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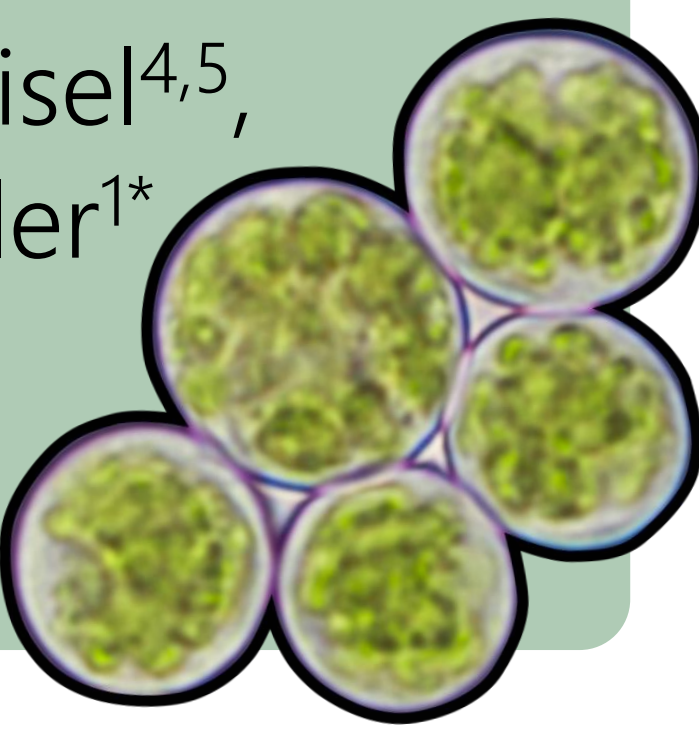
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# Phylogenomics reveals the evolutionary origin of lichenization in Chlorophytes algae

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## Introduction

Lichens are symbiotic organisms composed of a fungal partner and an photosynthetic partner which can either be a cyanobacteria or a chlorophyte alga. Within these latter, lichen forming algae (LFA) can be found in two distinct classes: the **Ulvophyceae** and the **Trebouxiophyceae** (Fig. 1). However, from the photobiont perspective, the evolutionary history of lichenization remains elusive. New approaches such as **comparative phylogenomics** can be used to test evolutionary hypotheses (ancestral gain, convergent evolution, Fig. 1) in order to understand how lichenization evolved and unravel its molecular bases.

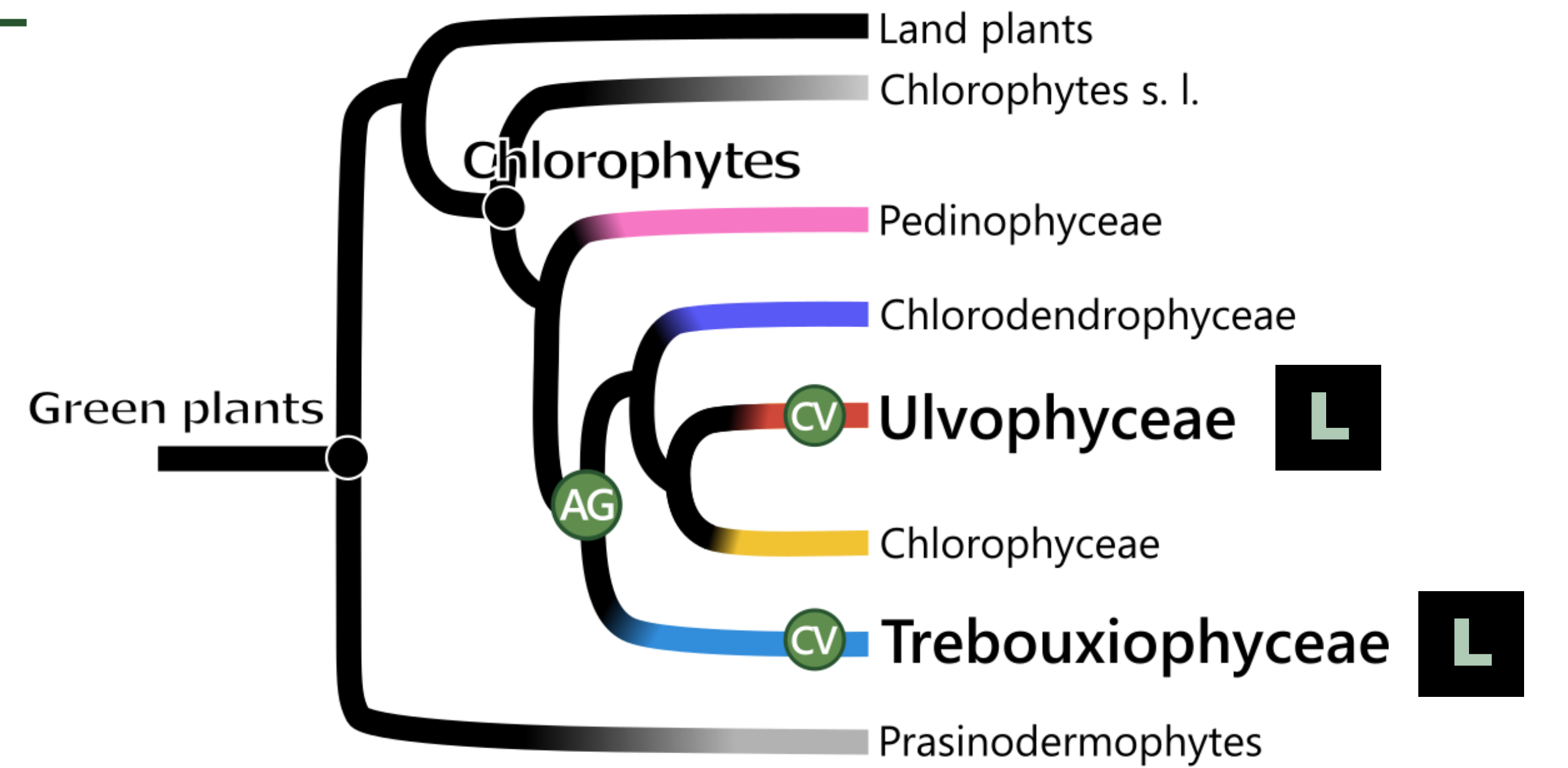


Fig. 1: Phylogenetic tree of the green plants (Viridiplantae). Clades that contains LFA are specified with the « L » letter. Potential evolutionary hypotheses are shown with green circles. AG: ancestral gain, CV: convergent evolution.

## Sampling and genomes sequenced to enable the comparative phylogenomics approach

12 species sequenced for this study (★ in Fig. 2)

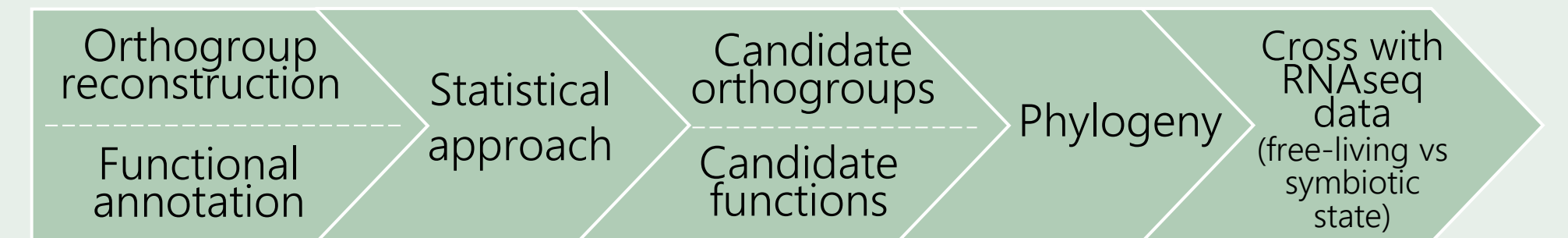
129 species from data mining (NCBI, 1KP)

Species	Ulvophyceae	Trebouxiophyceae
DilproSAG2392	●	■
DilpetSAG2240	●	■
EllbilSAG24580	●	■
CocpriSAG2167	●	■
SymirrSAG2036	●	■
ApalobSAG2145	●	■
ApafusSAG2523	●	■
MyrbisSAG2043	●	■
MyrbiSAG882	●	■
TrespOTU3	●	■
TrespOTU5	●	■
TrespOTU1	●	■

Fig. 2: BUSCO (completeness) of the species sequenced for this study.

## Ancestral state reconstruction (ASR) and phylogenomics supports the convergent evolution of lichenization in Chlorophytes

- The ASR supports at least 2 independent gains of lichenization (Fig. 3).
- A comparative phylogenomics workflow was used to detect the AG hypothesis (Fig. 1).



- None of the candidates identified (orthogroups/functions) can be linked to the AG hypothesis (Fig. 1).
- Candidates genes/functions associated with lichenization in Trebouxiophyceae
  - Stress tolerance (aquaporins, TspO/MBR)
  - Carbohydrates metabolism (GH8)

## The horizontal gene transfer of the Glycoside Hydrolase 8 (GH8) shaped the evolution of lichens

- The most significant candidate corresponds to the GH8 enzyme
- The GH8 originated from a horizontal gene transfer (Fig. 4)
- The GH8 degrades the lichenan (carbohydrates present in lichen-forming fungi) → LFA accommodation

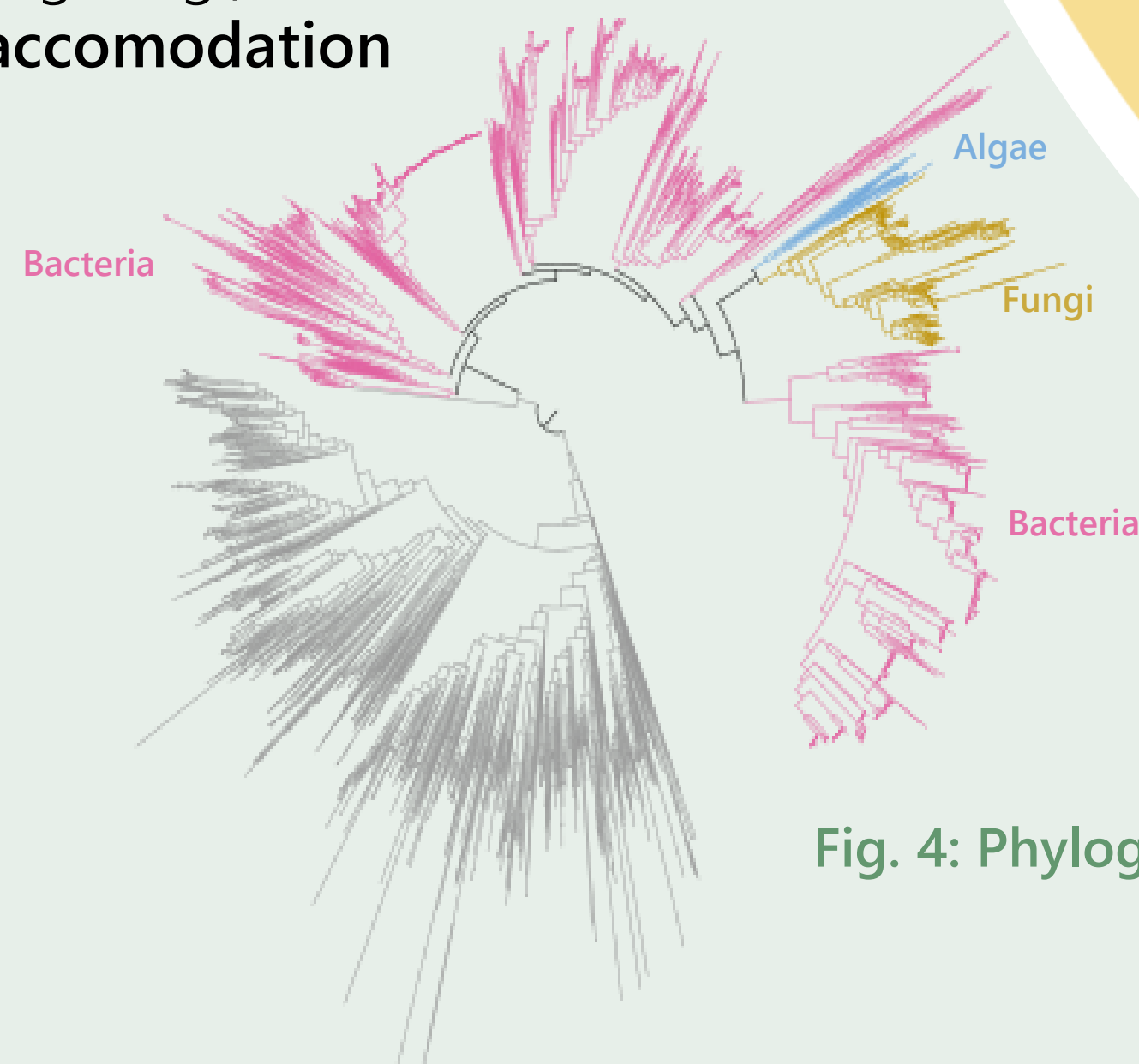


Fig. 4: Phylogenetic tree of the GH8

Fig. 3: Ancestral state reconstruction of lichenization in Chlorophytes (ARD model). Species are colored according to Fig. 1. Black: LFA, grey: nLFA. Stars: species sequenced for this study

## Conclusion

Using a combination of approaches, the evolution of lichenization in Chlorophytes was studied and according to the results, the convergent evolution hypothesis is currently favored. Candidates genes and functions were identified and might have provided the bases for lichenization to evolve. Following this study, it will be important to test the effects of these genes on the lichenization process.

