**Updates on Bioinformatics Database Resources for Plant Genomics**

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**ABSTRACT**

Advancement in genomic sequencing technologies causes a radical change in agricultural research. Currently, Plant biologists have simplest access to massive genome sequencing data to understand plant densities based on genetic deviation. Therefore, in contemporary plant genomic research, it is imperative to employ bioinformatics tools comprehensively to effectively manage and analyze omics data while maintaining a sympathetic approach. Numerous plant genomic databases have been acknowledged and are steadily growing in size in recent years. Simultaneously, bioinformatics-based analytical techniques have made significant advancements across various facets of plant genomic research. For example, prediction of evolutionary relationship, comparative genome based function prediction and whole genome wide association studies. However, the persistent challenge in plant genomic research remains the ongoing enhancement of IT infrastructure, including the development of high-capacity data storage and analysis software. This chapter highlights on the existing database resources for various plants that will potentially helps the plant scientists in the current era of plant genomics.

**Keywords:** Plant genomics, Databases for plant genomes, Bioinformatics, Comparative genomics, GWAS, sequencing technologies, Plant transcriptome databases.

1. **INTRODUCTION**

The researchers found that there are 4, 35,000 distinctive species of land plants and they discovered that 36.5 % of plant species are especially rare plants. The majority of plant genomes exhibit remarkable diversity, surpassing those of other biological kingdoms, with sizes ranging from approximately 10 megabytes to well over 100 gigabytes. Generally, plants play a crucial role in Earth's ecosystems as they serve as primary sources of nutrition, animal feed, medicines, and more [1, 2]. Additionally, they are frequently selected as model organisms for studying the role of epigenetics and heterochromatin elements [3]. An appreciative knowledge of variety of species genomes especially in plant genomes are primarily lagged, but have significantly improved with the advent of latest technologies in DNA sequencing and leads to an exponential growth of genomic data in wide variety of biological systems. In modern research, sequencing of a plant species genome is considered to be an important turning point. The advancement of automated sequencing techniques empowers researchers to delve into the molecular-level exploration of plant genetic material, a field commonly referred to as "Plant Genomics." Large volume of biological data especially plant genomic data obtained from various sequencing technologies will be effectively handled and significant findings will be extracted by applying various resources of bioinformatics that helps the scientists to have insight on the structural organization, positional arrangement, and functions of a gene in a genome unambiguously. In the year 2000, the sequencing of the first plant genome, that of Arabidopsis thaliana, marked a significant milestone and an approximate of 600 plant species genomes were completely sequenced and published [4] and it also includes many economically important crops genomes. These sequential data have been properly compiled and deposited in databases and are widely used in identification, breeding and conservation purposes. In recent years, a growing number of reviews have concentrated on updating plant sequencing projects and the advancement of crop plant databases [5 - 9]. Interestingly, the availability of notable resources of bioinformatics databases and tools facilitates to grow a fruitful environment for plant research [10].

In this chapter, various sequencing technologies in plant genomic research, features and applications of plant genomic databases, most accepted plant genomic resources will be elaborated. Currently, there are notable diversity of bioinformatics resources are available for plant research. Attention was primarily given to the databases which are hosted by government organizations and academic research centers and non commercial (freely available) analysis tools and software widely used in plants research.

1. **SEQUENCING TECHNOLOGIES IN PLANT RESEARCH**

In the past decade, almost all DNA sequencing process were restricted with some conventional methods of sequencing namely capillary based, modified and partially automated Sanger’s methods of sequencing [11 – 13]. These methods have been revitalized and flourished because of various scientific innovations which ultimately lead to the development of novel experiments [14].

It includes that the release of HTS (High - Throughput Sequencing) & NGS (Next Generation Sequencing) technologies. They are extensively used to assess wide range of biological phenomenon and are employed in resequencing and whole sequencing of genomes, RNA and ChIP sequencing, etc., The more sophisticated methods of NGS technologies are Sequencing By Synthesis (SBS) such as pyro 454 sequencing &Illumina, Sequencing-By-Ligation (SBL) (i.e. SOLiD), Non Optical Sequencing (i.e. Ion Torrent Semi Conductor), SMRT (HeliScope Single Molecule Real Time), DNA Nanoball, and Nanopore Sequencing etc., [15, 16]. They are all well suited for the present and future large scale sequencing demands.

1. **Sequencing by Synthesis (SBS)**
2. Pyro Sequencing

Make use of DNA polymerase enzyme to lengthen various DNA fragments in parallel. In the process of nucleotide integration, the release of pyrophosphate leads to the detection of a light signal emitted due to the cleavage of oxyluciferin by the enzyme luciferase [17]. The commercially available platform is Genome Sequencer from Roche /454 pyrosequencing.

1. llumina Sequencing (SOLEXA)

The principle involved in this sequencing technique is “Sequencing by Synthesis” (SBS) and clonal amplification. In this method, modified deoxy nucleotide triphosphates (dNTPs) i.e consisting of terminator is used, which stop further polymerization. Once, the modified dNTPs are incorporated, extension proceeds with one single base in each growing DNA copy strand [18]. Various upgraded versions of this technology consist of Miniseq series, Mi seq series, Nextseq series and Novaseq series [19].

1. **Sequencing-by-Ligation (SBL)**

SOLiD Sequencing

Starting in 2006, Applied Biosystems made this technology commercially accessible. DNA ligase is employed to enable consecutive ligation of dye-labeled oligonucleotides, facilitating the parallel sequencing of clonally amplified DNA strands [20]. The inconsistent nature of these amplified DNA helps to find out the concealed target sequence.

1. **Non Optical Sequencing**

Ion semiconductor sequencing involves the detection of hydrogen ions that are emitted during DNA polymerization. Commercially available sequencer is Ion Torrent from Life Science, Inc.

1. **Single Molecule Sequencing (SMS)**

HeliScope Single Molecule Real Time –an enzymatic degradation of fluorescently labeled single DNA molecule releases the monomer molecules with respect to their sequential order and they will be detected and identified [21, 22]. Commercial platforms currently accessible include those from Helicos Bioscience Corporation, which offers True single molecule sequencing, as well as the PacBio RS sequencers from Pacific Biosciences, providing Single molecule, real-time sequencing [23].

1. **Nanopore sequencing**

Using membrane lined protein nanopore, the individual nucleotides (one base at a time) will be identified by means of variation in the ion current [24]. A commercial platform readily accessible is the GridION, along with the miniaturized MinION sequencers, both offered by Oxford Nanopore Technologies for Nanopore sequencing.

Operation cost, sequence read length and specific model based error are the major differences between these systems [25 – 27]. However, the final results proved that, the sequencing data generated from these methods are similar. Hence, depends upon the research goal, the researcher can choose a suitable sequencing methods. These technologies are well applied in various plant genomic researches. For example, by exon sequencing method is well suited to study the quantitative trait loci (QTL) / genetic transmission of alleles. Further, it also facilitate to understand the biodiversity, to investigate the interactions between host – pathogens, to predict the crops evolution, to tests the genetic markers inheritance and to identify the genes involved in symbiotic systems [16]. Similarly, the single base sequencing technique provides epigenome of *A. thaliana* i.e. there is a relationship between the cytosine methylation and their abundance of sRNA targets [28]. Other important application of these high through – put and inexpensive methodsof sequencing technologies is genotyping which is especially used in the construction of genomic map and to identify the single nucleotide polymorphism (SNPs) [29]. For example, GBS analysis of 2815 maize inbred, resulted that the 6, 81,257 SNP markers were in positive association with trait related genes [30].With these novel genomic sequencing technologies, there is a fast growth in the genomic data availability. The development of numbers of databases will effectively help the scientists to store, handle and analyze these huge data.

1. **Applications of Plant Genomes**

Drastic changes in the history of plant genomics has been observed with the advent in the field of high-throughput genome sequencing technologies. Following the first release of whole genomic sequence of Arabidopsis thaliana in 2000, the Rice whole genome was successfully sequenced in 2002 [31, 32]. Merging of traditional breeding process and novel *insilico* or computational technologies resulted with the enhancement in the crops quality [33]. In the latest update, as of April 2019 (Release 7.1) of the Plant DNA-C Values Database, successful sequencing has been reported for approximately 12,273 species genomes [34]. Knowledge on genes involved in regulatory mechanisms and genome dynamics in the whole plant, influencing factors in plant development, plant group, ecosystem dynamics, evolutionary path and interactions between plant and other species are thoroughly analyzed [35 – 38]. The plant genomes used for various studies are listed in Table1.

**Table1: Examples for plant genomes used in various studies**

|  |  |  |
| --- | --- | --- |
| **S.No** | **Plant genomes** | **uses** |
|  | Arabidopsis [31] | Genomic models for drought tolerant plants [40] |
|  | Physcomitrella patens (moss) [39] |
|  | Setaria italic (millet) [41] |
|  | Brachypodiumdistachyon (grass) [42] |
|  | Oryza sativa (rice) [43] |
|  | Populustrichocarpa (poplar) [45] | Functional Models in crops [44] |
|  | Zea mays (maize) [46] |
|  | Utriculariagibba (bladderwort) [47] | Models to construct gene map, genome size variation and to analyze the evolutionary trajectories. [44] |

Likewise, the genomes of numerous horticultural plants, encompassing vegetables, fruits, beverage-producing plants, ornamental plants, and medicinal herbs, have been successfully sequenced. These plants have great impact in human health and lives globally by satisfying basic food demands, decorating the urban and rural background and enhancing personal esthetics. It also plays a role in balancing and improving of our biological environment by means of giving oxygen [48] which is given in Table 2.

**Table 2: Listing of database resources for horticulture plants**

|  |  |  |  |
| --- | --- | --- | --- |
| **S.No** | **Databases and their Website Address** | **Botanical Name** | **Common Name** |
|  | Phytozome 13https://phytozome-next.jgi.doe.gov/ | *Asparagus officinalis* | Garden asparagus |
| *Manihot esculenta* | Cassava |
| *Phaseolus vulgaris* | Common bean |
| *Manihot esculenta* | Cassava |
| *Phaseolus vulgaris* | Common bean |
| *Daucus carota* | Carrot |
| *Lactuca sativa* | Lettuce |
| *Solanum lycopersicum* | Tomato |
| *Solanum tuberosum* | Potato |
| *Asparagus officinalis* | Garden asparagus |
| *Ananas comosus*  | Pineapple |
| *Citrus clementina*  | Clementine citrus |
| *Vitis vinifera*  | Grape |
| *Aquilegia coerulea* | Colorado blue columbine |
| *Primula vulgaris* | Common primrose |
| *Mentha longifolia* | Horse mint |
| *Selaginellamoellendorffii,* | Spikemoss |
| *Selaginellatamariscina* | Little club moss |
| *Marchantia polymorpha* | Umbrella liverwort |
| *Amaranthushypochondriacus* | Prince’s feather |
| *Carnegiea gigantea* | Saguaro cactus |
| *Mimulusguttatus* | Seep monkeyflower |
| *Kalanchoefedtschenkoi* | Lavender-scallops |
|  | CoGe- https://genomevolution.org/coge/ | *Dioscorearotundata* | White Guinea yam |
| *Manihot esculenta* | Cassava |
| *Lagenaria siceraria* | Bottle gourd |
| *Cajanuscajan* | Pigeon pea |
| *Cicer arietinum; Cicerreticulatum* | Chick pea |
| *Chrysanthemum nankingense* | Juhuanao |
| *Brassica oleracea* | Cabbage |
| *Brassica rapa* | Chinese cabbage |
| *Capsella rubella* | Red shepherd’s purse |
| *Capsicum baccatum* | Berry-like pepper |
| *Solanum melongena* | Eggplant |
| *Dioscorearotundata*  | White Guinea yam |
| *Ananas comosus*  | Pineapple |
| *Castaneamollissima*  | Chinese chestnut |
| *Ziziphus jujuba*  | Jujube |
| *Malus domestica*  | Apple |
| *Prunus persica*  | Peach |
| *Actinidia chinensis*  | Kiwifruit |
| *Citrus clementina*  | Clementine citrus |
| *Vitis vinifera*  | Grape |
| *Rhizophoraapiculata* | Tall-stilt mangrove |
| *Aquilegia coerulea* | Colorado blue columbine |
| *Conyza canadensis* | Horseweed |
| *Catharanthus roseus* | Madagascar periwinkle |
| *Gnetummontanum* | Jointfir |
| *Phalaenopsis Aphrodite* | Aphrodite's phalaenopsis |
| *Phalaenopsis equestris* | Horse phalaenopsis |
| *Prunusmume*  | Mei |
| *Tarenayahassleriana* | Spider flower |
| *Amaranthushypochondriacus* | Prince’s feather |
| *Camptothecaacuminata* | Happy tree |
|  | Ensemble Plants - https://plants.ensembl.org/ | *Dioscorearotundata* | White Guinea yam |
| *Zizania latifolia* | Jiaobai |
| *Manihot esculenta* | Cassava |
| *Glycine max* | Soybean |
| *Medicagotruncatula* | Barrel clover |
| *Phaseolus vulgaris* | Common bean |
| *Vigna radiata* | Mung bean |
| *Daucus carota* | Carrot |
| *Brassica rapa* | Chinese cabbage |
| *Dioscorearotundata*  | White Guinea yam |
| *Musa acuminate, Musa balbisiana* | Wild banana |
| *Lupinusangustifolius* | Narrow-leaved lupine |
|  | Plant GDB - www.plantgdb.org;  | *Manihot esculenta* | Cassava |
| *Glycine max* | Soybean |
| *Medicagotruncatula* | Barrel clover |
| *Solanum tuberosum* | Potato |
| *Selaginellalepidophylla* | Resuscitation moss |
| *Mimulusguttatus* | Seep monkeyflower |
|  | Plaza - https://bioinformatics.psb.ugent.be/plaza/ | *Manihot esculenta* | Cassava |
| *Cajanuscajan* | Pigeon pea |
| *Cicer arietinum; Cicerreticulatum* | Chick pea |
| *Daucus carota* | Carrot |
| *Brassica oleracea* | Cabbage |
| *Brassica rapa* | Chinese cabbage |
| *Capsella rubella* | Red shepherd’s purse |
| *Moringa oleifera* | Moringa |
| *Beta vulgaris* | Sugar beet |
| *Capsicum annuum* | Spanish pepper |
| *Solanum lycopersicum* | Tomato |
| *Cucumis melo* | Muskmelon |
| *Citrulluslanatus*  | Watermelon |
| *Ziziphus jujuba*  | Jujube |
| *Malus domestica*  | Apple |
| *Prunus persica*  | Peach |
| *Pyrusbretschneideri*  | Chinese pear |
| *Carica papaya*  | Papaya |
| *Citrus clementina*  | Clementine citrus |
| *Vitis vinifera*  | Grape |
| *Trifolium pratense*  | Red clover |
| *Corchorusolitorius* | Chang shuohuang ma |
| *Marchantia polymorpha* | Umbrella liverwort |
| *Nelumbo nucifera* | Sacred lotus |
| *Tarenayahassleriana* | Spider flower |
| *Amaranthushypochondriacus* | Prince’s feather |
|  | CuGenDB - http://cucurbitgenomics.org/ | *Cucumissativus* | Cucumber |
| *Cucurbita argyrosperma* | Silver-seed gourd |
| *Cucurbita maxima* | Winter squash |
| *Cucurbita moschata* | Pumpkin |
| *Cucurbita pepo* | Summer squash |
| *Lagenaria siceraria* | Bottle gourd |
| *Cucumis melo* | Muskmelon |
|  | Brassicaceae Database (BRAD) - http://brassicadb.org/brad | *Cajanuscajan* | Pigeon pea |
| *Brassica juncea* | Zhacai |
| *Brassica oleracea* | Cabbage |
|  | **globe artichoke genome -** www.artichokegenome.unito.it | *Cynara cardunculus* | Cardoon |
|  | C. sativa (Cannabis) Genome Browser Gateway - http://genome.ccbr.utoronto.ca/cgi-bin/hgGateway | *Capsella bursa-pastoris* | Shepherd’s purse |
|  | Raphanus sativus Genome DataBase - http://radish.kazusa.or.jp/ | *Raphanus sativus* | Radish |
|  | Pennycress genomics - https://pennycress.umn.edu/ | *Thlaspiarvense* | Field pennycress |
|  | SpinachBase - http://spinachbase.org/ | *Spinacia oleracea* | Spinach |
|  | SolGenomics Network - https://solgenomics.net | *Solanum pimpinellifolium* | Currant tomato |
| *Solanum tuberosum* | Potato |
| *Nicotiana sylvestris* | Flowering tobacco |
|  | GiGa DB - http://gigadb.org/ | *Cocos nucifera* | Coconut palm |
| *Diospyros lotus*  | Date-plum |
| *Vaccinium macrocarpon*  | American cranberry |
| *Dimocarpuslongan*  | Longan |
| *Rhodiolacrenulata* | Tibetan Rhodiola |
| *Ginkgo biloba* | Ginkgo tree |
| *Salvia splendens* | Scarlet sage |
|  | Banana Genome Hub - https://banana-genome-hub.southgreen.fr/ | *Musa itinerans*  | Yunnan banana |
| *Musa acuminate, Musa balbisiana* | Wild banana |
|  | Herbalplant DB - http://herbalplant.ynau.edu.cn/ | *Siraitiagrosvenorii*  | Monk fruit |
| *Gastrodiaelata*  | Tianma |
| *Macleayacordata,* ,  | Plume poppy |
| *Papaver somniferum* | Opium poppy |
| Asian ginseng,  | *Panax ginseng,*  |
| Sanchi ginseng | *Panaxnotoginseng* |
| *Artemisia annua*  | Sweet wormwood |
|  | Hardwod Genomic DB - www.hardwoodgenomics.org | *Juglans nigra* | Eastern black walnut |
| *Juglans regia* | Common walnut |
| *Juglans sigillata* | Iron walnut |
| *Juglanscathayensis* | Chinese walnut |
| *Juglanshindsii* | Northern California walnut |
| *Juglansmicrocarpa* | Texas black walnut |
| *Macadamia integrifolia* | Macadamia nut |
| *Punica granatum*  | Pomegranate |
| *Liriodendron chinense* | Chinese tulip tree |
| *Casuarina equisetifolia* | Australian pine tree |
| *Handroanthusimpetiginosus* | Pink trumpet tree |
| *Fraxinus excelsior* | European ash |
|  | Artocarpus Genomics - http://sites.northwestern.edu/zerega-lab/research/artocarpus-genomics | *Artocarpuscamansi* | Breadnut |
|  | Strawberry GARDEN - https://strawberry-garden.kazusa.or.jp/ | *Fragariaiinuma* | Nogo strawberry, , , , ,  |
| *Fragarianipponica* | Japanese strawberry |
| *Fragarianubicola* | Tibet strawberry |
| *Fragariaorientalis* | Eastern strawberry |
| *Fragariavesca* | Woodland strawberry |
| *Fragaria* × *ananassa* | Strawberry |
|  | Morus DB – Mulberry Genome Database -https://morus.swu.edu.cn/ | *Morus notabilis*  | Mulberry |
|  | GDR – Genome Database for Rosaceae - www.rosaceae.org | *Prunus avium* | Sweet cherry |
| *Pyrus communis* | European pear |
| *Rubus occidentalis* | Black raspberry |
| *Prunusyedoensis* | Yoshino cherry |
| *Rosa* × *damascena* | Damask rose |
| *Rosa chinensis* | Chinese rose |
| *Rosa multiflora* | Many-flowered rose |
| *Rosa roxburghii* | Chestnut rose |
|  | GDV – Genome Database for Vaccinum - www.vaccinium.org | *Vacciniumcorymbosum* | Blueberry |
|  | Citrus Genome Databases -www.citrusgenomedb.org | *Citrus grandis* | Pummelo |
| *Citrus ichangensis* | Ichangpapeda |
| *Citrus paradisi* × *Poncirus trifoliate* | *C*itrumelo |
| *Citrus reticulate* | Mandarin orange |
| *Citrus sinensis* | Sweet orange |
| *Citrus unshiu* | Cold hardy mandarin |
| *Atalantiabuxifolia* | Jiu bingle |
| *Citrus medica* | Citron |
|  | Horticulture Plant Database - https://horticulture.eplant.org/ | *Echinochloa crus-galli* | Cockspur grass |
| *Enseteventricosum* | Ethiopian banana |
|  | Next Generation Genome Database - https://ngs-data-archive.psc.riken.jp/ | *Glycyrrhizauralensis*  | Chinese liquorice |
|  | Cacao Genome Daatabase - http://www.cacaogenomedb.org | *Trifolium pratense*  | Red clover |
|  | Portal for Parasponia Genomics Research - www.bioinformatics.nl/parasponia | *Parasponiaandersonii* | Caoyeshanhuangma |
| *Tremaorientalis* | Indian charcoal tree |
|  | GDPR - https://www.plabipd.de/  | *Cuscutacampestris* | Prairie dodder |
|  | Zoysia Genome Database - https://zoysia.kazusa.or.jp/ | *Zoysia japonica* | Japanese lawn grass, ,  |
| *Zoysiamatrella* | Manila grass |
| *Zoysiapacifica* | Mascarene grass |
|  |  Eschscholzia Genome DataBase - https://eschscholzia.kazusa.or.jp/ | Eschscholziacalifornica | California poppy |
|  | Carnation DB - https://carnation.kazusa.or.jp/ | *Dianthus caryophyllus* | Carnation |
|  | Orchidstra2.0 – A transcriptomic database for Orchid family - https://orchidstra2.abrc.sinica.edu.tw/ | *Phalaenopsis Aphrodite* | Aphrodite's phalaenopsis |
| *Phalaenopsis equestris* | Horse phalaenopsis |
|  | Medica Go Genome - www.medicagogenome.org | *Mimosa pudica* | Sensitive plant |
|  | Plant Genie Database - https://plantgenie.org/ | *Primula veris* | Cowslip |

The plant genomic sequence data enhances the process of recognition, classification and exploring of specific alleles as well as significant molecular markers were screened in order to enrich the plant breeding with desired features [49].

**Resources for Plant Genomic Research**

The landscape of plant genomics data has undergone a profound transformation due to the emergence of Expressed Sequence Tags (EST) sequencing, a high-throughput method for uncovering genetic information [50] and the publication of *A.thaliana* and Rice whole genomic sequence data in 2000 and 2002 respectively. These developments have left a lasting impact on both agricultural biotechnology and bioinformatics. In the pursuit of advancing our understanding, additional sequencing projects on vital plant species have been conducted by blending innovative *in-silico* techniques from genomic research with traditional breeding methods, further enhancing crop quality. Over time, these genes have offered invaluable tools for contemporary molecular genomics in plant research. As a result, numerous genes and important pathways' genetic and biological functions have been unveiled. With the availability of complete genome sequences and the proliferation of data systems, there has been an increasing demand for comprehensive cataloging and precise specification of DNA sequence databases.

The freely available sequencing projects, various plant genomic databases along with their URL were listed in Table 3.

|  |  |  |
| --- | --- | --- |
| **S.No** | **Sequencing projects** | **URL** |
|  | Tomato genome sequencing project [51] | https://solgenomics.net/organism/Solanum\_lycopersicum/genome |
|  | Potato genome sequencing consortium [52] | https://solgenomics.net/organism/Solanum\_tuberosum/genome |
|  | Papaya genome sequencing project [53] | https://hawaiipapaya.com/ |
|  | Grape genome sequencing project[54] | http://www.grapegenomics.com/ |
|  | Floral genome sequencing project[55] | http://fgp.bio.psu.edu/ |
|  | plant Genomic databases [56] | http://www.plantgdb.org/ |
|  | Genomes Online Database - GOLD [57] | https://gold.jgi.doe.gov/ |
|  | NCBI Genomes [58] | http://www.ncbi.nlm.nih.gov/genome/ |
|  | NCBI Assembly – [59] | http://www.ncbi.nlm.nih.gov/assembly/ |
|  | CoGepedia (plant genomes) [60] | https://genomevolution.org |
|  | plaBi | http://plabipd.de/ |
|  | Ensembl Plants [60] | http://plants.ensembl.org/ |
|  | Gramene[61] | http://www.gramene.org/ |
|  | PlantsDB[62] | http://pgsb.helmholtz-muenchen.de/ |
|  | Phytozome[63] | http://phytozome.jgi.doe.gov/ |
|  | PLAZA [64] | http://bioinformatics.psb.ugent.be/plaza/ |
|  | GreenPhylDB | http://www.greenphyl.org/ |
|  | PlantOrDB [65] | http://bioinfolab.miamioh.edu/plantordb/ |
|  | SALAD [66] | http://salad.dna.affrc.go.jp/ |
|  | PlantTribes [67] | http://fgp.bio.psu.edu/tribedb/ |
|  | PlantGenIE.org [68] | http://plantgenie.org/ |
|  | POGs2 [69] | http://pogs.uoregon.edu/ |
|  | GenomicusPlants [70] | http://www.genomicus.biologie.ens.fr/ |
|  | PIECE [71]  | http://wheat.pw.usda.gov/piece/ |
|  | PlantSEED [72] | http://bioseed.mcs.anl.gov/ |
|  | PGDBj[73, 74] | http://pgdbj.jp/ |
|  | ChloroplastDB [75] | http://chloroplast.cbio.psu.edu/ |
|  | KEGG [76] | http://www.genome.jp/kegg/ |
| **Plant species specialized genome databases** |
|  | The Arabidopsis Information Resource* TAIR (Arabidopsis) [77]
 | http://www.arabidopsis.org/ |
|  | Salk Institute Genomic Analysis Laboratory - SIGnAL (Arabidopsis)  | http://signal.salk.edu/ |
|  | Riken Arabidopsis + Genome Encyclopedia RARGE II(Arabidopsis) [78] | http://rarge.psc.riken.jp/ |
|  | RARGE II [79] | http://rarge-v2.psc.riken.jp/ |
|  | Rice Genome Annotation Project - RGAP v.7 (Rice)  | http://rice.uga.edu/ |
|  | Rice Annotation Project - RAP-DB (Rice)  | http://rapdb.dna.affrc.go.jp/ |
|  | Sol Genomic Network (SGN) (Solanaceae)  | https://solgenomics.net/solanaceae-project/index.pl |
|  | GrainGenes - A Database for Triticeae and Avena | https://wheat.pw.usda.gov/GG3/ |
|  | SoyBase (Soybean)  | http://soybase.org/ |
|  | MaizeGDB (Maize)  | https://www.maizegdb.org/ |
|  | CyanoBase – A Database for Cyanobacteria  | http://genome.microbedb.jp/cyanobase/ |
|  | Genome Database for Rosaceae - GDR  | https://www.rosaceae.org/ |
|  | Brassica Genome Gateway  | http://brassica.nbi.ac.uk/ |
|  | Cucurbit Genomics Database | http://www.icugi.org/cgi-bin/ICuGI/index.cgi |
| **Databases for comparative Genomics** |
|  | Golm Metabolome Database | http://gmd.mpimp-golm.mpg.de/ |
|  | A Database for co regulated genes - ATTED-II  | http://atted.jp/ |
| **Tools Resources for Plant Genome Analysis** |
|  | **GoMapMan – Annotation of Gene functions** | https://gomapman.nib.si/ |
|  | **NPACT – Database for plant derived anticancer compounds**  | http://crdd.osdd.net/raghava/npact |
|  | **PGDD – Identification tools for synteny relationship intra genomes** | http://chibba.agtec.uga.edu/duplication |
|  | **PlantRNA – Database consists of tRNA of photosynthetic Eukaryotes** | http://seve.ibmp.unistra.fr/plantrna/ |
|  | PMRD: plant microRNA database | http://bioinformatics.cau.edu.cn/PMRD/ |
|  | SALAD - database for systematic comparison of proteome data | https://salad.dna.affrc.go.jp/salad/en/ |

Available information in these public domain genome sequencing projects are considered as precious resources for comparative, evolutionary and functional studies [80]. For example, numbers of stress responsive factors of plants like soybean, sorghum, barley, maize and wheat were correctly predicted by comparative genomic approach in which the stress responsive transcription factors of Arabidopsis and Rice were selected as reference plant genomes [81, 82]. Likewise, numbers of functional genes and novel biosynthetic genes were discovered and annotated in newly sequenced plants by comparative genomics and co expression analysis [83, 84].

**Plant Transcriptomic Databases**

In general, the characterization and prediction of plant gene function is considered to be a difficult task because of availability of limited number of model plants, complexity in cultivation and lack of plants genomic transformation information. But, the available plant genome sequencing transcriptome data derived from different experiments and experimental treatments that capture the gene expression in tissues, organs and development phases and many bioinformatics approaches are considered to be a powerful resources for plant research scientific community. Understanding of the plant genes and their expressions will enhance the process of selection of desired plant traits [85, 86] and functional annotation of a novel gene. These gene expression data has immense values which provides significant information on the active state of the gene. Further, the expression data are used to predict gene function by comparative analysis [87]. With an exponential growing rate of available plant gene expression data, databases with different functionalities were emerged as a valuable contribution to the scientific community. Though there are huge numbers of online gene expression databases are available, only those databases used to predict gene function with unique approaches are given in Table 4.

|  |  |  |
| --- | --- | --- |
| **S.No** | **Databases**  | **URL** |
| **Databases for analysis of Expression** |
|  | Arabidopsis | http://www.ag.arizona.edu/microarray |
|  | Barley | http://www.barleybase.org |
|  | Rice | http://www.ricearray.org |
|  | Maize | http://www.maizearray.org |
|  | Soybean | http://soybeangenomics.cropsci.uiuc.edu |
|  | Tomato | http://ted.bti.cornell.edu |
|  | GENEVESTIGATOR | https://genevestigator.com/gv/start/start.jsp |
|  | ePlant by BAR | http://bar.utoronto.ca/ |
|  | CoNekT-Plants | https://evorepro.sbs.ntu.edu.sg/ |
|  | Expression Atlas | https://www.ebi.ac.uk/gxa/home |
| **Databases for analysis of Co-Expression** |
|  | Expression Angler by BAR | http://bar.utoronto.ca/ |
|  | CoNekT-Plants | https://evorepro.sbs.ntu.edu.sg/ |
|  | ATTED-II | https://atted.jp/ |
| **Databases for analysis of Differentially Expressed Genes (DGE)** |
|  | AtCAST | http://atpbsmd.yokohama-cu.ac.jp/cgi/atcast/home.cgi |
|  | Expression Atlas – Database of Gene expression crosswise species and biological condition | https://www.ebi.ac.uk/gxa/home |
|  | Genevestigator | https://genevestigator.com/gv/start/start.jsp |
| **Databases for analysis of Gene expression-specificity/stability** |
|  | RED - Rice Expression Database | http://expression.ic4r.org/ |
|  | CoNekT- Database for plant gene expression and co expression | https://evorepro.sbs.ntu.edu.sg/ |
|  | Genevestigator | https://genevestigator.com/gv/start/start.jsp |
| **Databases for analysis of Experiment correlation** |
|  | AtCAST – Tool for analysis of transcriptome data | http://atpbsmd.yokohama-cu.ac.jp/cgi/atcast/home.cgi |

**Resources for plant Genome – Wide Association Studies (PGWAS)**

Genome-wide association studies (GWAS) are a popular method to link genetic variation to phenotypic variation and are therefore important for plant genetics. The increasing wealth of publicly available genomic sequence information for crop plants provides an unprecedented opportunity to use GWAS for the identification of genes controlling a plethora of agronomic traits. However, lack of technical expertise and IT infrastructure still hinders the ability of plant breeders to conduct GWAS independently. However, more than 1300 different genes were genotyped and 107 phenotyped with respect to 2, 50,000 single nucleotide polymorphisms (SNPs) in a classic model plant Arabidopsis thaliana [88] With this ground work, there were frequent success in performing GWAS on some other qualities of interest in Arabidopsis, such as tolerance in heavy metal, salt, flowering time and heat resistance etc., [89]. Likewise, in Rice, another significant crop, mapping efforts were carried out intensively to understand the genetic variation responsible for starch quality, grain size, stress tolerance with respect to their ancestors [90, 91] In addition, the GWAS studies were performed on some other important crops for example Maize and Soybean [92, 93]. For better breeding, in GWAS, estimation of epistatic i.e. gene – gene interactions and gene environment interactions is considered to be an important task. Currently, the use of new bioinformatics approach, i.e. mixed linear model approach is widely used in the detection of epistatic and gene – gene interactions in Rice and the obtained results were also remarkable [94]. Similarly, to manage and make use of genetic association studies in plants, a special resource namely GnpIS – ASSo is available. Currently, this database dealt with GWAS in Tomato and Maize. It provides tools to study the linkage between traits and markers and the results were graphically visualized with devoted plots. Once, the best marker assisted the trait was selected, their location on chromosomes, their neighboring genes etc., were easily studied [95]. However, there is a need to enhance the speed, memory capacity and application of statistical test to make accurate results while using GWAS assisted tools.

**CONCLUSIONS**

Latest developments in bioinformatics application for plants Genomes offer enormous potential for large-scale genomics research among plant species along with several technical challenges. In near future, plant genetic data will be abundant with the application of NGS technologies and platforms.  The tools development for managing and examining these data are becoming more and more highly significant with the accessible genomic data. Undoubtedly, continuous establishment of several of plant specific genome databases facilitates retrieval and analysis of plant genomes. For example, specific information on functional genes, their evolutionary relationships within and between plant species will be identified by comparative genome and phylogenetic analysis respectively. Likewise, from the genome wide association studies loci and allelic variations related to valuable traits will be detected successfully. However, the researchers those who are working in plant genomic analysis are still facing the great demand for managing and manipulating the results obtained from plant genomic data by using the available bioinformatics resources. In summing up, for essential advances in crop improvement, the recent collection of plant genomic data have enabled plants research scientists to accomplish an essential and systematic understanding of economically important plants and plant processes by utilizing advances in bioinformatics resources. Besides these exciting results, there is a basic need for efficient tools and methods to advance plant biotechnology, solve difficult problems to address with recent approaches, and smooth the progress of the implementation of this innovative discovery of knowledge to attain excellent yield from plants,

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