

Resource Summary Report

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GreenPhylDB

RRID:SCR_002834

Type: Tool

Proper Citation

GreenPhylDB (RRID:SCR_002834)

Resource Information

URL: <http://www.greenphyl.org/>

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Description: A database designed for plant comparative and functional genomics based on complete genomes. It comprises complete proteome sequences from the major phylum of plant evolution. The clustering of these proteomes was performed to define a consistent and extensive set of homeomorphic plant families. Based on this, lists of gene families such as plant or species specific families and several tools are provided to facilitate comparative genomics within plant genomes. The analyses follow two main steps: gene family clustering and phylogenomic analysis of the generated families. Once a group of sequences (cluster) is validated, phylogenetic analyses are performed to predict homolog relationships such as orthologs and ultraparalogs.

Abbreviations: GreenPhylDB

Resource Type: service resource, data or information resource, production service resource, database, analysis service resource, data analysis service

Defining Citation: [PMID:20864446](#)

Keywords: comparative genomics, genome, functional genomics, genomics, gene family, homolog, bio.tools

Availability: Free, Freely available, Available for download

Resource Name: GreenPhylDB

Resource ID: SCR_002834

Alternate IDs: biotools:greenphylpdb, nif-0000-02928

Alternate URLs: <http://greenphyl.cirad.fr>, <http://www.greenphyl.org/v3/>, <https://bio.tools/greenphylpdb>

Record Creation Time: 20220129T080215+0000

Record Last Update: 20260813T054841+0000

Ratings and Alerts

No rating or validation information has been found for GreenPhylDB.

No alerts have been found for GreenPhylDB.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 20 mentions in open access literature.

Listed below are recent publications. The full list is available at [PRECISE-TBI](#) .

Tripathi L, et al. (2025) Loss of function of MusaPUB genes in banana can provide enhanced resistance to bacterial wilt disease. Communications biology, 8(1), 708.

Shi N, et al. (2025) Deciphering metabolic regulation in overripe grapes through multi-omics analysis of non-targeted metabolome, proteome, and transcriptome. BMC plant biology, 25(1), 1183.

Yang L, et al. (2023) From single- to multi-omics: future research trends in medicinal plants. Briefings in bioinformatics, 24(1).

Liu Y, et al. (2021) SorGSD: updating and expanding the sorghum genome science database with new contents and tools. Biotechnology for biofuels, 14(1), 165.

Dufayard JF, et al. (2021) RapGreen, an interactive software and web package to explore and analyze phylogenetic trees. NAR genomics and bioinformatics, 3(3), lqab088.

Valentin G, et al. (2021) GreenPhylDB v5: a comparative pangenomic database for plant genomes. Nucleic acids research, 49(D1), D1464.

O'Conner S, et al. (2020) Mitochondrial Fostering: The Mitochondrial Genome May Play a Role in Plant Orphan Gene Evolution. Frontiers in plant science, 11, 600117.

Bhuiyan F, et al. (2020) Characterizing fruit ripening in plantain and Cavendish bananas: A proteomics approach. Journal of proteomics, 214, 103632.

Duarte KE, et al. (2019) Identification and characterization of core abscisic acid (ABA) signaling components and their gene expression profile in response to abiotic stresses in Setaria viridis. Scientific reports, 9(1), 4028.

Cenci A, et al. (2017) Evolutionary Analyses of GRAS Transcription Factors in Angiosperms. *Frontiers in plant science*, 8, 273.

Santamar??a ME, et al. (2017) MATI, a Novel Protein Involved in the Regulation of Herbivore-Associated Signaling Pathways. *Frontiers in plant science*, 8, 975.

Clark JW, et al. (2017) Constraining the timing of whole genome duplication in plant evolutionary history. *Proceedings. Biological sciences*, 284(1858).

Sardos J, et al. (2016) A Genome-Wide Association Study on the Seedless Phenotype in Banana (*Musa spp.*) Reveals the Potential of a Selected Panel to Detect Candidate Genes in a Vegetatively Propagated Crop. *PloS one*, 11(5), e0154448.

Kroj T, et al. (2016) Integration of decoy domains derived from protein targets of pathogen effectors into plant immune receptors is widespread. *The New phytologist*, 210(2), 618.

Zorrilla-Fontanesi Y, et al. (2016) Differential root transcriptomics in a polyploid non-model crop: the importance of respiration during osmotic stress. *Scientific reports*, 6, 22583.

Ngaki MN, et al. (2016) Transcriptomic Study of the Soybean-*Fusarium virguliforme* Interaction Revealed a Novel Ankyrin-Repeat Containing Defense Gene, Expression of Whose during Infection Led to Enhanced Resistance to the Fungal Pathogen in Transgenic Soybean Plants. *PloS one*, 11(10), e0163106.

Dhanapal AP, et al. (2015) Unlimited Thirst for Genome Sequencing, Data Interpretation, and Database Usage in Genomic Era: The Road towards Fast-Track Crop Plant Improvement. *Genetics research international*, 2015, 684321.

Hyung D, et al. (2014) Cross-family translational genomics of abiotic stress-responsive genes between *Arabidopsis* and *Medicago truncatula*. *PloS one*, 9(3), e91721.

Kurowska M, et al. (2011) TILLING: a shortcut in functional genomics. *Journal of applied genetics*, 52(4), 371.

Sato K, et al. (2009) Development of 5006 full-length cDNAs in barley: a tool for accessing cereal genomics resources. *DNA research : an international journal for rapid publication of reports on genes and genomes*, 16(2), 81.