



Stress Combination and their Interactions in Plants (SCIP) Database

Website link- <http://www.nipgr.ac.in/scipdb.php>

How to use the search section

- Click on the 'Search' tab provided on the 'SCIPDb' home page to mine the datasets hosted in the database.

Stress Combinations and their Interactions in Plants (SCIP) Database

Home About **Search** Submit Connect Help

Control Drought stress Pathogen stress Combined stress

Photo credit: Ranjita Sinha, NIPGR, field experiment
SCIPDb@2022

Combined Stress: Omics data

- Phenomics
- Transcriptomics
- Metabolomics

Literature	939
Stress combinations	123
Organisms	408
Transcriptome	36
Combined stress genes	45169
Traits	107

- It redirects the user to a page as shown in below screenshot.
- This section provides extensive search options for users to mine the phenomics and transcriptomics datasets hosted in SCIP database.



- The background algorithm is based on fuzzy search, and any matches in the database with the keyword searched will be presented. The results can be further filtered out using the search bar provided above the interactive bootstrap table.
- Under each dataset, user can search the data in a category provided in the dropdown menu. For example, in the phenomics section, data can be retrieved pertaining to five categories: by name of plant, stress combination, parameters, pathogen or by user defined keywords.
- On clicking the “See an example” link, users are redirected to a page as shown in below screenshot which exemplifies, how to design search for each of these categories.

- 1) Plant: Arabidopsis thaliana, Rice, Adzuki bean, Soybean, Alfalfa, Pea, Onion, Red clover, Barley, Bayberry, Bell Pepper, Cajanus cajan, Chickpea, Common bean, Cucumber, Durum wheat, Bread wheat, Faba bean, Field bean, Field mustard, Wheat, White bean, white clover, white mustard /watercress Wild celery, Wild strawberry
- 2) Stress combination: Bacteria & fungus, Drought & bacteria, Drought & heat/high temperature, Drought & High light, Flooding/waterlogging/submergence/anoxia & cold/freezing/low temperature
- 3) Parameters: Spore per lesion, Spreading lesion, RWC/Relative water content, Total chlorophyll content, Bacterial number, Cell death quantification, Disease score/severity, Leaf symptoms/disease severity, Leaf bacterial population, Water potential, Biomass - Fresh and Dry weight, Leaf number, Stomata (L-W ratio)
- 4) Pathogen: Pseudomonas syringae pv. tomato DC3000, Alternaria brassicicola; Botrytis cinerea, Paenibacillus polymyxa, Pythium aphanidermatum
- 5) Keyword: 2016, 2011, 2020, Sequential stress, Simultaneous stress



Let's first discuss each of these five categories under phenomics dataset with an example.

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SCIP database- search

This section provides extensive search options for users to mine the phenomics and transcriptomics data hosted in SCIP database. The background algorithm is based on fuzzy search, and any matches in the database with the keyword searched will be presented. The results can be further filtered out using the search bar provided above the interactive bootstrap table.

Search Phenomics dataset
[See an Example](#)
Select category: Plant
Enter data:
Submit Reset

Search Transcriptomics dataset
I. Search by category: See an Example
Select category: Gene Id
Enter data:
Submit Reset

II. Search by Sequence (input sequence in Fasta Format):
Provides an option for search by sequence of interest using blastx or blastp server. The user's are expected to enter FASTA sequences starting with a greater than (>) symbol followed by the sequence ID. See example sequences through, "See an Example" link provided below to format your sequences

STEP I : PASTE YOUR SEQUENCE (Maximum 10 sequences): [See an Example](#)

- Under select category select plant, and then in the enter data box enter name of the plant of your choice, for example here we are searching rice. Finally, click submit.

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Search Phenomics dataset
[See an Example](#)
Select category: Plant
Enter data: Rice
Submit Reset



Stress Combination and their Interactions in Plants (SCIP) Database

Website link- <http://www.nipgr.ac.in/scipdb.php>

The screenshot shows the SCIP Database interface. At the top, there are navigation links: Home, About SCIP, Reach Us, Search SCIP, and Submit data. Below these is a search bar and a 'Download Result' button. The main content is a table with the following data:

Sl.no	Stress combination	Classification	Parameters	Plant	Cultivar	Pathogen	Reference
1	Drought & bacteria	Sequential stress	Lesion length, Bacterial count	Rice	IR64	Xanthomonas oryzae pv. oryzae	Dossa GS, Torres R, Henry A, Oliva R, Maiss R, Cruz CV, Wydra K. Rice response to simultaneous bacterial blight and drought stress during compatible and incompatible interactions. <i>Eur J Plant Pathol</i> 2016; DOI 10.1007/s10658-016-0985-8
2	Drought & cold/freezing/low temperature	Sequential stress	2-hydroxymelatonin content	Rice	Dongjin	N/A	Lee H-J and Back K. 2-hydroxymelatonin promotes the resistance of rice plant to multiple simultaneous abiotic stresses (combined cold and drought). <i>Journal of Pineal Research</i> 2016; 61, 303-316.
3	Drought & High light	Simultaneous stress	RWC/Relative water content, Leaf water potential, Maximum CO2 assimilation, Stomatal conductance, Intercellular CO2 concentration, Stomatal limitation, Membrane stability index, MDA/malondialdehyde content.	Rice	9311	N/A	Zhou Y, Lam HM, Zhang J. Inhibition of photosynthesis and energy dissipation induced by water and high light stresses in rice. <i>Journal of Experimental Botany</i> 2007, 58(5): 1207-1217
4	Heavy metal & ozone	Sequential stress	Root FW, shoot FW	Rice	Sakha 101	N/A	Tammam A, Badr R,

- User will see a page as shown in above screenshot, that will show all the entries for rice, in a tabular form. The results are depicted in the form of interactive bootstrap table which has nine columns, namely serial number, stress combination, type of combined stress (sequential or simultaneous), parameter studied, plant name, cultivar (if any) pathogen (if relevant), link to its reference article and its corresponding phenome data page hosted in the SCIPDb.



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				inter grain weight, yield, No. of J2/g root, No. of eggs/root, root galling index/disease severity, Multiplication factor				rice varieties grown in two soil types infested by the rice root-knot nematode <i>Meloidogyne graminicola</i> . Russian Journal of Nematology 23(2): 99 - 112.
10	Nematode & fungus	Sequential stress	H2O2 and MDA/malondialdehyde content, sporulating lesion, average lesion type, fungal DNA	Rice	Nipponbare	Meloidogyne graminicola, Magnaporthea oryzae	Kyndt T, Zemene HY, Haeck A, Singh R, De Vleeschauwer D, Denil S, De Meyer T, Hofte M, Demeestere K, Gheysen G (2017) Below-Ground Attack by the Root Knot Nematode <i>Meloidogyne graminicola</i> Predisposes Rice to Blast Disease. Mol Plant Microbe Interact 30: 255-266	

Showing 1 to 10 of 19 entries

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- Bottom of the page will show total number of entries available for rice

Stress Combinations and their Interactions in Plants (SCIP) Database

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SCIP database- search

This section provides extensive search options for users to mine the phenomics and transcriptomics data hosted in SCIP database. The background algorithm is based on fuzzy search, and any matches in the database with the keyword searched will be presented. The results can be further filtered out using the search bar provided above the interactive bootstrap table.

Search Phenomics dataset

[See an Example](#)

Select category Stress Combination

Enter data Drought & bacteria

Submit Reset

- On the selection of second select category, i.e., stress combination, in the enter data box user need to enter name of the desired stress combination, for example, enter for Drought & bacteria and click submit.



Stress Combination and their Interactions in Plants (SCIP) Database

Website link- <http://www.nipgr.ac.in/scipdb.php>

The screenshot shows the SCIP Database website interface. At the top, there are navigation links: Home, About SCIP, Reach Us, Search SCIP, and Submit data. Below these is a search bar and a 'Download Result' button. The main content is a table with the following columns: S.No, Stress combination, Classification, Parameters, Plant, Cultivar, Pathogen, Reference, and Phenon. The first row is highlighted with a red border.

S.No	Stress combination	Classification	Parameters	Plant	Cultivar	Pathogen	Reference	Phenon
1	Drought & bacteria	Sequential stress	RWC/Relative water content, Total chlorophyll content, Bacterial number, Cell death quantification, Disease score/severity	Arabidopsis	Col-0	Pseudomonas syringae pv. tomato DC3000	Gupta A, Dixit SK, Senthil-Kumar M. Drought stress predominantly endures Arabidopsis thaliana to Pseudomonas syringae infection. Frontiers in Plant Science 2016; 7:1-12. Doi: https://doi.org/10.3389/fpls.2016.00808	View Phenon Data
2	Drought & bacteria	Sequential stress	Hydraulic conductance, Embolism, vessels diameter and length	Virginia creeper	N/A	Xylella fastidiosa	McElrone AJ, Sberald JL, Forseth IN. Interactive effects of water stress and xylem-limited bacterial infection on the water relations of a host vine. J of Experimental Botany 2003; 54(381):419-430.	View Phenon Data
3	Drought & bacteria	Sequential stress	Total leaf area showing scorching symptoms/disease severity, Leaf area, Shoot length, Intermodal length, Number of nodes	Virginia creeper	N/A	Xylella fastidiosa	McElrone AJ. Effects of water stress on symptomatology and growth of Parthenocissus quinquefolia infected by Xylella fastidiosa. Plant Disease 2001;85(11):1160-1164.	View Phenon Data
4	Drought & bacteria	Sequential stress	Leaf symptoms/disease severity, Leaf bacterial population	Arabidopsis	Col-0	Pseudomonas syringae pv. tomato 1065	Mohar PG and Cahill DM. Abscisic acid influences the susceptibility of Arabidopsis thaliana to Pseudomonas syringae pv. tomato and Peronospora parasitic. Functional Plant Biol 2003:461-469	View Phenon Data
5	Drought & bacteria	Sequential stress	Disease incidence/severity (%), Wilt index (%), AUDIPIC- Total area under disease incidence progress curve, AUPSIPC- Total area under percentage severity progress curve	Banana	Mbwazirume	Xanthomonas compestris pv. musacearum	Ochola D, Ocimati W, Tinzaara W, Blomme G, Karamura EB. Effects of water stress on the development of banana Xanthomonas wilt disease. Plant Pathology 2015;64:552-558.	View Phenon Data
6	Drought & bacteria	Sequential stress	Stomatal conductance, Transpiration, Leaf water potential,	Grapevine	Chardonnaya and Cabernet	Xylella fastidiosa	Thorne ET, Stevenson JF, Rost TL, Labavitch JM, Matthews MA. Pierce's disease symptoms:	View Phenon Data

- User will see a page like this showing all the entries for drought & bacteria, in a interactive bootstrap tabular format.
- Here, again each entry will have results pertaining to name of stress combination, type of combined stress (sequential or simultaneous), parameter studied, plant name, cultivar (if any) pathogen (if relevant), link to its reference article and its corresponding phenome data page.



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Search Phenomics dataset

[See an Example](#)

Select category Parameters

Enter data biomass

Submit Reset

- On the selection of third select category, i.e., parameter, in the enter data box user will have to enter name of the parameter, for e.g., here we are searching for biomass. Finally, “click submit”.

Stress Combination and their Interaction in Plants (SCIP) Database

Home About SCIP Reach Us Search SCIP Submit data

Download Result

Show 10 entries Search:

Sl.no	Stress combination	Classification	Parameters	Plant	Cultivar	Pathogen	Reference
1	Drought & cold/freezing/low temperature	Simultaneous stress	Shoot and root length, shoot and root fresh weight/biomass, chlorophyll content, total soluble sugar, free proline	Maize	XD889, XD319, Yu13 and Yu37	N/A	Hussain HA, Men S, Hussain S, Ashraf U, Zhang Q, Anjun SA, Ali I and Wang L. Individual and concurrent effects of drought and chilli stresses on morpho-physiological characteristics and oxidative metabolism of maize cultivars. <i>BioRxiv</i> 201829309; doi: https://doi.org/10.1101/829309
2	Drought & cold/freezing/low temperature	Sequential stress	Relative growth rate, Leaf area ratio, Plant weight/biomass, Relative water content, Net assimilation rate, Specific transpiration rate	Maize	Errazu	N/A	Irigoyen JJ, Juan JPD and Sanchez-Diaz M. Drought enhances chilling tolerance a chilling-sensitive maize (Z Mays) variety. <i>New Phytologist</i> 1996; 134, 53-59
3	Drought & cold/freezing/low temperature	Sequential stress	Shoot length, Tiller number, Dry weight/biomass, Grain yield	Wheat	Yannong 19	N/A	Li X, Cai J, Liu F, Dai T, Cao and Jiang D. Physiological, proteomic and transcription responses of wheat to combination of drought or waterlogging with late spring low temperature. <i>Functional Plant Biology</i> 2014; 41, 690-703.
4	Drought & heat/high temperature	Sequential stress	Water potential, Biomass - Fresh and Dry weight, Leaf number, Stomata (L-W ratio)	Arabidopsis	N/A	N/A	Prasch CM, Sonnwald U. Simultaneous Application of Heat, Drought, and Virus to Arabidopsis Plants Reveals Significant Shifts in Signaling Networks. <i>Plant Physiology</i> 2013; 162: 1849-1866.
5	Drought & heat/high temperature	Sequential stress	Days to flowering, Days to podding, Days to maturity, shoot/aboveground biomass	Chickpea	ICC4567, ICC5912, ICC3776	N/A	Awasthi R, Kaushal N, Vade V, Turner NC, Berger J, Siddique KHM, Nayyar H. Individual and combined effects of temperature and drought



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- User will see a page like this showing all the entries for biomass, in the same tabular form as explained above. Here, again each entry will have link to its reference article and its phenome data page hosted in the SCIPDb.

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SCIP database- search

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Search Phenomics dataset

[See an Example](#)

Select category Pathogen

Enter data Pseudomonas syringae

Submit Reset

- Under the fourth select category, user can mine the datasets based on pathogen. In the enter data box they will have to enter the name of the pathogen, for e.g., on searching for *Pseudomonas syringae* and clicking submit, results are displayed.

Stress Combination and their Interaction in Plants (SCIP) Database

Home About SCIP Reach Us Search SCIP Submit data

Download Result

Show 10 entries Search:

Sl.no	Stress combination	Classification	Parameters	Plant	Cultivar	Pathogen	Reference
1	Bacteria & fungus	Sequential stress	Disease measurement, Enzyme assays/Activities of phenylalanine ammonia lyase (PAL), coniferyl alcohol dehydrogenase (CAD) and peroxidase (PO), Chitinase and 7-1,3-glucanase levels	Rice (Oryza sativa cv. nohrin)	nohrin	Pseudomonas syringae pv. syringae, Pyricularia oryzae; race 283	Smith JA and Metraux JP. Pseudomonas syringae pv. induces systemic resistance to Pyricularia oryzae in r Physiological and molecular plant pathology 1991; 39 https://www.sciencedirect.com/science/article/pii/0881223235 .doi: https://doi.org/10.1016/S0885-5765(05)80223-235
2	Bacteria & fungus	Sequential stress	Peroxidase activity, Lesion diameter	Cucumber (Cucumis sativus L. var. SMR-58)	SMR-58	Pseudomonas syringae pv. syringae, Colletotrichum lagenarium; race 1	Smith JA, Hammerschmidt R, Fulbright DW. Rapid induced systemic resistance in cucumber by Pseudomonas syringae. Physiological and molecular plant pathology 223-235. doi: https://doi.org/10.1016/S0885-5765(05)80223-235
3	Bacteria & fungus	Sequential stress	Spore per lesion, Spreading lesion	Arabidopsis	Col-0	Pseudomonas syringae pv. tomato DC3000, Alternaria brassicicola; MUCL20297 strain	Spoel SH, Johnson JS, Dong X. Regulation of tradeoff plant defenses against pathogens with different lifestyles. Proceedings of the national academy of science USA 2007 ; 104: 18842-18847. doi: 10.1073/pnas.07081
4	Bacteria & mites	Sequential stress	Leaf damage/injury, Egg production by adult female	Bean	N/A	Spider mite (Tetranychus urticae), Pseudomonas syringae, Pantoea ananatis	Karamanoli K, Kokalvas V, Koveos DS, Junker RR, Fan (2020) Bacteria Affect Plant-Mite Interactions Via Alter Emissions. J Chem Ecol. 46:782-792
5	Drought & bacteria	Sequential stress	RWC/Relative water content, Total chlorophyll content, Bacterial	Arabidopsis	Col-0	Pseudomonas syringae pv. tomato DC3000	Gupta A, Dixit SK, Senthil-Kumar M. Drought stress p endures Arabidopsis thaliana to Pseudomonas syring Frontiers in Plant Science 2016; 7:1-12. Doi: https://doi.org/10.3389/fpls.2016.00808



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- User will see a page like in above screenshot showing all the entries for *Pseudomonas syringae*, in a tabular form. Also again, each entry will have link to its reference article and its phenome data page hosted in the SCIPDb.

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SCIP database- search

This section provides extensive search options for users to mine the phenomics and transcriptomics data hosted in SCIP database. The background algorithm is based on fuzzy search, and any matches in the database with the keyword searched will be presented. The results can be further filtered out using the search bar provided above the interactive bootstrap table.

Search Phenomics dataset

[See an Example](#)

Select category By Keyword

Enter data 2011

Submit Reset

- Under the fifth select category “By keyword”, user can enter any keyword, in the enter data box. Here suppose we are searching by year 2011 and on clicking submit button results are displayed as shown in below screenshot.



Stress Combination and their Interactions in Plants (SCIP) Database

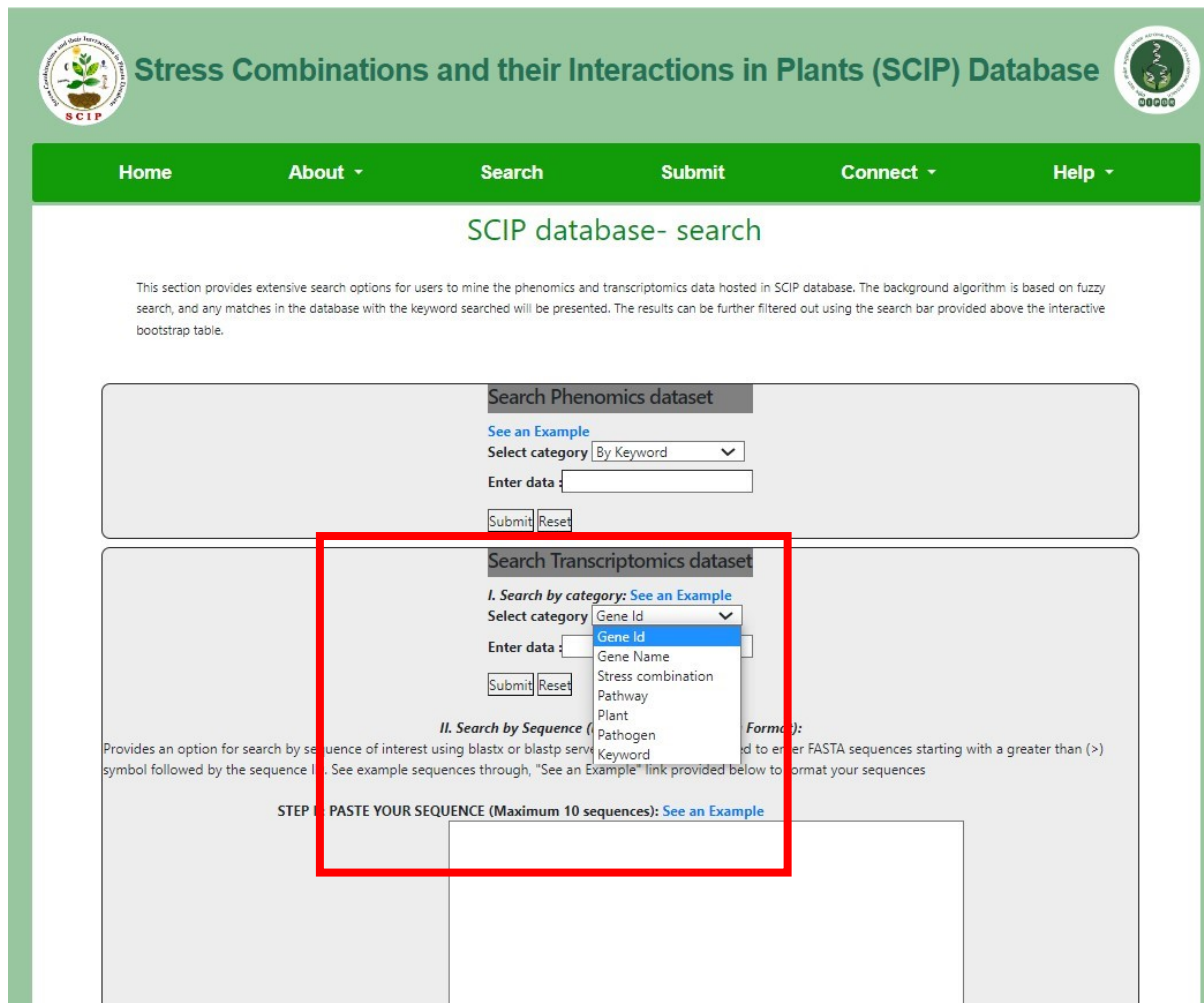
Website link- <http://www.nipgr.ac.in/scipdb.php>

The screenshot shows the SCIP Database website interface. At the top, there are navigation links: Home, About SCIP, Reach Us, Search SCIP, and Submit data. Below these is a search bar with a 'Download Result' button and a 'Show 10 entries' dropdown. The main content is a table with 9 columns: Sl.no, Stress combination, Classification, Parameters, Plant, Cultivar, Pathogen, Reference, and Phenome. Three entries are visible, with the first entry highlighted by a red box.

Sl.no	Stress combination	Classification	Parameters	Plant	Cultivar	Pathogen	Reference	Phenome
1	Drought & cold/freezing/low temperature	Sequential stress	Net photosynthetic assimilation, Transpiration rate, Stomatal conductance	Creosote bush	N/A	N/A	Medeiros JS and Pockman WT. Drought increases freezing tolerance of both leaves and xylem of Larrea	View Phenome Data
2	Flooding/waterlogging/submergence/anoxia & insects	Sequential stress	Kaempferol (Flavanoid content)	Broccoli	italica Plenck	Aphid	Khan MAM, Ulrichs C, Mewis I (2011) Effect of water stress and aphid herbivory on flavonoids in broccoli (Brassica oleracea var. italica Plenck). Journal of Applied Botany and Food Quality 84, 178 - 182.	View Phenome Data
3	Heavy metal & nematode	Sequential stress	Shoot weight/biomass, Shoot length, Root weight/biomass, Root length, Root knot index/disease severity	Tomato	Rutgers	Meloidogyne incognita	Park BY, Lee JK, Ro HM, Kim YH. Effects of heavy metal contamination from an abandoned mine on tomato growth and root-knot nematode development. Plant Pathology Journal 2011,	View Phenome Data

- User's will see a page like this showing all the entries for 2011 in a tabular form. Here again, each entry will have link to its reference article and its phenome data page hosted in the SCIPDb.

- Now let's see each category under transcriptomics dataset with an example.



- In the transcriptomics section, data can be retrieved using the categories or using the FASTA sequence. Here, search can be done under seven categories: by gene ID, gene name, stress combination, pathway, plant, pathogen or by any keyword.
- On clicking the “See an Example” link, users are redirected to a page as shown in below screenshot which exemplifies, how to design search for each of these categories.

- 1) Gene Id: AT5G16440, BRADI2g10830, CATMA4a03730, 101248621
- 2) Gene Name: auxin-responsive protein SAUR19-like, SNF2 domain-containing protein CLASSY 4-like, ABC transporter
- 3) Stress combination: Nematode and Water, Cold and Drought, Drought and nonhost pathogen, B. brassicae and P. brassicae
- 4) Pathway: Metabolic pathways, Glutathione metabolism, Arachidonic acid metabolism, MAPK signaling pathway, Plant hormone signal transduction
- 5) Plant: Brachypodium distachyon, Arabidopsis thaliana, Triticum Aestivum, Brassica nigra, Solanum lycopersicum, V. vinifera, Camellia sinensis, Hordeum vulgare, Sorghum bicolor, Cicer arietinum, Glycine max, Rice, Solanum peruvianum
- 6) Keyword: RING/FYVE/PHD zinc finger superfamily protein, vacuolar-sorting receptor 7

- Let's see an example in each category.



Stress Combination and their Interactions in Plants (SCIP) Database

Website link- <http://www.nipgr.ac.in/scipdb.php>

The screenshot shows the search interface for the SCIP database. A red box highlights the search options. Under the heading "I. Search by category: See an Example", there is a dropdown menu for "Select category" with "Gene Id" selected, and an input field for "Enter data" containing "AT5G16440". Below these are "Submit" and "Reset" buttons. A second heading "II. Search by Sequence (Input sequence in FASTA Format)" is partially visible. Below the search options, there is a text box for "STEP I : PASTE YOUR SEQUENCE (Maximum 10 sequences): See an Example".

- Under the first category, “Gene Id”, users need to enter “Gene ID” in the Enter data section. For e.g., here we are searching for AT5G16440.

The screenshot shows the search results page for the SCIP database. A red box highlights the results table. The table has eight columns: Sl.no, Gene ID, Gene Name, Stress combination, Plant, Pathogen, Log FC, and Pathway & Metadata. The first row shows the results for Gene ID AT5G16440.

Sl.no	Gene ID	Gene Name	Stress combination	Plant	Pathogen	Log FC	Pathway & Metadata
1	AT5G16440	Isopentenyl-diphosphate Delta-isomerase I	Salt and heat	Arabidopsis thaliana	NA	-0.55	ath01100 Metabolic pathways ath01110 Biosynthesis of secondary metabolites ath00900 Terpenoid backbone biosynthesis

- On clicking submit, user will see a page as shown in above screenshot showing the entry for AT5G16440, in an interactive bootstrap tabular format.
- The results displayed above has eight columns namely the serial number, Gene ID, Gene name, Stress combination, Plant, Pathogen (if applicable), Log FC (Log Fold change) and link to pathways & metadata (KEGG pathway or KEGG genes link).
- Here, each entry will have link to its pathway and metadata hosted on the SCIPDb.



Stress Combination and their Interactions in Plants (SCIP) Database

Website link- <http://www.nipgr.ac.in/scipdb.php>

Search Transcriptomics dataset

I. Search by category: [See an Example](#)
Select category
Enter data

II. Search by Sequence (input sequence in Fasta Format):
Provides an option for search by sequence of interest using blastx or blastp server. The user's are expected to enter FASTA sequences starting with a greater than (>) symbol followed by the sequence ID. See example sequences through, "See an Example" link provided below to format your sequences

STEP I : PASTE YOUR SEQUENCE (Maximum 10 sequences): [See an Example](#)

- Under the second category, i.e., Gene Name, in the enter data box user will have to enter gene name of their choice, For e.g., on searching for auxin responsive protein and clicking submit, results are presented as shown below.

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Download Result
Show 10 entries Search:

Sl.no	Gene ID	Gene Name	Stress combination	Plant	Pathogen	Log FC	Pathway & Metadata
1	BRADI3g54610	auxin-responsive protein IAA9	Salinity, drought and heat	Brachypodium distachyon	NA	1.70	bdi04075 Plant hormone signal transduction
2	BRADI3g50080	auxin-responsive protein SAUR36	Salinity, drought and heat	Brachypodium distachyon	NA	-0.75	bdi04075 Plant hormone signal transduction
3	BRADI1g55370	auxin-responsive protein IAA24	Salinity, drought and heat	Brachypodium distachyon	NA	-0.72	bdi04075 Plant hormone signal transduction
4	BRADI2g16850	auxin-responsive protein IAA19	Salinity, drought and heat	Brachypodium distachyon	NA	-0.71	bdi04075 Plant hormone signal transduction
5	BRADI4g36945	auxin-responsive protein SAUR36	Salinity, drought and heat	Brachypodium distachyon	NA	-1.27	KEGG Genes Link
6	AT4G32280	auxin-responsive protein IAA29	Chilling and larval feeding	Arabidopsis thaliana	Pieris brassicae	3.90	ath04075 Plant hormone signal transduction
7	AT3G09870	SAUR-like auxin-responsive protein	Chilling and larval feeding	Arabidopsis thaliana	Pieris brassicae	-1.26	ath04075 Plant hormone signal transduction
8	AT3G61900	SAUR-like auxin-responsive protein	Chilling and larval feeding	Arabidopsis thaliana	Pieris brassicae	-1.50	ath04075 Plant hormone signal transduction
9	AT5G18060	SAUR-like auxin-responsive protein	Insect-eggs and larval-feeding	Arabidopsis thaliana	Pieris brassicae	-1.18	ath04075 Plant hormone signal transduction
10	AT1G72430	SAUR-like auxin-responsive protein family	Insect-eggs and larval-feeding	Arabidopsis thaliana	Pieris brassicae	-1.53	KEGG Genes Link

Showing 1 to 10 of 122 entries

Previous 1 2 3 4 5 ... 13 Next

- User will see a page like this showing the entries for auxin responsive protein, in a tabular form. Here, each entry will have a serial number, Gene ID, Gene name, Stress combination, Plant, Pathogen (if applicable), Log FC (Log Fold change) and link to pathways & metadata (KEGG pathway or KEGG genes link).



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- Bottom of the page will show total number of entries (here 122). At a time only 10 entries are displayed for quicker display and the results are segregated into several pages, which can be assessed by clicking the pagination function (as shown in above screenshot by red arrow).

Search Transcriptomics dataset

I. Search by category: [See an Example](#)
Select category: Stress combination
Enter data :Cold and Drought

II. Search by Sequence (input sequence in Fasta Format):
Provides an option for search by sequence of interest using blastx or blastp server. The user's are expected to enter FASTA sequences starting with a greater than (>) symbol followed by the sequence ID. See example sequences through, "See an Example" link provided below to format your sequences

STEP I : PASTE YOUR SEQUENCE (Maximum 10 sequences): [See an Example](#)

- The third category pertains to “Stress combination”, in the enter data box the name of desired stress combination can be entered. For e.g., on searching for cold and drought, and clicking submit, results are depicted as shown below.

Download Result

Sl.no	Gene ID	Gene Name	Stress combination	Plant	Pathogen	Log FC	Pathway & Metadata
1	112942136	uncharacterized protein At3g17950 isoform X2	Cold and drought	Solanum lycopersicum	NA	-3.04	KEGG Genes Link
2	112942122	putative F-box protein At1g32420	Cold and drought	Solanum lycopersicum	NA	-4.77	KEGG Genes Link
3	112942062	uncharacterized protein LOC112942062	Cold and drought	Solanum lycopersicum	NA	2.11	KEGG Genes Link
4	112942062	uncharacterized protein LOC112942062	Cold and drought	Solanum lycopersicum	NA	2.11	KEGG Genes Link
5	112942019	uncharacterized protein LOC112942019	Cold and drought	Solanum lycopersicum	NA	6.42	KEGG Genes Link
6	112941859	skin secretory protein xP2-like	Cold and drought	Solanum lycopersicum	NA	-6.78	KEGG Genes Link
7	112941852	G-type lectin S-receptor-like serine/threonine-protein Kinase At4g27290	Cold and drought	Solanum lycopersicum	NA	4.85	KEGG Genes Link
8	112941695	uncharacterized protein LOC112941695	Cold and drought	Solanum lycopersicum	NA	-2.42	KEGG Genes Link
9	112941556	uncharacterized protein LOC112941556	Cold and drought	Solanum lycopersicum	NA	-2.04	KEGG Genes Link
10	112941248	uncharacterized protein LOC112941248	Cold and drought	Solanum lycopersicum	NA	5.56	KEGG Genes Link

Showing 1 to 10 of 1,130 entries

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Stress Combination and their Interactions in Plants (SCIP) Database

Website link- <http://www.nipgr.ac.in/scipdb.php>

- User will see a page like above and results are presented in the same way as explained above. Here again, each entry will have a serial number, Gene ID, Gene name, Stress combination, Plant, Pathogen (if applicable), Log FC (Log Fold change) and link to pathways & metadata (KEGG pathway or KEGG genes link).

Search Transcriptomics dataset

I. Search by category: [See an Example](#)

Select category Pathway

Enter data Metabolic pathways

II. Search by Sequence (input sequence in Fasta Format):

Provides an option for search by sequence of interest using blastx or blastp server. The user's are expected to enter FASTA sequences starting with a greater than (>) symbol followed by the sequence ID. See example sequences through, "See an Example" link provided below to format your sequences

STEP I : PASTE YOUR SEQUENCE (Maximum 10 sequences): [See an Example](#)

- Under the fourth category, "Pathway", in the enter data box on entering the name of pathway, for e.g., "Metabolic pathways", and clicking submit results are presented.

Stress Combination and their Interaction in Plants (SCIP) Database

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Show 10 entries

Search:

Sl.no	Gene ID	Gene Name	Stress combination	Plant	Pathogen	Log FC	Pathway & Metadata
1	BRADI1g17790	peroxidase P7	Salinity, drought and heat	Brachypodium distachyon	NA	-0.97	bdi01100 Metabolic pathways bdi01110 Biosynthesis of secondary metabolites bdi00940 Phenylpropanoid biosynthesis
2	BRADI3g52680	9-cis-epoxycarotenoid dioxygenase NCED1, chloroplastic	Salinity, drought and heat	Brachypodium distachyon	NA	-0.79	bdi01100 Metabolic pathways bdi01110 Biosynthesis of secondary metabolites bdi00906 Carotenoid biosynthesis
3	BRADI3g13590	peroxidase 47	Salinity, drought and heat	Brachypodium distachyon	NA	-2.41	bdi01100 Metabolic pathways bdi01110 Biosynthesis of secondary metabolites bdi00940 Phenylpropanoid biosynthesis
4	BRADI1g34180	UDP-sugar pyrophosphorylase	Salinity, drought and heat	Brachypodium distachyon	NA	-0.59	bdi01100 Metabolic pathways bdi01110 Biosynthesis of secondary metabolites bdi00040 Pentose and glucuronate interconversions bdi00052 Galactose metabolism bdi00053 Ascorbate and aldarate metabolism bdi00520 Amino sugar and nucleotide sugar metabolism
5	BRADI1g70620	mannose-1-phosphate guanyltransferase alpha	Salinity, drought and heat	Brachypodium distachyon	NA	-0.75	bdi01100 Metabolic pathways bdi01110 Biosynthesis of secondary metabolites bdi01240 Biosynthesis of cofactors bdi00051 Fructose and mannose metabolism bdi00520 Amino sugar and nucleotide sugar metabolism

- User will see a page like above and results are presented in the same way as explained above. Here again, each entry will have a serial number, Gene ID, Gene name, Stress



Stress Combination and their Interactions in Plants (SCIP) Database

Website link- <http://www.nipgr.ac.in/scipdb.php>

combination, Plant, Pathogen (if applicable), Log FC (Log Fold change) and link to pathways & metadata (KEGG pathway or KEGG genes link).

- Under the fifth category “Plant”, in the enter data box user need to enter name of the plant for e.g., on searching for *Sorghum bicolor*, and clicking submit, results pertaining to sorghum are presented as shown below, in the same manner as explained above (see below screenshot).

Sl.no	Gene ID	Gene Name	Stress combination	Plant	Pathogen	Log FC	Pathway & Metadata
1	Sb09g028880.1	RLK (receptor lectin kinase); kinase	Drought and heat	Sorghum bicolor	NA	52.83	NA
2	Sb01g013990.1	pentatricopeptide (PPR) repeat-containing protein	Drought and heat	Sorghum bicolor	NA	52.72	NA
3	Sb09g001420.1	lipase class 3 family protein	Drought and heat	Sorghum bicolor	NA	50.18	NA
4	Sb08g018920.1	unknown protein	Drought and heat	Sorghum bicolor	NA	32.04	NA
5	Sb01g030785.1	calcineurin-like phosphoesterase family protein	Drought and heat	Sorghum bicolor	NA	42.03	NA
6	Sb09g021640.1	calcineurin-like phosphoesterase family protein	Drought and heat	Sorghum bicolor	NA	43.77	NA
7	Sb01g015450.1		Drought and heat	Sorghum bicolor	NA	35.21	NA
8	Sb08g020290.1	PIF4 (phytochrome interacting factor 4); DNA binding / protein binding / transcription factor	Drought and heat	Sorghum bicolor	NA	33.25	NA
9	Sb09g001620.1	unknown protein	Drought and heat	Sorghum bicolor	NA	28.34	NA
10	Sb08g022720.1		Drought and heat	Sorghum bicolor	NA	24.81	NA



Stress Combination and their Interactions in Plants (SCIP) Database

Website link- <http://www.nipgr.ac.in/scipdb.php>

Search Transcriptomics dataset

I. Search by category: [See an Example](#)
Select category: Pathogen
Enter data: Pseudomonas

II. Search by Sequence (input sequence in Fasta Format):
Provides an option for search by sequence of interest using blastx or blastp server. The user's are expected to enter FASTA sequences starting with a greater than (>) symbol followed by the sequence ID. See example sequences through, "See an Example" link provided below to format your sequences

STEP I : PASTE YOUR SEQUENCE (Maximum 10 sequences): [See an Example](#)

- Under the sixth category, i.e., Pathogen, in the enter data box user will have to enter name of the pathogen, for e.g., here on searching for *Pseudomonas*, and clicking submit, results showing the entries for *Pseudomonas* are presented in the same way as detailed above (see below screenshot).

Stress Combination and their Interaction in Plants (SCIP) Database

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Show 10 entries

Sl.no	Gene ID	Gene Name	Stress combination	Plant	Pathogen	Log FC	Pathway & Metadata
1	AT1G01080	RNA-binding (RRM/RBD/RNP motifs) family protein	Drought and nonhost pathogen	Arabidopsis thaliana	Pseudomonas syringae pv. tabaci	-1.10	KEGG Genes Link
2	AT1G01290	cofactor of nitrate reductase and xanthine dehydrogenase 3	Drought and nonhost pathogen	Arabidopsis thaliana	Pseudomonas syringae pv. tabaci	0.50	ath01100 Metabolic pathways ath00790 Folate biosynthesis ath04422 Sulfur relay system
3	AT1G01440	Protein of unknown function (DUF3133)	Drought and nonhost pathogen	Arabidopsis thaliana	Pseudomonas syringae pv. tabaci	0.70	KEGG Genes Link
4	AT1G01470	Late embryogenesis abundant protein	Drought and nonhost pathogen	Arabidopsis thaliana	Pseudomonas syringae pv. tabaci	0.60	KEGG Genes Link
5	AT1G01480	1-amino-cyclopropane-1-carboxylate synthase 2	Drought and nonhost pathogen	Arabidopsis thaliana	Pseudomonas syringae pv. tabaci	0.60	ath01100 Metabolic pathways ath01110 Biosynthesis of secondary metabolites ath04016 MAPK signaling pathway ath00270 Cysteine and methionine metabolism
6	AT1G01510	NAD(P)-binding Rossmann-fold superfamily protein	Drought and nonhost pathogen	Arabidopsis thaliana	Pseudomonas syringae pv. tabaci	-0.50	KEGG Genes Link
7	AT1G01540	Protein kinase superfamily protein	Drought and nonhost pathogen	Arabidopsis thaliana	Pseudomonas syringae pv. tabaci	-0.60	KEGG Genes Link
8	AT1G01550	Protein of unknown function (DUF793)	Drought and nonhost pathogen	Arabidopsis thaliana	Pseudomonas syringae pv. tabaci	0.50	KEGG Genes Link
9	AT1G01620	plasma membrane intrinsic protein 1C	Drought and nonhost pathogen	Arabidopsis thaliana	Pseudomonas syringae pv. tabaci	-0.60	KEGG Genes Link
10	AT1G01650	SIGNAL PEPTIDYL PEPTIDASE-LIKE 4	Drought and	Arabidopsis	Pseudomonas	0.70	KEGG Genes Link



Stress Combination and their Interactions in Plants (SCIP) Database

Website link- <http://www.nipgr.ac.in/scipdb.php>

Search Transcriptomics dataset

I. Search by category: [See an Example](#)
 Select category
 Enter data

II. Search by Sequence (Input sequence in Fasta Format):
 Provides an option for search by sequence of interest using blastx or blastp server. The user's are expected to enter FASTA sequences starting with a greater than (>) symbol followed by the sequence ID. See example sequences through, "See an Example" link provided below to format your sequences

STEP I : PASTE YOUR SEQUENCE (Maximum 10 sequences): [See an Example](#)

- Under the last category, "Keyword", in the enter data box user will have to enter keyword of their choice, for e.g., on searching for zinc finger and clicking submit, results matching to the "zinc finger" as presented in the same way as detailed above (see below screenshot).

Stress Combination and their Interaction in Plants (SCIP) Database

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Download Result

Show 10 entries Search:

Sl.no	Gene ID	Gene Name	Stress combination	Plant	Pathogen	Log FC	Pathway & Metadata
1	BRADI1g26570	dof zinc finger protein DOF1.4	Salinity, drought and heat	Brachypodium distachyon	NA	-0.55	KEGG Genes Link
2	BRADI4g08050	zinc finger CCOH domain-containing protein 66 isoform X1	Salinity, drought and heat	Brachypodium distachyon	NA	-0.73	KEGG Genes Link
3	BRADI3g03060	B-box zinc finger protein 32	Salinity, drought and heat	Brachypodium distachyon	NA	-1.35	KEGG Genes Link
4	AT5G22920	ring finger and CHY zinc finger domain-containing protein 1	Chilling and larval feeding	Arabidopsis thaliana	Pieris brassicae	3.60	ath04120 Ubiquitin mediated proteolysis
5	AT5G44260	zinc finger CCOH domain-containing protein 61	Chilling and larval feeding	Arabidopsis thaliana	Pieris brassicae	3.28	KEGG Genes Link
6	AT1G02610	RING/FYVE/PHD zinc finger-containing protein	Chilling and larval feeding	Arabidopsis thaliana	Pieris brassicae	2.57	KEGG Genes Link
7	AT1G49130	zinc finger protein CONSTANS-LIKE 8	Chilling and larval feeding	Arabidopsis thaliana	Pieris brassicae	1.43	KEGG Genes Link
8	AT3G57480	zinc finger AN1 and C2H2 domain-containing stress-associated protein 13	Chilling and larval feeding	Arabidopsis thaliana	Pieris brassicae	1.13	KEGG Genes Link
9	AT1G29160	Dof zinc finger protein	Chilling and larval feeding	Arabidopsis thaliana	Pieris brassicae	1.08	KEGG Genes Link
10	AT1G51700	DOF zinc finger protein 1	Chilling and larval feeding	Arabidopsis thaliana	Pieris brassicae	-1.23	KEGG Genes Link

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Stress Combination and their Interactions in Plants (SCIP) Database

Website link- <http://www.nipgr.ac.in/scipdb.php>

- User can also search transcriptomic datasets using FASTA sequences.
- This section of search, provides users with an option to search by sequence of interest using the standalone blastx or blastp server hosted.
- The users are expected to enter FASTA sequences starting with a greater than (>) symbol followed by the sequence ID.
- Clicking example sequences through, "See an Example" link provided will aid users to format their sequences.

Search Transcriptomics dataset

I. Search by category: [See an Example](#)
Select category
Enter data :

II. Search by Sequence (Input sequence in Fasta Format):
Provides an option for search by sequence of interest using blastx or blastp server. The user's are expected to enter FASTA sequences starting with a greater than (>) symbol followed by the sequence ID. See example sequences through, "See an Example" link provided below to format your sequences

STEP I : PASTE YOUR SEQUENCE (Maximum 10 sequences): [See an Example](#)



Stress Combination and their Interactions in Plants (SCIP) Database

Website link- <http://www.nipgr.ac.in/scipdb.php>

Search Transcriptomics dataset

I. Search by category: [See an Example](#)
 Select category:
 Enter data:

II. Search by Sequence (input sequence in Fasta Format):
 Provides an option for search by sequence of interest using blastx or blastp server. The user's are expected to enter FASTA sequences starting with a greater than (>) symbol followed by the sequence ID. See example sequences through, "See an Example" link provided below to format your sequences

STEP I : PASTE YOUR SEQUENCE (Maximum 10 sequences): [See an Example](#)

```
>AT5G16930
MAQKIAIGVISALAAASLAPSKFAAADGPFPTFGFSTSPSASIPQQGSTPPASES
INNSAHAKKVFESIKTREETRQAEFTAKAQEFKAMQSQAERQRVIYEEQKLAQ
RREVARRATEEEIQARRQTEREKAEIERETIRVKAMAEAEGRARESKLSEOVNRRN
LTALAAGIYTTREGAKVIWVSYVDRILGQPSLIRESSRGKYPWGSASRVLSTLRGGG
ILFYGPPGTGKTMAAARELARRSGLDYALMTGGDVAPLGAQAVTKIHQLFDWSKKS
VLLATNRPGDLDSAVADRIDETLEFPLPGEERFKLLNLYLEKYISKTNLKKPGLLQS
QAAVYGSANCLLDANLFREVIDYKVAEHQQRKKLAGTDAGNKKK
```

Autofill this form

Select BLAST program :

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- In the form provided above users need to paste the FASTA sequence in single or batch mode (maximum 10), and then click submit button.

Stress Combination and their Interactions in Plants (SCIP) Database

Home Phenome Transcriptome Meta-phenome

Download complete Blast hits in SCIPDb

Download

Sl.no	Query	Subject	Percentage identity	Plant	Stress combination	Gene name	Log FC
1	AT5G16930	AT5G16930.1	100.000	Arabidopsis thaliana	Heat and highlight	AAA-type ATPase family protein	0.10
2	AT5G16930	AT5G16930.1	100.000	Arabidopsis thaliana	Drought and Pieris rapae	AAA-type ATPase family protein	-1.09
3	AT5G16930	AT5G16930.1	100.000	Arabidopsis thaliana	Heat & drought	AAA-type ATPase family protein (Uncharacterized protein At5g16930)	1.60

Showing 1 to 3 of 3 entries Previous1Next

- The results are presented as an interactive bootstrap table, which shows the number of hits, Query, Subject, Percent identity, Plant, Stress combination, Gene name and Log fold change as shown in above screenshot.