GreenPhylDB: a plant comparative genomics platform

http://greenphyl.cirad.fr

Matthieu.G CONTE, Mathieu ROUARD, Sylvain GAILLARD, Nadège LANAU and Christophe PERIN*.

*Corresponding author: perin@cirad.fr CIRAD: French Agricultural Research Center for International Development .

➢ Overview

The increasing amount of sequence data provided by full or partial genome sequencing projects urgently needs a way to transfer information from model species to new sequenced ones. Orthologous and paralogous genes identification is now a major objective for gene function prediction as orthologous sequences are more likely to share the same function than paralogous sequences.

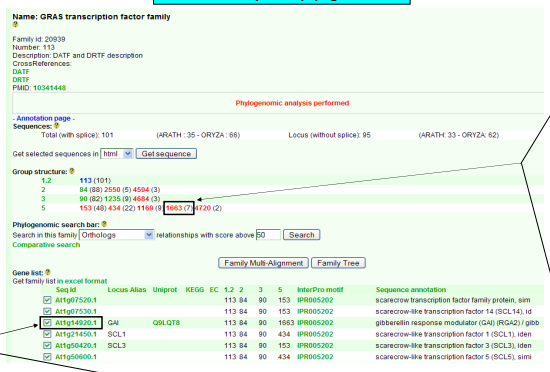
➢ Results

We developed **GreenPhylDB**, a comprehensive platform for comparative genomics analyses of ***Arabidopsis thaliana*** and ***Oryza sativa*** full genomes. First **GreenPhylDB offers the most complete plant family list with 6423 manually curated families. Most of these families have been analyzed with our optimized phylogenomic pipeline (4425 families).** Thus GreenPhylDB is the only plant database that provides an indicator of phylogenomic accuracy prediction.

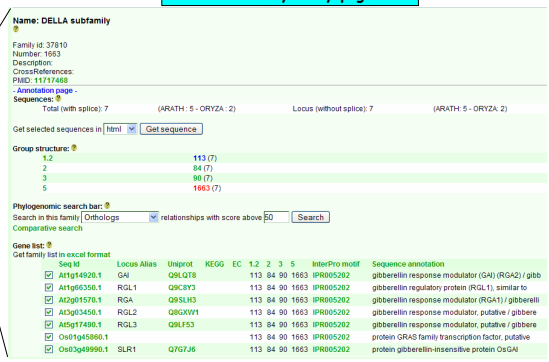
➢ GreenPhylDB

Example of GreenPhylDB family entry pages for GRAS transcription factor family

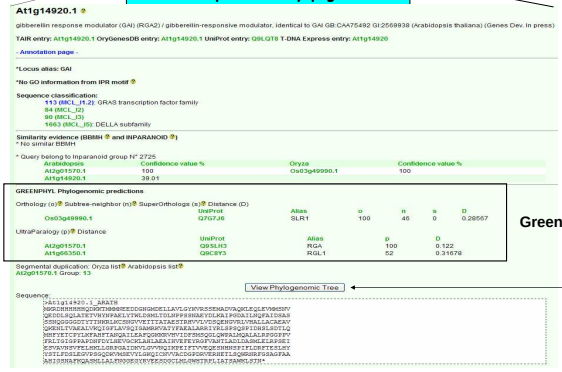
Family entry page



Sub-Family entry page

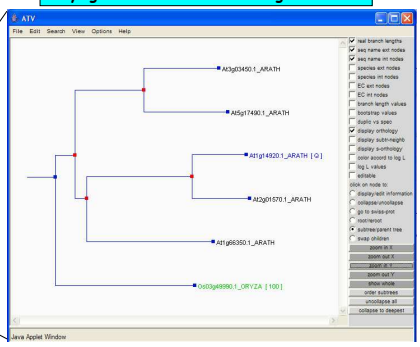


Sequence entry page



GreenPhyl Phylogenomic prediction field

Phylogenomic tree with orthologous scores

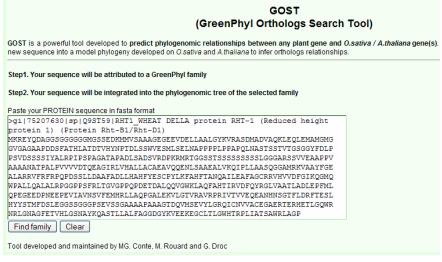


➢ GOST: GreenPhyl Orthologs Search Tool

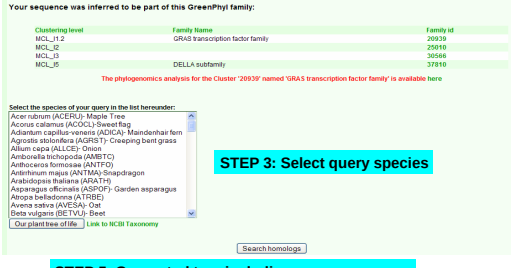
GOST is a powerful tool developed to predict phylogenomic relationships between any plant gene and *O. sativa* / *A. thaliana* gene(s). This tool rapidly integrates a new sequence into a precomputed phylogenic tree developed on *O.sativa* and *A.thaliana* to infer orthologs relationships.

Phylogenomic prediction on RHT1 wheat gene from GRAS transcription factor family:
This gene have been published to be ortholog to *Arabidopsis thaliana* Gibberellin Insensitive (GAI) gene involved in gibberellin transduction.
PMID: 10421366

STEP 1: Paste your protein sequence

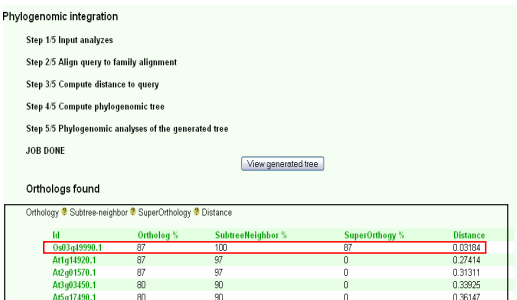


STEP 2: Integration of your query into a GreenPhylDB family

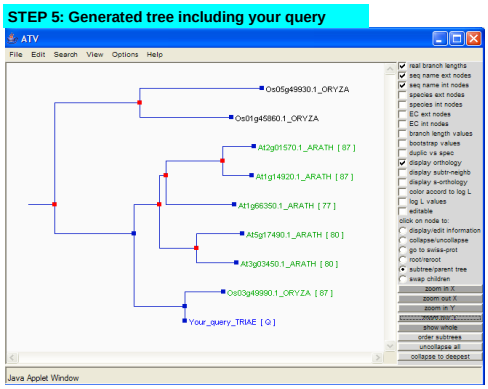


STEP 3: Select query species

STEP 4: Phylogenomic integration of your sequence into the selected family



STEP 5: Generated tree including your query



GOST
Phylogenomic predictions