

Plant Molecular Biology Databases

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Abstract

Many of plant biological database comprise data from study fields including metabolomics, proteomics, genomics, microarray gene expression, and phylogenetic. Information in biological databases involves the role of genes, composition, chromosomal location, clinical impacts of mutations, and similarity of biological sequences and characteristics. We are here targeting to review and rank some of plant databases according to their use and feature. Hoping that scientists could use this study to pick, combine and correlate distinct databases, based on their study needs and objective specifications.

Keywords: plant biological database, bioinformatics, software, phylogenetic, metabolomics, proteomics, genomics.

Introduction

Many of plant databases were constructed from some biological fields including metabolomics, proteomics, genomics, microarray gene expression, and phylogenetic(1). With bioinformatics tools the number of plant database were growing (2), so here we described many of plant database such as RicyerDB, PlantRGDB, Functional trait databases, ERISdb, HaloDom, PlantProm DB, CTDB, CmMdb, CicArMiSatDB, eHALOPH, MSDB, Kazusa Marker DataBase , PMDBase, SnoRNA database , OGDD, PlantRNA, PRGdb, PineElm SSRdb , SBMDb, SpinachDB, SisatBase, Sinbase, Ricebase, ReprOlive, and Planteome database

RicyerDB

The Rice Yield-related Database (RicyerDB) was developed to complement associated influence rice research (*Oryza sativa* L.) yield in various aspects by manually curating associated databases and literature and information on genomics and proteomics that can be helpful for a detailed knowledge of rice biology. RicyerDB offers a more useful resource for researching, browsing and



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analyzing genes related to yield efficiently. You can readily query and download the entire information collection through the webpage. Furthermore, RicyerDB also built a network of communication between protein and protein with biological assessment. The intermingled rice database opens a fresh path for scientists to obtain rice gene data in terms of its impacts on rice breeding traits. At <http://server.malab.cn/Ricyer/index.html>, the web server is publicly accessible (3).

PlantRGDB

PlantRGDB (Plant Retrocopied Gene DataBase) was built as the first plant retrocopy database to provide a supposedly full unified catalog of plant genomic retrocopies. Free access to the database is <http://aegilops.wheat.ucdavis.edu/plantrgdb>. It included 49 species of plants and 38,997 retrocopies along with data on classification. PlantRGDB offers a user-friendly internet interface to search, browse and download the data base retrocopies. PlantRGDB also provides graphical viewer-integrated sequence data to display each retrocopy's composition. Report the retrocopy characteristics of each species using a browse feature. Furthermore, helpful instruments such as sophisticated search and BLAST are accessible to more conveniently search the database (4).

Functional trait databases

Tavşanoğlu and Pausas (5) depicted a functional database of traits that emerged as key instruments for a broad spectrum of ecological studies worldwide. Their database of functional characteristics for *Mediterranean Basin* vascular plant species. The database contains 25,764 personal documents of 44 characteristics from 2,457 plant taxa dispersed in 119 taxonomic families. Trait information were acquired from an extensive survey of literature, along with some field and experimental findings. All documents are fully mentioned and include geographic coordinates in many instances. The database is organized to include various concentrations of character data precision for each input. BROT 2.0 should promote the testing of plant functional ecology hypotheses within the *Mediterranean Basin* and compare this region with other ecosystems around the world. The BROT2.0 is offline database as well as its trait definitions can be used in other areas of the globe as a model to create comparable trait databases.

ERISdb

Kabza et al. (6) conducted a large-scale assessment of splice sites in eight species of plants using new algorithms and tools. The analyzes included orthological splice sites,

polypyrimidine sections, and branch locations being identified. They also recognized putative intronic and exonic-regulatory motifs, U12 introns and splice sites in 5 plant species in 45 microRNA genes. In the form of expressed sequence tag and RNA-Seq information, they also provide experimental proof for plant splice sites. All information is deposited in a novel ERISdb database and is freely available at <http://lemur.amu.edu.pl/share/ERISdb/>.

HaloDom

Loukas et al. (7) documented from scientific literature more than 1000 halophilic species. Of these, 21.9% correspond to archaea, 50.1% to bacteria and 27.9% in eukaryotes. Their documents comprise fundamental data such as the salinity discovered by a specific organism, its taxonomy and genomic data through NCBI and other connections. You can access the internet database called "HaloDom" at <http://www.halodom.bio.auth.gr>.

PlantProm

Shahmuradov et al. (8) obtained a plant promoter repository, is an annotated, non-redundant set of RNA polymerase II proximal promoter sequences with experimentally determined transcription start site(s), TSS, from different plant species. PlantProm DB includes 305 records from monocot, dicot and other crops, including 71, 220 and 14 promoters. It offers TSS, promoter type ranking of promoters and Nucleotide Frequency Matrices (NFM) DNA sequence of promoter areas for promoter components: TATA-box, CCAAT-box and TSS-motif (Inr). Analysis of TSS motifs disclosed that their structure is distinct in dicots and monocots, as well as in promoters without TATA and TATA. The database acts as a instructional base for the development of forecast programs for plant promoters. You can find PlantProm DB at <http://mendel.cs.rhul.ac.uk/>.

CTDB

Verma et al. (9) designed an incorporated Chickpea Transcriptome Database (CTDB) that offers a extensive internet interface for visualizing and easily retrieving chickpea transcriptome information. The database includes numerous resources for searching for similarities, searching for functional annotations, and assessment of relative gene expression. The database contains a catalog of transcription factor relatives and their chickpea expression profiles. In order to study the expression profiles of chickpea transcripts in major tissues/organs and various stages of flower development, the gene expression data were integrated. To enable relative genomic research between distinct legumes

and *Arabidopsis*, utilities such as similarity search, orthology recognition and relative gene expression have also been introduced in the database. In addition, the CTDB is a tool for finding functional molecular markers (microsatellites and single nucleotide polymorphisms) between distinct kinds of chickpea. The CTDB can be found at <http://nipgr.res.in/ctdb.html>.

CmMDb

The first entire genome based microsatellite DNA marker repository of *Cucumis melo* L was created by Bhawna et al. (10). And a extensive internet resource that helps to identify varieties and map the *Cucurbitaceae* family physically. Microsatellite repository of The *Melo Cucumis* L. includes 39,072 SSR markers along with repeat motif, sequence length, motif sequence, marker ID, motif type and chromosomal location. The database features a new automated plant primer design tool to satisfy the requirements of wet laboratory scientists. At <http://65.181.125.102/cmmdb2/index.html>, CmMDb is readily accessible.

CicArMiSatDB

Doddamani et al. (11) reported a user-friendly relational database called the Chickpea Microsatellite Database to support genetic research and apps for reproduction. This database offers comprehensive data about SSRs as well as their genome characteristics. SSRs were categorized and rendered available via a internet interface that was easy to use. At <http://cicarmisatdb.icrisat.org>, CicArMiSatDB the database is readily accessible.

eHALOPH

A database of salt-tolerant plant-halophytes was built by Santos et al. (12). Data of plant species tolerant of salt levels of about 80 mM or more sodium chloride have been gathered, together with information on plant species, life form, ecotypes, highest tolerated salinity, existence or lack of salt glands, photosynthetic pathways, antioxidants, secondary metabolites, compatible solutes, habitat, financial use and whether germination, microbial articles are available. The eHALOPH database may be used to analyze tolerance-related traits and to inform selection of species that may be used for saline farming, bioremediation or environmental recovery and rehabilitation of decayed wetlands or other regions. The database available at <http://www.sussex.ac.uk/affiliates/halophytes/>.

MSDB

A MSDB (Microsatellite Database) of > 650 million SSRs from 6,893 species such as archaea, fungi, bacteria, plants and animals was founded by Avvaru et al. (13). This database is the most comprehensive tool for various species accessing and analyzing SSR information. In addition to researching information in a customizable tabular format, the interactive plotting scheme allows users to display and compare various species information concurrently. Using the Django framework and MySQL, MSDB is created. It can be found at <http://tdb.ccmb.res.in/msdb>.

Kazusa Marker DataBase

A database was developed by Shirasawa et al. (14), the Kazusa Marker DataBase. This database involves DNA marker data such as SSR and SNP markers, genetic association maps, and physical maps. This database also provides keyword searches for markers, sequence information used to develop markers, and experimental environments. There are mainly 10 specific crop species: pepper, tomato, strawberry, soybean, radish, peanut, red clover, white clover, and eucalyptus. This DataBase is a helpful instrument for fundamental and advanced sciences like genomics, genetics, and crop molecular breeding. Database link <http://marker.kazusa.or.jp>.

PMDBase

A database, PMDBase, was established by Yu et al. (15), which integrates large quantities of microsatellite DNAs out of genome-sequenced species of plants and involves a web service for microsatellite DNAs. PMDBase recognized 26 230 099 microsatellite DNAs covering 110 species of plants. For each microsatellite DNA, up to three combinations of primers were provided. For 81 species, the microsatellite DNA genomic characteristics were provided with the respective genes or transcripts from various databases. Microsatellite DNAs could be studied with a user-friendly internet interface and tailored software by browsing and locating modules. In addition, they constructed MISAwEB and embedded Primer3web to help users recognise microsatellite DNAs of their own online molecular sequences and construct corresponding primers. All microsatellite DNA datasets can be easily downloaded. PMDBase will be updated with the latest genome data on a regular basis and can be accessed via the <http://www.sesame-bioinfo.org/PMDBase>

Plant snoRNA database

The Plant SnoRNA database (16) offers data from *Arabidopsis* and eighteen other plant species on small nucleolar RNAs. Information involves genes, information on transcription, target alteration sites for methylation and pseudouridylation, primary gene association, and number of versions of genes. The *Arabidopsis* data is split by target locations in rRNA, snRNA or unidentified, into box C / D and box H / ACA snoRNAs, and within all of these groups. For many snoRNA genes, alignments of orthological genes and gene variations from various plant species are accessible. It is accessible via http://www.scri.sari.ac.uk/plant_snoRNA/.

OGDD

An Olive Genetic Diversity Database (OGDD) (17) is therefore provided <http://www.bioinfo-cbs.org/ogdd/>. It is a worldwide olive tree as well as oil genetic, morphological and chemical database with a dual function. In reality, it offers users with extra morphological and chemical data for each recognized cultivar in addition to being a reference system produced to identify unknown olive or virgin olive oil cultivars depending on their microsatellite allele size. Using a number of effective query interfaces and evaluation instruments, OGDD is currently intended to allow users to readily collect and visualize biologically significant data.

PlantRNA

Database of PlantRNA (18) <http://plantrna.ibmp.cnrs.fr/> compiles gene sequences of RNA (tRNA) transformation from completely annotated nuclear, plastidial as well as mitochondrial genomes. For highest performance and certainty, the array of annotated tRNA gene sequences was manually selected. This database's novelty lies in the incorporation of biological data appropriate to all the tRNAs stored in the library. This involves 30- and 50-flank sequences, transcription initiation region, A and B box sequences, and tRNA intron sequences, aminoacyl-tRNA synthetases, poly(T) transcription termination extends, and tRNA maturation and alteration enzymes. The present annotation includes the full genomes of 11 species: 5 flowering plants (*Oryza sativa*, *Arabidopsis thaliana*, *Medicago truncatula*, *Populus trichocarpa*, and *Brachypodium distachyon*), 2 red fungi (*Ostreococcus tauri* and *Chlamydomonas reinhardtii*), 1 purple fungus (*Ectocarpus siliculosus*), 1 glauco-phyte (*Cyanophora paradoxa*) and 1 pennate diatom.

PRGdb

The Plant Resistance Genes database (19) <http://prgdb.org> has been modernized with a new software, new sections, new instruments and fresh genetic improvement information, enabling convenient entry not only to the plant science society but also to breeders who want to enhance resistance to plant disease. The home page provides an overview of easy-to-read search boxes for streamlining data queries and showing directly plant species for which candidate or cloned gene data were collected. For each host plant species, bulk information files and curated gene annotations are produced accessible. In order to show shared features with other genes, the fresh Gene Model view provides comprehensive data on each cloned resistance gene structure. PRGdb provides 153 genes of reference resistance and Pathogen Receptor Genes (PRGs) annotated applicant 177072. Compared to the earlier publication, the amount of putative genes from 76 sequenced Viridiplantae and algae genomes has been improved from 106 to 177 K.

PineElm_SSRdb

A total of 359511 SSRs were recognized in pineapple (chromosome sequence 356385, chloroplast sequence 45, mitochondrial sequence 249, and EST sequence 2832) (20). The database contains the list of EST-SSR tags and their information. Conclusions: PineElm SSRdb is a non-commercial academic database accessible at <http://app.bioelm.com/> with a mapping instrument that can create circular maps of the chosen target collection. For breeders, scientists and graduates operating on *Ananas* spp, this repository will be of enormous use. And others operating on cross-species marker transferability, diversity research, mapping and fingerprinting of genetic material.

SBMDb

Iquebal et al. (21) Using the Primer3 core, integrated at the backend in SBMDb, embedded markers and correlating location information of the selected chromosome, location / interval and primers could be produced. They as well reported 2027 polymorphic markers in a panel of five genotypes depending on e-PCR identification. These indicators can be used in variety enhancement program for DUS screening of variety recognition and MAS / GAS. The current database provides a broad source of probable markers for the development and implementation of fresh molecular breeding methods needed to boost the industrial use of this plant, particularly for sugar, health care goods, medications and color coloring. URL of the database: <http://webapp.cabgrid.res.in/sbmdb/>.

SpinachDB

Yang et al. (22) has been created to effectively record, annotate, mine and evaluate the datasets of genomics and genetics. All 21702 spinach genes have also been annotated. A total of 1,5741 spinach genes have been cataloged into 4,351 families, including a significant number of transcription factors being identified. To build a high-density genetic map, 11 grown and wild spinach cultivars recognized a total of 131592 SSRs and 1125743 prospective SNPs situated in 548801 loci of spinach dna. The SpinachDB page includes seven primary parts, including the homepage; the GBrowse map integrating genes, genome, SNP and SSR marker data; the Blast alignment service; the search tool for gene family classification; the search tool for orthological and concurrent gene pairs; and the download and helpful contact data. In addition to the related data mining and assessment instruments, SpinachDB will be continuously extended to include freshly created solid genomics and genetic data sets. URL of your database: <http://222.73.98.124/spinachdb>.

SisatBase

Dossa et al. (23) recognized 138,194 genome-wide SSRs, 76.5% of which have been physically linked to the 13 pseudo-chromosomes. Within these SSRs, up to three primers combinations were provided for 101,930 SSRs and used together with two freshly sequenced sesame accessions to amplify the reference genome in silico. A total of 79,957 SSRs (78%) were polymorphic among the three genomes indicating their successful use in various breeding implementations assisted by genomics. Of 48 sesame accessions from various growing areas of Africa, 23 of these polymorphic SSRs were chosen and evaluated to have high polymorphic potential. In addition, SisatBase has established a user-friendly internet database that offers free access to SSR information as well as an embedded functional analysis tool. All in all, the SSR and SisatBase reference would serve as useful resources for genetic evaluation, genomic studies, and advancement of sesame breeding, particularly in developing countries. URL of the database: <http://www.sesame-bioinfo.org/SisatBase/>.

Sinbase

Sinbase was intended by Wang et al. (24), a internet-based database with extensive genomic, genetic and relative genomic data on sesame. Sinbase involves pseudo-molecular chromosomal sequences of constructed sesame, transposable elements (372,167), protein-coding genes (27,148), and non-coding RNAs (1,748). With multiple plant genomes as well

as for *Arabidopsis thaliana*, *Glycine max*, *Vitis vinifera*, and *Solanum lycopersicum*, Sinbase offers distinctive and useful data on colinear areas. Sinbase also offers helpful search and data mining instruments, including a quest for keywords and local BLAST service. Is available free of charge at <http://ocri-genomics.org/Sinbase/>.

Ricebase

Edwards et al. (25) created a Ricebase database and an integrative genomics database for rice (*Oryza sativa*) with a focus on merging datasets in a manner that retains important connections between previous and present genetic research. Ricebase involves information on DNA sequence, gene annotations, and data on nucleotide variety and statistics on molecular fragment size markers. Rice study has benefited from early acceptance and comprehensive use of easy sequence repetition (SSR) markers; however, most of the rice SSR models were created prior to the most recent rice pseudo-molecule assembly. The interpretation of recent studies using SNPs in the light of the literature quoting SSRs needs a common coordination scheme. SSR markers and laboratoroly tested amplicons sizes are provided in a web-based relationship database and are accessible as a map placed in a genome browser with connections between the browser and the database. The merged capacities of Ricebase connect genetic markers, genome background, alleles throughout rice germplasm and possibly user-curated phenotypic interpretations as a community tool for genetic exploration and breeding in rice. It is publicly available at <http://ricebase.org>.

ReprOlive

Claros (26) provided an olive tree reproductive transcriptome database containing samples of pollen and pistil at separate phases of development, as well as leaf and root as a control of vegetative tissues. It was created from 2,077,309 pure reads to 1,549 Sanger sequences. Using a predefined workflow centered on open-source instruments, sections were pre-processed, compiled, mapped, and annotated with expression information, GO terms, descriptions, InterPro tags, KEGG pathways, EC numbers, ORFs, and SSRs. Tentative transcripts (TTs) have also been annotated with the respective orthologists in the *Arabidopsis thaliana* of the TAIR and RefSeq records to allow the inclusion of LinkedData. The result is a reproductive transcriptome of 72,846 contigs with an median duration of 686 bp, of which 63,965 (87.8 per cent) included at least one functional annotation, and 55,356 (75.9 per cent) had an orthologist. ReprOlive offers these outcomes with free access and download capacity. Retrieval processes for sequence as

well as transcript annotations are given. Graphical location of annotated enzymes in KEGG processes is also feasible. It freely available at <http://reprolive.eez.csic.es>.

Planteome database

The Planteome initiative (27) <http://www.planteome.org> offers a suite of reference and species-specific ontologies for crops and annotations of genes as well as phenotypes. Ontologies act as popular norms for the semantic integration of a wide and increasing body of plant phenomics, genomics, and genetic data. Reference ontologies involve Plant Ontology, Plant Treatment Ontology and Plant Experimental Conditions Ontology created by the Planteome initiative, along with Gene Chemical Entities in Biological Interest, Ontology, Attribute Ontology, Phenotype, and others. The initiative also offers access to species-specific Crop Ontologies created by multiple plant breeding and study groups around the globe. It also offers incorporated information on plant characteristics, phenotypes, and gene function and activity from 95 plant taxa, annotated with reference ontological terms.

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