

Exchange your knowledge on plant gene families



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ABSTRACT: Every year, hundreds of **gene families** are characterized through peer-review publications but their structure and classification is hardly captured by dedicated databases such as Phytozome, Plaza, Ensembl or GreenPhylDB. To address this situation, we developed a user-friendly interface allowing either to customize pre-computed protein sequence clusters or to create new ones based on prior knowledge of a given gene family. Information can be then **shared with collaborators and/or reviewers with a unique URL**.

1. Rationale

Many studies on plant gene families...

...but is there any repository?

Get started with **GreenPhyl** to add value to your gene families!

- easy gene family creation
- feature management
- nice display

What is GreenPhyl?

A published public web resource designed for **comparative and functional genomics** in plants:

- 4th release
- 37 complete plant genomes
- 1 300 000 gene sequences
- 8 300 sequence clusters
- 2 900 annotated clusters

3. Display

a. Species composition

b. Phylogeny analysis display

2. Searching

Family directory

Family search

to my list

d. Sequence export and mapping

to my list

External tools: **Galaxy**

to galaxy

c. (Sub)family relationship

a. Relationship management

to display

b. Phylogeny analysis

to display

4. Creation

a. Building gene family from GreenPhyl data using "My List" feature

"My List" is a clipboard-like space storing a set of sequences. This set can be modified using another set of selected sequences or gene families by applying some basic operations:

Selection My List
Merge Replace Intersect Subtract

b. Building gene family from FASTA sequences

step 1: Multiple-FASTA import

step 2: Species validation

supports all plant UniProt codes (>4000 species)

5. Management

a. Sequence management

to gene family management

Properties

dynamic edition

Access control

Designed for **peer-review process**

restricted (read or read/edit) for **publication review process, collaboration, ...**

private for **work in progress**

public access (read or read/edit) for **visibility or wiki-style gene family**

"private" URL or password

User account

Free, required for gene family creation, **OpenID** supported: use your **Google**, **Yahoo!**, etc. account to log in!

References:

1. Cenci A, Guignon V, Roux N, Rouard M. **Genomic analysis of NAC transcription factors in banana (*Musa acuminata*) and definition of NAC orthologous groups for monocots and dicots.** Plant Mol Biol. 2014 Feb 26.
2. Jourda, C., Cardi, C., Mbégué-A-Mbégué, D., Bocs, S., Garsmeur, O., D'Hont, A. and Yahiaoui, N. (2014), **Expansion of banana (*Musa acuminata*) gene families involved in ethylene biosynthesis and signalling after lineage-specific whole-genome duplications.** New Phytologist. doi: 10.1111/nph.12710.
3. Rouard, M., Guignon, V., Aluome, C., Laporte, M.-A., Droc, G., Walde, C., Zmasek, C.M., Perin, C. et Conte, M.-G. (2011) **GreenPhylDB v2.0: comparative and functional genomics in plants.** Nucleic Acids Research, 39, D1093-D1102, 10.1093/nar/gkq811.
4. Waterhouse, A.M., Procter, J.B., Martin, D.M.A, Clamp, M. and Barton, G. J. (2009), **Jalview Version 2 - a multiple sequence alignment editor and analysis workbench.** Bioinformatics25 (9) 1189-1191 doi: 10.1093/bioinformatics/btp033
5. Zmasek C.M., Eddy S.R. **ATV: display and manipulation of annotated phylogenetic trees.** Bioinformatics. 2001, Apr;17(4):383-4.