

Hunting for nuclear markers in green algal lineages: Molecular evolution of glucose-6-phosphate isomerase

Ellen Cocquyt, Frederik Leliaert, Heroen Verbruggen & Olivier De Clerck

EllenE.Cocquyt@UGent.be

Research Group Phycology and Center for Molecular Phylogenetics and Evolution (CeMoFE), Biology Department, Ghent University, K.L. Ledeganckstraat 35, 9000 Gent, Belgium

Introduction

- The Chlorophyta exhibit a remarkable cytological diversity
→ Fig 1
- Unravelling the evolutionary history of this diverse group is a difficult task, due to:
 - antiquity of the major defining lineages
 - considerable rate variation among lineages
 - scarcity of useful molecular phylogenetic markers
- examination of several independent nuclear markers is needed, therefore:
 - different genes with known function and sequence data available are tested
 - a cDNA library is screened to search for new useful genes



Fig 1: Remarkable cytological diversity in the Chlorophyta ranging from unicellular microscopic algae with a single nucleus, over multicellular filaments and foliose blades, to coenocytic and siphonous life forms that are essentially composed of a giant cell containing thousands of nuclei.

Chlorococcal	Chlorococcal	Chlorococcal	Chlorococcal	Chlorococcal
Chlorococcal	Chlorococcal	Chlorococcal	Chlorococcal	Chlorococcal
Chlorococcal	Chlorococcal	Chlorococcal	Chlorococcal	Chlorococcal
Chlorococcal	Chlorococcal	Chlorococcal	Chlorococcal	Chlorococcal
Chlorococcal	Chlorococcal	Chlorococcal	Chlorococcal	Chlorococcal

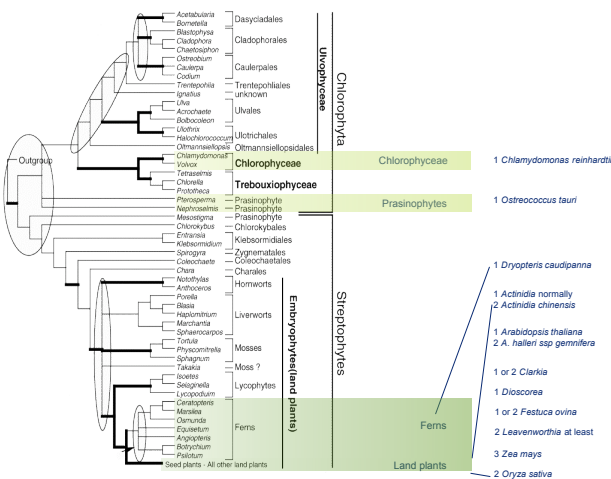


Fig 2: Evolution and copy number of G6PI in the Chloroplastida Tree after D. Mandoli et al. Toward resolution of the "Fuzzy Nodes" in green plant phylogeny (<http://faculty.washington.edu/mandoli/fuzzy.ph>)

Aims of the study

- Identification of nuclear genes useful for phylogenetic reconstruction in the Chlorophyta
- Investigation of the G6PI gene(s) useful as a phylogenetic marker in the Chlorophyta

Methods

- Primer design based on the G6PI genome sequences of *Arabidopsis thaliana*, *Oryza sativa*, *Chlamydomonas reinhardtii* and *Ostreococcus tauri*
- DNA extraction → PCR → Cloning → Sequencing
- RNA extraction → RT-PCR → PCR → Sequencing

Conclusions

- Epiphytic or endophytic bacteria interfere with direct DNA amplification of nuclear genes
- Information content of G6PI depends on taxonomic level
 - deep phylogenies require exclusion of 3rd codon pos
 - species level relationships are generally well-supported
 - introns at fixed positions may offer opportunities towards studies at the intraspecific level
- Most likely only one (functional) copy of G6PI gene is present in the taxa tested

Glucose-6-phosphate isomerase (G6PI)

- Enzyme of the carbohydrate biosynthesis pathway, after the Calvin cycle, in photosynthetic organisms and of the glycolysis in all living organism
- Genome sequences of *C. reinhardtii* and *O. tauri* revealed that both have a single copy of G6PI → Fig 2

Results

- G6PI phylogenetic tree of several green algae

