

Navigate HIDAP



Highly Interactive Data Analysis Platform

HIDAP

Highly Interactive
Data Analysis Platform



RESEARCH
PROGRAM ON
Roots, Tubers
and Bananas

International Potato Center
RESEARCH INFORMATICS UNIT



This Installation Handbook contains all essential information for the user to use HIDAP. It includes step-by-step procedures on how to create material lists, fieldbooks, reports and graphics.

Once this document has been read and revised, the user will be capable to navigate HIDAP effectively.



Contents

Navigate HIDAP	3
Chapter I: Introduction.....	3
Objective.....	3
Related documents	3
System Requirements	3
Chapter II: HIDAP's structure	4
View: About	4
View: Phenotype	5
View: Geographic Information	8
View: Documentation	8
Chapter III: Material management	9
How to create material lists using accession numbers (families) from the Institutional database ..	9
How to create material lists using accession numbers (clones) from the Institutional database ..	13
How to create material lists using accession numbers (clones) from the Local database	17
Chapter IV: Geographic information	21
Add trial sites.....	21
Check locations table	25
Chapter V: Fieldbook management.....	27
How to create fieldbooks	27
Calculate variables in fieldbooks	34
Chapter VI: Single trial analysis	37
Single report	37
Chapter VII: MET (multi-environment trial) analysis.....	40
MET Trial analysis report	40



Navigate HIDAP

Chapter I: Introduction

Objective

This document aims to provide a step-by-step guide for using HIDAP (Highly Interactive Data Analysis Platform) on desktop computers or laptops.

Related documents

Id	Nombre	Descripción
01	Installation - Install HIDAP.pdf	It is the main support document for installing HIDAP

System Requirements

Computer Processor:	Desktop: x86, 2.33 GHz or higher Laptop: Intel® Atom™ 1.6 Ghz or higher
Memory:	1 GB RAM or higher
Hard drive:	3 GB of free space
Operating system:	Windows 7 or higher, 64-bit
Graphics card:	1024 x 768 Screen resolution
Prerequisite:	Microsoft Excel 2007 or higher
Internet access (optional):	High-speed connection, at least 512kbps (a slower connection won't suffice)



Chapter II: HIDAP's structure

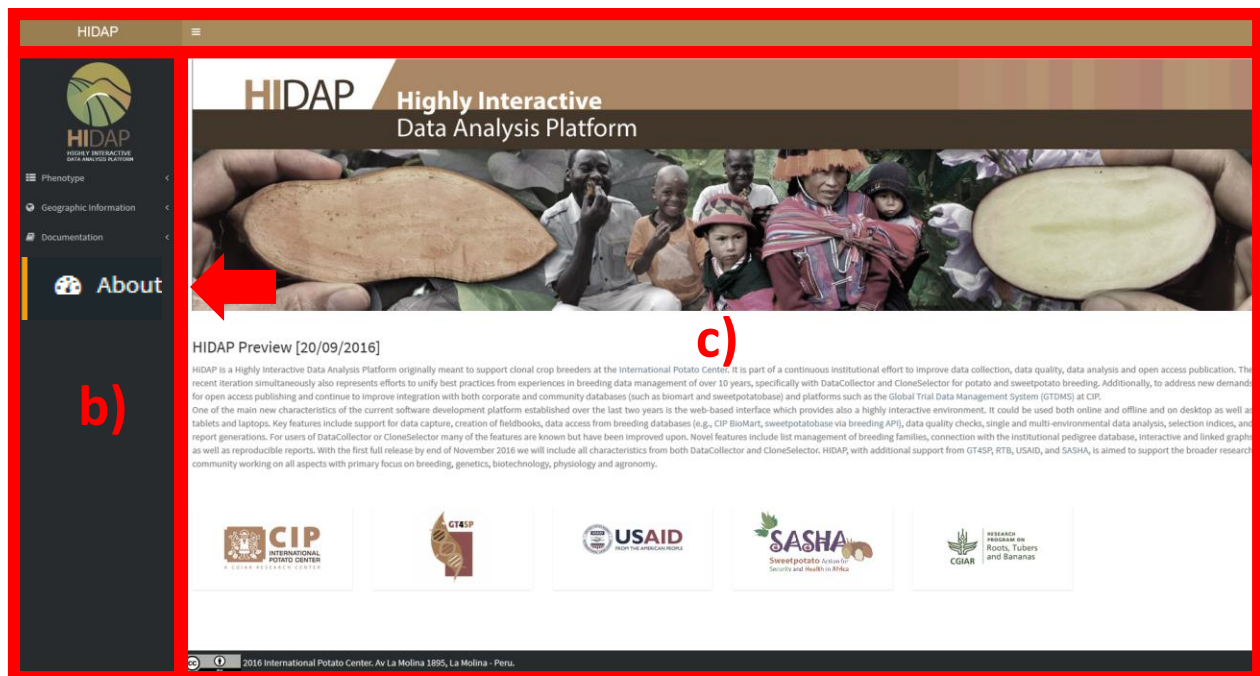
This document describes the structure of HIDAP software; focusing in its layout and how the user interacts with it

View: About

This is the general layout of HIDAP software, there are three main areas identified with red boxes around them:

- a) **Header:** the content area can be minimized or maximized
- b) **Left-side bar:** holds HIDAP's main menu
- c) **Content area:** shows the area where the user will work with different types of information

a)

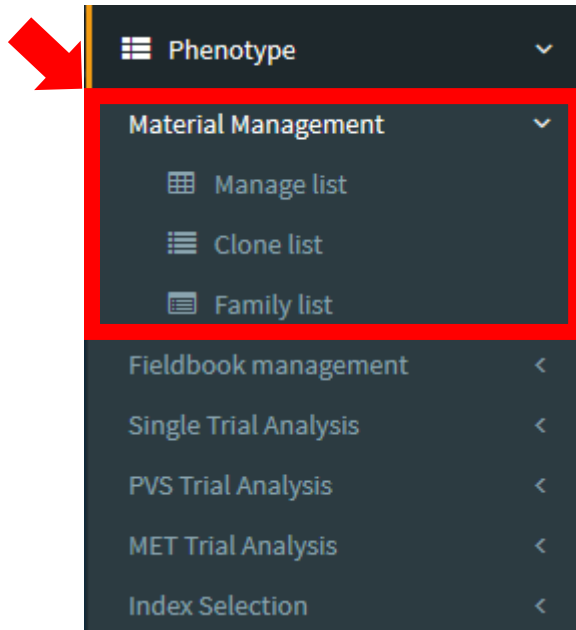




View: Phenotype

Each item from the “**Phenotype**” menu will be briefly described:

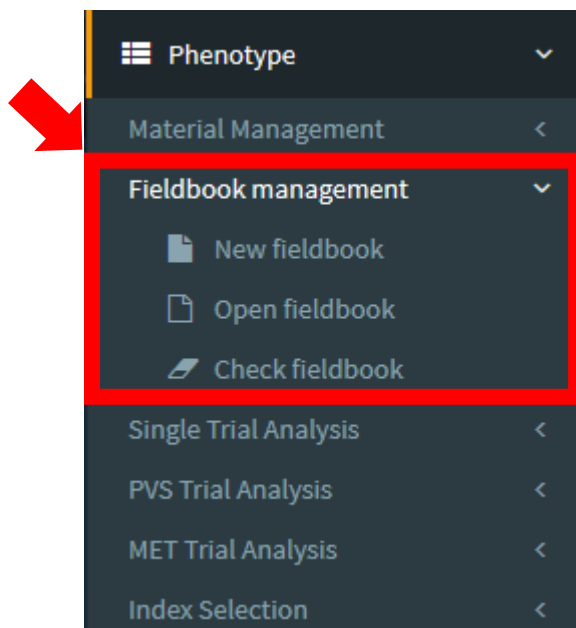
a) Material Management



Manage list: displays the lists created by the user and the synchronization of the institutional databases

Clone list: Enables the creation of new lists of clones and lists from lists. Besides, opens lists already created and exports them

b) Fieldbook Management



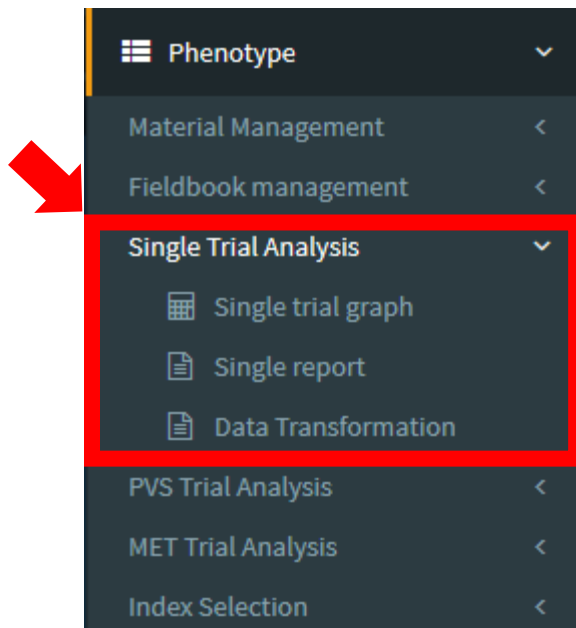
New fieldbook: Enables the creation of fieldbooks using a statistical design and metadata about the localities and installation

Open fieldbook: manages the fieldbooks created using HIDAP

Check fieldbook: calculates and checks traits from fieldbooks and generates a statistical summary



c) Single Trial Analysis

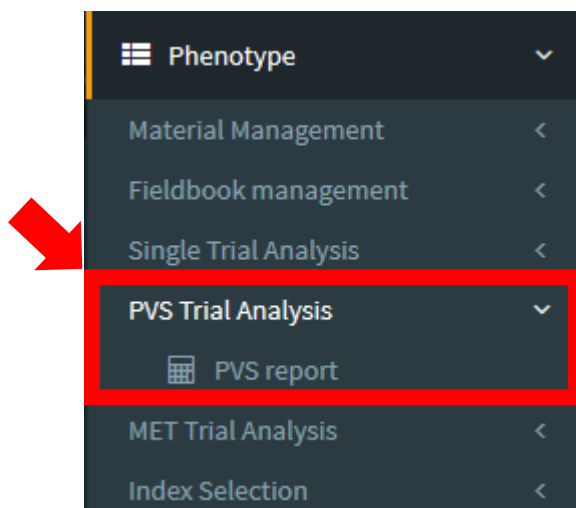


Single trial graph: shows interactive graphics using fieldbooks from a single environment

Single report: creates statistical reports from fieldbooks, including the analysis of variance (ANOVA) according to the statistical design

Data Transformation: Transforms fieldbook data using square root, arcsene, and logarithm conversions.

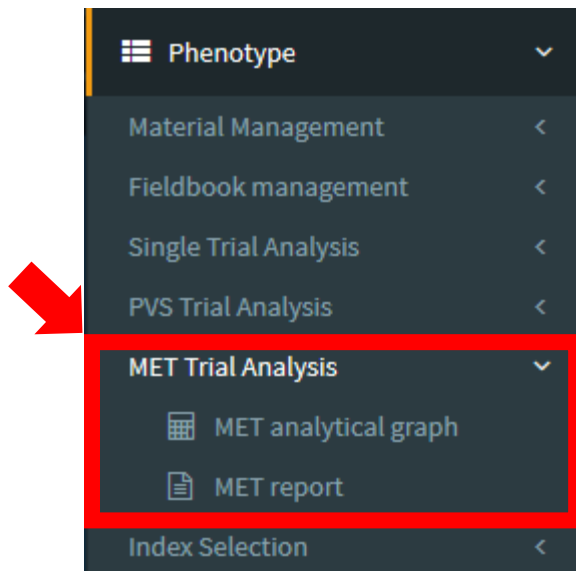
d) PVS Trial Analysis



PVS report: creates statistical reports from participatory varietal selection fieldbooks, including analysis of variance (ANOVA) and Principal component analysis (PCA)



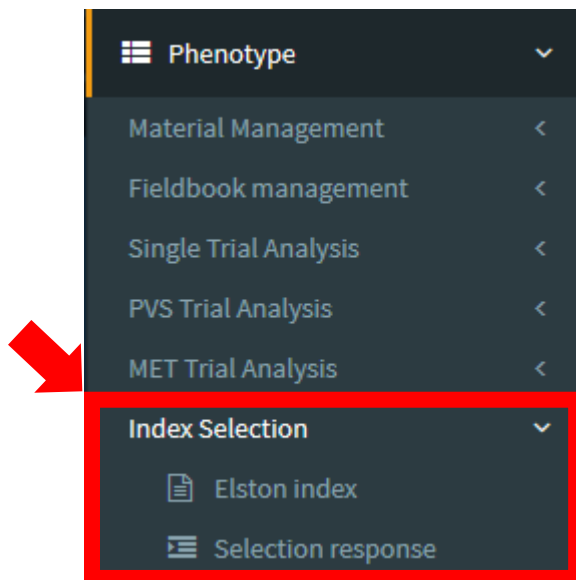
e) MET Trial Analysis



MET analytical graph: shows interactive graphics using fieldbooks from different environments

MET report: creates statistical reports from multiple environments under the Randomized Complete Block Design (RCBD)

f) Index Selection



Elston index: calculates the Elston index for the material selection in the field

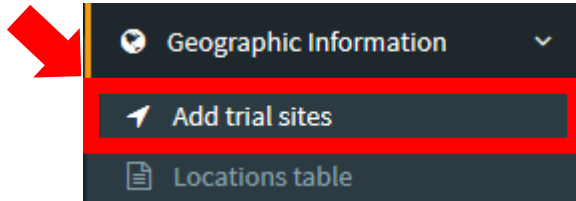
Selection response: shows an interactive graphic of how a population will respond to the selection of a particular environment



View: Geographic Information

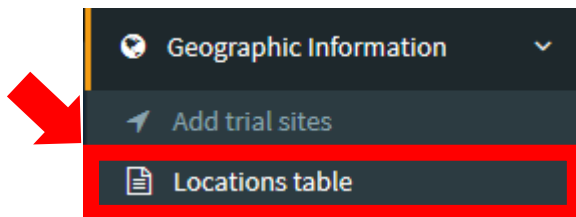
Each item from the “**Geographic information**” menu will be briefly described:

a) Add trial sites



Adds new localities created by the user, georeference is needed

b) Locations table

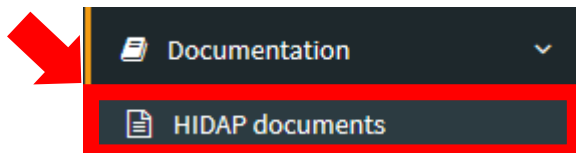


Displays all experimental localities that have been added to HIDAP either from the database or manually by the user

View: Documentation

Each item from the “**Documentation**” menu will be briefly described:

a) HIDAP documents



Hold the handbooks, manuals and fieldbook examples of HIDAP

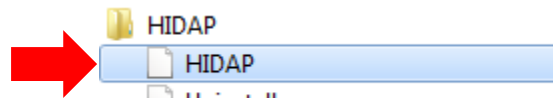


Chapter III: Material management

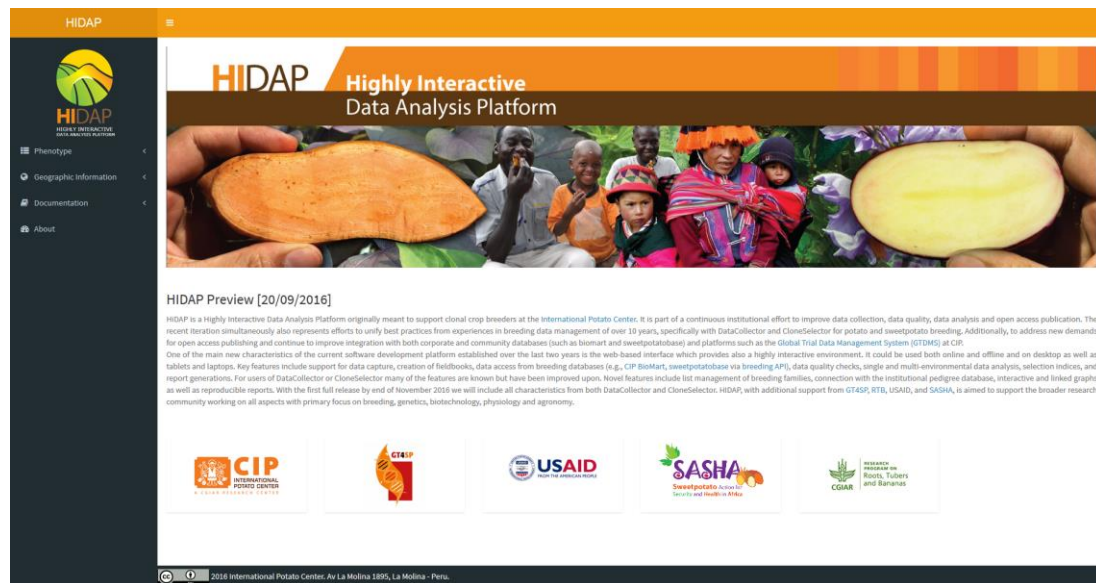
This document provides a step-by-step guide for creating material lists, those which will be used when creating fieldbooks

How to create material lists using accession numbers (families) from the Institutional database

1. Locate and select **HIDAP's shortcut** in the start menu from the taskbar of Windows and wait a few seconds until it loads completely

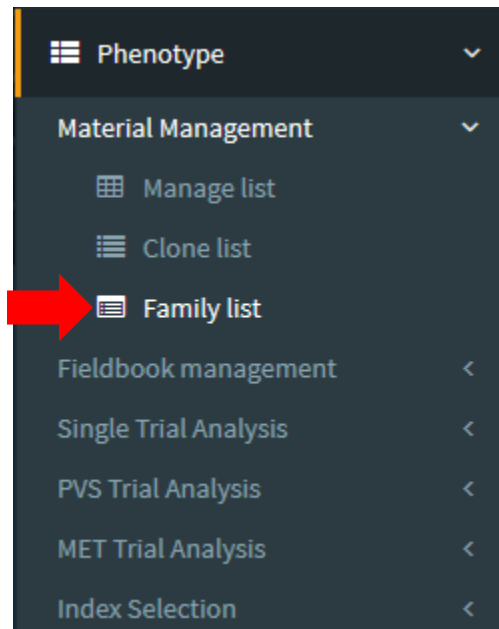


2. Check that HIDAP's main interface (**About**) shows in the default browser





3. In the left sidebar locate and click “**Phenotype**”, then select “**Material Management**” and next “**Family list**”



4. The following interface will come into view; select the **crop** (potato or sweetpotato), the **database** (Institutional) and the **list** (potato_pedigree.rds). Then click “**Connect**”

Family List

Select crop

potato

sweetpotato

Select database

Institutional

Select list

potato_pedigree.rds

Connect



- Copy a list of accession numbers (**families**) you wish to work with, and click “**Select marks**” to create a new material list

Paste a list of families

CIP315028
CIP315029
CIP315030
CIP315031
CIP315032

Search Results

Accession_Number	Female_AcceeNumb	Female_codename	Male_AcceeNumb	Male_codename	Population	Cycle	IDX
CIP315028	CIP300056.33	LR00.014	CIP506131.4	PL-4	UCDAVIS - DH		24739
CIP315029	CIP300056.33	LR00.014	CIP800951	IVP-35	UCDAVIS - DH		24740
CIP315030	CIP300093.14	LR00.026	CIP506131.4	PL-4	UCDAVIS - DH		24741
CIP315031	CIP300093.14	LR00.026	CIP800951	IVP-35	UCDAVIS - DH		24742
CIP315032	CIP300093.14	LR00.026	CIP801037	IVP-101	UCDAVIS - DH		24743

Showing 1 to 5 of 5 entries

Select marks

- Next, complete the form with the required information: new list name, researcher name, continent, country and breeder code.

Fill your Material List Information

New List Name

Write a List Name

Researcher Name

Write Researcher Name

Select Continent

Please select a country below

Select Country

Please select country below

Breeder Code

Write Breeder Code



7. Now, type the number of clones in every family that you have selected and click “**Save List**” button

The screenshot shows a web form titled "Material Selected". It contains five rows, each with a material ID and a corresponding input field for the number of clones. Red arrows point to each of these input fields. At the bottom of the form is a "Save List" button, also indicated by a red arrow.

Material ID	Clones
CIP315028	100
CIP315029	150
CIP315030	100
CIP315031	100
CIP315032	200

Save List

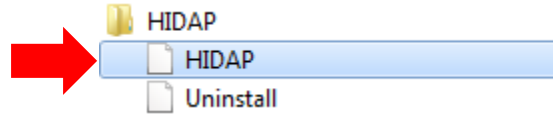
8. Lastly, a green message will be displayed: “**Material List successfully created**”

Material List successfully created! success



How to create material lists using accession numbers (clones) from the Institutional database

1. Locate and select **HIDAP's shortcut** in the start menu from the taskbar of Windows and wait a few seconds until it loads completely

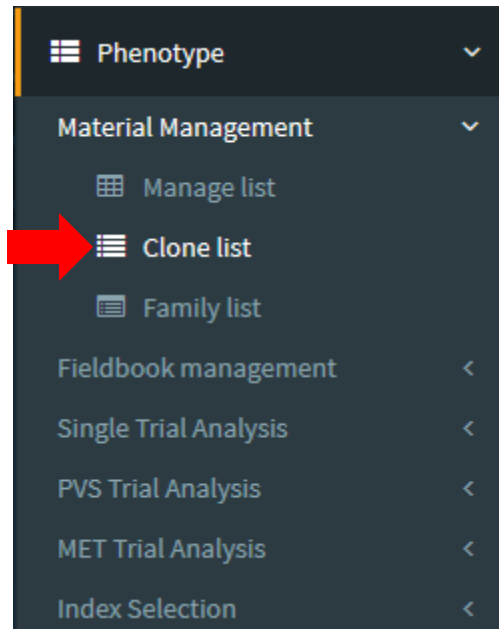


2. Check that HIDAP's main interface (**About**) shows in the default browser





3. In the left sidebar locate and click “**Phenotype**”, then select “**Material Management**” and next “**Clone list**”



4. The following interface will come into view; select the **crop** (potato or sweetpotato), the **database** (Institutional) and the **list** (dspotatortials_dpassport.rds or potato pedigree.rds). Then click “**Connect**”

Clone List

The screenshot shows a form titled 'Clone List'. It contains three dropdown menus and a 'Connect' button. The first dropdown, 'Select crop', has 'potato' selected and is highlighted with a dashed orange box and a red arrow. The second dropdown, 'Select database', has 'Institutional' selected and is pointed to by a red arrow. The third dropdown, 'Select list', has a dropdown arrow and is pointed to by a red arrow; its open state shows two options: 'dspotatortials_dpassport.rds' and 'potato_pedigree.rds'. A red arrow points to the blue 'Connect' button.



- Copy a list of accession numbers (**clones or families**) you wish to work with, and click “**Select marks**” to create a new material list

The screenshot shows the HIDAP interface. On the left, a dialog box titled "Paste a list of clones" is open, displaying a list of accession numbers: CIP392797.22, CIP397006.18, CIP397012.20, CIP397012.22, and CIP397014.2. A red arrow points from this list to the "Search Results" table on the right. The table has columns: Accession_Number, Accession_Name, Accession_Code, Female_AcceptNum, Male_AcceptNum, Population, and IDX. The table contains 5 rows of data. Below the table, there are several "All" buttons and a "Select marks" button, which is highlighted with a red arrow.

Accession_Number	Accession_Name	Accession_Code	Female_AcceptNum	Male_AcceptNum	Population	IDX
CIP392797.22	UNICA	C92.140	387521.3	APHRODITE	Cycle 0	11009
CIP397006.18		102.18	389468.3-(92.119)	88.052		13963
CIP397012.20		319.2	391846.5-(L893.309)	88.052		13970
CIP397012.22		104.22	391846.5-(L893.309)	88.052		13971
CIP397014.2		506.2	392738.4-(92.062)	88.108		13975

- Next, complete the form with the required information: new list name

The screenshot shows the "Fill your material list information" form. It has a title bar "Fill your material list information" and a main content area. The main content area has a heading "New list name" and a text input field with the placeholder text "Write a list name". A red arrow points to the input field.



7. Now, click **“Save List”** button

Material Selected

Show 10 entries

	Accession_Number	Accession_Name	Accession_Code	Female_AcceNumb	Male_AcceNumb	Population	IDX
11009	CIP392797.22	UNICA	C92.140	387521.3	APHRODITE	Cycle 0	11009
13963	CIP397006.18		102.18	389468.3=(92.119)	88.052		13963
13970	CIP397012.20		319.2	391846.5=(LR93.309)	88.052		13970
13971	CIP397012.22		104.22	391846.5=(LR93.309)	88.052		13971
13975	CIP397014.2		506.2	392739.4=(92.062)	88.108		13975

Showing 1 to 5 of 5 entries

Previous

1

Next

Save list

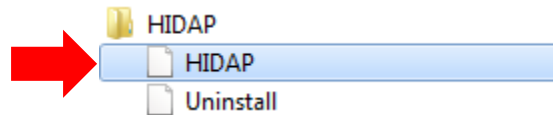
8. Lastly, a green message will be displayed: “Material List successfully created”

Material List successfully created! success



How to create material lists using accession numbers (clones) from the Local database

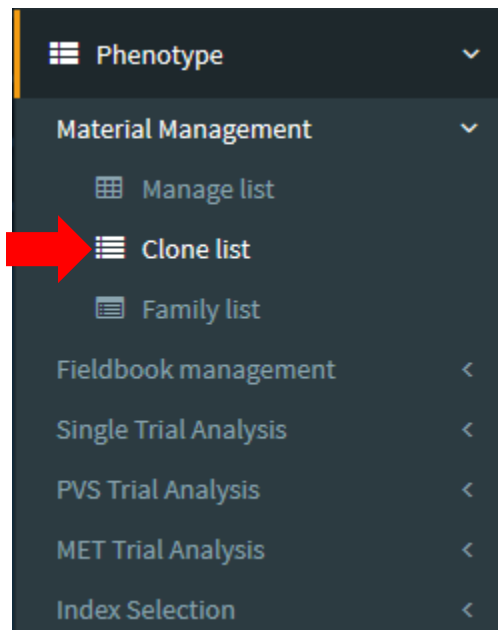
1. Locate and select **HIDAP's shortcut** in the start menu from the taskbar of Windows and wait a few seconds until it loads completely



2. Check that HIDAP's main interface (**About**) shows in the default browser



3. In the left sidebar locate and click **“Phenotype”**, then select **“Material Management”** and next **“Clone list”**



4. The following interface will come into view; select the **crop** (potato or sweetpotato), the **database** (Local) and a list (PT_clone_Material_list_clones.rds) or lists, previously created. Then click “Connect”

A screenshot of the 'Clone List' interface. The title 'Clone List' is at the top. Below it are four input fields and a button. The first field is 'Select crop' with a dropdown menu showing 'potato' and 'sweetpotato'. The second field is 'Select database' with a dropdown menu showing 'Local'. The third field is 'Select list' with a text input showing 'PT_clone_Material_list_clones.rds'. The fourth field is a blue button labeled 'Connect'. Red arrows point to each of these four elements: the 'Select crop' dropdown, the 'Select database' dropdown, the 'Select list' text input, and the 'Connect' button.

5. From the chosen list or lists, select the accession numbers (clones) needed and then click “**Select marks**”



Search Results

Download Search:

Numeration	Accession_Number	Accession_Name	Accession_code	Female_AcceNumb	Female_codename	IDX
1	CIP315028.001		bb028.001	CIP300056.33	LR00.014	1
2	CIP315028.002		bb028.002	CIP300056.33	LR00.014	2
3	CIP315028.003		bb028.003	CIP300056.33	LR00.014	3
4	CIP315028.004		bb028.004	CIP300056.33	LR00.014	4
5	CIP315028.005		bb028.005	CIP300056.33	LR00.014	5
6	CIP315028.006		bb028.006	CIP300056.33	LR00.014	6
7	CIP315028.007		bb028.007	CIP300056.33	LR00.014	7
8	CIP315028.008		bb028.008	CIP300056.33	LR00.014	8
9	CIP315028.009		bb028.009	CIP300056.33	LR00.014	9
10	CIP315028.010		bb028.010	CIP300056.33	LR00.014	10

Showing 1 to 10 of 650 entries

Previous 1 2 3 4 5 ... 65 Next

6. Next, complete the form with the required information: new list name

Fill your material list information

New list name

7. Now, click “Save List” button



Material Selected

Show 10 entries

	Numeration	Accession_Number	Accession_Name	Accession_code	Female_AcceNumb	Female_codename	Male_Acc
1	1	CIP315028.001		bb028.001	CIP300056.33	LR00.014	CIP596131.0
2	2	CIP315028.002		bb028.002	CIP300056.33	LR00.014	CIP596131.0
3	3	CIP315028.003		bb028.003	CIP300056.33	LR00.014	CIP596131.0
4	4	CIP315028.004		bb028.004	CIP300056.33	LR00.014	CIP596131.0
5	5	CIP315028.005		bb028.005	CIP300056.33	LR00.014	CIP596131.0

Showing 1 to 5 of 5 entries

Previous

1

Next

Save list

- Lastly, a green message will be displayed: **“Material List successfully created”**

Material List successfully created! success

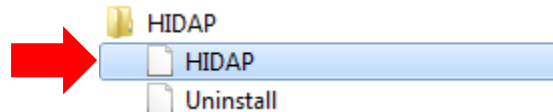


Chapter IV: Geographic information

This document provides a step-by-step guide on how to add trial sites to the local HIDAP database, those which will be used when creating fieldbooks

Add trial sites

1. Locate and select **HIDAP's shortcut** in the start menu from the taskbar of Windows and wait a few seconds until it loads completely

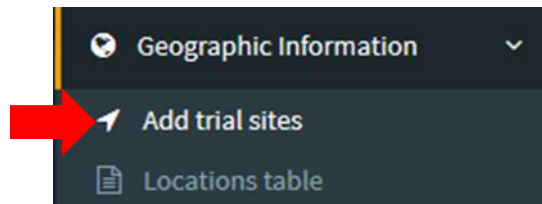


2. Check that HIDAP's main interface (**About**) shows in the default browser





3. In the left sidebar locate and click “**Geographic Information**”, then select “**Add trial sites**”



4. The following interface will come into view **Geographic Data**; complete the **required information**: continent, country and region. Then click “Connect”

Geographic Data

Select Continent

Please select continent

Select Country

Please select country

CIP Region

Please select the crop

5. To continue, complete the form **New Locality**: type the Admin1 (Región), Admin2 (Province), Admin3 (Distrit), locality, locality full name and the abbreviation

New Locality

Admin1 (Region)

Admin2 (Province)

Admin3 (District)

Locality

Locality Full Name

Locality Short Name (Abbreviation)



6. Lastly, complete the form **Geographic Coordinates**: Select the type of coordinates system (decimal or sexagesimal) and then fulfil the information: latitude, longitude and elevation (masl)

Decimal system

Geographic Coordinates

Type of coordinates system

☒ Decimal ☐ Sexagesimal

Latitude

0

Longitude

0

Elevation (m.s.n.m)

2000

Sexagesimal system

Geographic Coordinates

Type of coordinates system

☐ Decimal ☒ Sexagesimal

Longitude

Grades (°)

10

Minutes (')

10

Seconds (")

10

Orientation

E

Latitude

Grades (°)

10

Minutes (')

10

Seconds (")

10

Orientation

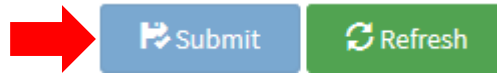
N

Elevation (m.s.n.m)

2000



7. Now, click **“Submit”** button to save the new locality in the database. And then click **“Refresh”**, to be able to select it from now on



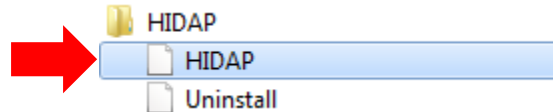
8. At last, this message will be displayed: **“Your new locality has been successfully added”**

Your new locality has been successfully added.



Check locations table

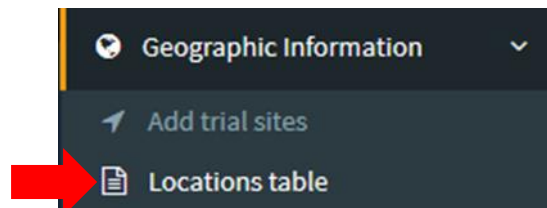
1. Locate and select **HIDAP's shortcut** in the start menu from the taskbar of Windows and wait a few seconds until it loads completely



2. Check that HIDAP's main interface (**About**) shows in the default browser



3. In the left sidebar locate and click “**Geographic Information**”, then select “**Locations table**”





4. The following interface will come into view **List of trial sites**; there the entire list of trial sites is displayed

List of trial sites

	id	shortn	altern	fulln	local	latd	lond
1	1.00	CHIARA		Chiara	Chiara	-13.2734	-74.206
2	2.00	CIPSRM-1		Experimental station San Ramon (CIP)	San Ramon	-11.1275	-75.356389
3	3.00	CIPSRM-2		San Ramon	San Ramon	-11.16116	-75.34171
4	4.00	COMAS		Comas	Comas	-11.7178	-75.0814
5	5.00	ETMB-2		Experimental station INIEA	El Tambo	-12.012381	-75.221558
6	6.00	CIPHYO		Experimental station Santa Ana (CIP)	Santa Ana	-12.010394	-75.224111
7	7.00	MRSCLC		Mariscal Castilla	Mariscal Castilla	-12.14529	-75.18793
8	8.00	HUANCN		Huancani	Huancani	-11.8628	-75.4144
9	9.00	LAVICT		La Victoria	La Victoria	-12.0264	-75.2449
10	10.00	CIPHQ	CIPLM	Experimental station CIP headquarters	La Molina	-12.076289	-76.948417
11	11.00	OXAPMP		Oxapampa	Oxapampa	-10.57745	-75.4043
12	12.00	BARAKA		Baraka	Baraka	-0.2	35.0333
13	13.00	LIMURU		Limuru	Limuru	-1.1333	36.7333
14	14.00	KISIMA		Kisima	Kisima	0.1166	37.4
15	15.00	KIBRCH		Kibirichia	Kibirichia	0.1	37.5166
16	16.00	OLJORO		Oljoro Orok	Oljoro Orok	0.0666	36.3666
17	17.00	NAROK		Narok	Narok	-1.0833	35.8666
18	18.00	MODZI		Ntengo umodzi	Ntengo umodzi	-14.5473	34.185283
19	19.00	SUSSD		Sussundenga	Sussundenga	-19.32245	33.226067
20	20.00	NAMACH		Namaacha	Namaacha	-25.95855	32.026483
21	21.00	TSANG		Tsangano	Tsangano	-15.234333	34.49985
22	22.00	LULIM		Lulimile	Lulimile	-13.3325	35.25108333
23	23.00	GURUE		Gurue	Gurue	-15.4669	36.9777
24	24.00	MUTUL		Mutuali	Mutuali	-14.8275	37.0141

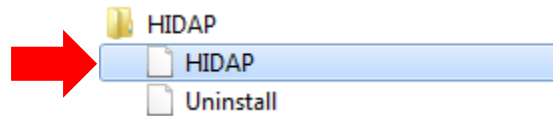


Chapter V: Fieldbook management

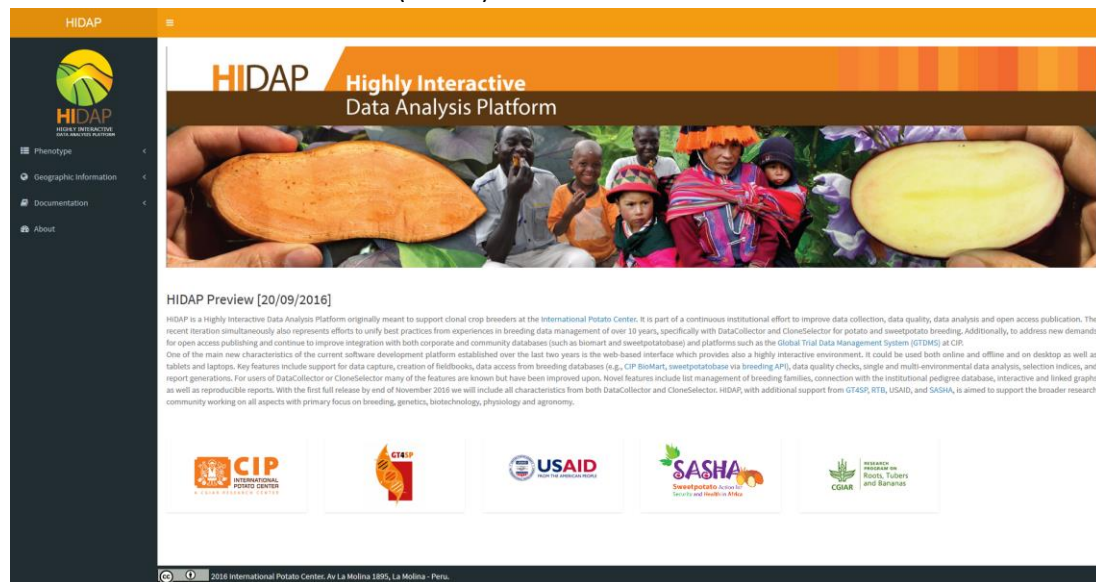
This document provides a step-by-step guide on how to create fieldbooks for breeding experiments and how to revise them

How to create fieldbooks

1. Locate and select **HIDAP's shortcut** in the start menu from the taskbar of Windows and wait a few seconds until it loads completely

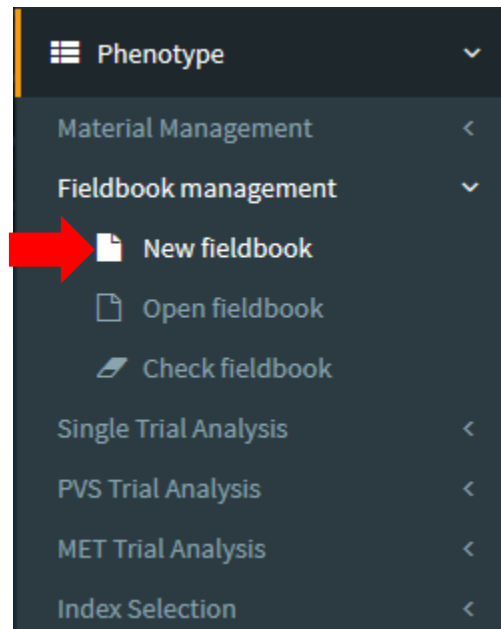


2. Check that HIDAP's main interface (**About**) shows in the default browser



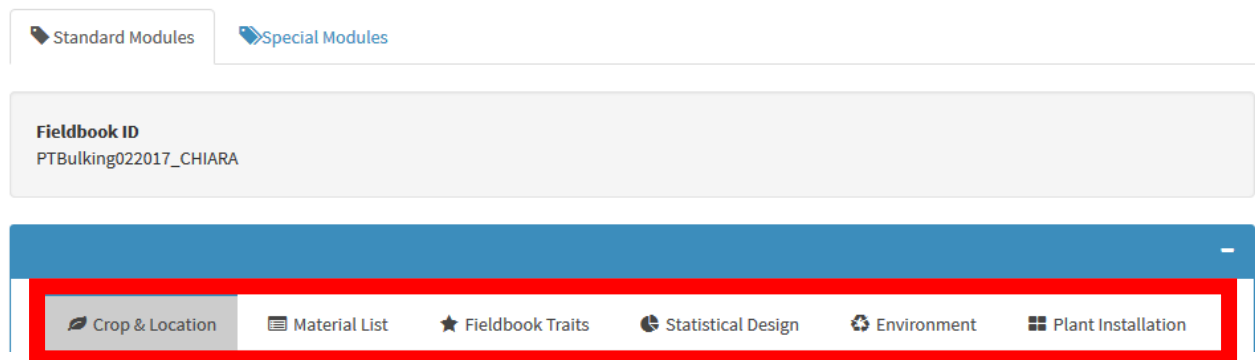


3. In the left sidebar locate and click “**Phenotype**”, then select “**Fieldbook management**” and next “**New fieldbook**”



4. Next, in the top content area the **Design of Field Experiments** will be displayed; here six tabs need to be completed in order to create your fieldbook: Crop & Location, Material List, Fieldbook Traits, Statistical Design, Environment and Plant Installation

Design of Field Experiments





5. First complete the information in **Crop & Location** tab: Select the crop (potato or sweetpotato), type of trial, dates of experiment (from and to), country, location and the experiment number

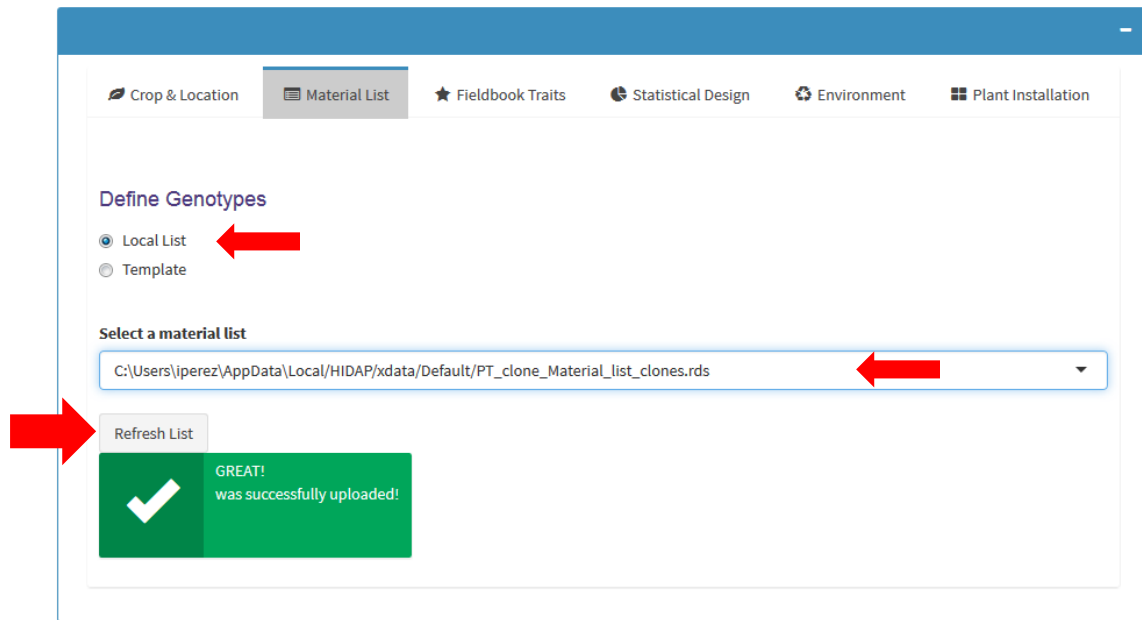
The screenshot shows the 'Crop & Location' tab in the HIDAP interface. The form includes the following fields:

- Crop:** A dropdown menu with 'potato (PT)' selected.
- Types of trial:** A dropdown menu with 'Bulking (PTBM)' selected.
- Date of experiment:** Two date input fields. The first field contains '15/02/2017' and the second field contains '09/03/2017', separated by a 'to' label.
- Field country:** A dropdown menu with 'Peru' selected.
- Field locations:** A dropdown menu with 'Chiara (CHIARA)' selected.
- Experiment number:** A dropdown menu with '-' selected.

6. Next, complete the information in the **Material List** tab, two options are available: **Local** list or **Template**

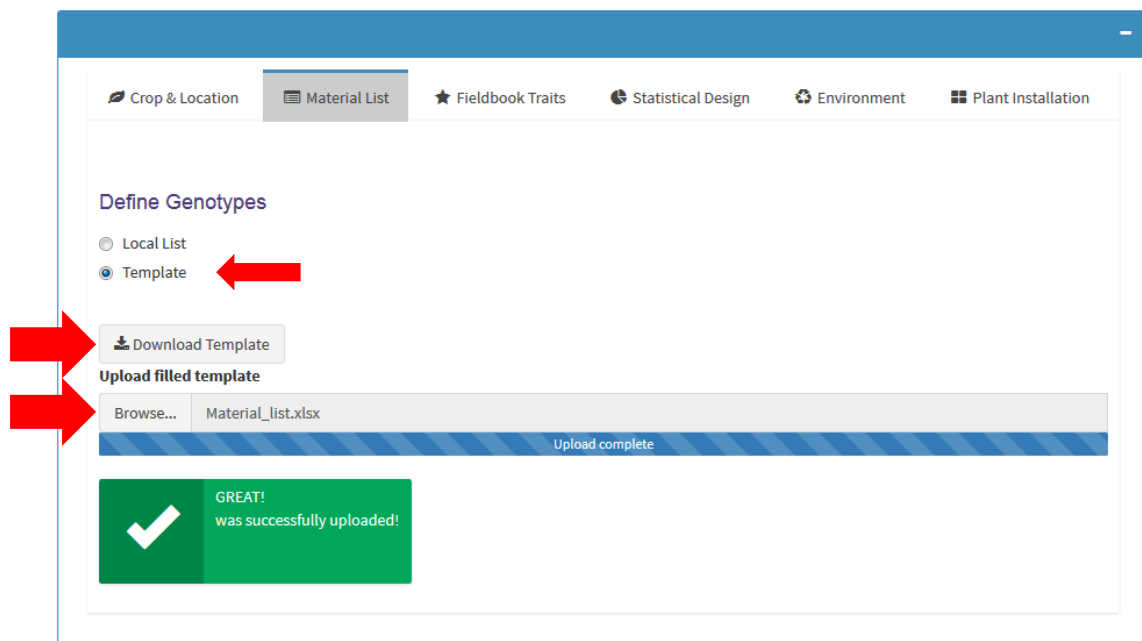
Local list

Under **Define Genotypes** choose “**Local List**”, then click “**Refresh List**” and select any material list previously created. After that, the message “Great! Was successfully uploaded!” will be displayed



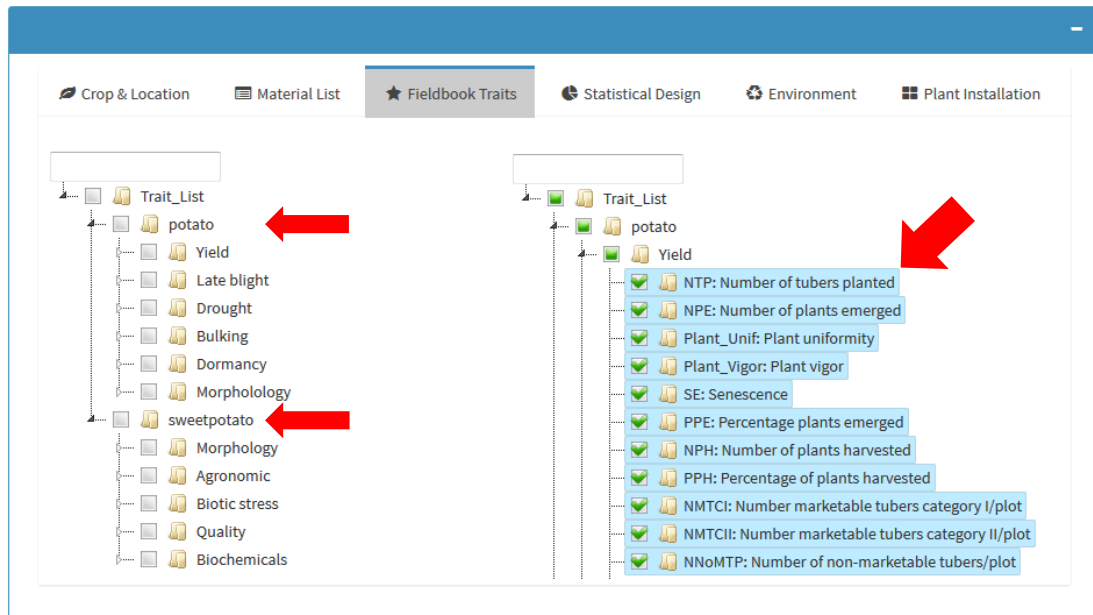
Template

Under **Define Genotypes** choose “**Template**”, then click “**Download Template**” this will cause for the template file to open automatically. Next, this template needs to be completed and saved in the PC. After that, click “**Browse**” to select the file and the message “GREAT! Was successfully uploaded” will be displayed

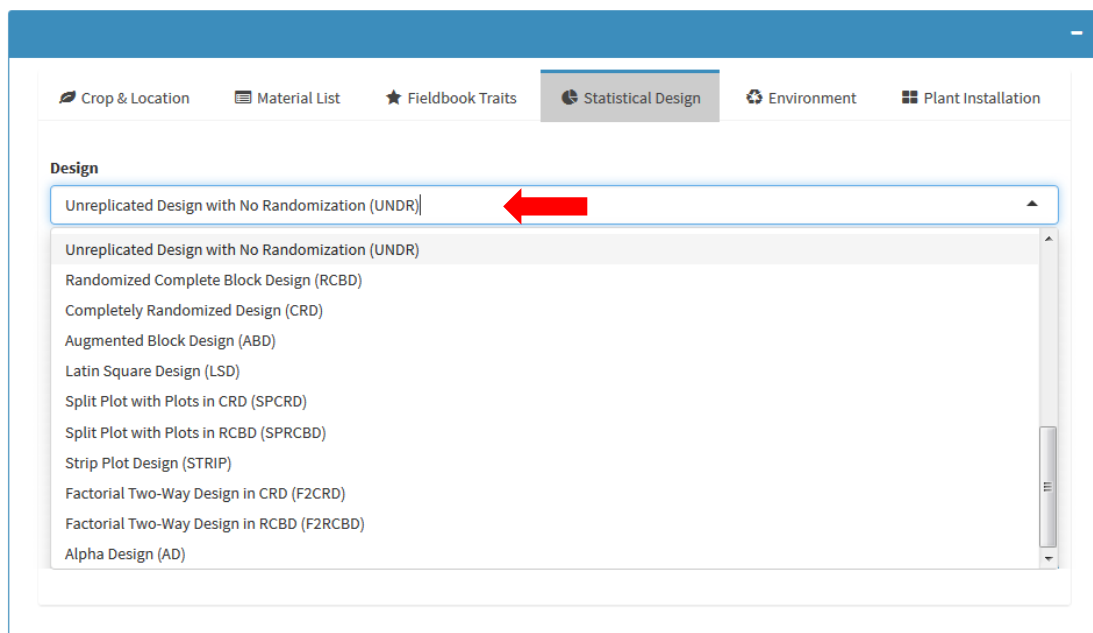




- Continue to the third tab **Fieldbook Traits**: select the crop (potato or sweetpotato) and the traits needed (for potato: yield, late blight, drought, bulking, dormancy and/or morphology; and for sweetpotato: morphology, agronomic, biotic stress, quality and/or biochemical).



- Now in the fourth tab **Statistical Design**, select one design to use in the experiment, these are the available options:





9. To continue complete the information in **Plant Installation**, select zigzag plantation if desired, choose the label series, the environment type and tick the checkbox if weather or soil data is going to be registered

Plant Installation

☒ Zigzag

Label series

☒ 1 ☐ 2 ☐ 3

Environment type

☒ Field ☐ Greenhouse ☐ Screenhouse

☒ Register weather data

☒ Register soil data

Label series

There are three options available to choose from:

Label series: 1

	PLOT	REP	INSTN
1	1	1	CIP397030.31
2	2	1	CIP397060.19
3	3	1	CIP397036.7
4	4	1	CIP397054.3
5	5	1	CIP397073.15
6	6	1	CIP397069.11
7	7	1	CIP397099.6
8	8	1	CIP397016.7
9	9	1	CIP397012.20
10	10	1	CIP397012.22
11	11	1	CIP397065.28
12	12	1	CIP397079.26
13	13	1	CIP397077.16
14	14	1	CIP397006.18
15	15	1	CIP397078.12
16	16	1	CIP380389.1

Label series: 2

	PLOT	REP	INSTN
1	101	1	CIP397060.19
2	102	1	CIP397098.12
3	103	1	CIP397073.7
4	104	1	CIP397012.22
5	105	1	CIP397069.11
6	106	1	CIP800048
7	107	1	CIP380389.1
8	108	1	CIP397065.2
9	109	1	CIP397100.9
10	110	1	CIP397065.28
11	111	1	CIP397030.31
12	112	1	CIP397029.21
13	113	1	CIP397055.2
14	114	1	CIP392797.22
15	115	1	CIP397073.15
16	116	1	CIP397006.18

Label series: 3

	PLOT	REP	INSTN
1	1001	1	CIP397054.3
2	1002	1	CIP397014.2
3	1003	1	CIP397079.26
4	1004	1	CIP397077.16
5	1005	1	CIP397078.12
6	1006	1	CIP800048
7	1007	1	CIP397006.18
8	1008	1	CIP397079.6
9	1009	1	CIP392797.22
10	1010	1	CIP380389.1
11	1011	1	CIP397016.7
12	1012	1	CIP397098.12
13	1013	1	CIP397035.26
14	1014	1	CIP397067.2
15	1015	1	CIP397099.6
16	1016	1	CIP397073.7



10. To finish complete the **Plant Installation**: fill the information according to your experiment conditions. Except the Plot size and Plant density, these two are calculated automatically.

Crop & Location Material List Fieldbook Traits Statistical Design Environment **Plant Installation**

Number of plants per plot/pot
10

Number of plants per row
10

Number of rows per plot/pot
1

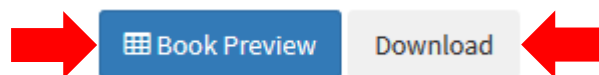
Distance between plants (m)
0.3

Distance between rows (m)
0.9

Plot size (m2)
2.7

Plant density (plants/Ha)
37037.037037037

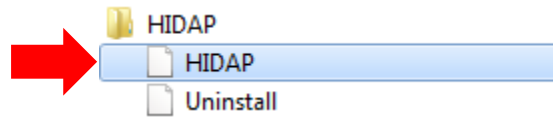
11. Once all tabs have been completed, “**Book Preview**” enables a preview of the fieldbook with all the variables selected. At last, click “**Download**” to download the fieldbook to the PC





Calculate variables in fieldbooks

1. Locate and select **HIDAP's shortcut** in the start menu from the taskbar of Windows and wait a few seconds until it loads completely

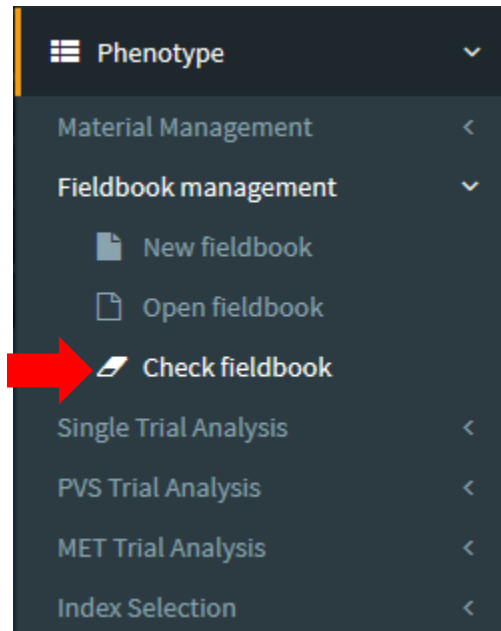


2. Check that HIDAP's main interface (**About**) shows in the default browser

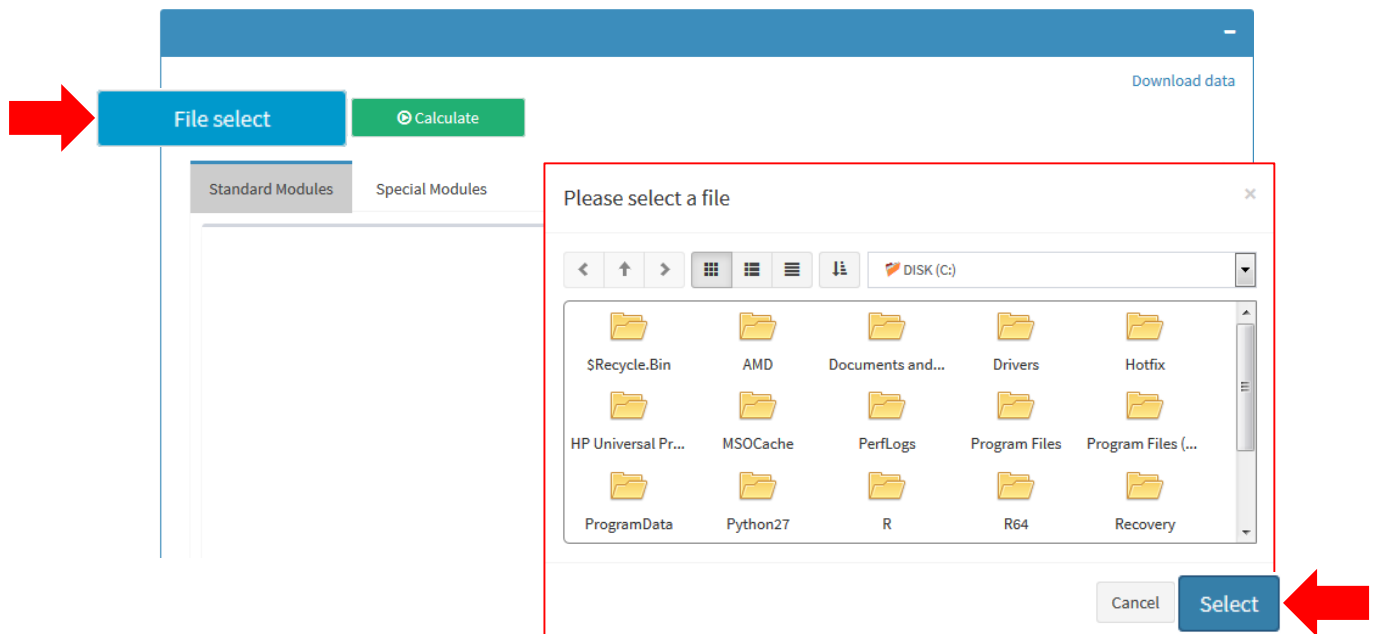




3. In the left sidebar locate and click **“Phenotype”**, then select **“Material Management”** and next **“Check fieldbook”**



4. The following interface will come into view; click **“File select”** to locate the fieldbook in the PC, once selected click **“Select”**





5. A preview of the selected fieldbook will come into view. Next, click **“Calculate”** so that the missing values are calculated by HIPAD.

Pink cells: mean that these values are outside allowed ranges. Whereas

yellow cells: mean that these particular values are outliers

The screenshot shows the HIDAP interface with a blue header bar. Below the header, there are two buttons: 'File select' (blue) and 'Calculate' (green). A red arrow points to the 'Calculate' button. Below the buttons, there are two tabs: 'Standard Modules' (selected) and 'Special Modules'. Below the tabs, there is a table with 11 columns: PLOT, REP, INSTN, NTP, Plant_Vigor, SE, NPH, PPH, NMTP, and MTWP. The table contains 8 rows of data. The 'SE' column has a pink cell with the value '2' in the first row. The 'PPH' column has a yellow cell with the value '300' in the fourth row.

	PLOT	REP	INSTN	NTP	Plant_Vigor	SE	NPH	PPH	NMTP	MTWP
1	1	1	CIP397006.18	10	7	2	10	100	36	4.7
2	2	1	CIP397012.22	10	9	7	10	100	76	14.6
3	3	1	CIP397030.31	10	9	5	10	100	110	8.4
4	4	1	CIP397065.28	10	9	5	10	100	300	17.45
5	5	1	CIP397079.26	10	9	5	10	100	66	13.45
6	6	1	CIP397100.9	10	5	7	10	100	56	7.45
7	7	1	CIP397060.19	10	9	5	10	100	50	7.7
8	8	1	CIP397069.11	10	7	7	10	100	86	14.7

6. Lastly, click on **“Download data”** and your book will be downloaded and opened automatically

The screenshot shows the HIDAP interface with a blue header bar. Below the header, there are two buttons: 'File select' (blue) and 'Calculate' (green). A red arrow points to the 'Download data' button, which is located to the right of the 'Calculate' button. Below the buttons, there are two tabs: 'Standard Modules' (selected) and 'Special Modules'. Below the tabs, there is a table with 11 columns: PLOT, REP, INSTN, NTP, Plant_Vigor, SE, NPH, PPH, NMTP, and MTWP. The table contains 8 rows of data. The 'SE' column has a pink cell with the value '2' in the first row. The 'PPH' column has a yellow cell with the value '300' in the fourth row.

	PLOT	REP	INSTN	NTP	Plant_Vigor	SE	NPH	PPH	NMTP	MTWP
1	1	1	CIP397006.18	10	7	2	10	100	36	4.7
2	2	1	CIP397012.22	10	9	7	10	100	76	14.6
3	3	1	CIP397030.31	10	9	5	10	100	110	8.4
4	4	1	CIP397065.28	10	9	5	10	100	300	17.45
5	5	1	CIP397079.26	10	9	5	10	100	66	13.45
6	6	1	CIP397100.9	10	5	7	10	100	56	7.45
7	7	1	CIP397060.19	10	9	5	10	100	50	7.7
8	8	1	CIP397069.11	10	7	7	10	100	86	14.7

Now, the fieldbook has a new sheet named **Summary**. In it, every trait has been analyzed by clone

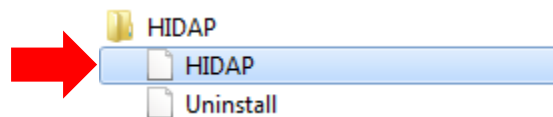


Chapter VI: Single trial analysis

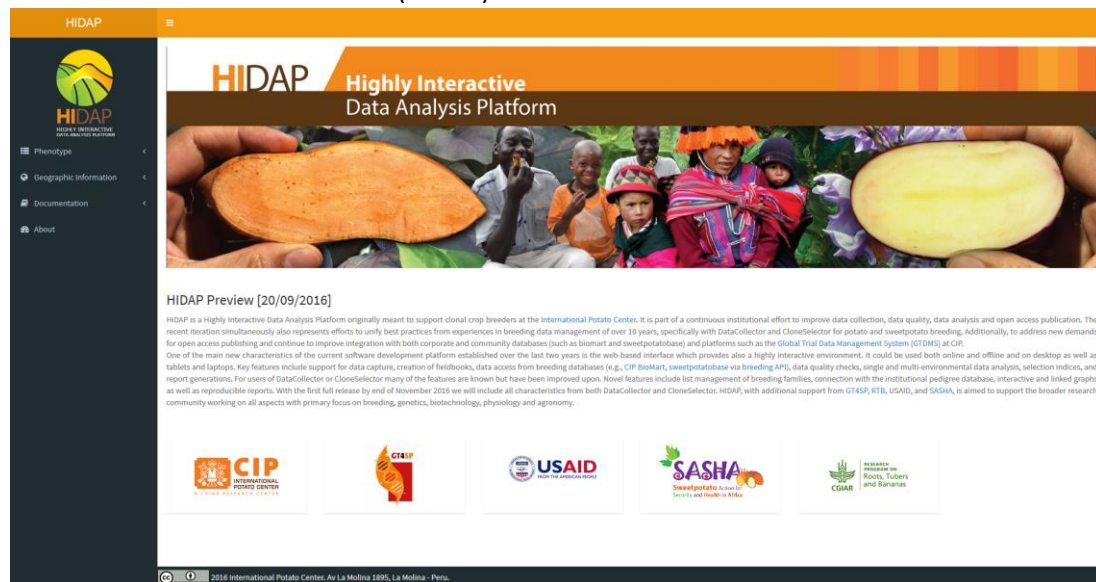
This document provides a step-by-step guide on how to create calculate traits from fieldbooks for breeding experiments

Single report

1. Locate and select **HIDAP's shortcut** in the start menu from the taskbar of Windows and wait a few seconds until it loads completely

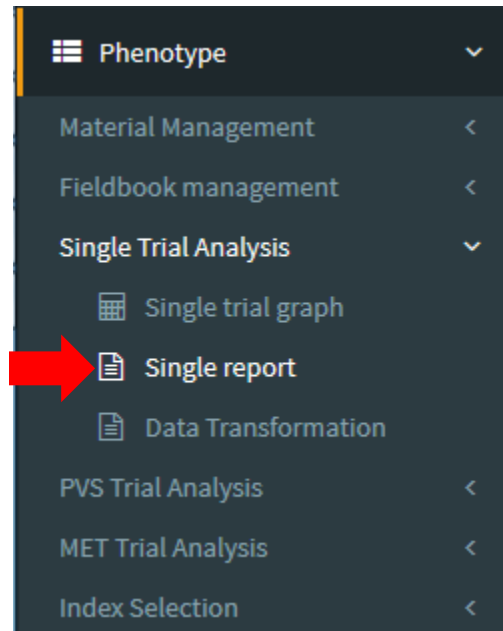


2. Check that HIDAP's main interface (**About**) shows in the default browser

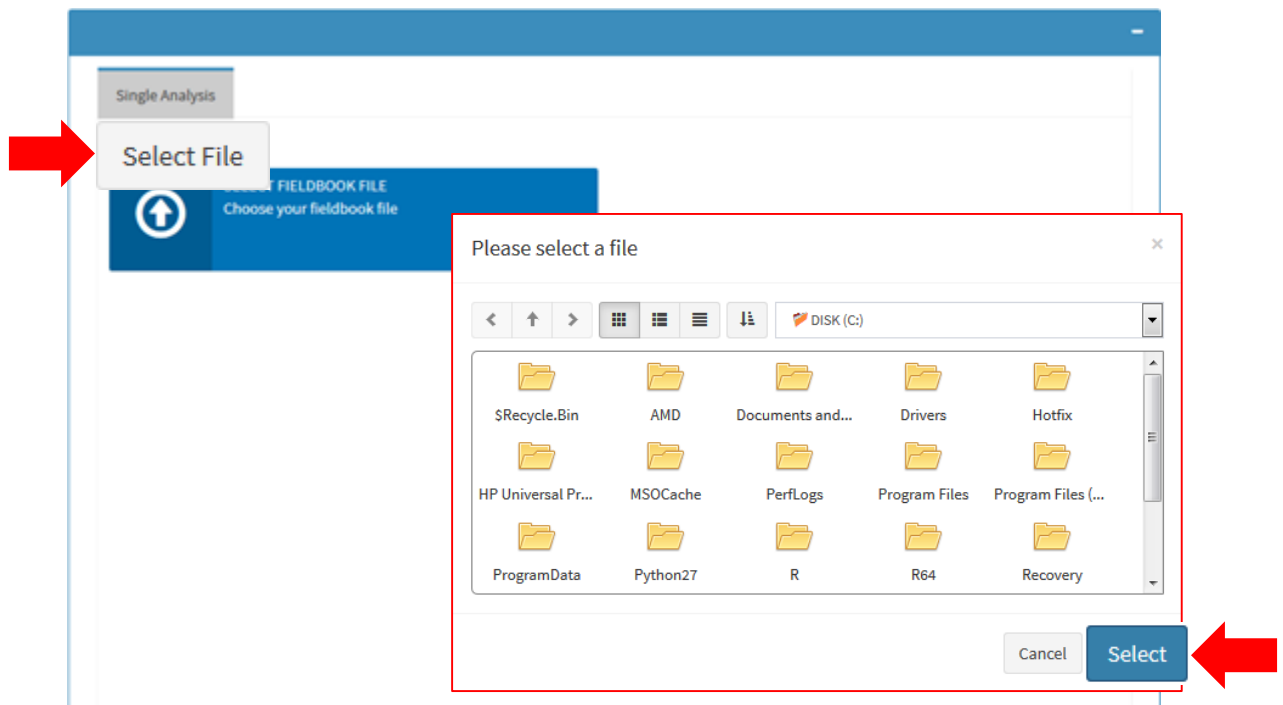




3. In the left sidebar locate and click “**Phenotype**”, then select “**Single Trial Analysis**” and next “**Single report**”

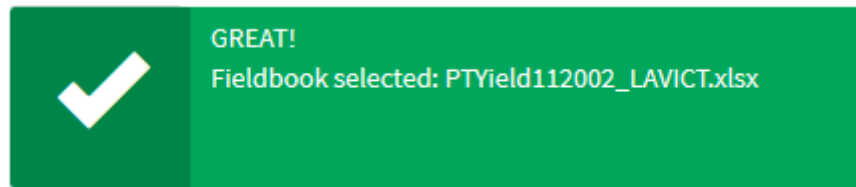


4. The following interface will come into view; click “**Select file**” to locate a fieldbook, once selected click “**Select**”





5. Next, this message will be displayed: **“GREAT” Fieldbook selected: PTYield112002_LAVICT.xlsx**



6. To continue, complete the requested information using the drop-down menus: select statistical design of your experiment, genotypes (INSTN), traits (those to be analyzed), repetitions (REP) and select the report format (html or word) and after that click **“Analyze”**

A screenshot of the "Single Analysis" form in the HIDAP application. The form has a blue header bar. Below the header, there is a "Select File" button. A green success message box is displayed below the button. The form contains several sections with drop-down menus and radio buttons, each with a red arrow pointing to it: "Select statistical design of your experiment" (showing "Randomized Complete Block Design (RCBD)"), "Select Genotypes" (showing "Choose"), "Select Trait(s)" (showing "Choose"), "Select Repetitions" (showing "Choose"), and "Report format" (with "html" selected). At the bottom, there is an "Analyze" button with a play icon, which is also pointed to by a red arrow.

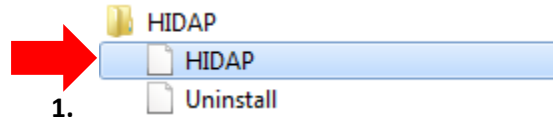


Chapter VII: MET (multi-environment trial) analysis

This document provides a step-by-step guide on how to do multi-environment trials for breeding experiments

MET Trial analysis report

1. Locate and select **HIDAP's shortcut** in the start menu from the taskbar of Windows and wait a few seconds until it loads completely

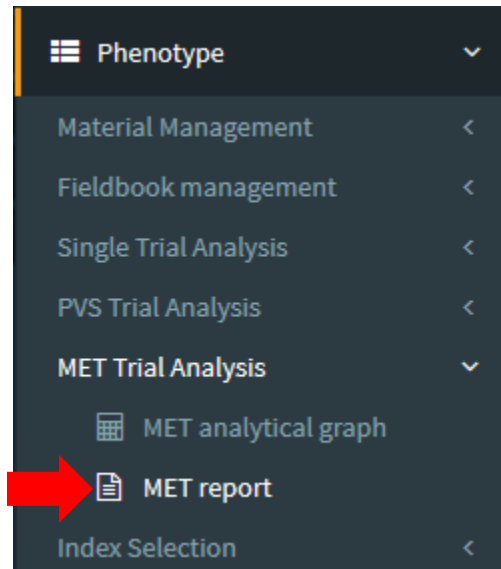


2. Check that HIDAP's main interface (**About**) shows in the default browser

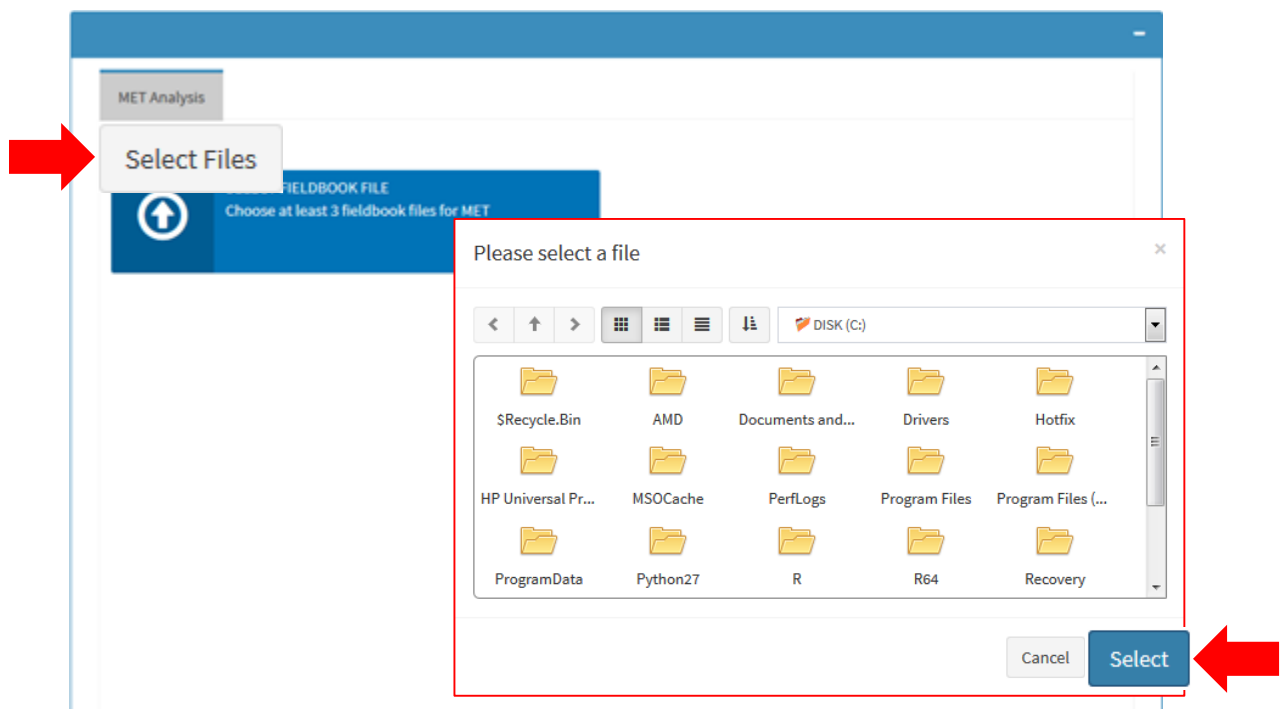




3. In the left sidebar locate and click “**Phenotype**”, then select “**MET Trial Analysis**” and next “**MET report**”

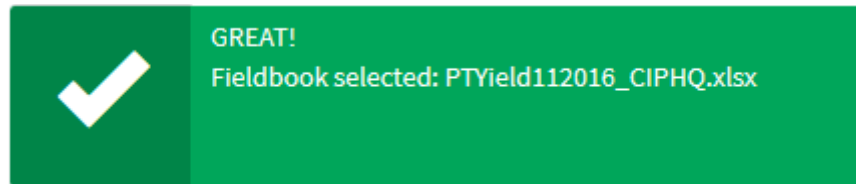


4. The following interface will come into view; click “Select Files” to locate at least three fieldbooks, and once selected click “**Select**”





5. Next, the message “**GREAT! Fieldbook select: PTYield112016_CIPHQ.xlsx**” will be displayed



6. Now, complete the form **MET Analysis** with the required information: genotypes

To finish, complete the requested information using the drop-down menus: select genotypes (INSTN), environments (**leave it blank**), repetitions (REP) and choose the traits (those to be analyzed) and after that click “**Analyze**”