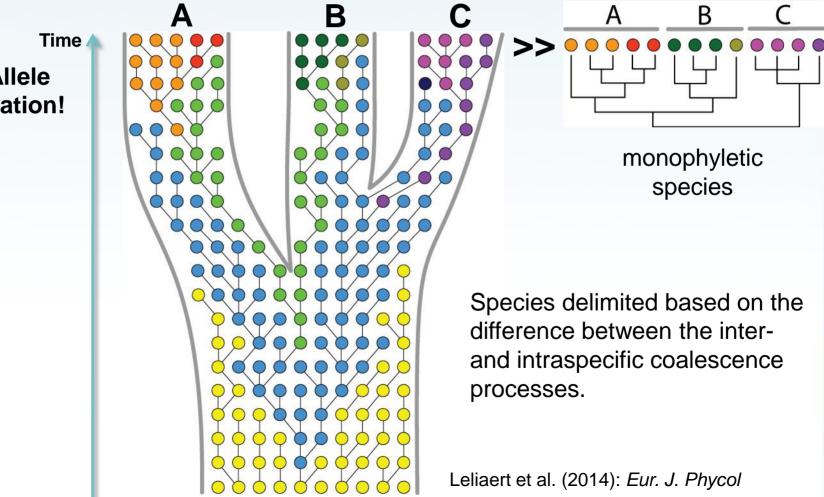
Leliaert et al. (2014): Eur. J. Phycol

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



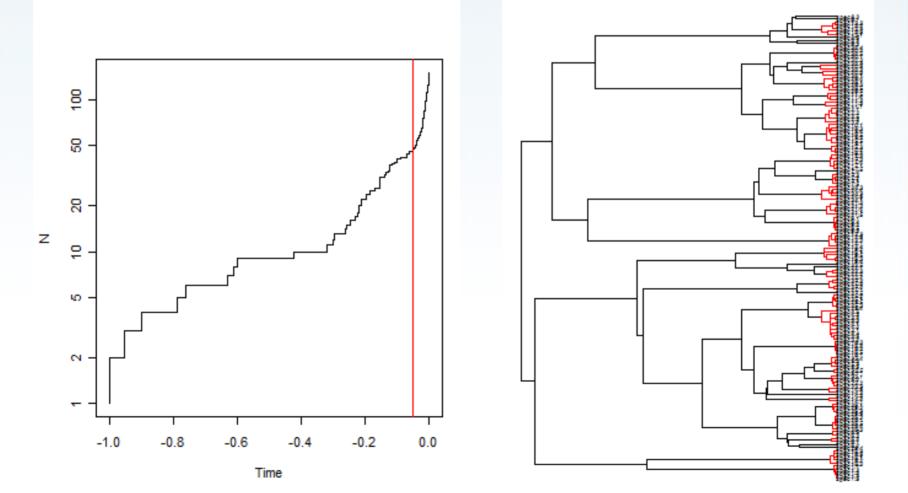
- Coalescence processes(Wright-Fisher) •
 - > during the coalescence, gene tree topologies resolve the species as polyphyletic, paraphyletic, and monophyletic

Allele fixation!



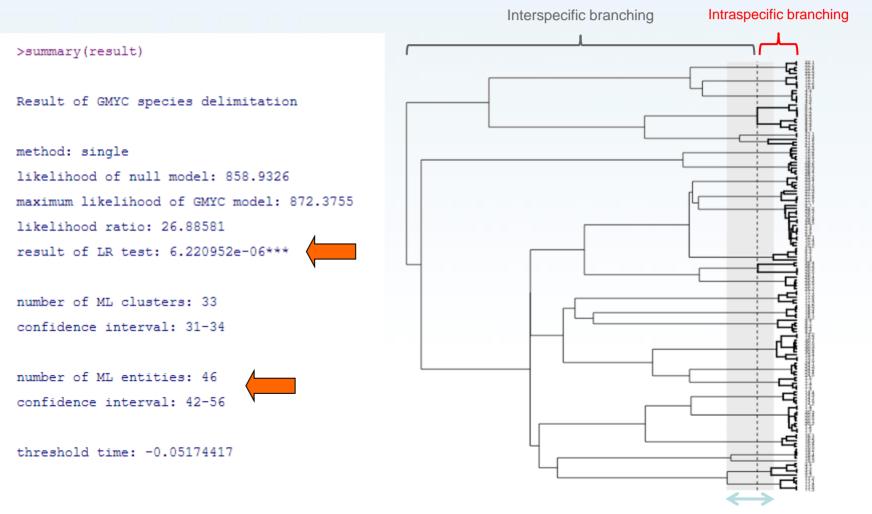
GMYC method

- 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



Confidence interval

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

```
<sup>29</sup> SAG_216_1_HG972999_Coccomyxa_arvernensisWien_C19_HG973000_Coccomyxa_sp
          CR2 4 HE586519 Monodus sp
            <sup>02</sup>SAG_2127_HG973005
               0.00 SAG_2325
                                            Choricystis snSAG 2040 HG973004 Coccomyya sr
      0,02-SAG 2104_HG973003_
<sup>0,99</sup> KN_2011_C4_HE586508_Coccomyxa
99 UTEX B SNO83 HE586506 Monodus sr
    SAG 49 84 HG972998 Coccomyxa
 ASIB V16 HG972994 Coccomvxa confluent
      CAUP H103 HE586505 Pseudococcomyxa simplex SS
  <sup>1,00</sup> CCAP 211 97 FN298928 Coccomyxa spCCAP 812 5 HG972995 Pseudococcomyxa atd
     <sup>QQ</sup> ACCV1 HE617183_Coccomyxa_onubensis_SS
       PPKN 2011 T3 HE586515 Coccomyxa
            <sup>),03</sup>-KN 2011 T2
             <sup>18</sup>CCAP 216 25 FR850476 Coccomvxa actinabiotis SS
            <sup>0,18</sup>-KN 2011 T4 HE586516 Coccomyxa
          <sup>0,04</sup> NIES_2252_HG972973_Coccomyxa_dis
                CCAP 812 3 HG972972 Pseudococcomyxa simplexNIES 2166 AGSI00000000 atd
               B GF 12 KM020052 Cocco
          <sup>2.78</sup> CAUP_H5105_HG972974_Choricystis
                  Wien C20 HG972975 Cor
                                           Coccomyxa_pringsheimii_KN_2011_U2_KN_2011_C13_KN_2011_C14_SAG_216_13
  1.00 GA5a_SS_AB917140_Coccomyxa_s
      <sup>1.00</sup> CCAP_216_24_FN298927_Coccomyxa_spCCAP_812_2A_HG972992_Pseudococcomyxa_atd
     1.00 Coccomyxa_SCCA048_SS
      <sup>1,00</sup> CCAP_211_60_FR865679_Chlorella_saccharophila_S
                           H102 HE586504 Pseudococcomy
                                                              SAG 216 9a FN298926 Pseudococcomyxa simplex
                     SAG 216 2 HG972989 Coccomyxa chodat
                   <sup>40</sup>CAUP H5107 HG972981 Choricystis spSAG 216 3b HG972980 Coccomyxa elongata
                   <sup>40</sup> UTEX LB 2460 AY422078 Paradoxia multiseta
                 AG 216 6 HG972988 Coccomyxa
                     <sup>0.00</sup>-SAG_216_10_HG972986_Coccomyxa
                           SAG 216 12 HG972987 Coccomyxa
                          CCAP 216 15 HG972985 Coccomyxa subellipsoideaSAG 216 11a HG972983 atc
```

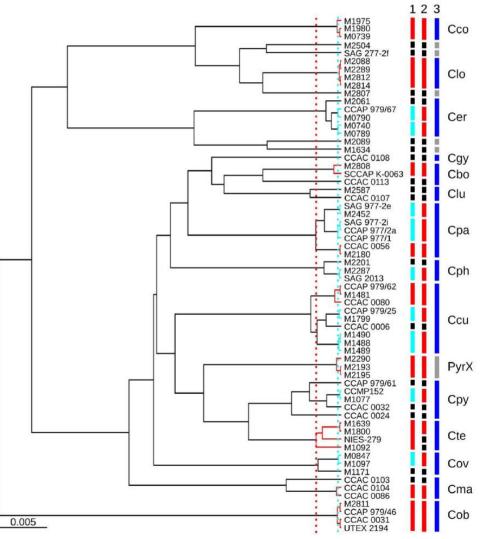
DNA-based species delimitation methods

De ferrer en	Existing	Species after	No. of	No. of	Diamana dar	Validation
Reference	species	delimitation	samples	loci	Discovery approaches	approaches
Avila et al. (2006)	6	>12	293	1	Statistical parsimony (NCA)	None
Barrett & Freudenstein (2011)	3	3	162	5	Morphological cluster analysis, PCA	BPP
Burbrink et al. (2011)	1	1	45	3	Structurama	BPP
Camargo et al. (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 et al. (2012)	Unknown	Unstated	103	7	Morphometric clustering; structure	None
Esselstyn et al. (2012)	13	18-19	413	1	GMŶC	None
Florio et al. (2012);	1	2	111	1	Canonical variates analysis	None
Flot et al. (2010)	1		74	3	Haplowebs	None
Hamilton et al. (2011)	4	3	147	1	Combo WP and barcoding gap, monophyly, GMYC	
Kelly et al. (2008)	39	1	114	1	WP	None
Leaché & Fujita (2010)	1	3	51	6	Structure	BPP
Leavitt et al. (2012)	19	2	414	6	Structure	BPP, mean genetic distance
Leliart et al. (2009)	19	13	175	1	GMYC, statistical parsimony (NCA)—clades that exceed 95% cut off	None
Niemiller et al. (2012)	1	19	135	9	O'Meara clustering	BPP
Pons et al. (2006)	24	54	468	1	Parsimony network, PAA, CHA, WP, GMYC	None
Puillandre et al. (2009)	1	4	44	2	Elliptic Fourier analysis on shape to the mollusc shell; qualitative phylogenetic evidence	None
Puillandre et al. (2012)	43	27	1000	2	GMYC, ABGD Carstens et al. (2013)	None Mol. Ecol. 22: 43

Pitfalls of DNA-based species delimitation

Incongruence between species delimited by GMYC and by those delimited by a combined 12 3 M1975 M1980 Cco molecular and morpho-M0739 M2504 SAG 277-2f M2088 M2289 Clo logical aproach M2812 M2814 M2807 M2061

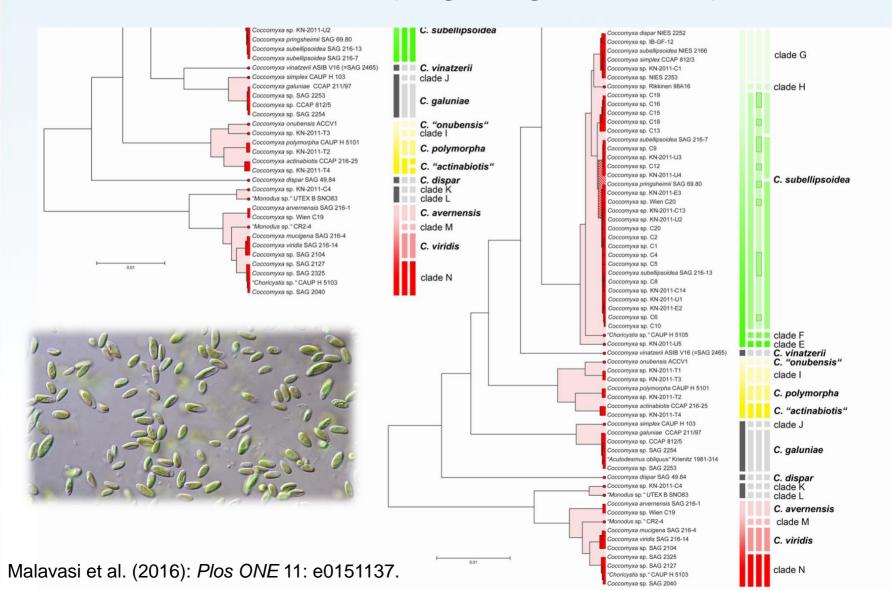




Hoef-Emden (2012): Plos ONE 7(8): e43652.

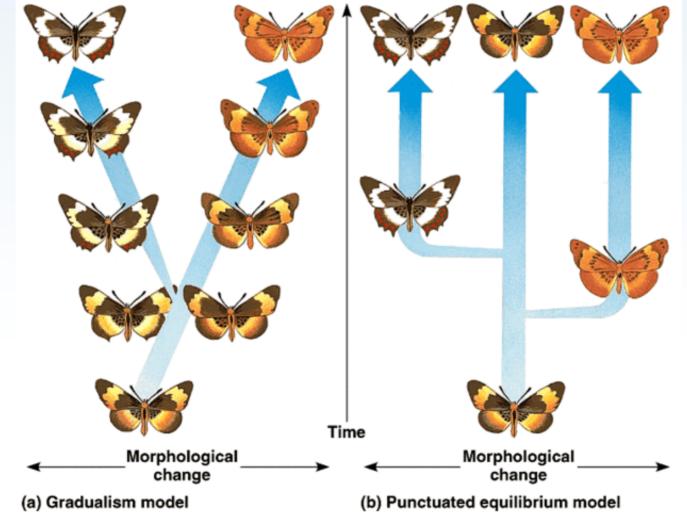
Pitfalls of DNA-based species delimitation

• Problems with taxon sampling, using identical sequences



Universal species concept?

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

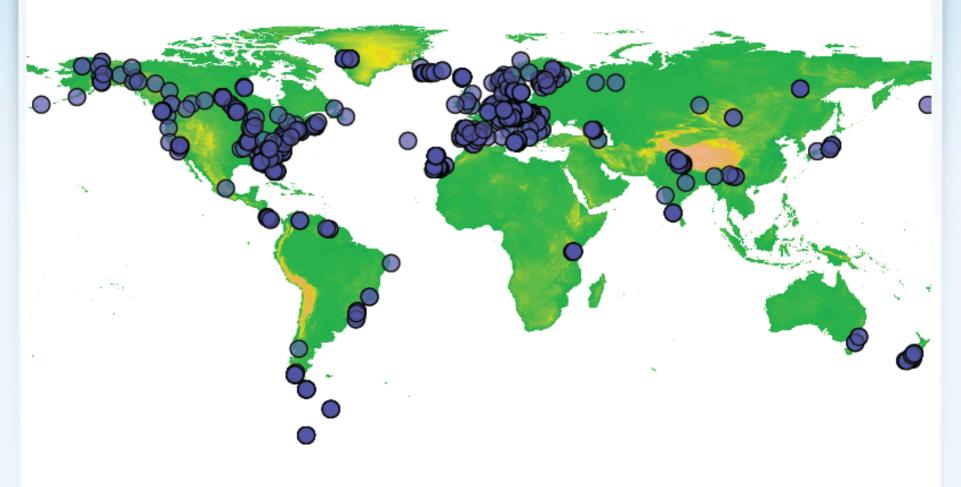


Copyright @ Pearson Education, Inc., publishing as Benjamin Cummings.

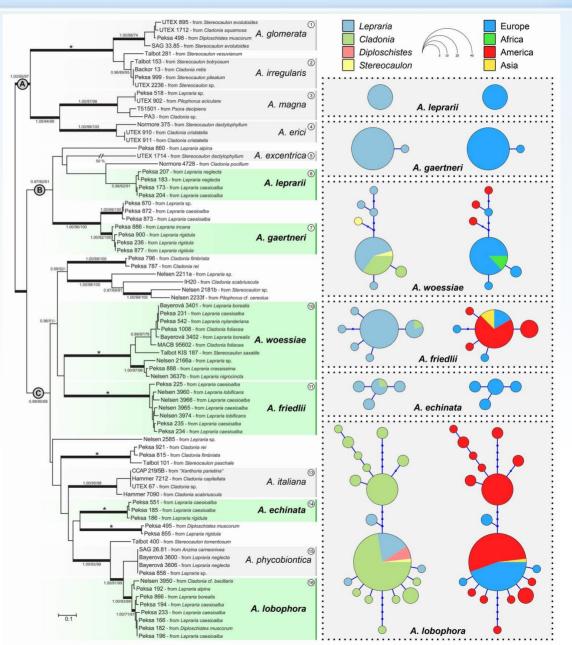
• Asterochloris – one of the most common lichen symbionts



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



 molecular data (ITS rDNA + actin)

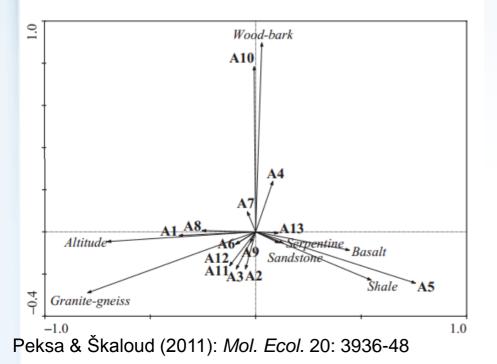


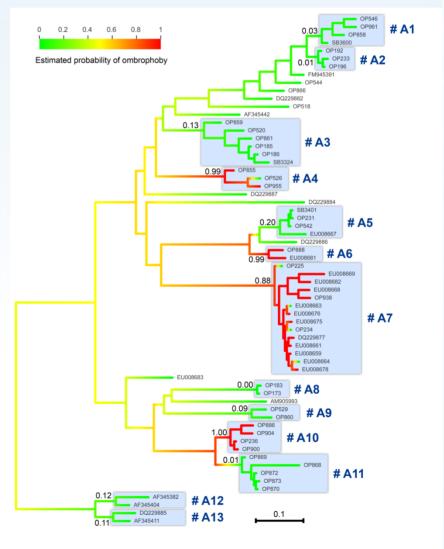
Škaloud et al. (2015): *J. Phycol.* 51: 507-27

ecology

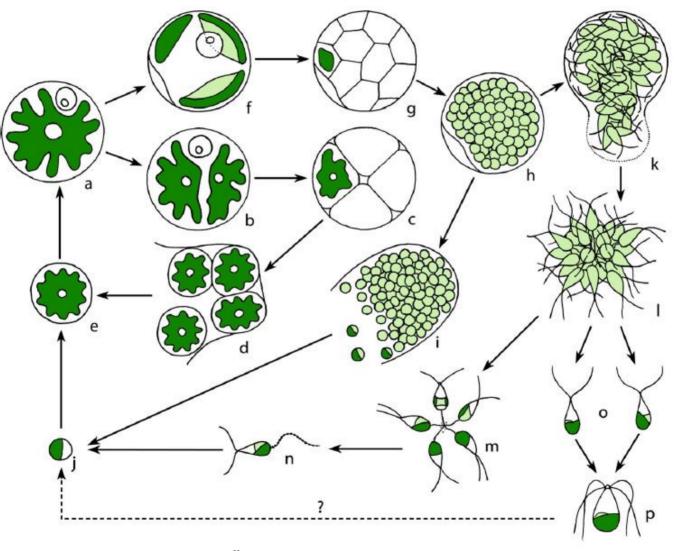
substrate specificity, altitude, ombrotrophy

	Pagel's λ				
Trait	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		



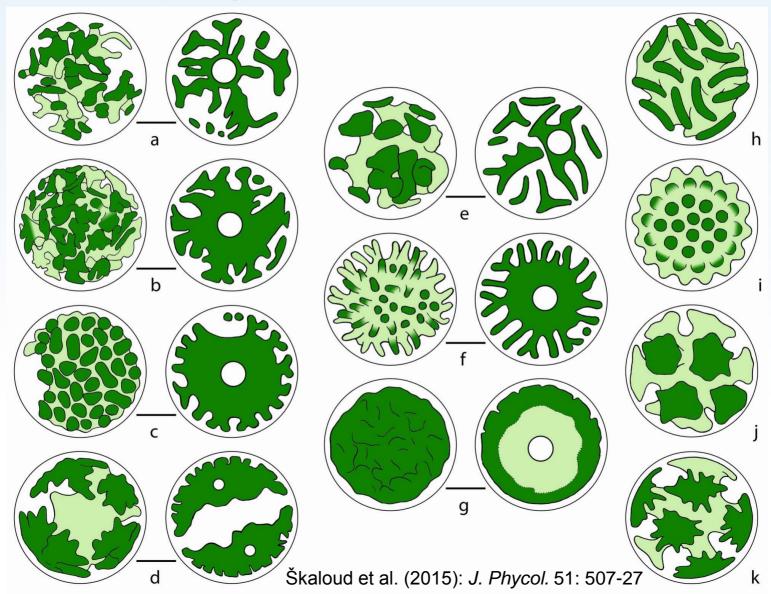


• Ontogeny

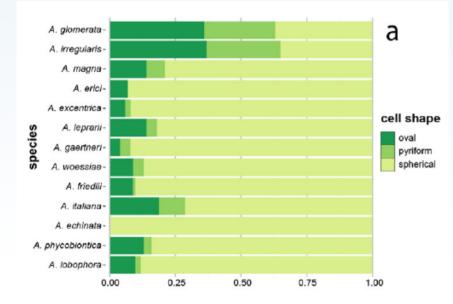


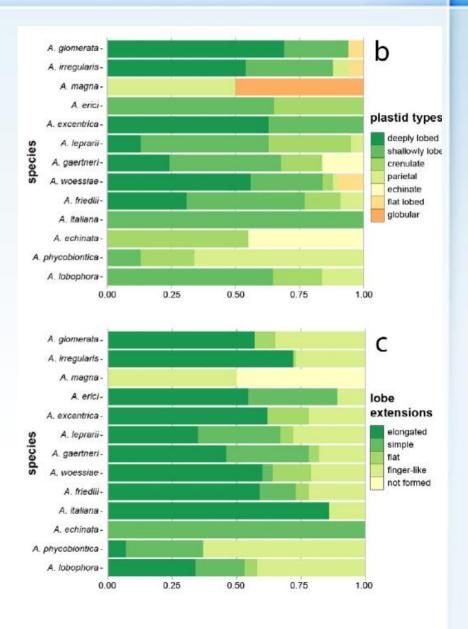
Škaloud et al. (2015): *J. Phycol.* 51: 507-27

Chloroplast morphology



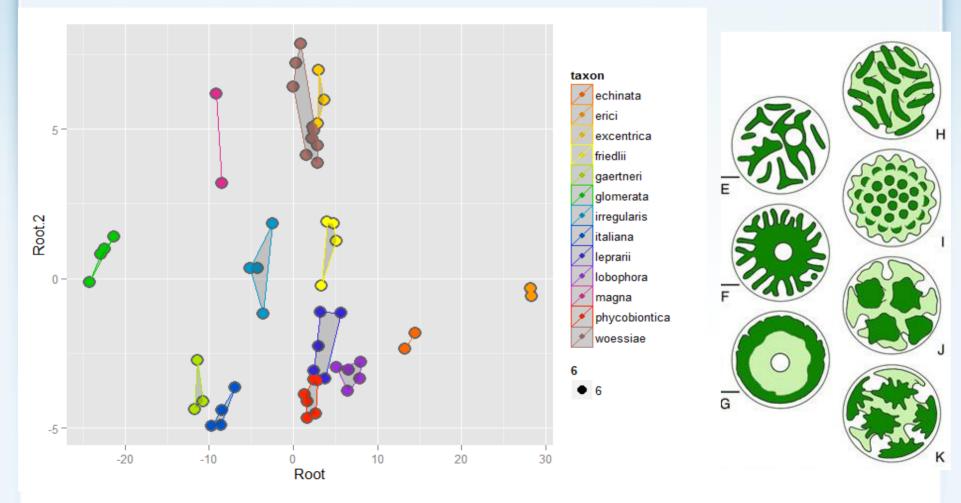
- Morphology
 - cell shape, cell dimensions, chloroplast shape, number of zoo- and aplanospores

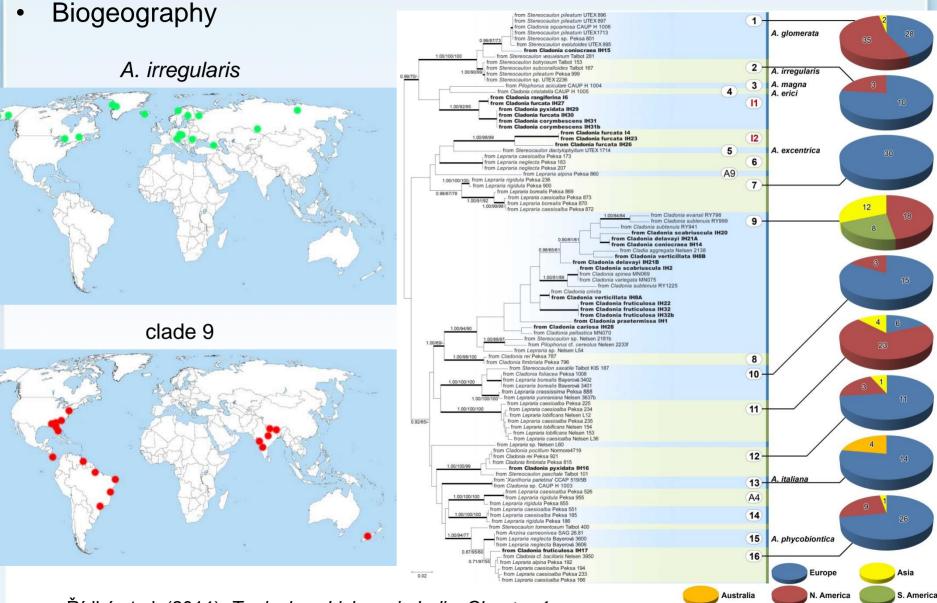




Škaloud et al. (2015): J. Phycol. 51: 507-27

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





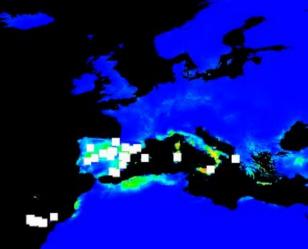
Řídká et al. (2014): Terricolous Lichens in India, Chapter 4

• Biogeography: niche modelling

0,54 0,46 0,38 0,31 0,23 0,15

0,62 0,54 0,46 0,38 0,31 0,23 0,15

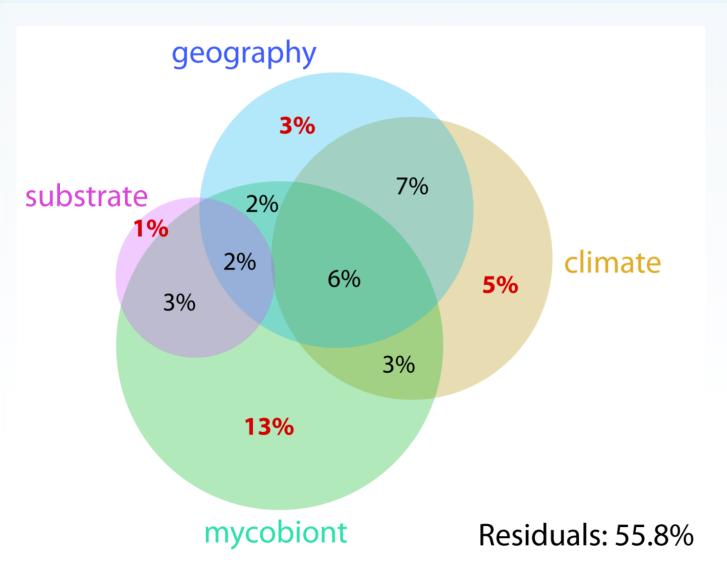
A. irregularis



A. mediterranea

A. friedlii

• Mycobiont selectivity









species boundary line (ABGD, GMYC, bPTP)

- At the moment, 48 species lineages recognized
- Species delimitation:
 - Morphology
 - Ecology
 - Distribution
 - Mycobiont selectivity

