



# Stress Combination and their Interactions in Plants (SCIP) Database

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

The user can go to the Meta-phenome tab by selecting any of the two tabs which are highlighted (Phenomics and Transcriptomics).

The screenshot shows the main navigation bar with tabs: Home, About, Search, Submit, Connect, and Help. Below it, a grid of four images shows plant growth under different stress conditions: Control, Heat stress, Drought stress, and Combined stress. To the right, a section titled "Combined Stress: Omics data" contains two tabs: "Phenomics" (highlighted in red) and "Transcriptomics" (highlighted in green). An arrow points to these tabs with the text "Click any of the two tabs". Below the tabs is a table:

Literature	1088
Stress combinations	100
Organisms	325
Transcriptome	24
Traits	107

Welcome to SCIP database:

A comprehensive database for understanding combined stress response in plants

Under natural conditions, plants are exposed to a wide range of abiotic and biotic stress combinations, affecting their growth and yield. In most cases, the simultaneous or sequential occurrence of two different type of combined stresses affects a plant's performance more severely than single stresses. For example, a combination of drought and heat stress caused more significant damage worth \$200 billion to U agriculture than the \$50 billion loss caused by drought alone (Mittler 2006:8...

If the user clicks the Transcriptomics tab, then the user will be redirected to the corresponding transcriptomics web page. By clicking on the "Meta-phenome" tab which is highlighted below, the user will be redirected to the corresponding Meta-phenome section.

The screenshot shows the "Meta-phenome" section of the database. The navigation bar highlights "Meta-phenome" in red. Below it, the title "Combined stress: Transcriptome data" is displayed. The section contains a search form with two steps:

Search unique/common genes based on Plant

STEP I : Select a plant species:

Choose a Plant:

STEP II: Select a stress combination:

Choose a Stress combination:

On the right side, there are four bullet points describing the data:

- SCIP database hosts a comprehensive collection of combined stress responsive differentially expressed genes (DEGs) identified in publically available transcriptomic data from various plant species.
- Transcriptomic data represented here includes a list of DEGs, log fold change and absolute fold change over control, obtained after in-house analysis of the combined stress transcriptome available in the public domain.
- This section provides an option for browsing transcriptomics data, based on drop down based selection of plants and stress combination.
- Result is presented in the form of interactive bootstrap table, that displays informations about list of differentially expressed genes (DEGS) genes expressed uniquely and commonly under individual and combination of stresses along with gene annotation and fold change in expression.
- The data also includes information about DEGs nature of change in expression i.e whether it is expressed uniquely or common or

Shown below is the Meta-phenome section, which shows the user the net impact of the stress combination in plant performance. The user needs to select a maximum of 3 individual stresses



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(result will be displayed if such a triple stress combination data exists or otherwise provide 2 stresses) and the plant species which they are interested to check from the highlighted portion shown below and click on the “Go” button which is also highlighted.

The screenshot shows the SCIP database interface. At the top, there is a green navigation bar with the following tabs: Home, Phenome, Transcriptome, and Meta-phenome. Below the navigation bar, the page title is "Combined stress: Meta-Phenome data". A paragraph of text explains the interactive view, stating that it shows the net impact of stress combinations on plant performance. Below the text, there is a search form with the following fields: "Stress 1", "Stress 2", "Stress 3", and "Plant species", each with a "Make a se" dropdown menu. A "Go" button is located to the right of the search form. An arrow points to the "Stress 1" dropdown menu, and another arrow points to the "Go" button. The text "Click Here to Submit" is written above the "Go" button.

Step 1 : Select the stress 1 from the highlighted drop down menu as shown below

The screenshot shows the SCIP database interface with the "Stress 1" dropdown menu open. The dropdown menu lists the following stress combinations: Salt, Drought, Nutrient deficiency/toxicity, Light, High/low temperature, Ozone, Flood/waterlog/submergence, Heavy metal, Shade/plant competition, UV, Weed, Nematode, Insect, Fungus, Virus, Bacteria, Oomycete, and Wound. The "Go" button is highlighted. The text "©2022. National Institute Of Plant Genome Research" and the number "0042858" are visible at the bottom of the page.

Step 2 : Select the stress 2 from the highlighted drop down menu as shown below.



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## Combined stress: Meta-Phenome data

The interactive view represented below shows the net impact of stress combinations on plant performance. Positive (green colour or its graded shade) and negative (red colour or its graded shade) interactions indicate that the plant parameter is less and more affected under combined stress as compared to individual stresses, respectively. Once the user selects stress 1 from the drop-down menu, automatically stress 2 drop-down menus will show the list of stresses that are reported interaction with stress 1. Option to choose stress 3 is also provided if such a combination is reported in the literature. Once stresses are selected user can choose the plant species, and after that, the outcome will be displayed. The display will show the plant species name, stress combination, whether the interaction is positive or negative, along with the number of studies reported the trend and the measured parameter, which was considered to conclude. Finally, one representative graph for one of the listed parameters showing the actual values under different stress treatments, along with control, will also be displayed

Choose the combination and plant species:

Stress 1 Salt Stress 2 Make a selection Stress 3 Make a selection Plant species Make a selection Go

Step 3 : Select the plant species from the drop down menu as highlighted below.

## Combined stress: Meta-Phenome data

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Choose the combination and plant species:

Stress 1 Salt Stress 2 heat Plant species Make a selection Go

Step 4 : Click on the “Go” button which is highlighted and shown below.

Home Phenome Transcriptome Meta-phenome

## Combined stress: Meta-Phenome data

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Choose the combination and plant species:

Stress 1 Salt Stress 2 Heat Plant species Quinoa Go

If the user selects the Stress 1 as “Salt”, Stress 2 as “Heat” and Plant species as “Quinoa” corresponding Meta-phenome page will be displayed. A colour bar will be shown which is highlighted below to indicate whether the stress combination is deleterious or not. If it’s deleterious



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the colour will be red, if not it will be green.

## Combined stress: Meta-Phenome data

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Choose the combination and plant species:

Stress 1 Salt Stress 2 heat Plant species Quinoa Go

### Quinoa

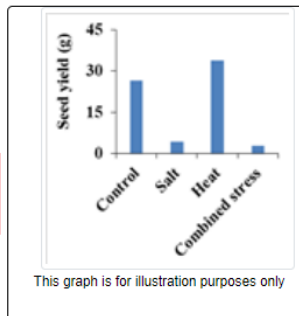
#### Salt+heat stress combination

Net impact of combined stress

Study showed negative interaction

(\*Parameters considered: Seed yield)

For details/other parameters, visit the phenome section of the SCIPdb



[Download result \[PDF\]](#)  
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Yield graph and the image of the plant species will also be displayed which is highlighted below.



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## Combined stress: Meta-Phenome data

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Choose the combination and plant species:

Stress 1: Salt    Stress 2: heat    Plant species: Quinoa    [Go](#)

### Quinoa

#### Salt+heat stress combination

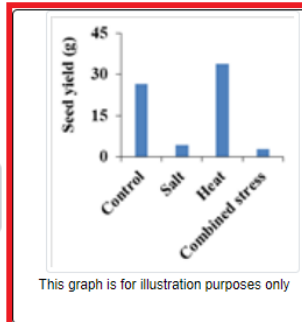
Net impact of combined stress



Study showed negative interaction

(\*Parameters considered: Seed yield)

For details/other parameters, visit the phenome section of the SCIPdb



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