



Short Communication

NTDBPlant: Nutrient Transporters Database for Plants

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Abstract

Ion transporters are the proteins localized in the plasma membrane and play a vital role in the transport of ions, maintenance of pH and cell expansion. NTDBPlant is a database that provides a web interface in order to access information related to ion transporter genes in *Arabidopsis thaliana*, a small flowering plant. This database contains data of genomic sequences, coding sequences, transcriptomic data, protein sequences, domain annotations, scientific literature and external links to other databases for 233 transport-related genes from 37 gene families in genus *Arabidopsis*. The current database is the very first of its kind for plants. It will provide significant information on a single platform related to the ion transporters and is publicly available through <http://ntdbplant.net/>. In future, more data related to other ion transport related gene families will be added and will be helpful for the researchers around the globe. © 2018 Friends Science Publishers

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Introduction

Nutrient transport proteins play an important role in the supply of energy, uptake and sequestration of ions into vacuoles, in cell expansion and maintenance of pH in the cell environment. Plants acquire mineral nutrients from the soil (Grennan, 2009). The plant cell plasma membrane (PM) has a selective permeability that confirms selective metabolites and ions to enter into the cell. Together with tonoplast, the selectively permeable plasma membrane of plant cell facilitates cytoplasm to sustain intracellular homeostasis. These membranes are comprised of phospholipid bilayers along with transmembrane proteins and enable the passage of metabolites, ions and water molecules in order to maintain the pH of cytosol. Channel proteins, ATP powered pumps, co-transporters are required for the transport of organic solutes, inorganic ions and protons across the plasma membrane (Sze, 1999).

Electrophysiological studies revealed the presence of various transport pathways like ion channels and ion carriers for the uptake and translocation of cations. Identification of transporters at gene level revealed involvement of a number of genes and gene families in uptake and distribution of specific ions (Rodríguez-Navarro, 2000; Nieves-Cordones *et al.*, 2016; Azeem *et al.*, 2018). Analysis of *Arabidopsis thaliana* genome has revealed that gene families encoding

for particular ion transporters are surprisingly large (Hawkesford, 2003) (Table 1).

Earlier several databases have been developed for multiple plant species such as PlnTFDB (Pérez-Rodríguez *et al.*, 2010), PlanTAPDB (Richardt *et al.*, 2007), GRASSIUS (Yilmaz *et al.*, 2009), LegumeTFDB (Mochida *et al.*, 2010), TreeTFDB (Mochida *et al.*, 2013) and DATFAP (Fredslund, 2008). Similarly databases like AGRIS (Yilmaz *et al.*, 2011), TOBFAC (Rushton *et al.*, 2008) and SoyDB (Wang *et al.*, 2010) are available for individual organisms. Most of these databases are publicly available for identification and annotation of plant TFs. By keeping in mind the importance and vast use of these databases, we have developed a database named as Nutrient Transporters database for plants “NTDBPlant” (<http://ntdbplant.net/>), that provides complete primary information related to ion transporter gene families in *Arabidopsis*. It is first of its kind database that provides basic data related to nutrient transporter genes at one place. It could be a promising resource of information for the understanding of ion transporter gene families at a single forum. The NTDBPlant contains 233 gene members from 37 gene families of *Arabidopsis thaliana*. To provide comprehensive information for each gene member involved in nutrient transport, we have provided its DNA sequence, cDNA sequence, protein sequence, thousand base pairs promoter sequence and the CDS sequence.

Table 1: Basic information of 37 nutrient transporters gene families of *Arabidopsis thaliana* currently present in NTDBPlant database

Ion Transporter Gene families	Members	Ion Transporter Gene families	Members
Shaker family	9	Putative zinc transporter ZIP2 - like family	2
KCO-like protein 3 family	1	Putative potassium transporter family	3
KCO5 protein family	5	Fe(II) transporter isolog family	11
Glutamate Receptor (ATGLR) Family**	20	High affinity nitrate transporter family	7
Cyclic nucleotide gated channel family	20	Nramp2 family	6
Anion channel protein family	5	Putative sulfate transporter family	12
Putative calcium channel	1	Putative sulfate transporter family	2
Cation-chloride co-transporter family	2	Zinc transporter (ZAT) family	4
Ammonium transporter family	5	Putative potassium transporter family	3
Inorganic phosphate transporter family	9	Copper transport protein-like family	5
Ammonium transporter	1	Sodium transporter	1
<i>Arabidopsis thaliana</i> Antiporter Superfamily	28	Putative phosphate permease	1
Phosphate/triose-phosphate translocatorfamily	8	Putative Na ⁺ /H ⁺ antiporter family	26
Low affinity calcium antiporter CAX2 family	6	Putative Na ⁺ /H ⁺ antiporter family	2
Sodium proton exchanger family	4	Putative potassium proton antiporter family	3
Putative anion exchange protein family	7	Na ⁺ /H ⁺ antiporter-Putative family	2
ADP, ATP carrier-like Protein family	4	2-oxoglutarate/malate translocator precursor-like	3
sodium-calcium exchanger like-family	3	Putative Na ⁺ /Ca ²⁺ antiporter	1
Putative carnitine/acylcarnitinetranslocase	1	Potassium-dependent sodium-calcium exchanger like-family	3

Both the sequences and detailed annotations for each gene are available at NTDBPlant. We have also identified functional domains in proteins to aid functional analysis and annotations of various nutrient transport proteins.

Data Sources and Methods

The main steps involved in the construction of NTDBPlant database include data integration, nutrient transporters sequence information, and gene annotations.

Sequence Data

The sequences for each gene member *i.e.*, DNA sequence, cDNA sequence, protein sequence, CDS sequence and a thousand base pair promoter sequence were downloaded from The Arabidopsis Information Resource (TAIR, <https://www.arabidopsis.org>), Joint Genome Institute (JGI, <https://phytozome.jgi.doe.gov/pz/portal.html>) and National Center for Biotechnology Information (NCBI, <http://www.ncbi.nlm.nih.gov/>).

Gene Annotations

In order to offer comprehensive information for the different nutrient transport genes, we made extensive annotations at family and gene levels. On the page having list of ion transporter families, for each ion transporter family, a brief introduction and key references were listed. The annotations for each gene were made accessible and were gathered from multiple databases which include Kyoto Encyclopedia of Genes and Genomes (KEGG, <http://www.genome.jp/kegg/>), Gene Ontology Consortium (GO, <http://www.geneontology.org/>), Protein Analysis Through Evolutionary Relationships (Panther, <http://www.pantherdb.org/>) and PFAM (<https://pfam.xfam.org/>). The database also includes the detailed protein information. Gene location and protein lengths were also provided based on Phytozome and NCBI information.

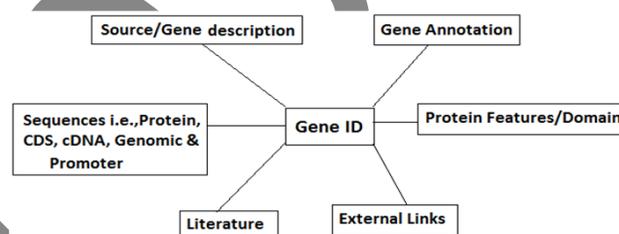


Fig. 1: Flowchart shows the basic information required for each gene member in NTDBPlant database

The domains in each protein sequence are listed in NTDBPlant which were primarily gathered from Uniprot (www.uniprot.org/).

The gene descriptions (Fig. 1) were collected from NCBI (<https://www.ncbi.nlm.nih.gov/>), TAIR (<https://www.arabidopsis.org/>), Phytozome (<https://phytozome.jgi.doe.gov>) Ensembl plants (<https://plants.ensembl.org/index.html>) and PGSB (<http://pgsb.helmholtz-muenchen.de/plant/index.jsp>) databases. NTDBPlant database also contains related literature about each gene member of all the transporter families. Additionally, the database was linked to the other resources such as TAIR (<https://www.arabidopsis.org/>), phytozome (<https://phytozome.jgi.doe.gov/>), NCBI (<https://www.ncbi.nlm.nih.gov/>), Ensembl plants (<https://plants.ensembl.org/index.html>), PGSB (<http://pgsb.helmholtz-muenchen.de/plant/index.jsp>), PGDD (<http://chibba.agtec.uga.edu/duplication/>), e-FP browser (<http://bar.utoronto.ca/efp/cgi-bin/efpWeb.cgi>), Bio-grid (<https://thebiogrid.org/>), Atted-II (<http://atted.jp/>), Plaza (<https://bioinformatics.psb.ugent.be/plaza>), Gene visible (<https://genevisible.com/search/>), plant genome database (<http://www.plantgdb.org>) and many other databases.

Web Construction

We used relational database model for the construction of NTDBPlant database in Microsoft Access 2007. The data have been divided into 9 relations (Fig. 2) named as Gene_Description, Other names, Protein_information, Protein_Features, Annotations, Gene Accessions, Sequences, Publications and External_links. Each of these 9 tables is connected with main relation "Information". For each gene, information relation stores Gene ID, chromosomal location, gene model, its family and family abbreviations for query purpose. Relation Gene_description stores description of each gene as reported in published biological databases with a source of information. Similarly, relation Annotation has been used to store different functional annotations regarding ion transporter gene with a brief description as mentioned in different sources (*i.e.*, PFAM, a database of protein families), KEGG (Kyoto Encyclopedia of Genes and Genomes), PANTHER (Protein Analysis Through Evolutionary Relationships), annotation ID and navigation links. Associated protein features such as protein length, domains and external links have been stored in two relations Protein_information and Protein_features. Two relations "Accessions" and "Sequences" contain protein, cDNA, CDS, genomic and promoter sequences and their unique accession numbers as specified in TAIR database. To provide references to original work relation "Publications" have been used which stores publication details (*i.e.*, paper title, journal, authors, PUBMED ID). However, we used relation External_links to provide external database navigational links. This relation provides minimum 15 external sources for each gene.

Implementation and Web Interface

Apache Server (LAMP) has been used for the implementation and testing NTDBPlant. Web languages such as HTML, PHP, JAVA, C++, CSS and MySQL have been used to design freely accessible web interface. NTDBPlant provides two browsing facilities, browse by chromosome and browse by family (Fig. 3). Browse by chromosome allows the user to have a view of different gene families on a particular chromosome with a number of genes as recorded in the database. Browse by family provides an overview of all gene families in our database and a navigation link. This link provides all genes with chromosomal position in a respective gene family (Fig. 4). Search interface facilitates three types of inquiries, Search by chromosome, Search by Family and Search by Gene. All of these search options ultimately takes the user to a Gene information interface. This Gene information interface provides gene location, other names used for gene, brief description of a gene, annotations, related protein domains and sequences (protein, cDNA, CDS, genomic and promoter) which can be downloaded, related publications and links to external

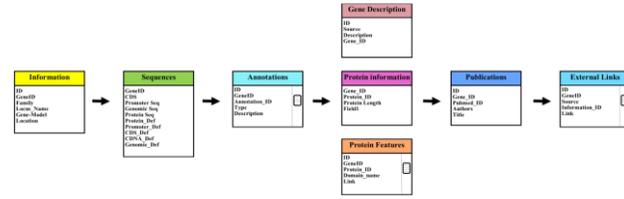


Fig. 2: The flowchart for construction of NTDBPlant

Gene ID:	Chromosome No.:	Gene Location:
AT5G17850	chr5	Chr5:5899253-5900938 forward
AT5G17860	chr5	Chr5:5902394-5904380 reverse
At1g08960	chr1	Chr1:2879642-2882231 forward

Fig. 3: Screenshot of a web page displaying information about nutrient transporters gene families in NTDBPlant. Web page in NTDBPlant displays basic information about gene families to search either by chromosome or by a gene family

databases such as TAIR, T-DNA Express, Plant Genome and Systems Biology, Ace view, Plant Proteome Database, Phytozome, Salk SNP Viewer, Plaza, NCBI-Entrez Gene, BioGRID, Araport, AtGDB View, e-FP Browser and EVEX.

Future Perspectives

There has been an increasing trend of transporter gene identification that are further isolated and then cloned to reveal understandings of the mechanism of ion transport across the membrane. The findings are handy for further research. The database we developed is just a beginning of an important resource. We intend to gradually expand the database with membrane transport gene families of other plant genomes as well.

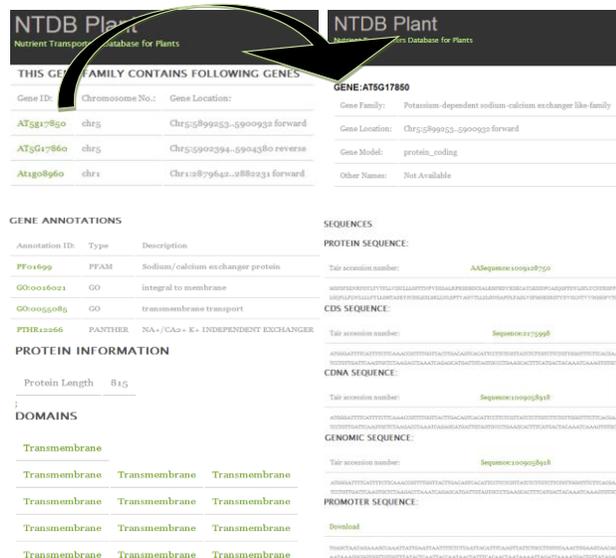


Fig. 4: Every gene page in NTDBPlant displays the basic information for a typical nutrient transporter gene. The annotation information of a typical entry of the NTDBPlant displaying the rich annotation of a nutrient transporter gene (AT5g17850) of the Potassium-dependent sodium-calcium exchanger like-family. The annotation contains four major categories: (A) Basic information (B) Gene Annotations (C) Protein Information: domains are linked to the original domain databases and protein length is also provided for each gene member (D) Sequence Information: all sequence information with TAIR accession numbers is provided

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