



PHENOPSIS DB

User guide



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1. Description

PHENOPSIS DB is the Web interface associated to the PHENOPSIS automated platforms and to the LEPSE growth chambers concerning *Arabidopsis thaliana* platform.

URL: <http://bioweb.supagro.inra.fr/phenopsis/>

Local URL: <http://lps-junior.supagro.inra.fr/phenopsis/>

1.1 Functionalities

This interface allows:

- to get documentation about the experiments and the information system associated to PHENOPSIS platforms and other *Arabidopsis thaliana* growth chambers,
- to browse and download data from experiments performed in PHENOPSIS platforms and other *Arabidopsis thaliana* growth chambers,
- to insert data concerning the experiments in PHENOPSIS platforms and other *Arabidopsis thaliana* growth chambers (only LEPSE users),
- to update data (only LEPSE users),
- to delete data (only administrators),
- to visualise and perform statistical analyses on data from the experiments in PHENOPSIS platforms and other *Arabidopsis thaliana* growth chambers,
- to analyse images of plants grown in PHENOPSIS platforms and other *Arabidopsis thaliana* growth chambers,
- *Arabidopsis thaliana* growth chambers ,
- to download tools for data and image analyses,
- to manage users and access to data (only administrators).

1.2 Data ownership

1.2.1 Metadata

All metadata are **publicly open** without any restriction or authentication request. Metadata are:

- growth chamber features,

- experiment features and protocol files,
- pot features,
- genotype features,
- list of the variables and associated protocols,
- list of the plant parts,
- comments about the experiments,
- meteorological data.

1.2.2 Phenotyping and pot irrigation data

Phenotyping and pot irrigation data issued from public experiments and public genotypes are open to the public without any restriction or authentication request.

Phenotyping and pot irrigation data issued from private experiments or genotypes require user authentication and their access depend on the user rights.

2. Home page, connection and user rights

2.1 Home page

URL: <http://bioweb.supagro.inra.fr/phenopsis/Accueil.php>

Access: public

2.1.1 Language selection

PHENOPSIS DB is accessible in French or in English. Choose you language by clicking on the corresponding flag (Fig 1).

2.1.2 Menu

The vertical menu (Fig 1) presents the different accessible functionalities.

2.1.3 Log in / Log out

To log on, please fill in the connection form (Fig 1) the *Login* and *Password*.

To get your connection parameters, please follow the links in the bottom of the connection form.

To log out, please click on the *Log out* link in the top right corner of the **home page** (Fig 2).

Languages



Fig 1: Home page

2.2 User rights and accounts

URL: <http://bioweb.supagro.inra.fr/phenopsis/Compte.php>

Access: logged on user

2.2.1 User account validity duration

Start and end dates of account validity are given by the administrator.

2.2.2 Groups

One user can belong to one or more user groups giving him access to data owned by these groups.

There are 2 special groups:

- ADMIN group: only users from this group can delete data and have access to pages for user and group management,

- INSERTION group: only users from this group can insert and update data.

2.2.3 Special users

A « special » user owns particular access to one or more genotypes and / or to one or more experiments. He may not belong to any group.

2.2.4 Consultation of user account parameters

Once logged on, users can consult their account parameters by clicking on the *My account* link in the top right corner of the **home page** (Fig 2).



Fig 2: Logout and account properties

3. PHENOPSIS Documentation Section

URL: <http://bioweb.supagro.inra.fr/phenopsis/InfoBDD.php>

Access: public

The *PHENOPSIS Documentation* section provides informations on PHENOPSIS platforms and the experiments that are performed on these platforms, on the PHENOPSIS database and on the information system associated to the platforms. User guide and documentation on data

insertion are also downloadable.

This section finally lists publications associated to the platforms and emails of LEPSE staff in charge of the platforms and the information system.

4. Data Download and Browsing Section

URL: <http://bioweb.supagro.inra.fr/phenopsis/Consultation.php>

Access: public

4.1 Access to data

A user without account can only access **metadata and public data**.

A user with account can browse and download public data but also data issued from experiments and from genotypes corresponding to the **groups** he belongs to. In summary, to access datasets, the user should have access to the corresponding experiment AND genotype.

Note: When logged in, the user can consult its account parameters by clicking on the *My account* link in the top right corner of the **Home page** (Fig 2). User rights are also displayed on restricted consultation pages.

4.2 Data selection criteria

4.2.1 Search selection

In some consultation pages, basic or advanced searches are suggested.

The basic search only provides the main selection criteria, while advanced search provides all available selection criteria.

4.2.2 Drag-down menu

Data selection criteria are suggested in drag-down menus.

To select more than one selection criteria in a multiple drag-down menu, the user should keep the CTRL key pressed.

If no entry is selected in a drag-down menu, the default choice is « all values », i.e. no selection is processed.

4.3 Results: display, download and export format

4.3.1 SQL request

Result pages first display the run SQL requests.

4.3.2 Data tables

Results are displayed in tables.

For results of hundreds of lines, only the first and last 15 lines are displayed.

A **description** of columns is displayed by pointing on table column names.

All data tables can be downloaded in CSV format. For large data tables, the user can choose to export data in only one CSV file, or in as many 60.000 lines maximum CSV files as necessary.

Note to Open Office users: CSV files should be imported in Open Office with the Occidental Europe (Windows-1252/WinLatin 1) character set, and not with the UTF8 character set (by default).

4.3.3 Files

All files referenced in the database can be downloaded: experiment or genotype Excel files, comment files, scans or plant images.

Plant image files (leaf scans, leaf sections, images taken by the automatons, etc) can be downloaded in ZIP files. The number of data downloadable in one request is limited to 40.000.

Other files (experiment protocol files, genotyping files, comment files, etc) can be downloaded from the displayed data table.

4.4 Data update and deletion

4.4.1 Data update

Data update can only be performed on LEPSE **local server**.

During the display of most data tables, an  icon is displayed at the end of lines for users from the INSERTION or ADMIN groups.

Users can update data **record per record** (growth chamber, experiment, pot, genotype, variable or organ) by clicking on this icon .

Users from the INSERTION or ADMIN groups can also update **pot sets** data. An *Update all*


pots link is displayed during the pot data table display.

To update other **data sets** (meteorological data, irrigation data or data measured on plants), they should be first deleted and then inserted again. Only ADMIN group users are allowed to update these data sets.

4.4.2 Data deletion

Data deletion can only be performed on LEPSE **local server**.

ADMIN group users can delete data **record per record** (growth chamber, experiment, pot, genotype, variable or organ), or delete **data sets** (meteorological data, irrigation data or data measured on plants).

To delete data record per record, an  icon is displayed at the end of lines of the data tables.

To delete data sets, the *Delete data* link is displayed during the data table display.

4.5 Phenotypic data browsing

4.5.1 Data measured on plants

These data are measured by the experimenters on different parts of the plants at various stages of their development.

For each variable, the rank of the measured organ and the phenological stage of the measure are also displayed.

Both variables and organs are referenced – when possible - with existing ontologies: PO, TO, PATO, etc, or combination of these ontologies following the EQ (Entity Qualifier) model. See http://www.gramene.org/plant_ontology/ and http://obofoundry.org/wiki/index.php/PATO:Main_Page.

4.5.2 Plant images

Depending on the experiment, several image files for each plant are produced: different parts of the plants are scanned (rosette, whole plant, roots, etc), images of plant are taken by the experimenters (histological sections), etc.

For experiments performed in PHENOPSIS, images are automatically taken either in the visible or in the infrared.

4.6 Experimental data browsing

4.6.1 Experiment features

Available features are: the growth chamber where the experiment took place, the experiment manager, the start and end dates, the experiment title, the list of publications related to the experiment, the possible stresses applied to the plants during the experiments, the group of users with access to the data, and an Excel file describing the protocol.

The data table only displays experiment main information. User can get all detailed information of one experiment by clicking on the experiment identifier.

Links: The experiment consultation card gives access to the list of pots in the experiment, the studied genotypes and variables, and environmental conditions.

Available downloadable files: experiment protocol Excel file

Pot features of one experiment

Available features are: the pot identifier, its position in the growth chamber, the experimental block in which it was included, the weights of perforated and non-perforated pots, the weight of dry soil in the pot, the number of plants, the sowing date and the genotype, the substrate used, and finally the target humidity levels of the pot during the experiment (i.e. the humidity instructions that have to be compared to the real humidity levels measured by weighing the pots afterwards).

Links: the page with Experiment pot features gives also access to features of genotypes sown in each pot.

Genotype features

Available features are: the genotype identifier, its common name, its code (international reference as NASC), its type (accession, RIL, mutant..), its genetic background, its origin (laboratory providing it), its reference (publications mentioning it), its function, the group of users with access to the genotype data, and a genotyping file (in case of RILs, HIFs, etc).

Available downloadable files: genotyping file

4.6.2 Variable list

2 types of browsing are available:

- browse the features of the variables by choosing their nature (environmental instructions, meteorological variables, ...) or their type,
- browse the features of the variables measured on plants of a given experiment.

Available features are: the variable identifier, its nature (automaton, meteorological or organ), its definition, its units, its maximal and minimal values, its type (numeric, character or file), its protocol, and its reference in existing ontologies (see 4.5.1).

Available downloadable files: protocol file

4.6.3 Organ list (plant measured parts)

Available features are: the organ identifier, its definition and its reference in existing ontologies (see 4.5.1).

4.6.4 Comment list

Comment list contains: the identifier of the chamber to which the comment is referring, the comment date, its author, its category, its subject, the date of the event to which the comment is referring, its content and an miscellaneous file.

Available downloadable files: comment file

4.7 Environmental data browsing

4.7.1 Irrigation data

Irrigation data concern pot soil humidity over experiments.

4.7.2 Meteorological data

The meteorological data (humidity, temperature, etc.) are collected by sensors in the growth chambers.

It is possible to browse only **corrected** data: experimenters can correct meteorological data with different coefficients when necessary.

5. Graphs and Descriptive Statistics Section

URL: <http://bioweb.supagro.inra.fr/phenopsis/Statistiques.php>

Access: public

5.1 General

This section provides visualisation and statistical analysis tools for meteorological data, pot

irrigation data and phenotypic data measured on plants.

Graphs and analyses are performed thanks to R scripts.

5.2 Meteorological data

This module allows to visualise and download graphs and statistics on growth chamber meteorological data.

In the case the user wants to download meteorological data from an experiment that is still running (the experiment end date has not been supplied), the *Experiment still running* corresponding option has to be checked.

If the *Experiment still running* option is checked, another option is displayed to visualise only data of the **last 2 days**.

Produced results

- Selected data table to download,
- If an experiment has been selected: the list of environmental instructions of this experiment,
- The selected meteorological data curves: a graph showing VPD and air temperature, a graph for air humidity and a graph for radiation. Graphs can be downloaded under PDF format, or under PNG format by using *right click* → *Record the image as*.
- A table with mean, minimum and maximum values of the different meteorological variables, computed per day and night periods. Day / night periods are determined from environmental instructions of photoperiod and day start time. This table can be downloaded.

5.3 Pot irrigation data

5.3.1 Visualisation of pot humidity curves

This module allows to visualise and download graphs and statistics of soil water content over time for one or more pots in one experiment.

If the selected experiment is **still running** (the experiment end date has not been supplied), then the *Experiment still running* option has to be checked.

If the *Experiment still running* option is checked, another option is displayed to visualise only irrigation data of the **last 3 days**.

It is also possible to visualise only irrigation data of pots for which there is at least one **alarm** on the selected period.

An alarm corresponds to an irrigation cycle of a pot for which the humidity level after watering differs from the target humidity level by at least 10%.

Caution: To visualise pot soil humidity information such as « perforated pot weight », « non-perforated pot weight » and « dry soil weight » must have been provided for all concerned pots (to allow calculations of soil water contents from pots weighing)!

Produced results

- The table of computed water content data of selected pots to download,
- For each genotype a graph showing changes in water content over time in each pot. For each pot 2 kinds of periods can be distinguished: **water deficit** periods showed in dot lines (the soil is drying and to allow homogeneous drying, there is just one pot, i.e. the perforated pot) and periods during which the pot is **watered** (the target soil water content is reached and there are two pots, i.e. the perforated pot in the non-perforated pot) in full lines. **Cruces** indicate data for which the pot humidity level after watering differs from the target humidity level by at least 10%. Graphs can be downloaded under PDF format, or under PNG format by using *right click* → *Record the image as*.
- The **alarm list** to download providing data to identify pots with a humidity level after watering that differs from the target humidity level by at least 10%.
- The downloadable table with computed statistics on the selected irrigation data: for each pot and per period (succession of periods of stress or not) mean, minimum and maximum humidity are provided with the period duration in days.

5.3.2 Visualisation of pot humidity levels in PHENOPSIS for a given date

This module allows to visualise and download graphs of pot water content in a PHENOPSIS growth chamber for each cycle, before and after irrigation.

Caution: To visualise pot soil humidity data informations « perforated pot weight », « non-perforated pot weight » and « dry soil weight » must have been provided for all pots!

If these informations have not been provided for some of the selected pots, the file containing the list of these pots and their missing features can be downloaded.

Produced results

- The table of computed water content data of selected pots to download,
- For each cycle, a graph showing the hydric state of each pot before and after irrigation in the selected PHENOPSIS growth chamber. Graphs can be downloaded under PDF format, or under PNG format by using *right click* → *Record the image as*.

5.4 Phenotypic data

This module allows to perform graphs and statistic analyses on univariate data (variable per variable) and to download R scripts for data analyses.

5.4.1 Univariate analyses

The user first chooses selection criteria for the data set to analyse.

He selects:

- one or more **variables**,
- **analyses** to perform on each variable (histogram, boxplot, non-linear fitting of growth curves, ...),
- the analysis level, that is to say the **factor** to use (no factor, analysis per genotype, analysis per pot, analysis per plant, ...).

Produced results

- the downloadable table of data selected for analyses,
- graphs corresponding to the selected analyses and factors, to be downloaded in PDF format,
- depending on the selected analyses, a statistic table to download.

5.4.2 R script download

This module provides R data analysis tools.

For each suggested kind of analysis, a ZIP archive can be downloaded with the analysis R script, a testable R script, test datasets and outputs of analyses on these test datasets.

6. Image Analyses and ImageJ Macros Section

URL: <http://bioweb.supagro.inra.fr/phenopsis/Imagerie.php>

Access: public

6.1 General

This module provides tools to analyse image sets thanks to ImageJ macros. [ImageJ](http://rsbweb.nih.gov/ij/) (<http://rsbweb.nih.gov/ij/>) is a free software for image analysis.

6.2 ImageJ tool download

This module allows to download ImageJ macros to analyse rosette images coming from PHENOPSIS automatons, and leaf scan sets done on plants.

An ImageJ software version with all of these macros integrated in it can also be downloaded.

A use guide of these tools can be downloaded.

6.3 Online leaf scan analyses

This module allows to automatically analyse leaf scan sets of plants of one experiment, i.e. to automatically get for each scan the areas of each individual leaf.

For the moment these analyses are only available on LEPSE **local server**.

Produced results

- a downloadable ZIP file of analysed scans,
- a downloadable leaf area data table,
- text file of messages sent during the macro execution,
- the downloadable ZIP file of analysed scan masks.

7. Data Insertion and Upload Section

URL: <http://lps-junior.supagro.inra.fr/phenopsis/Saisie.php>

Access: INSERTION group users

7.1 General

Data insertion can only be performed on LEPSE **local server**.

Data can be inserted record per record via forms, and datasets can be uploaded in CSV files:

- **record per record**: insert a growth chamber, an experiment, a genotype, an organ, a variable or comments on an event,
- **CSV files**: insert one experiment pot list, a genotype list, meteorological data, irrigation data and images or data measured on plants.
- It is also possible to **correct** meteorological data with coefficients for day and night.

To upload data CSV files, a document describing the required format of files and their data can be downloaded. Model Excel files can also be downloaded.

NB: In case of PHENOPSIS growth chambers, meteorological data, irrigation data and images are **automatically** inserted into the database and transferred on the server.

7.2 Procedure

7.2.1 Experiments in PHENOPSIS automatons

– Before to start an experiment in the PHENOPSIS platform, it is necessary to declare the experiment in the database. Only a few fields have to be filled at the onset of the experiment (required fields) and the others have to be completed later on only fill required fields, and to complete then other informations by **updating** the experiment (*Browse experiments* ⇒ *Update*).

– Insert new studied genotypes, organs or variables.

Caution!! It is essential that any insertion of new genotypes, organs or variables has been validated before by a scientific manager!

– Pot identifiers are **automatically** inserted into the database as soon as the data_in file has been provided to the automaton (i.e. only if the experiment has been previously inserted!). The user can then complete pot informations: genotypes, weights, etc .. via the pot consultation page (*Browse the experiment* ⇒ *Browse pots* ⇒ *Update all pots*)

– Upload plant measurement files. This operation can be performed in **as many steps as necessary** (variable per variable, all variables at the same time, etc ...).

– Insert comments (problems, pot transfer, etc).

– Users can add new environmental instructions at any time (for example in case of changing environmental instructions during an experiment) by browsing the instructions of one experiment : a link is displayed there to add new instructions.

7.2.2 Experiments in other growth chambers than PHENOPSIS

For experiments performed in other growth chambers than PHENOPSIS (classic growth chambers, hydraulic bench, etc):

- Insert the experiment. It is possible to only fill required fields, and to complete then other informations by **updating** the experiment (*Browse experiments* ⇒ *Update*).
- Insert new studied genotypes, organs or variables.

Caution!! It is essential that any insertion of new genotypes, organs or variables has been validated before by a scientific manager!

- Insert pots.
- Upload plant measurement files. This operation can be performed in **as many steps as necessary** (variable per variable, all variables at the same time, etc ...). Upload irrigation and meteorological data.
- Insert comments (problems, pot transfer from a position in the chamber to another, etc).
- Users can add new environmental instructions at any time (for example in case of changing environmental instructions) by browsing the instructions of one experiment : a link is displayed to add new instructions.

7.3 Insertion record per record

During the record per record data insertion, if data provided by the user are not in accordance with required formats or are already present in the database, the list of problematic elements is displayed in the top of the form.

7.4 CSV file upload

7.4.1 CSV file format

A document describing the required format for CSV files to be uploaded is available on the home page of the *Insertion* section and on CSV file upload pages.

During the submission of CSV files not in accordance with required formats or containing data already present in the database, the list of problematic elements is available in downloadable text file.

7.4.2 Request execution time

Checking and insertion of thousands of lines CSV files (meteorological or irrigation data) can

require time.

For meteorological data, it takes less than 1 minute to upload files of 1000 lines coming from PHENOPSIS automatons, and about 15 minutes for a file of 1000 lines coming from classic growth chambers.

For irrigation data, it takes about 2h for a file of 15.000 lines.

It is essential not to close the Web browser and not to touch at the Web window while the result page has not been displayed!

7.4.3 Error management during CSV file upload

If a message of error (see example below) is displayed during data CSV file upload:

"Error!! data have not been inserted!! [...] If the problem continues please contact the administrator!!

Then the CSV file has maybe been corrupted during the saving process.

Procedure to locate problems:

- Open the CSV file with a classic text editor.
- Check that all fields are not surrounded with quotes. If they are, save again the Excel file as CSV by specifying that text separator is an empty string.
- Check that all fields are separated by semi commas. If they are not, save again the Excel file as CSV by specifying that field separator is semi comma.
- Check that the last column has been taken into account. Indeed, if the file last column is empty, Excel may not recognize it. If it is the case, select in Excel the column and apply the correct format (*Format* ⇒ *Cells* ⇒ *Text* for example). Save again the Excel file as CSV.
- If none of these actions is successful, contact the administrator!

8. Group and User Management Section

Access: ADMIN group user

8.1 User management

URL: <http://bioweb.supagro.inra.fr/phenopsis/GestionUtilisateur.php>

8.1.1 Create a user

User management page allows inserting a new user.

When the user has been created, it is possible to associate him with a **special access** to one or more genotypes and / or to one or more experiments by following the *Define special access* link, or to assign him to one or more user **groups** by following the *Assign user to user groups* link (see 8.2.2 *Browse, update, delete a group*).

8.1.2 Special users

A « special » user owns **specific** access to one or more genotypes and / or to one or more experiments.

To define special access to a user, an entry by genotype or by experiment should be chosen.

If **genotype** entry is selected, the administrator has to choose a genotype in the drag-down menu. Once the genotype has been selected, the list of experiments in which the genotype has been grown is displayed, and the administrator checks in this list the experiments for which he wants to give a special access to the user.

If **experiment** entry is selected, the administrator has to choose an experiment in the drag-down menu. Once the experiment has been selected, the list of genotypes grown during this experiment is displayed, and the administrator checks in this list the genotypes for which he wants to give a special access to the user.

8.1.3 Browse, update and delete an user

User management page allows to browse the list of users of one group, or of all users if no group is selected.

The table displays the user list and provides links to browse or define their special access, update the user features or delete users.

8.2 Group management

URL: <http://bioweb.supagro.inra.fr/phenopsis/GestionGroupe.php>

8.2.1 Create a group

Group management page allows creating a new user group by providing its identifier.

8.2.2 Update or delete a group

It is possible to update one group identifier on the group management page.

The administrator can also add or remove users to / from a selected group. To do this, the administrator selects a group in the drag-down menu and then chooses in the « Group users » and « Out-of-group users » drag-down menus the user(s) to add or to remove.

Finally the administrator can delete a user group. Caution! Experiments and genotypes having as group identifier the group the administrator wants to delete will be then assigned to the PUBLIC group.

9. Modification and Deletion Management Section

URL: <http://bioweb.supagro.inra.fr/phenopsis/GestionLOG.php>

Access: ADMIN group users

This page allows to download the **LOG file** listing all events on PHENOPSIS DB database linked to deletion or modification of data or files.

Each line contains the date of the event and the login of the user who did the action.

To modify this file, the administrator should edit it after connection on the local server.