



Endosymbiosis and kleptoplasty in the evolution of complex algae

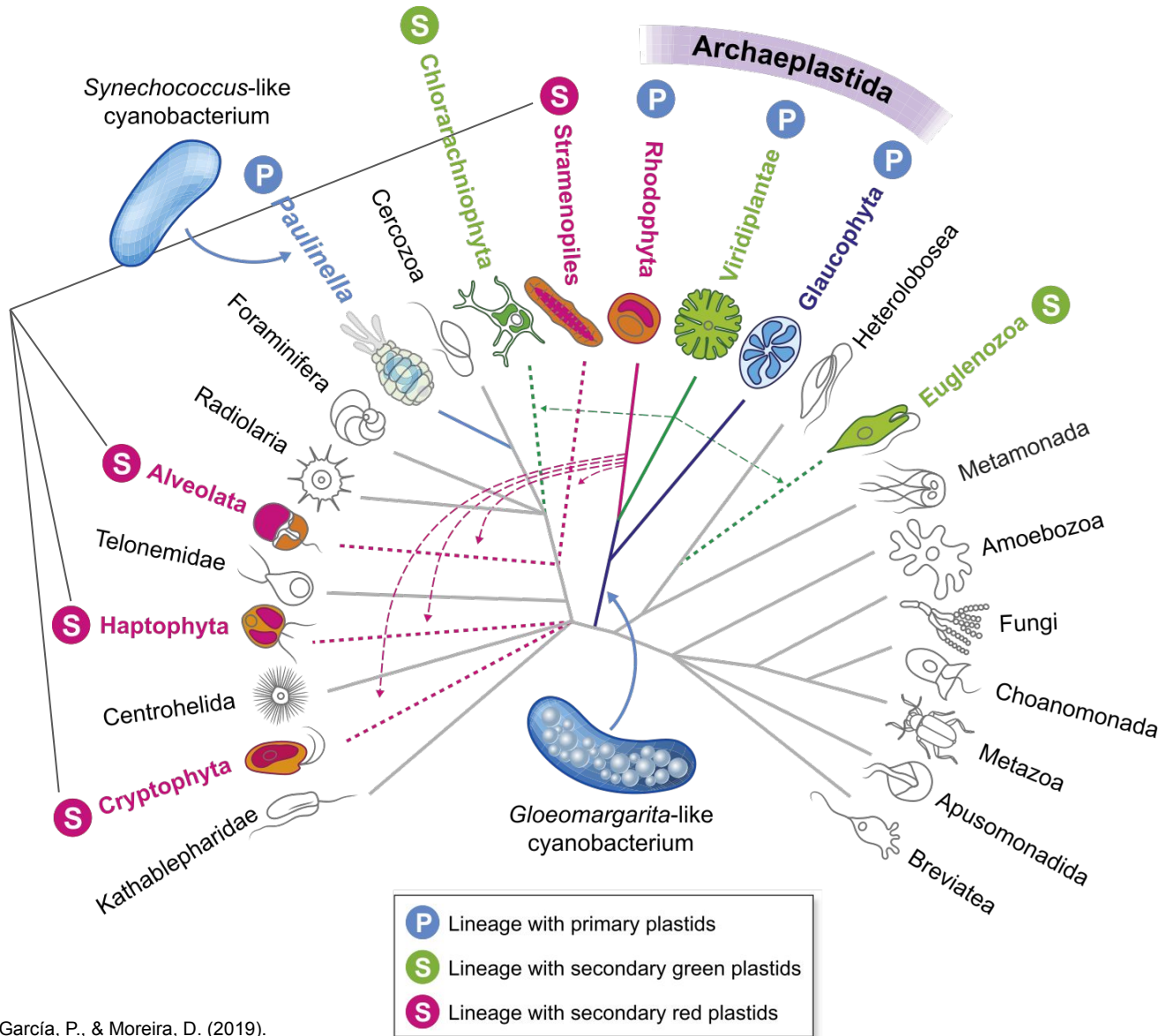
Mick Van Vlierberghe (mvanvlierberghe@doct.uliege.be) and Denis Baurain (denis.baurain@uliege.be)

InBioS – PhytoSYSTEMS, Eukaryotic Phylogenomics, University of Liège, Liège, Belgium

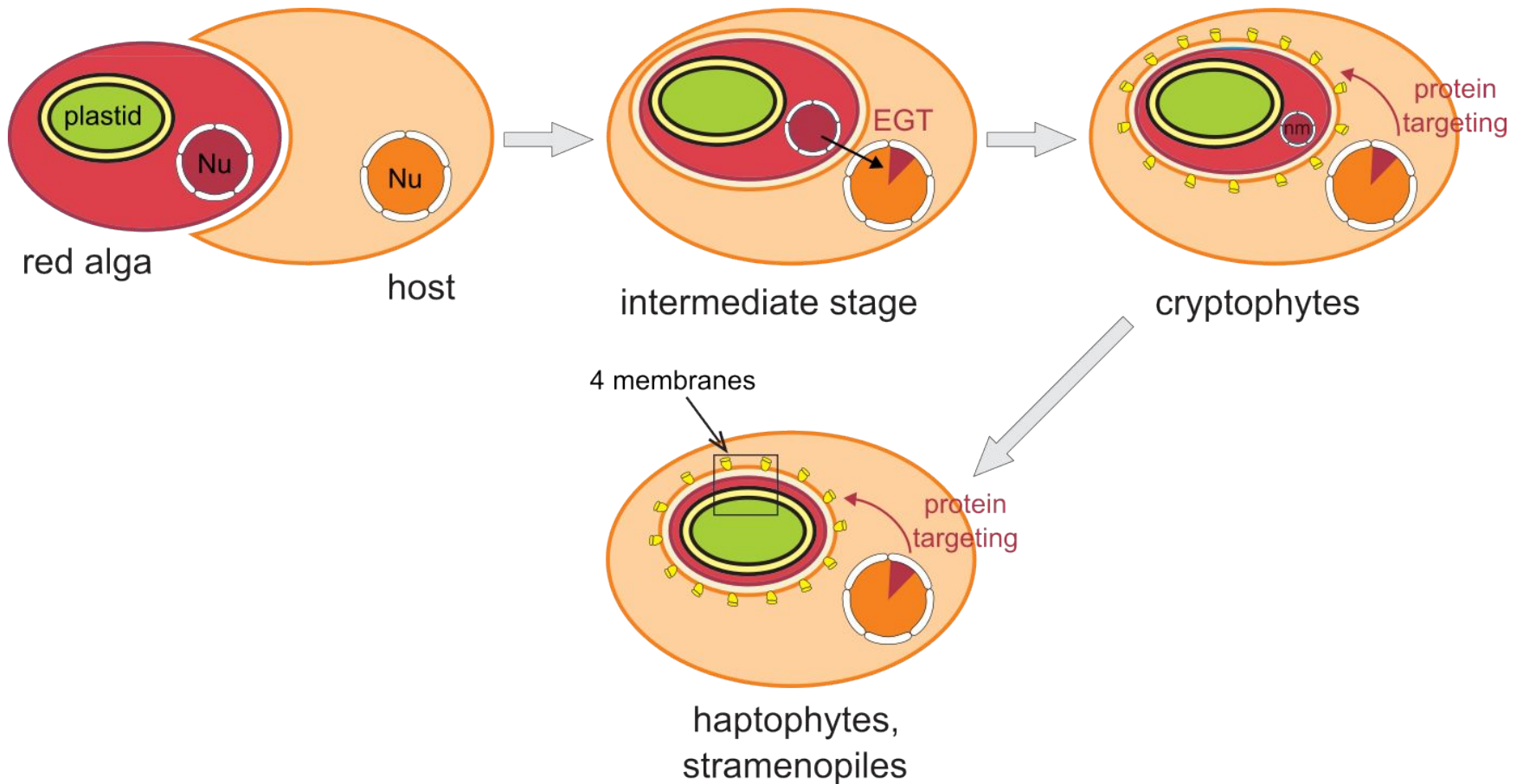
AMPEE7
Tuesday, 14th November
Liège, Belgium

Complex Algae - Panorama

CASH
lineages



Endosymbiosis/Single source EGT



Gene mosaicism

REPORTS

Genomic Footprints of a Cryptic Plastid Endosymbiosis in Diatoms

Ahmed Moustafa,^{1*} Bánk Beszteri,^{2*} Uwe G. Maier,³ Chris Bowler,^{4,5}
Klaus Valentin,² Debashish Bhattacharya^{1,6†}

ARTICLE

OPEN

doi:10.1038/nature11681

Algal genomes reveal evolutionary mosaicism and the fate of nucleomorphs

Bruce A. Curtis^{1,2,3}, Goro Tanifuji^{1,2,3}, Fabien Burki^{3,4}, Ansgar Gruber^{5,6}, Manuel Irimia⁶, Shinichiro Maruyama^{1,2,3}, Maria C. Arias⁷, Steven G. Ball⁷, Gillian H. Gile^{1,2,3}, Yoshihisa Hirakawa^{3,4}, Julia F. Hopkins^{1,2,3}, Alan Kuo⁸, Stefan A. Rensing^{9,†}, Jeremy Schmutz^{8,10}, Aikaterini Symeonidi⁹, Marek Elias¹¹, Robert J. M. Eveleigh^{1,2,12}, Emily K. Herman¹³, Mary J. Klute¹³, Takuro Nakayama^{1,2,3}, Miroslav Obornik^{14,15,16}, Adrian Reyes-Prieto^{3,17}, E. Virginia Armbrust¹⁸, Stephen J. Aves¹⁹, Robert G. Beiko²⁰, Pedro Coutinho²¹, Joel B. Dacks²², Dion G. Durnford¹⁷, Naomi M. Fast⁴, Beverley R. Green⁴, Cameron J. Grisdale⁴, Franziska Hempel²², Bernard Henrissat²³, Marc P. Höppner²³, Ken-Ichiro Ishida²⁴, Eunsoo Kim²⁵, Luděk Kořený^{14,15}, Peter G. Kroth²⁶, Yuan Liu^{19,26}, Shehre-Banoo Malik^{1,2,3}, Uwe G. Maier²², Darcy McRose²⁷, Thomas Mock²⁸, Jonathan A. D. Neilson²⁹, Naoko T. Onodera^{1,2,3}, Anthony M. Poole²⁹, Ellen J. Pritham³⁰, Thomas A. Richards²⁶, Gabrielle Rocap¹⁸, Scott W. Roy³¹, Chihiro Sarai³², Sarah Schaeck³³, Shu Shirato²⁴, Claudio H. Slamovits^{1,2,3}, David F. Spencer^{1,2,3}, Shigekatsu Suzuki²⁷, Alexandra Z. Worden²⁷, Stefan Zauner²⁷, Kerrie Barry⁸, Callum Bell³³, Arvind K. Bharti³³, Jane Grimwood^{8,10}, Robin Kramer³³, Erika Lindquist⁸, Susan Lucas⁸, Asaf Salamov⁸, Geoffrey I. McFadden³⁴, John A. Crow³³, Christopher E. Lane^{1,2,3,35}, Patrick J. Keeling^{1,4}, Michael W. Gray^{1,2,3}, Igor V. Grigoriev⁸ & John M. Archibald^{1,2,3}



RESEARCH ARTICLE



Chimeric origins of ochrophytes and haptophytes revealed through an ancient plastid proteome

Richard G Dorrell^{1*}, Gillian Gile², Giselle McCallum¹, Raphaël Méheust³,
Eric P Bapteste³, Christen M Klinger⁴, Loraine Brillet-Guéguen⁵,
Katalina D Freeman², Daniel J Richter^{6,7}, Chris Bowler^{1*}

PNAS

RESEARCH ARTICLE

EVOLUTION

OPEN ACCESS

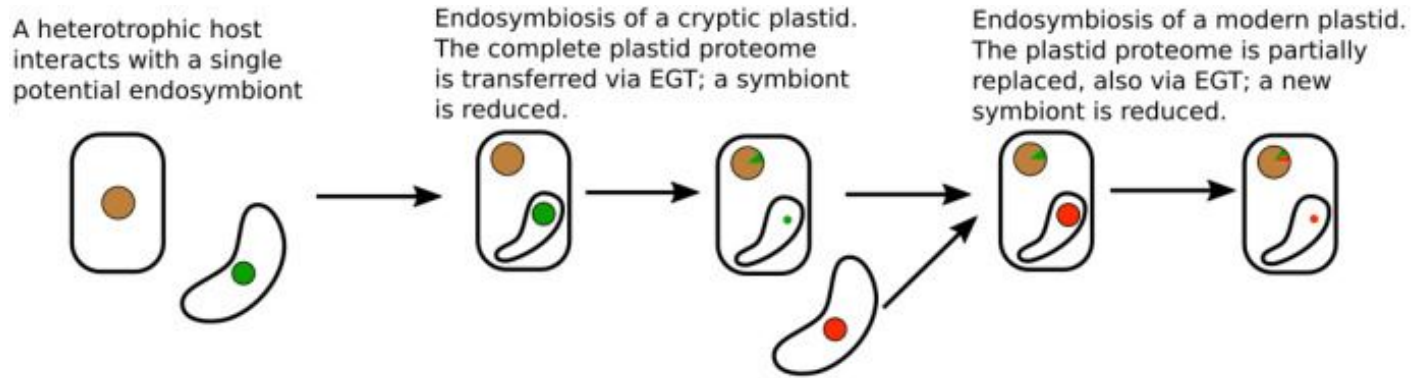


Euglenozoan kleptoplasty illuminates the early evolution of photoendosymbiosis

Anna Karnkowska^{a,b,c,1,2} , Naoji Yubuki^{a,b,1}, Moe Maruyama^{d,e,1} , Aika Yamaguchi^f , Yuichiro Kashiyama^{d,e,2} , Toshinobu Suzaki^g , Patrick J. Keeling^a, Vladimir Hampel^h, and Brian S. Leander^{a,h,2} 

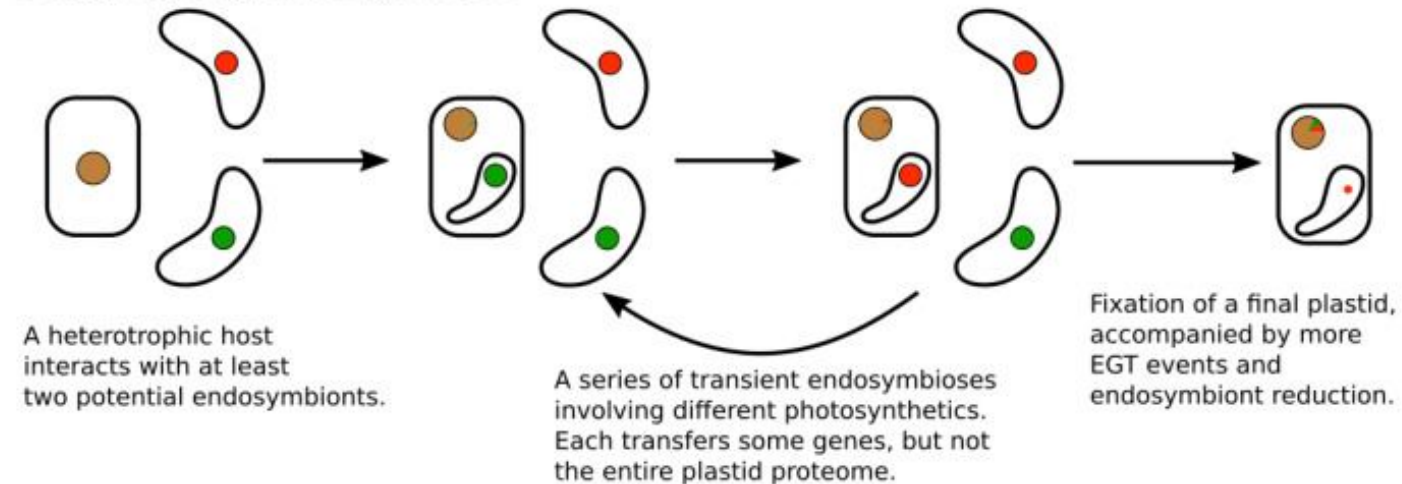
Edited by Edward DeLong, University of Hawai'i at Manoa, Honolulu, HI; received November 30, 2022; accepted February 14, 2023

MODELS



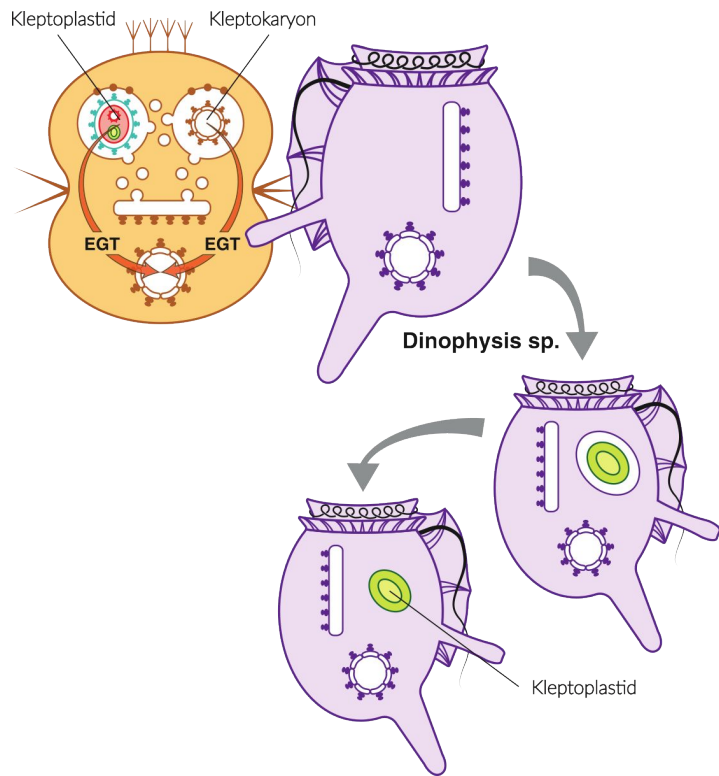
Serial endosymbioses

Shopping bag endosymbiosis

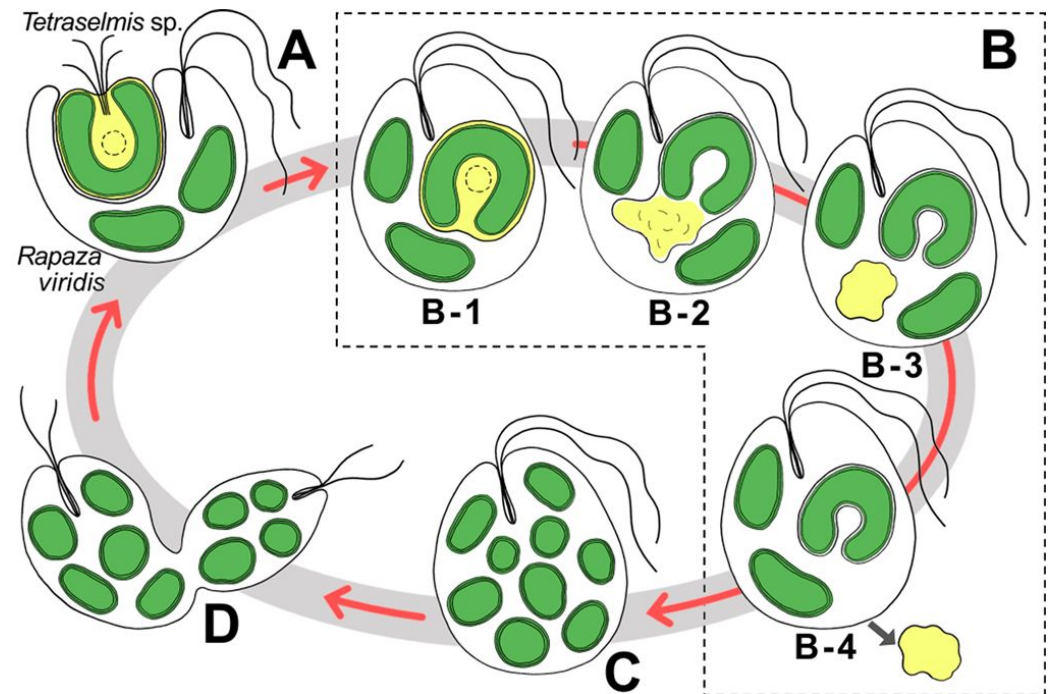


“Shopping bag” by kleptoplasty

Kleptoplasty by myzocytosis



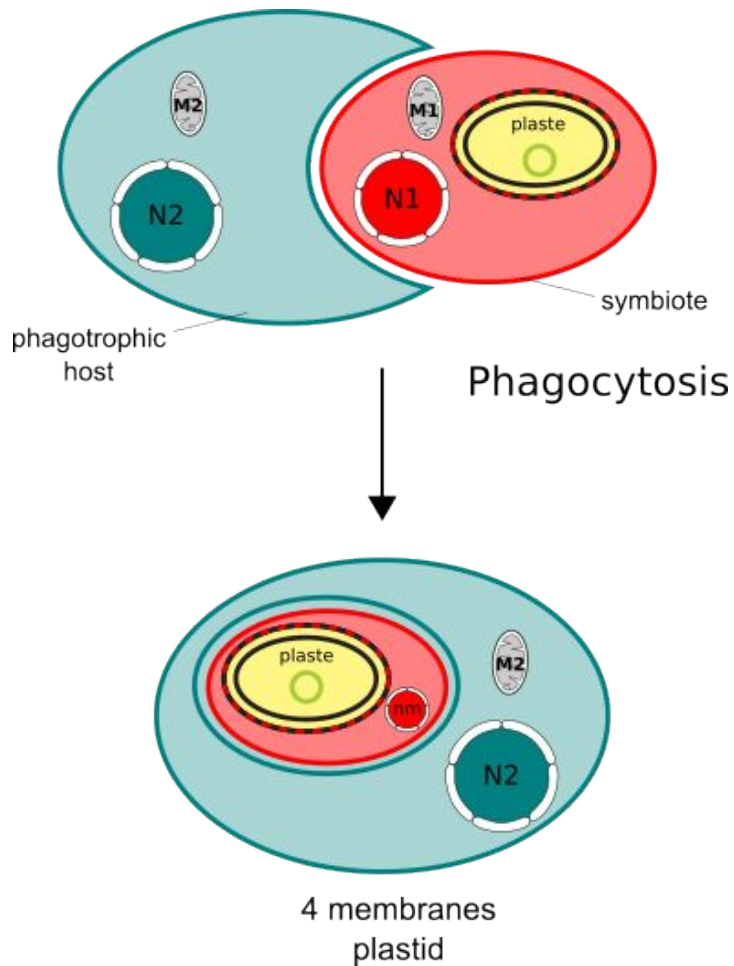
Kleptoplasty by phagocytosis



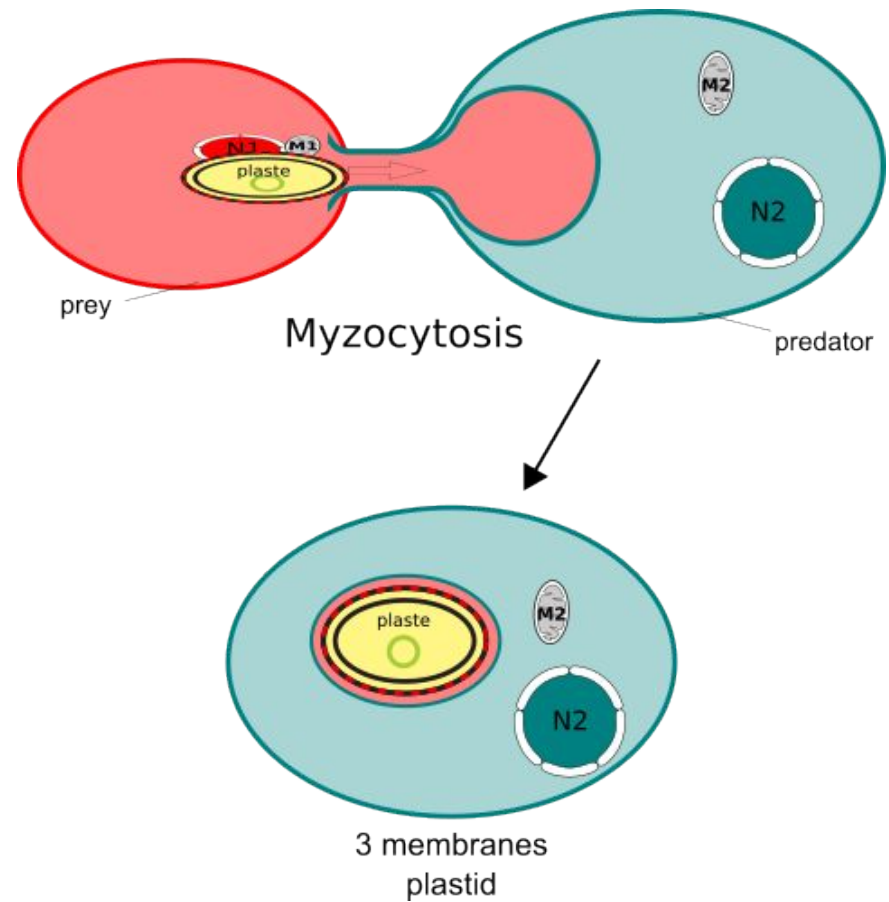
Strong selection pressure !

Origin of 3-membrane plastids?

Endosymbiosis (conservative)



Kleptoplasty (non-conservative)



AIM

Use **nuclear-encoded** and **plastid-targeted** gene **diversity** as an **indicator** of **kleptoplasty's** contribution to plastid acquisition among complex algae

Methods

Datasets

Data note | [Open access](#) | [Published: 17 April 2021](#)

Broadly sampled orthologous groups of eukaryotic proteins for the phylogenetic study of plastid-bearing lineages

[Mick Van Vlierberghe](#), [Hervé Philippe](#) & [Denis Baurain](#) 

[BMC Research Notes](#) **14**, Article number: 143 (2021) | [Cite this article](#)

1577 Accesses | 5 Citations | 2 Altmetric | [Metrics](#)

- ★ 73 high quality proteomes
- ★ ~ 40 000 photosynthetic clans

Data note | [Open access](#) | [Published: 09 August 2021](#)

Decontamination, pooling and dereplication of the 678 samples of the Marine Microbial Eukaryote Transcriptome Sequencing Project

[Mick Van Vlierberghe](#), [Arnaud Di Franco](#), [Hervé Philippe](#) & [Denis Baurain](#) 

[BMC Research Notes](#) **14**, Article number: 306 (2021) | [Cite this article](#)

1862 Accesses | 7 Citations | 2 Altmetric | [Metrics](#)

- ★ redundancy [678 -> 260]
- ★ contaminations [260 -> 224]

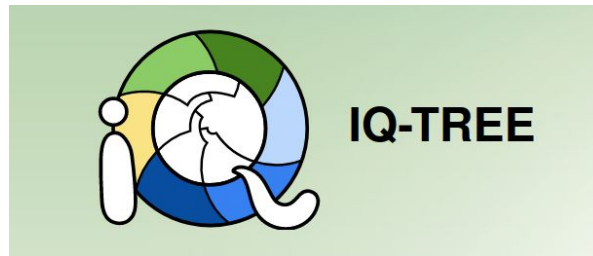
Dataset (1+2)

★ Clans [proteomes] enrichment [transcriptomes]

- orthology engine
- <https://metacpan.org/pod/Bio::MUST::Apps::FortyTwo>

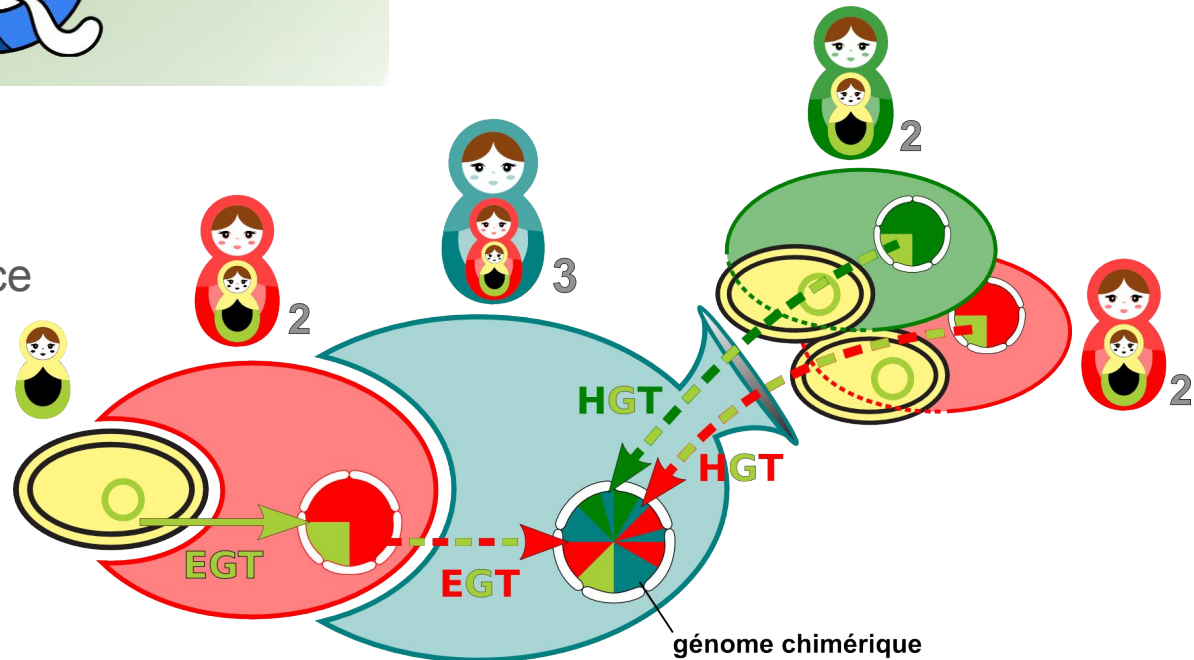


★ Tree building



★ Automatic tree analysis

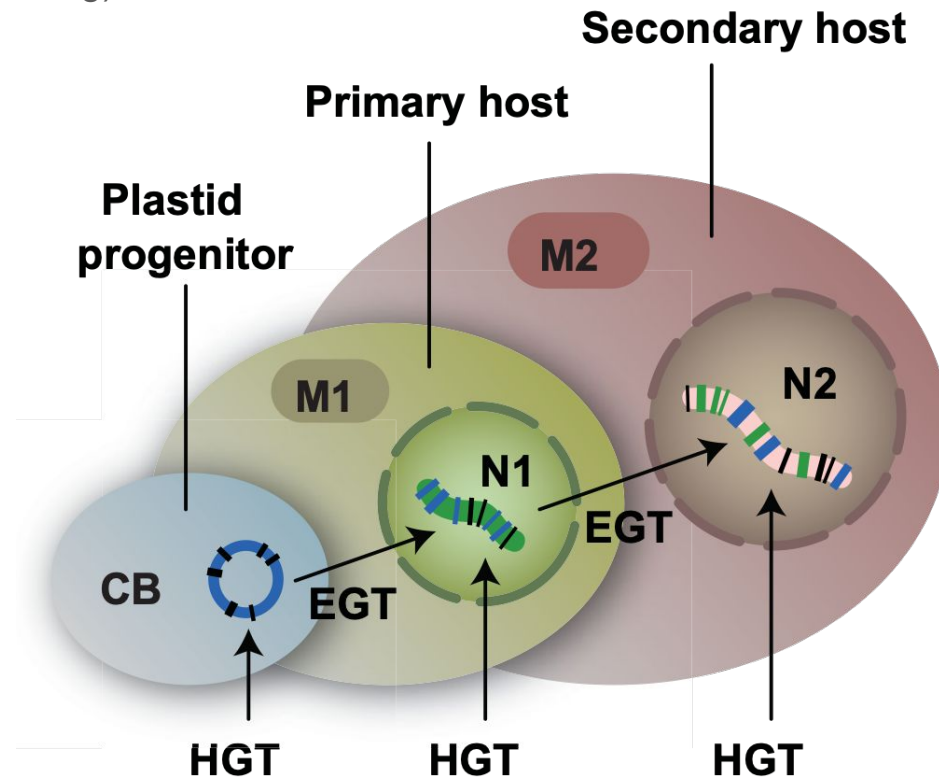
- Gene transfer inference



Automatic tree-parsing and gene transfer inference

★ Time constraints

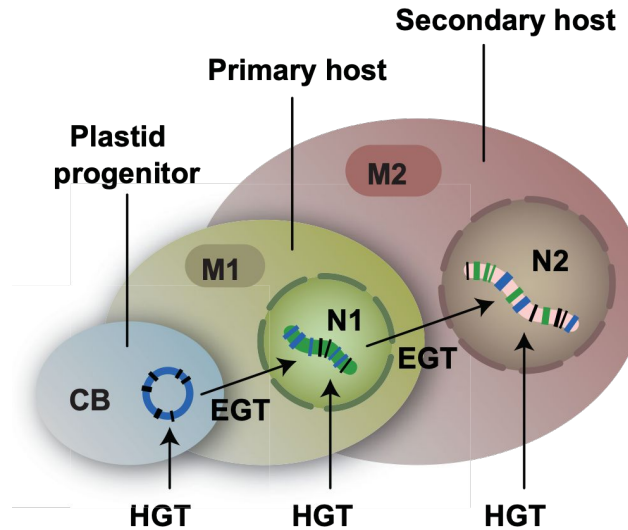
- primary algae (Archaeplastida)
- secondary algae (nm-bearing)
- higher-order algae



Automatic tree-parsing and gene transfer inference

★ Time constraints

- primary algae (Archaeplastida)
- secondary algae (nm-bearing)
- higher-order algae



★ Inference by paraphyly detection VS neighbourhood

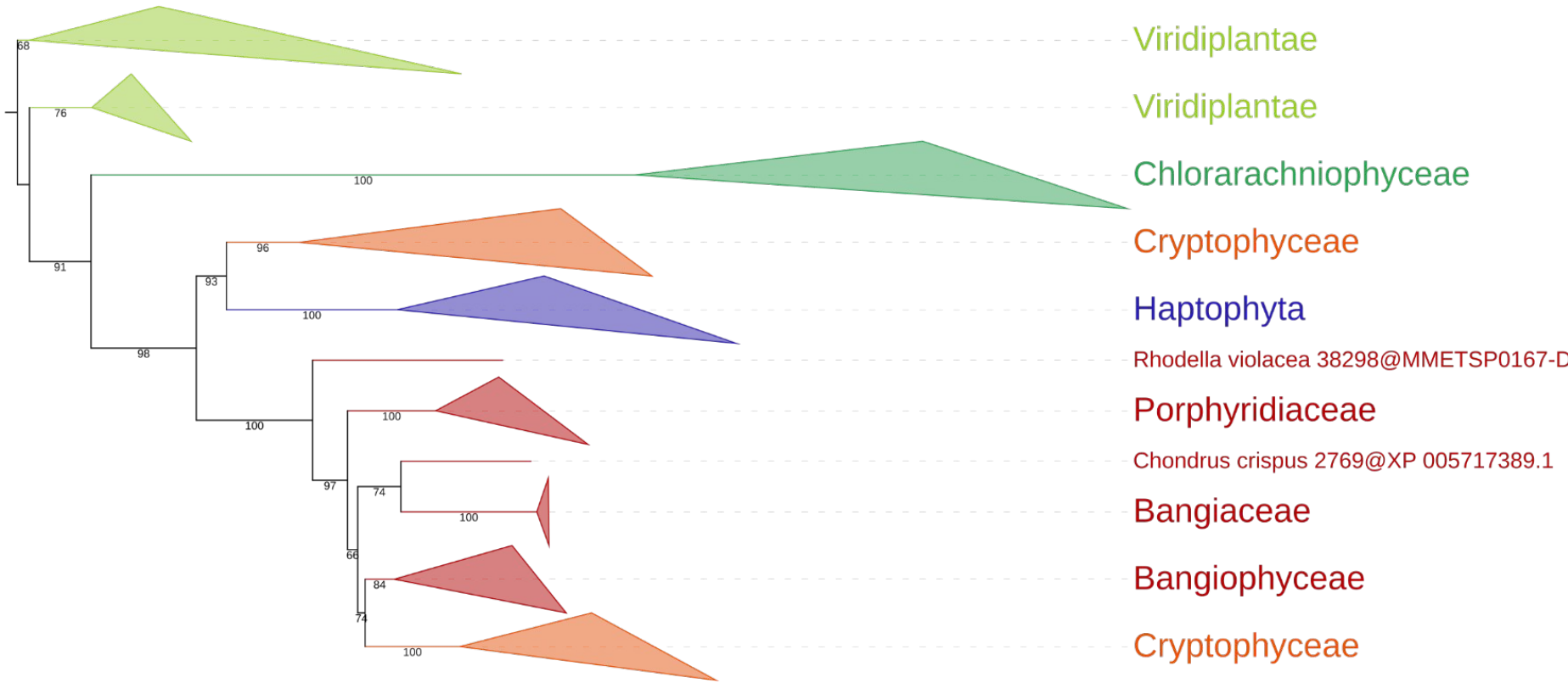
- exclusive/inclusive

★ Transfer event labelling [receiver tag/donor tag]

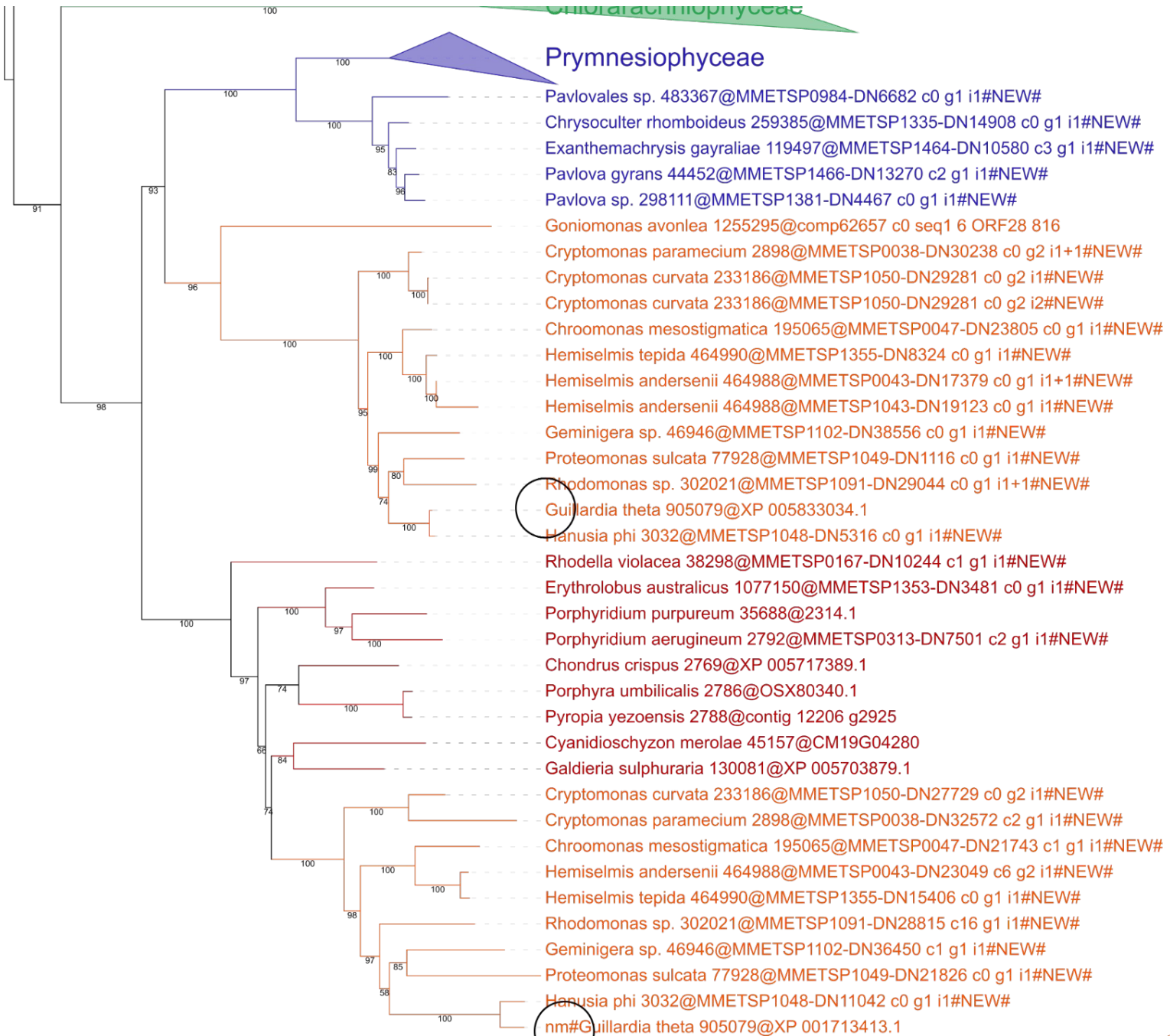
- cpcpt#, nm#, nucpt#...

OG0000267-17-IQ-TREE-C20

Tree scale: 0.1



Prymnesiophyceae



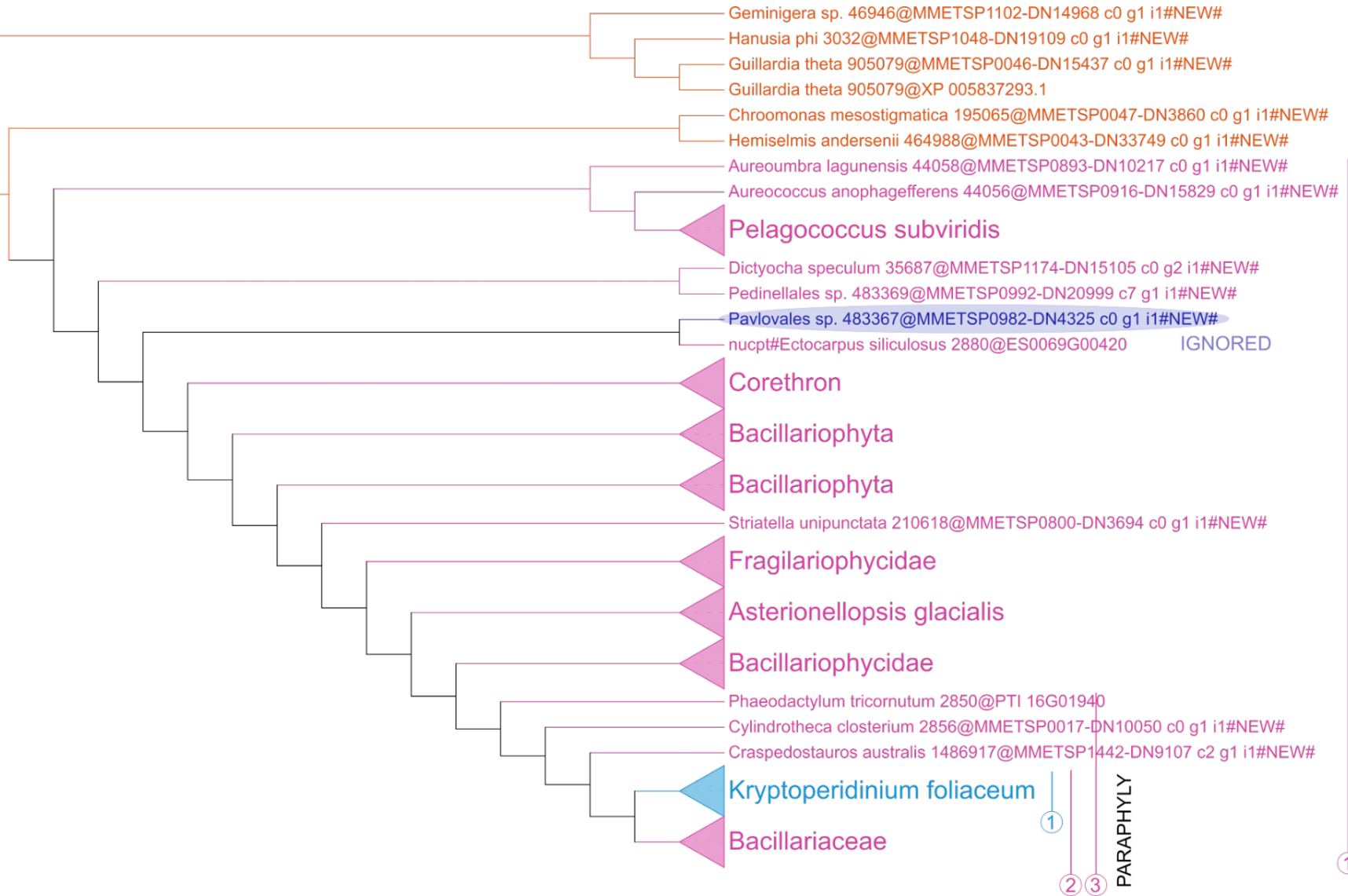
SISTER GROUP
RELATIONSHIP

PARAPHYLY

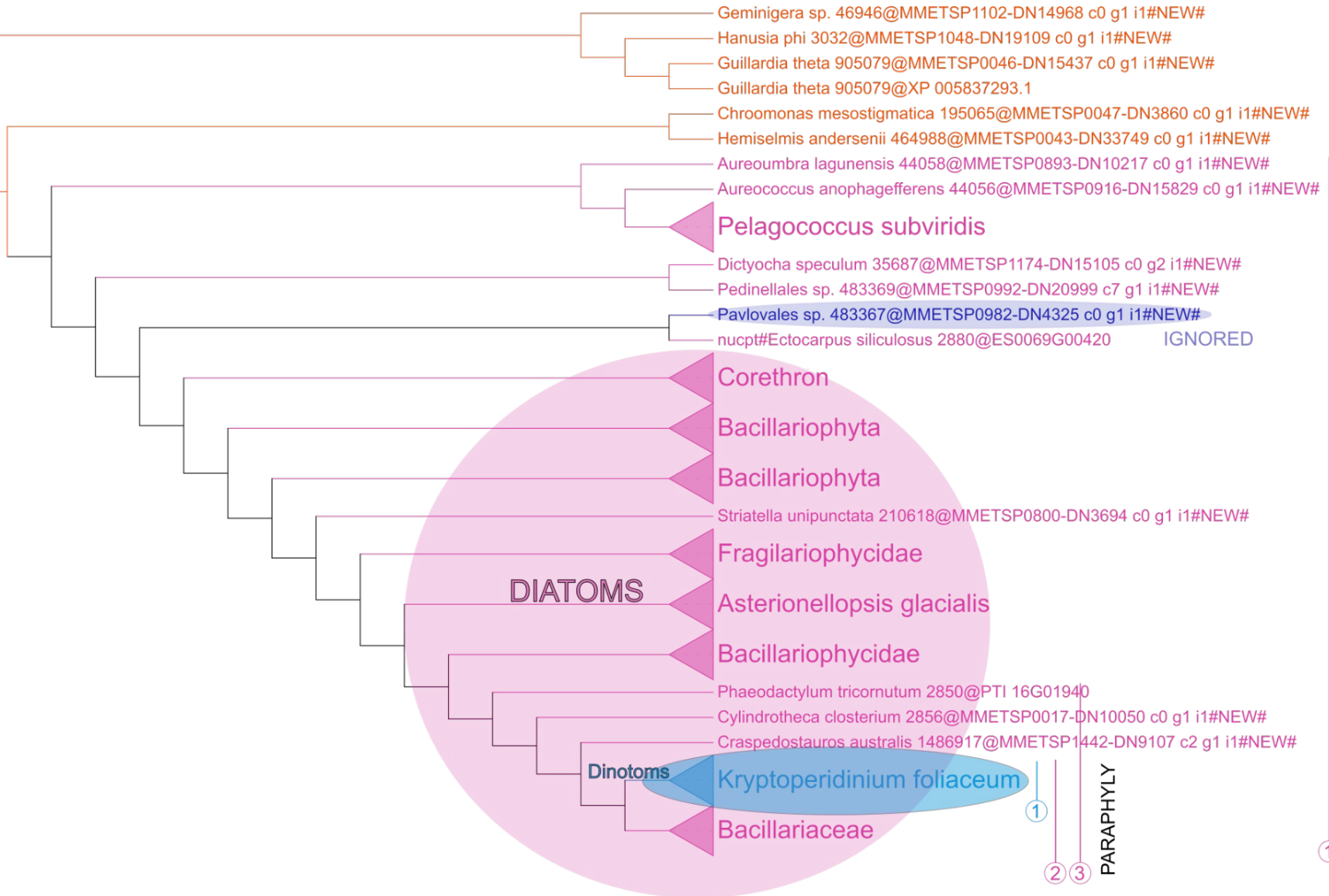
① ② ③

TAG

OG0015365-0-IQ-TREE-C20



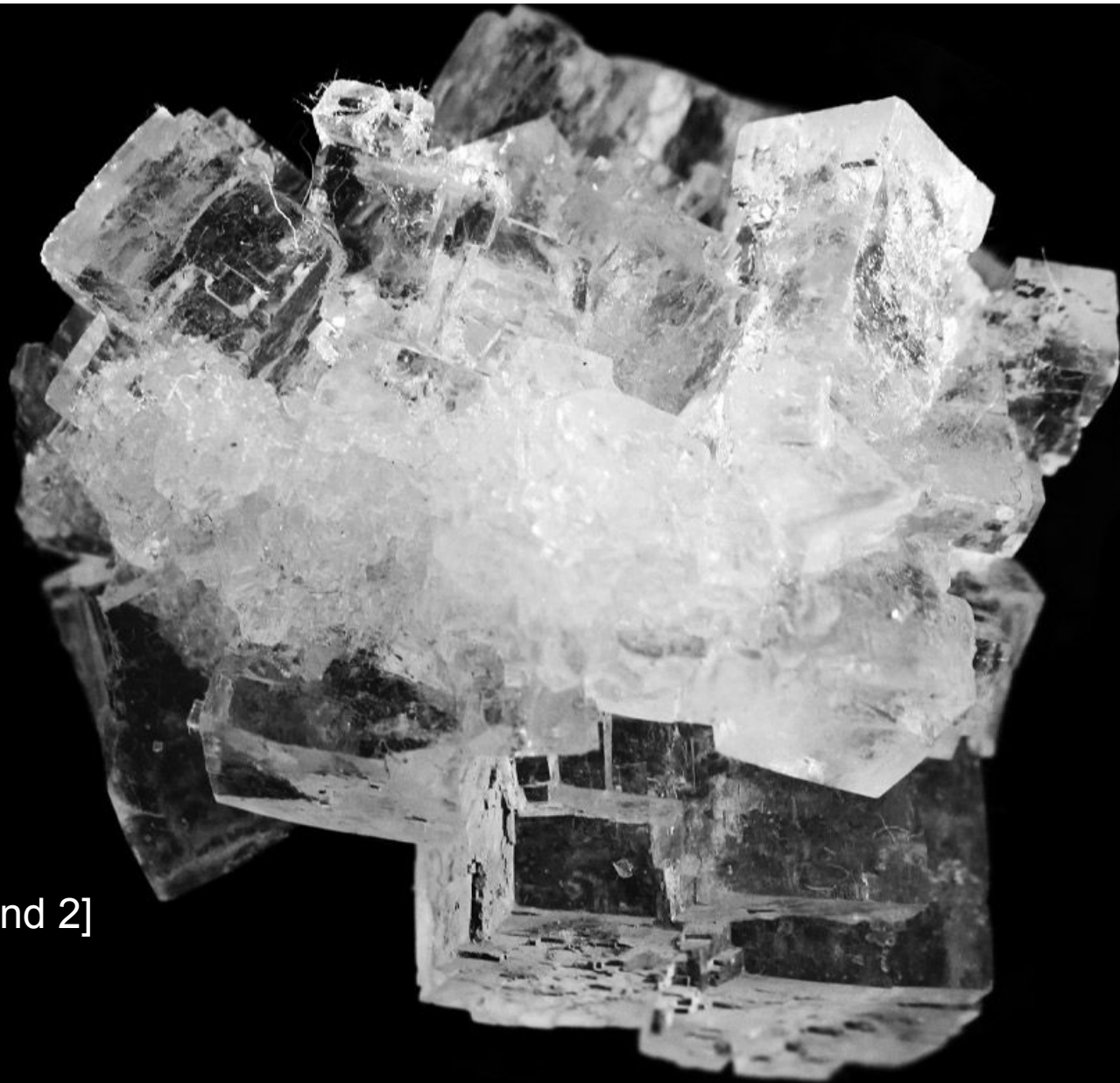
OG0015365-0-IQ-TREE-C20



PARAPHYLY

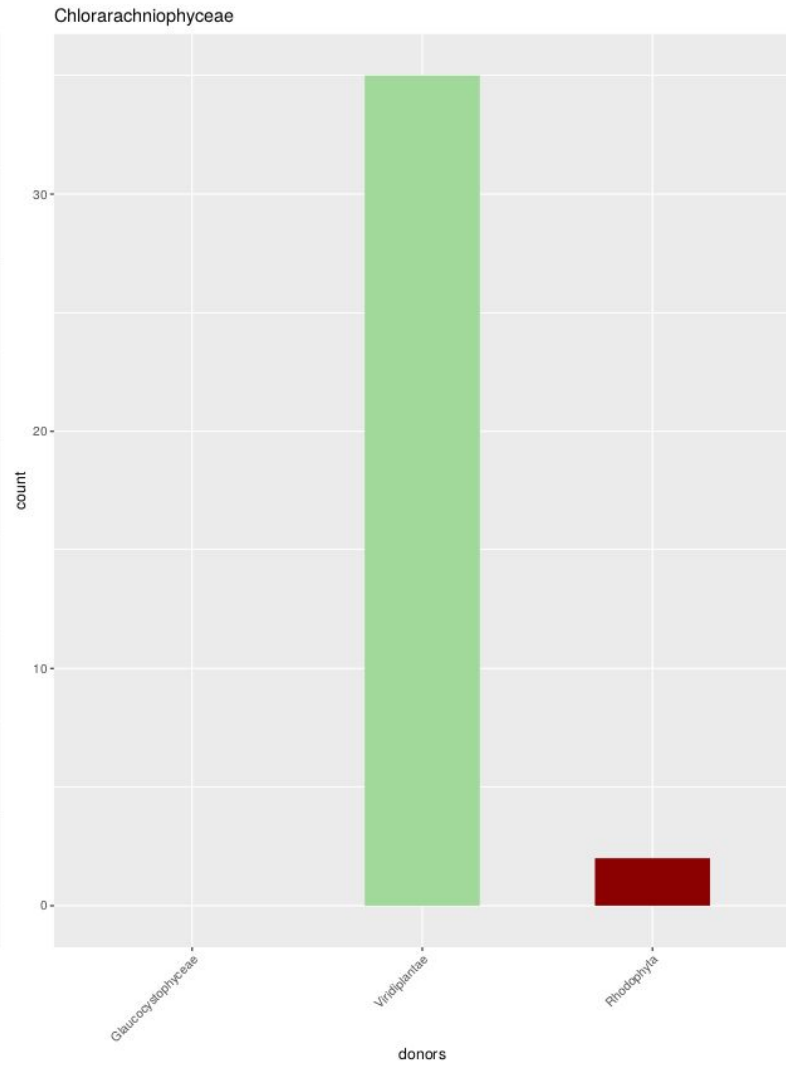
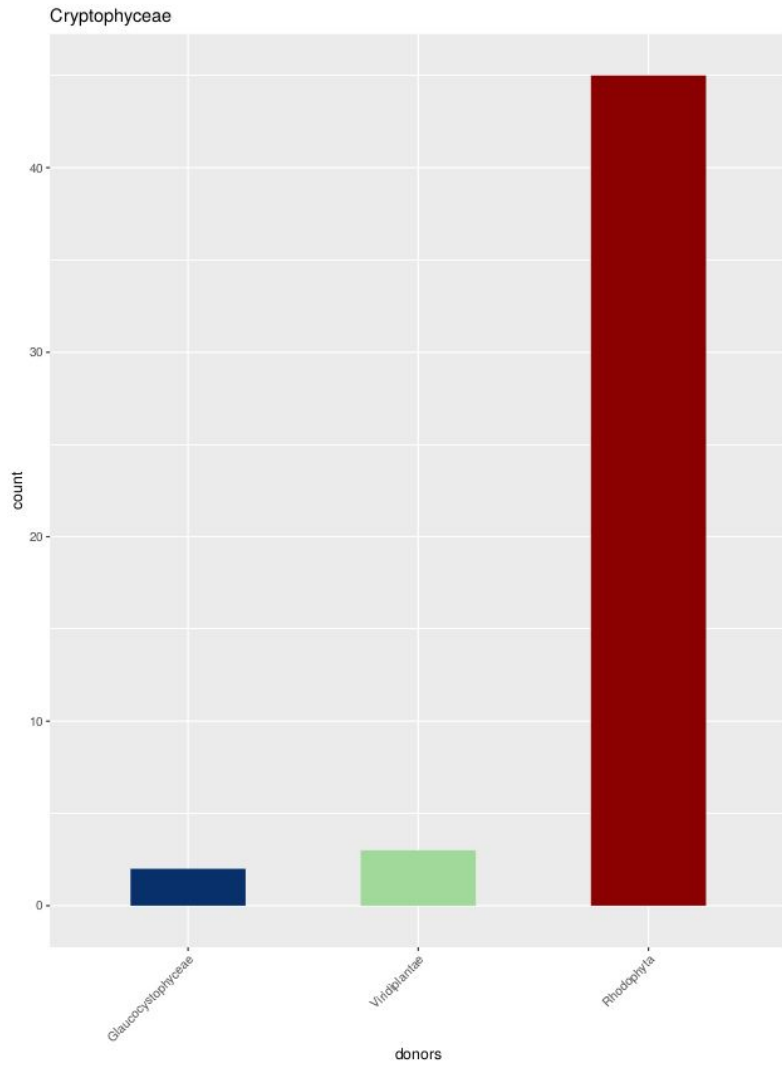
1 2 3

1
2 3
PARAPHYLY

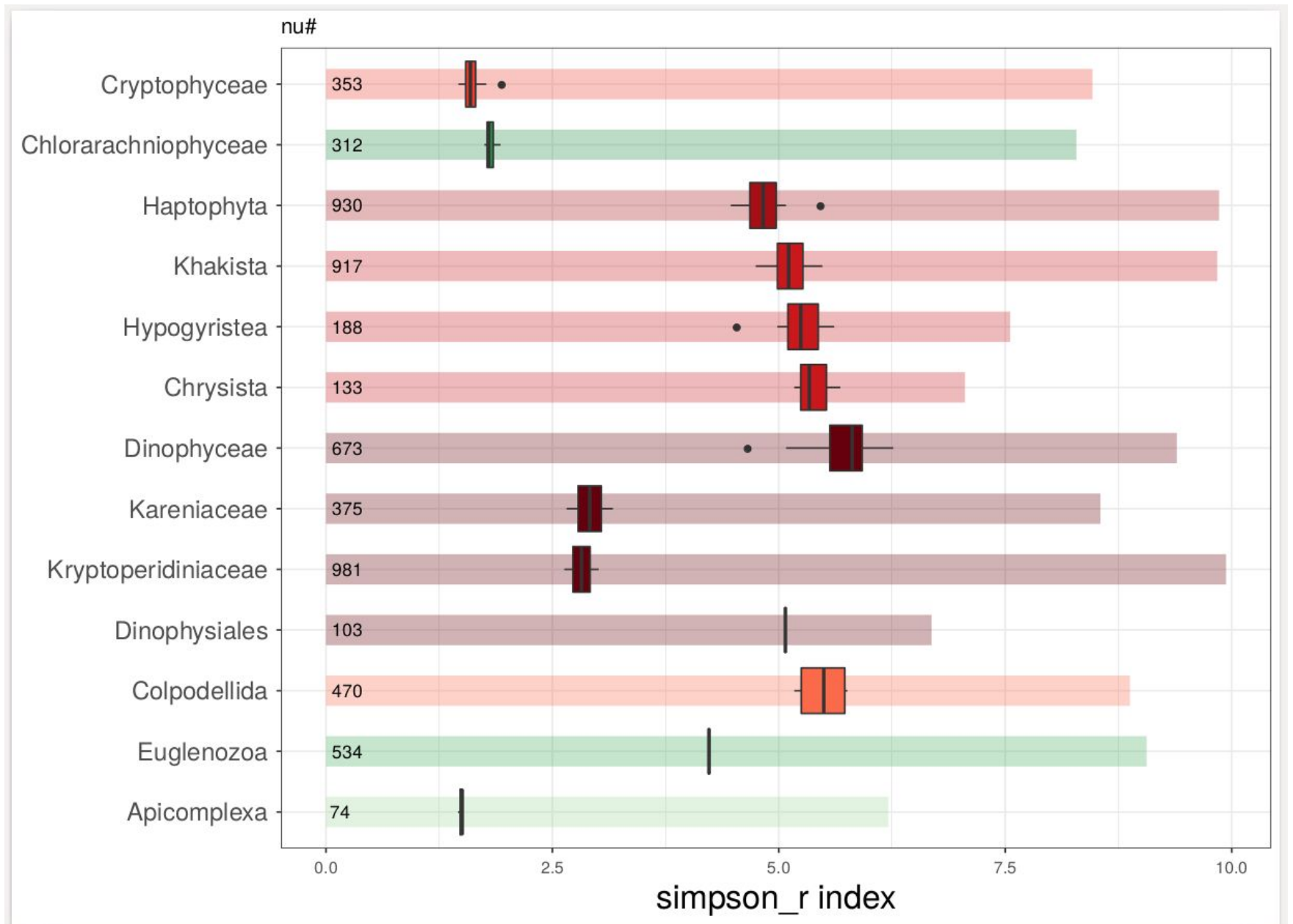


Preliminary results [round 2]

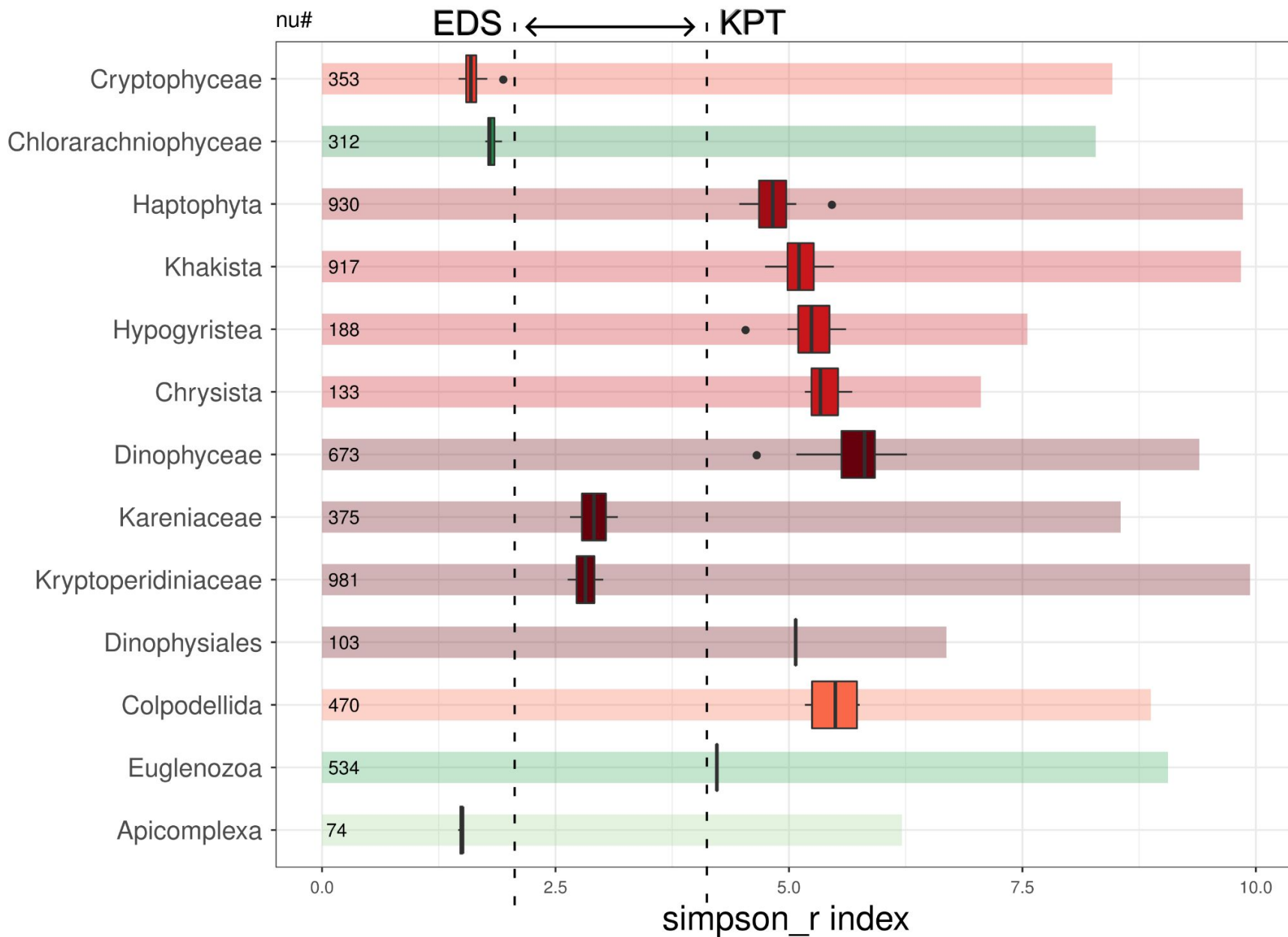
Control set : cpcpt#



nucpt# : alpha-diversity



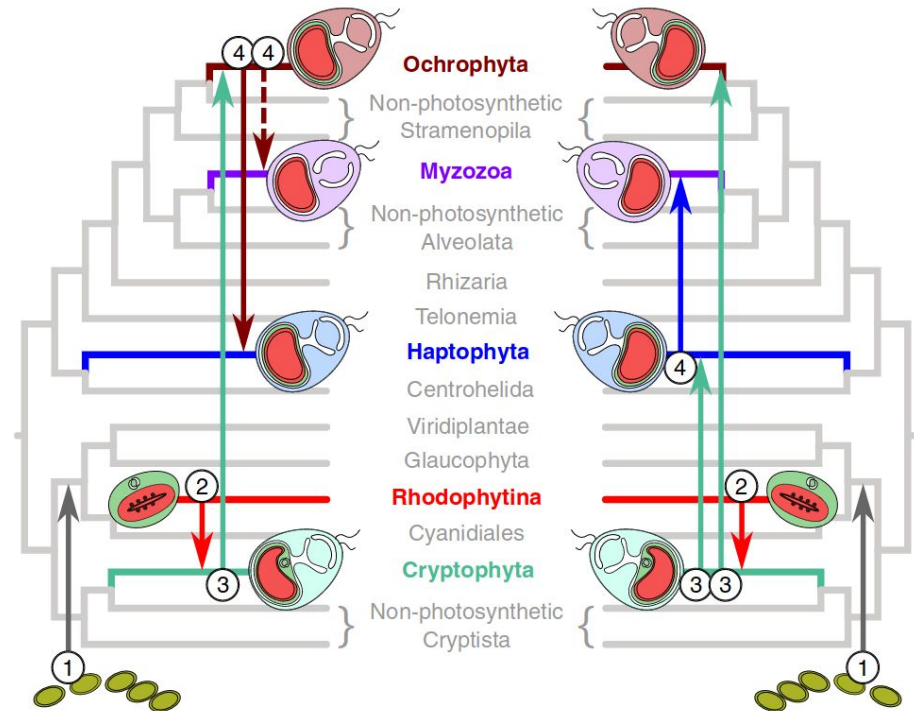
nucpt# : alpha-diversity



Can't wait for round 3 ...

Test robustness

- ★ naive time constraints
- ★ functional annotation
- ★ neighbourhood ?
- ★ sampling bias ?





Denis Baurain

Durandal

