QuercusMap Guide

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Validate by	Antoine Kremer, Frederic Raspail

Structured walkthroughs			
Date	**Version**	**By**	**Remarks**
13/12/2007	V 1.0	Mélina Millox	
17/01/2008	V2.0	Mélina Millox	First part of A.K modification. (orthography and vocabulary)
22/01/2008	V2.2	Mélina Millox	Second part of A.K. modification (harmonisation of terms)

Version 2.2

Summary

Introduction

QuercusMap allows to manage molecular and phenotypic data used for the construction of genetic maps or for detecting QTLs. The software was developed for oaks, where offsprings of the mapping pedigree are vegetatively propagated.
All along this tutorial, many capture screens allow to visualize software's options.

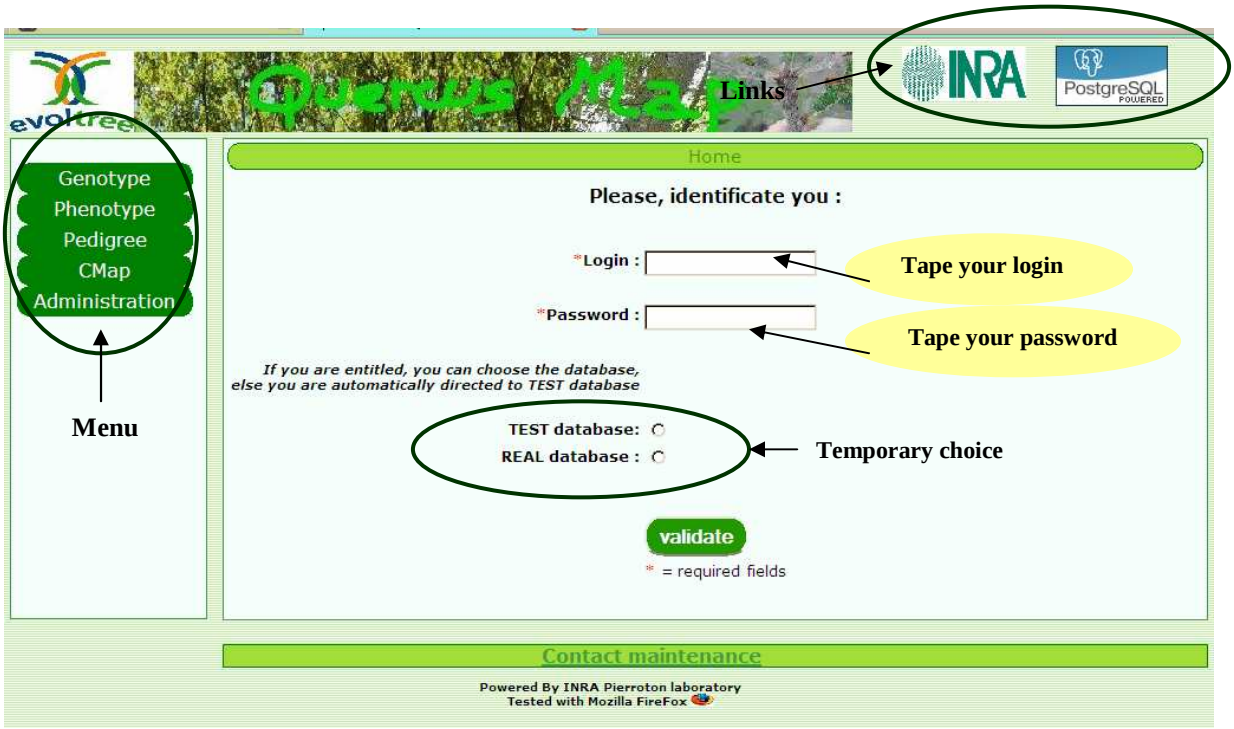
1- Software Organisation & Technical information

* Technical information:

This software was tested with mozilla firefox.
The databases (Test and Real) are managed by PostgreSQL.

* First stage:

The first step is to log in.



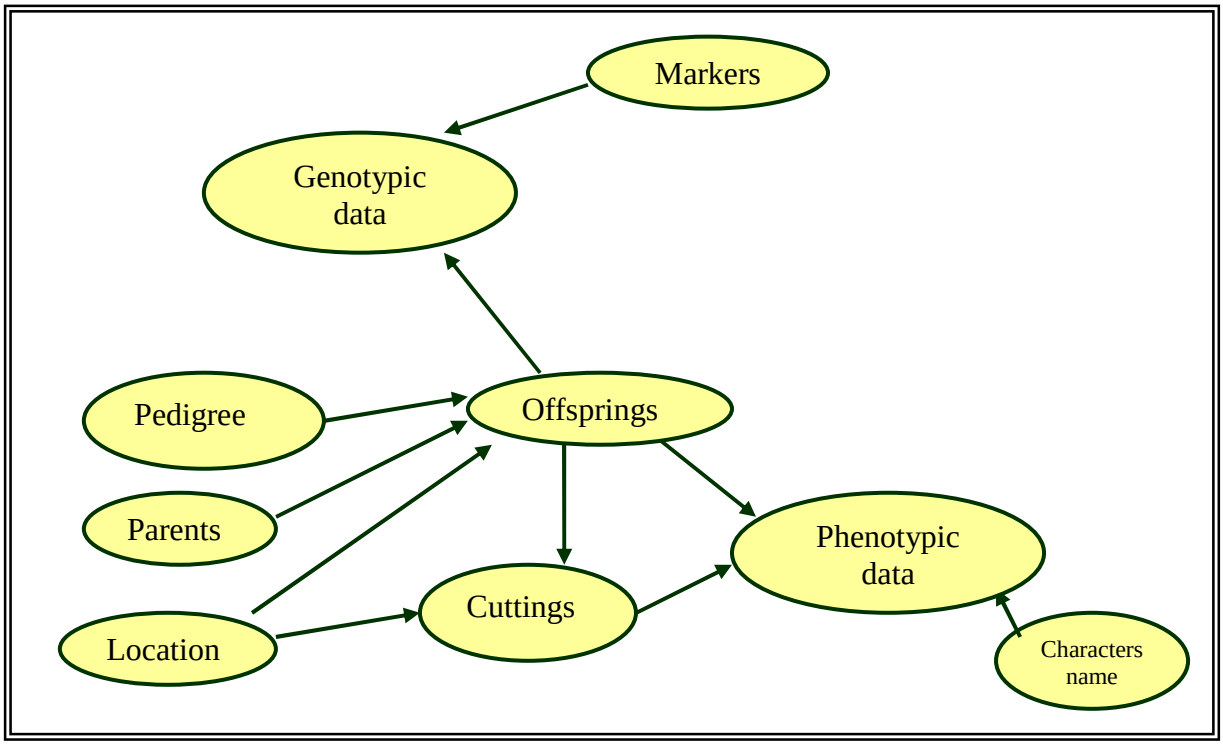
The login is composed with the first letter of your first name + your surname with the first letter capitalized (ex: AKremer). Uppercases are considered for the login and password.
Of course we must make sure your administrator create your account.
Temporary, you have to choose the database where you are working.
By default, you are connected on test database.

*** More information**

All the fields to which a red asterisk "*" is attached, indicate that the fields have to be filled.

2- Routing

This scheme depicts the interrelationship between the different data sets contained in the database.



In case you want to insert a new offsring:

The location, pedigree, parents have to already exist in the database.

Go to "Pedigree"."Offsprings"."Add Offsprings".

In case you want to insert a cutting:

The location and the ortet have to already exist in the database.

Go to "Pedigree"."Cuttings"."Add Clones".

In case you want to insert phenotypic data:

The ortet or cutting, character name have to be already in the database.

You go to "Phenotype"."Add or View Phenotypics Data"."Phenotypic Data Acquisition".

In case you want to insert genotypic data:

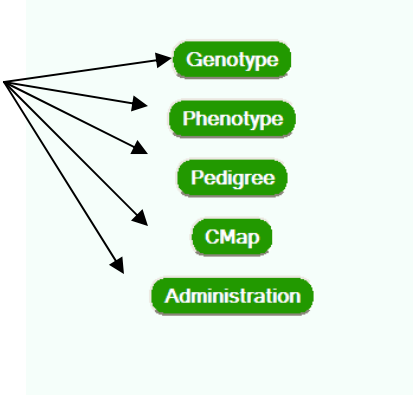
The ortets and the marker have to already exist in the database.

You go to "Genotype"."Genotype Data"."Add Measure".

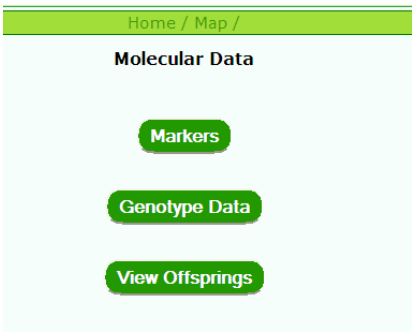
To insert location, pedigree, markers type, first parent, category of phenology, users you have for the moment to contact the administrator.

3- Principals parts

The data base is composed of 5 main parts:

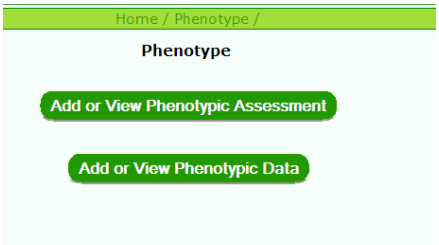


a) Molecular data, "Genotype":



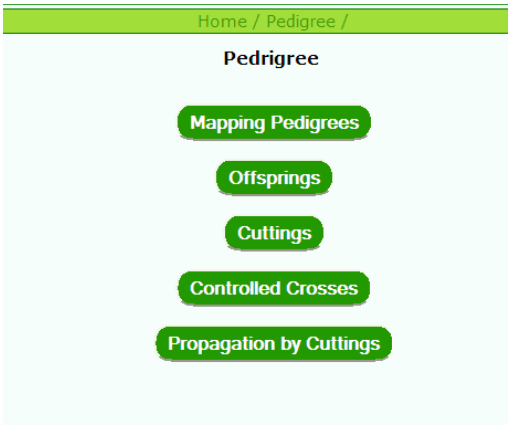
This part allows to add, to modify or to consult information about molecular data.
It contains 3 sections: "Markers": information about marker types, "Genotype Data": the genotypic arrays by markers and by pedigrees, "View Offsprings" abstract of existing pedigrees.

b) Phenotypics data, "Phenotype" :



This part allows to add, to modify or to consult information about phenotypic data of the offsprings.
It contains 2 sections: "Add or View Phenotypic Assessment": information about the phenotypic character, "Add or View Phenotypic Data" measures of each phenotypic character by pedigree, by category of phenotypic characters, by characters…

c) Pedigrees, "Pedigree":



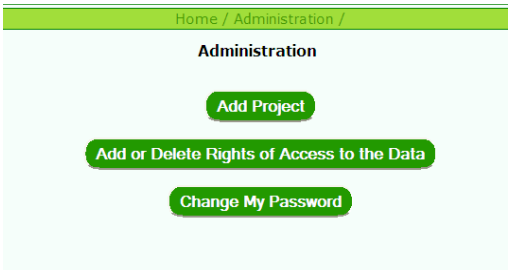
This part allows to add, modify or consult all the information about the pedigree.
- "Mapping Pedigrees": overall information about all the pedigrees integrated in the database: number of offsprings, number of cuttings …
- "Offsprings": add, modify or check data about a given ortet (offspring of a given pedigree)
- "Cuttings": add, modify or check data about cuttings of a given ortet.
- "Controlled Crosses": yields of controlled crosses made each year.

- "Propagation by cuttings": yields of vegetative propagation of the offsprings by year and by offspring.

d) CMap, "CMap" :

CMap is a GMod tool who allows to view graphically the genetic maps.

e) Administration, "Administration":



- "Add Project": allows to add a new project
- "Add or Delete rights of Access to the Data": allows to manage the rights according to your data.
- "Change My Password": if you want to change your password…

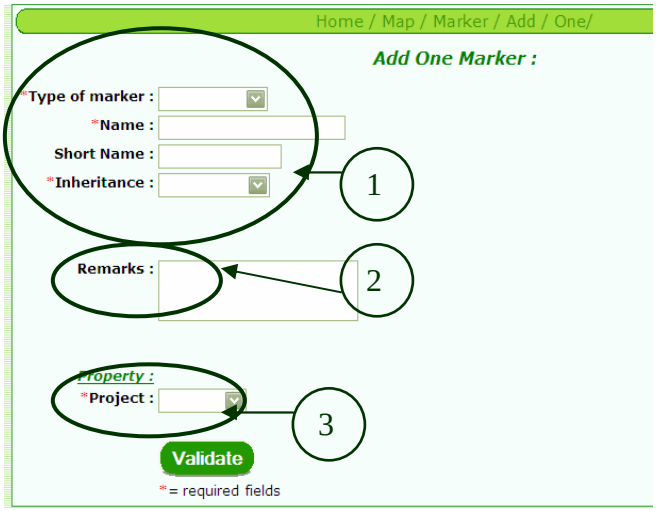
4- Molecular Data

It is composed of 3 parts.

4.1. Markers

a) Add markers

** Add one marker:*



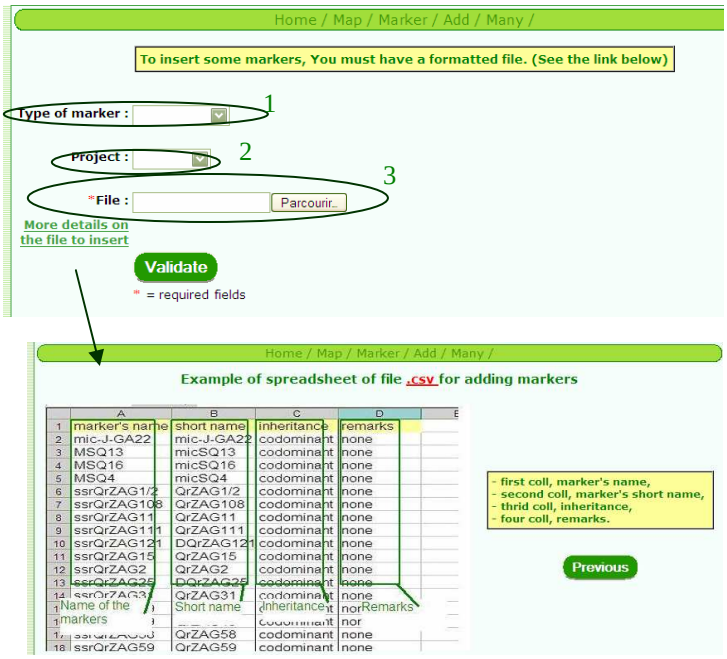
① Required fields: you have to select the type of marker, to tape the name, eventually the short name and to select the type of inheritance ('codominant', 'dominant') of your new marker.

② You can insert some remarks about your new marker.
③ You have to select the project associated to this marker (Evoltree or older project).

You cannot use the same name of markers for the different category of marker. In addition a marker has to be assigned to a project in order to manage the data rights. You can tape whatever you want in the "Remarks fields" as additional info to the marker. You can eventually indicate a

short name for the marker but it is not necessary because all markers have not a short name associated, for example of short name (ssrQpZAG112, his short name is Qp112…).
If the name of the marker already exists in the database an error message will appear!!

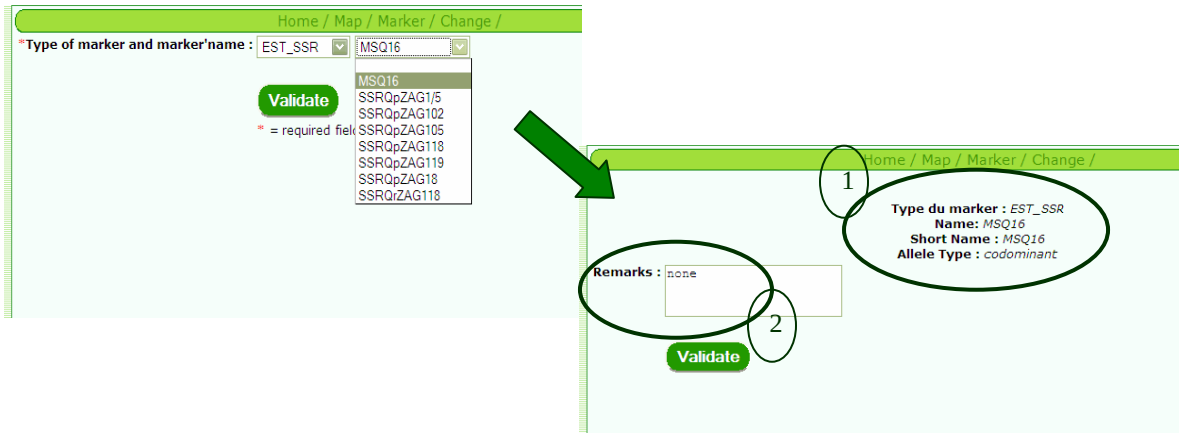
** Add many markers:*



1 =you have to select the type of marker concerned by this insertion.
2 = you have to select the project associated to this data
3 = you have to select the file who contains the data to insert in the database.

A format of the file has to be defined more precisely. First column, the marker's name, second column the short name of the marker, third column the type of inheritance, fourth column the remarks.

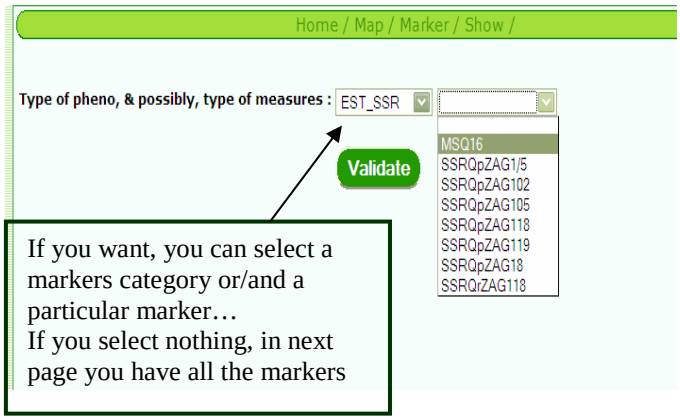
b) Change markers

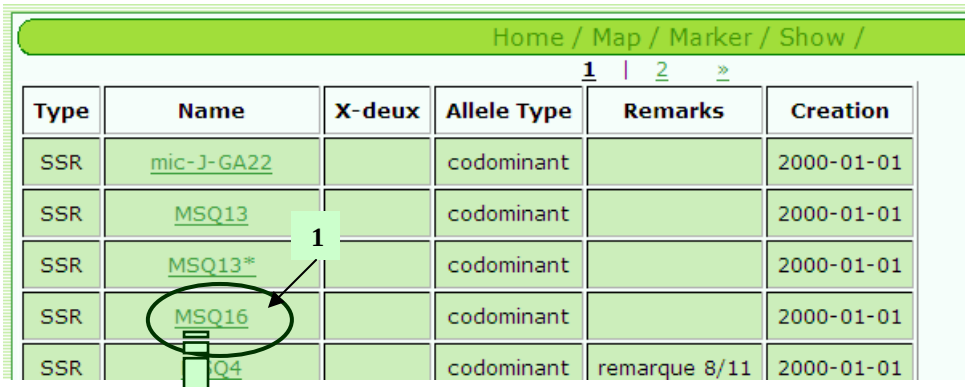


First you have to select the category of the marker to which the marker belongs. When you select the category of marker, the list of all available markers corresponding to this category will be displayed. Choose within this list the marker's name you want to modify.

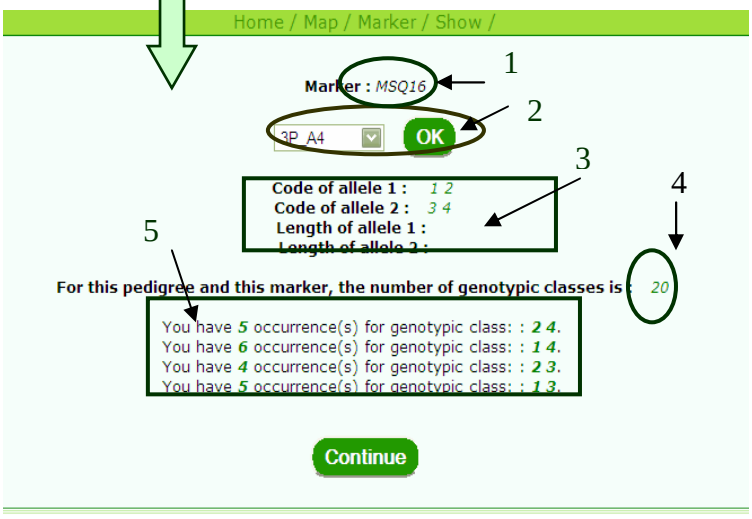
The marker information is then displayed on the screen (1). You can only make changes in the remarks field (2).

c) Show Markers





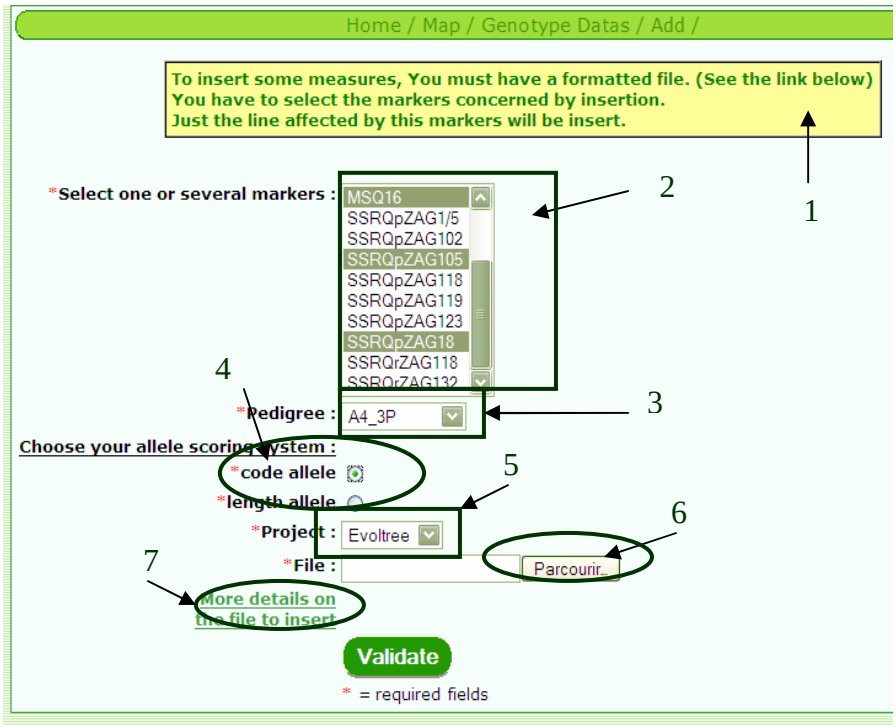
1 = this is a link to get more information about the genotypic arrays and coding in the database.



1 = marker's name
2 = you can choose the pedigree associate to have an abstract of all measures obtains.
3 = allele codes and the allele lengths of the parents of the chosen pedigree.
4 = number of genotypic classes existing in the database
5 = number of occurrences (trees) for each genotypic array existing in the data base

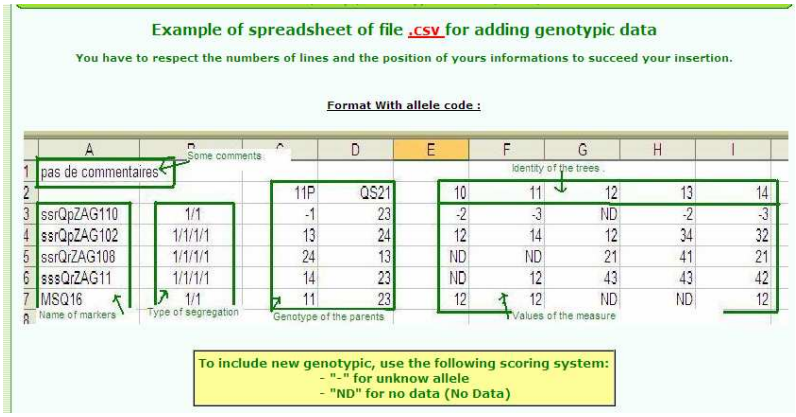
4.2. Genotypic Data

a) Add genotypic data:



1 = prerequisite info on this page.
2 = select the markers, For example here I want to add new genotypic data for markers: "MSQ16, SSRQpZAG18, SSRQrZAG132. Names of markers for which data are added need to be included in the list beforehand.
3= select the pedigree
4 = select the project or contract supporting the activity
5 = select the way alleles are scored, either by allele length or codes
6 = browse your directory to indicate the location of the files containing the data to be inserted.
7 = link to a commentary page that explains the format of the file

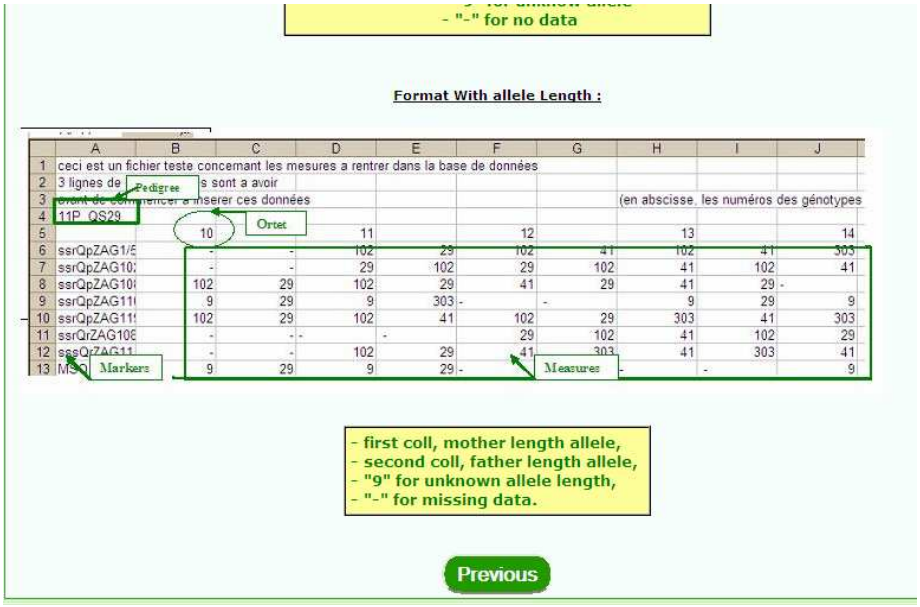
Here is an example of a file:



- 1 row of comments (only 1 row is allowed for comments)
- line number 3 corresponds to the offsprings belonging to the pedigree ;

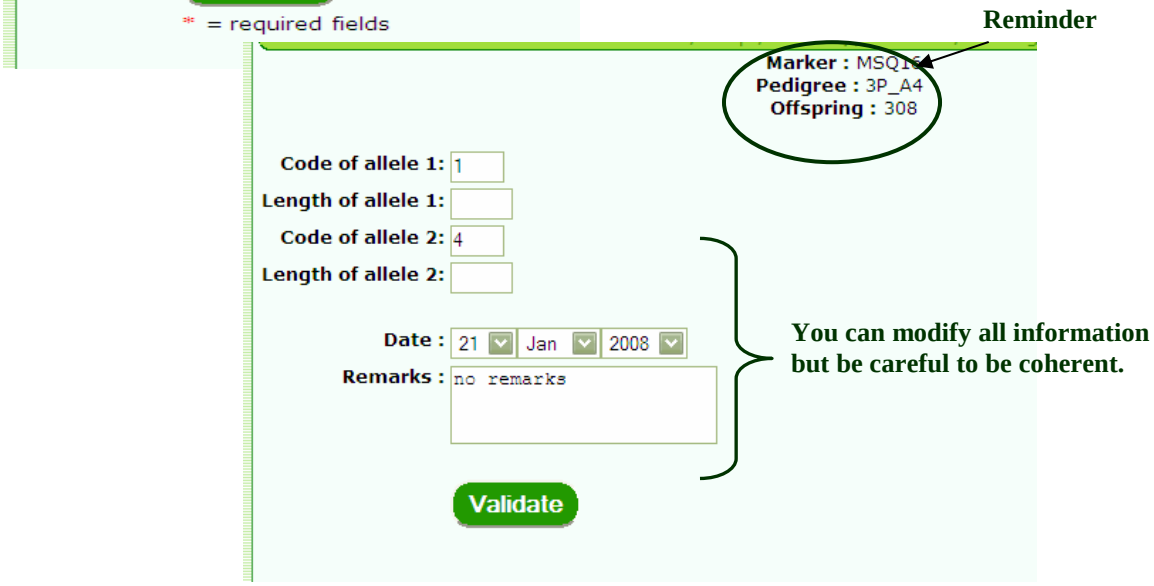
You have to care about the orthography of the markers and the pedigree (uppercase, space, punctuation …).

This is another example of a file where alleles are scored by using their size (in bp).

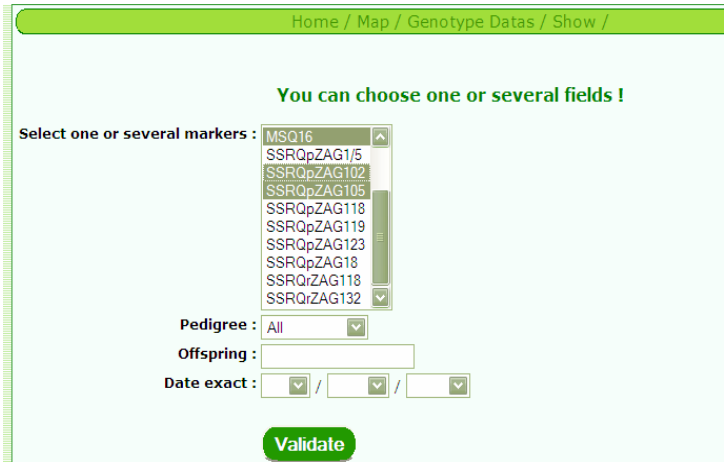


b) Change genotypic data

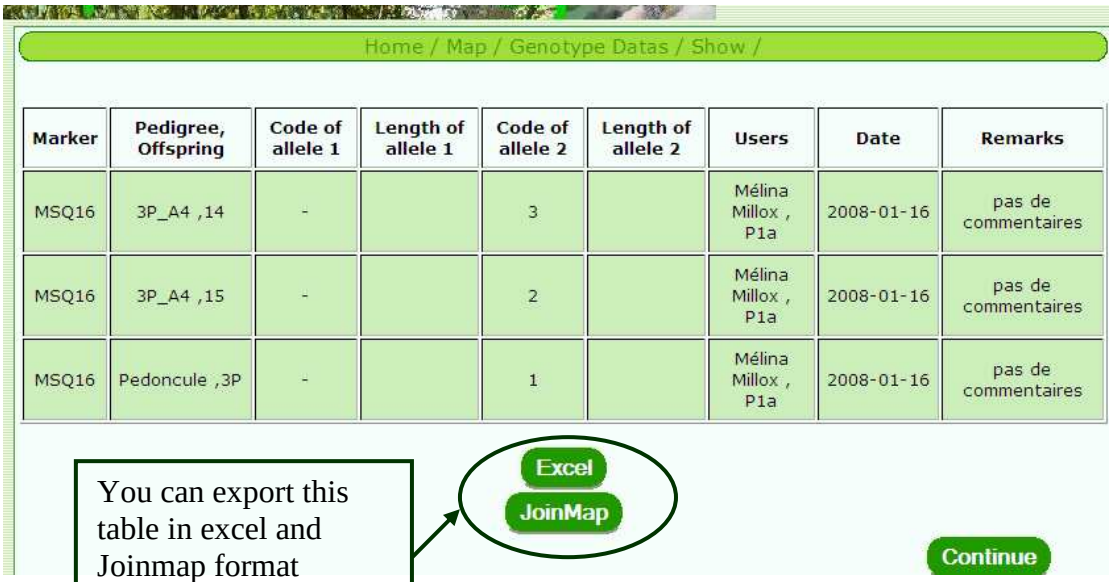
You can change genotypic data only one by one.
This means that you need to identify the offspring whose genotypic score need to be changed, the marker concerned and the name of the pedigree.



c) Show genotypic data

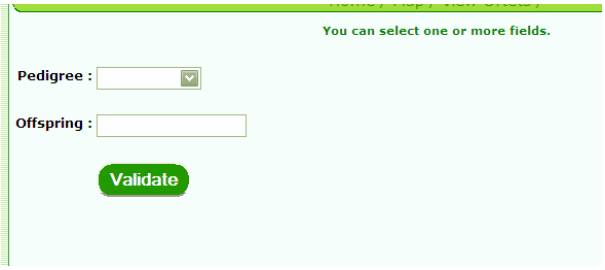


If you do not select any marker, all genotypic arrays will be shown on the table.
Further, you can select subsets of data by pedigrees, particular genotypic classes or dates of scoring.

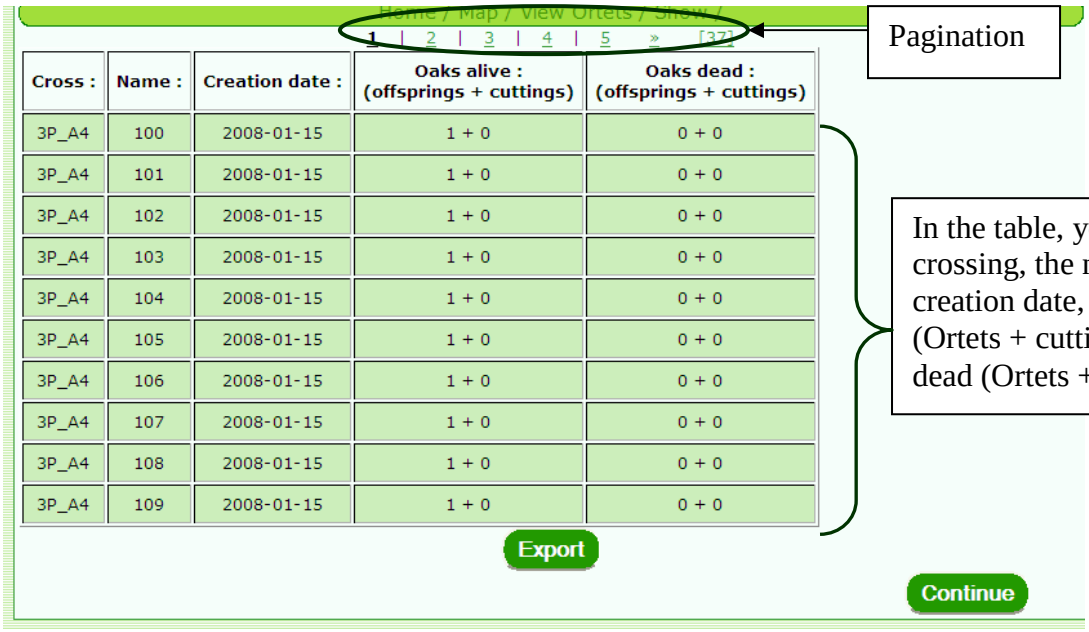


You can export this table in excel and Joinmap format

4.3 View Offsprings



This menu provides an overview of all the offsprings that belong to the pedigree (number of existing cuttings in case they were vegetatively propagated).

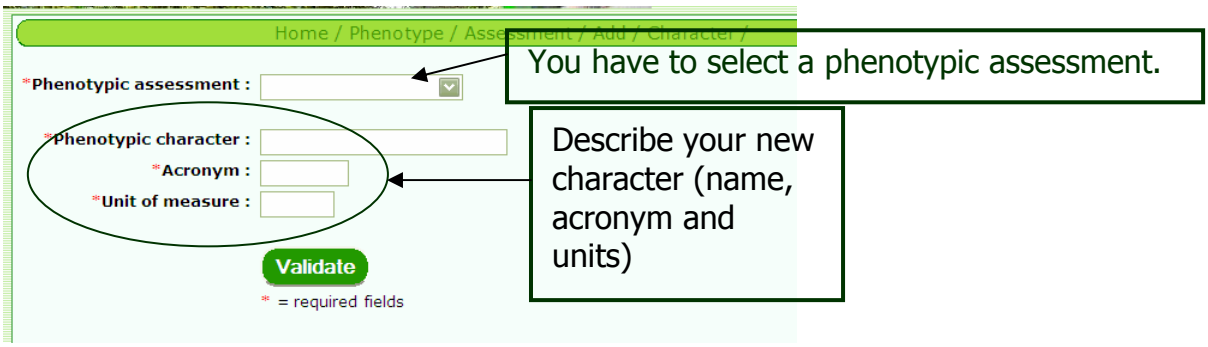


In the table, you can see the crossing, the name (Ortets), the creation date, the oaks alive (Ortets + cuttings), the oaks dead (Ortets + cuttings).

5- Phenotypic Data

5.1. "Add or View Phenotypic Assessments":

a) Add a new character:



b) View Existing Characters

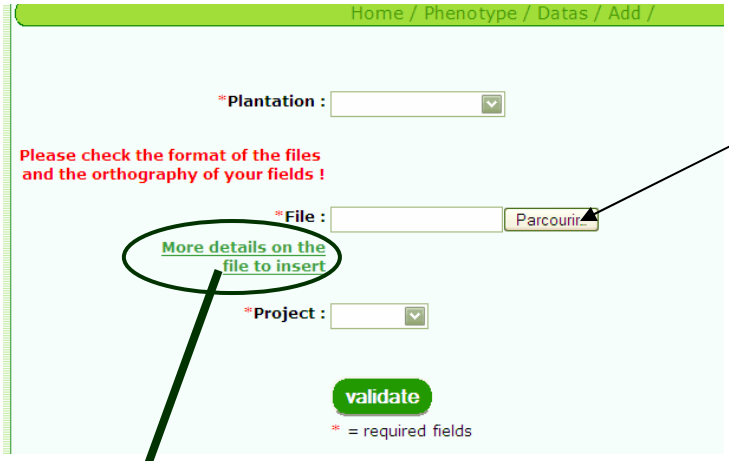
1 = here you can select the different among the different assessments. If you click on a given assessment, you can see all the characters that were measured
2 = = link to documents giving more details on the protocols used to measure the various characters (publications, thesis or other documents in pdf formats) . If you click on the link, a new window will open with the content of the document
3 = if you can you can export this table in an excel file.

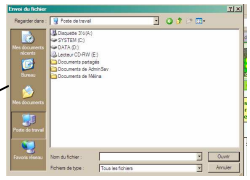
This table indicates the names of the various characters measured for a given assessment,

5.2. "Add or view Phenotypic Data"

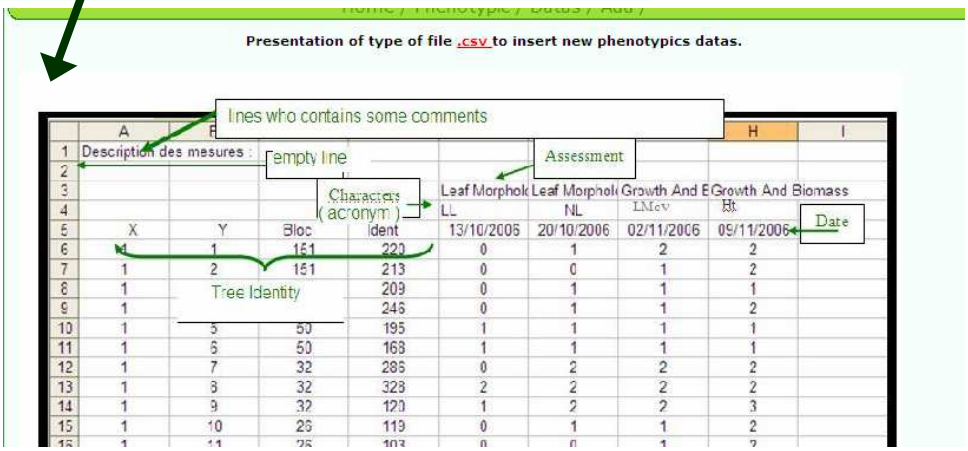
In this section you can introduce or view existing "raw" phenotypic data, eg the measurements made for each offspring (or a vegetative propagule of the offspring) in a giving plantation used for QTL detection.

a) Adding new phenotypic data :

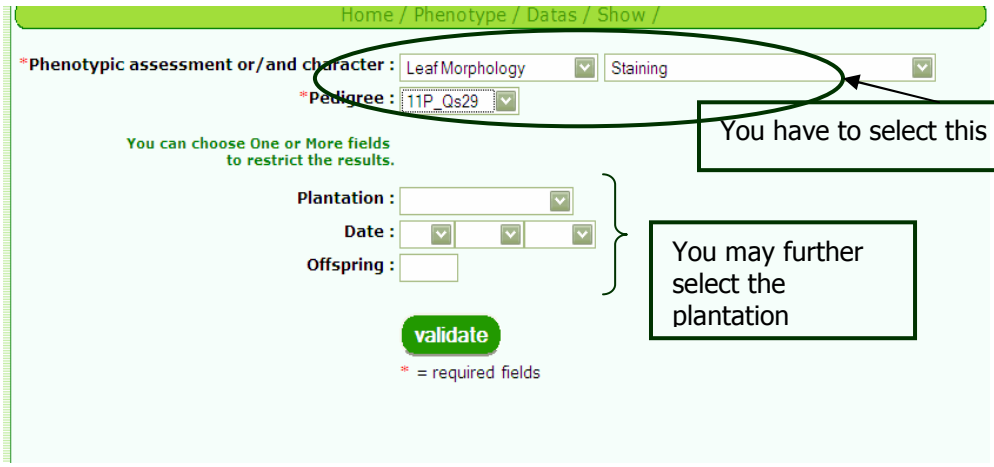




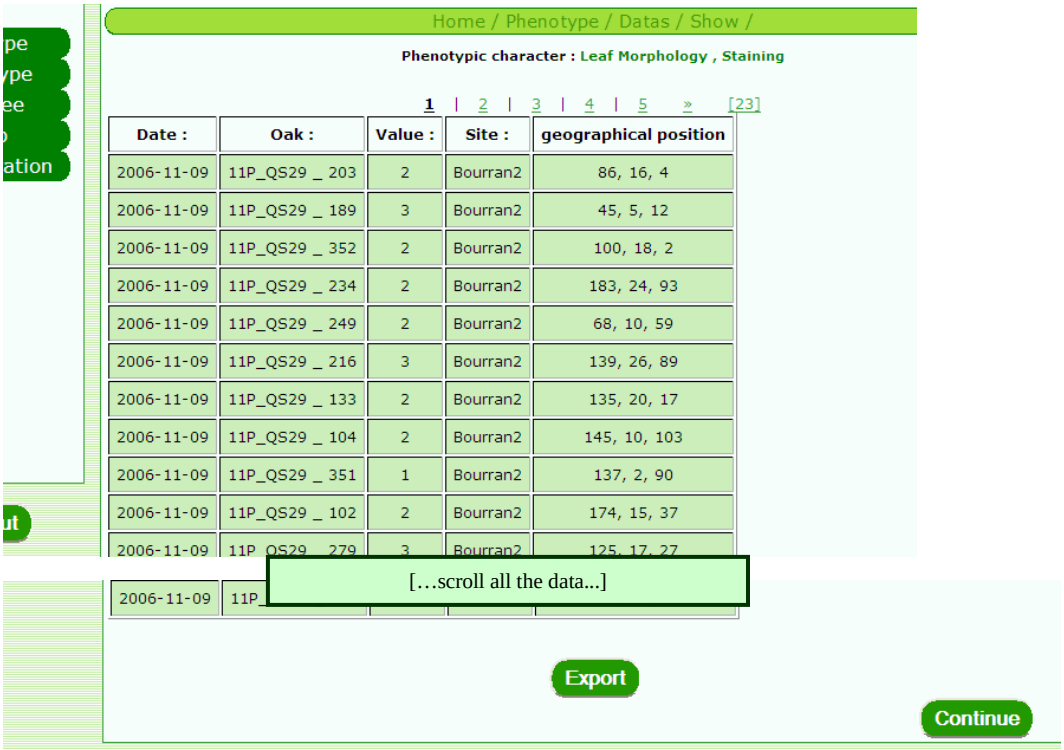
You have to select the site, the file and the project. The green link will provide you the format of the file.



b) Show existing phenotypic data:



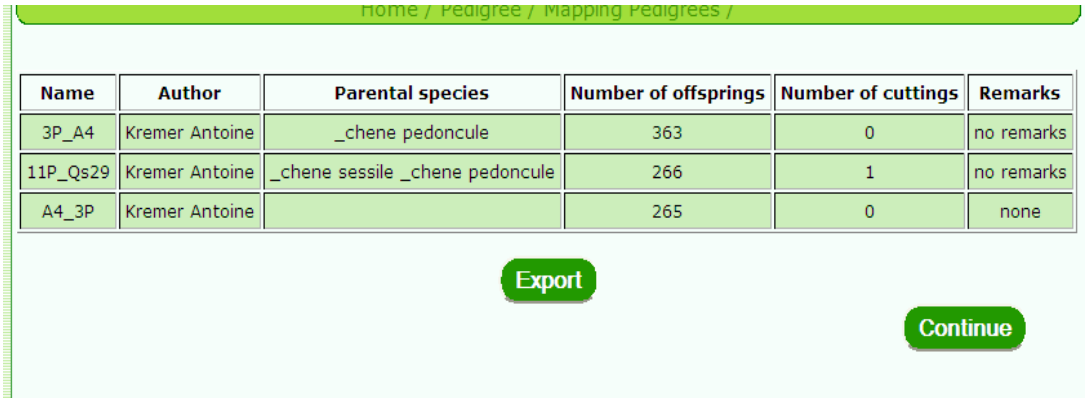
You have to select a phenotypic character and a pedigree.
You may use additional criteria to screen your data.



You can navigate within the file and export the table as a Excel file.

6- Pedigree

6.1. Mapping Pedigrees:



This is a summary table of all pedigrees in the database, and their corresponding number of offsprings and cuttings.

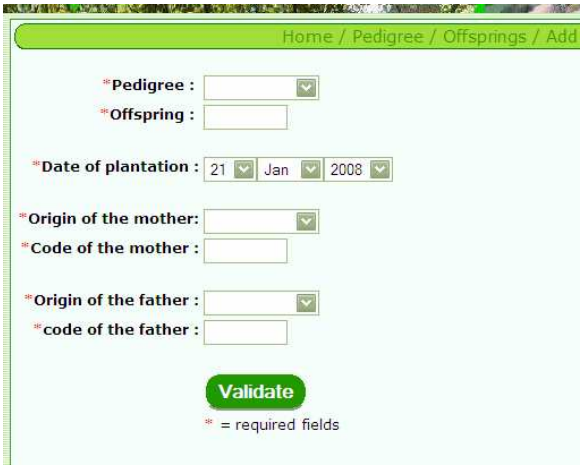
6.2. Offsprings:

In this section, you can add new offsprings, modify information about existing offsprings or view data about the offsprings

a) Add Offspring:

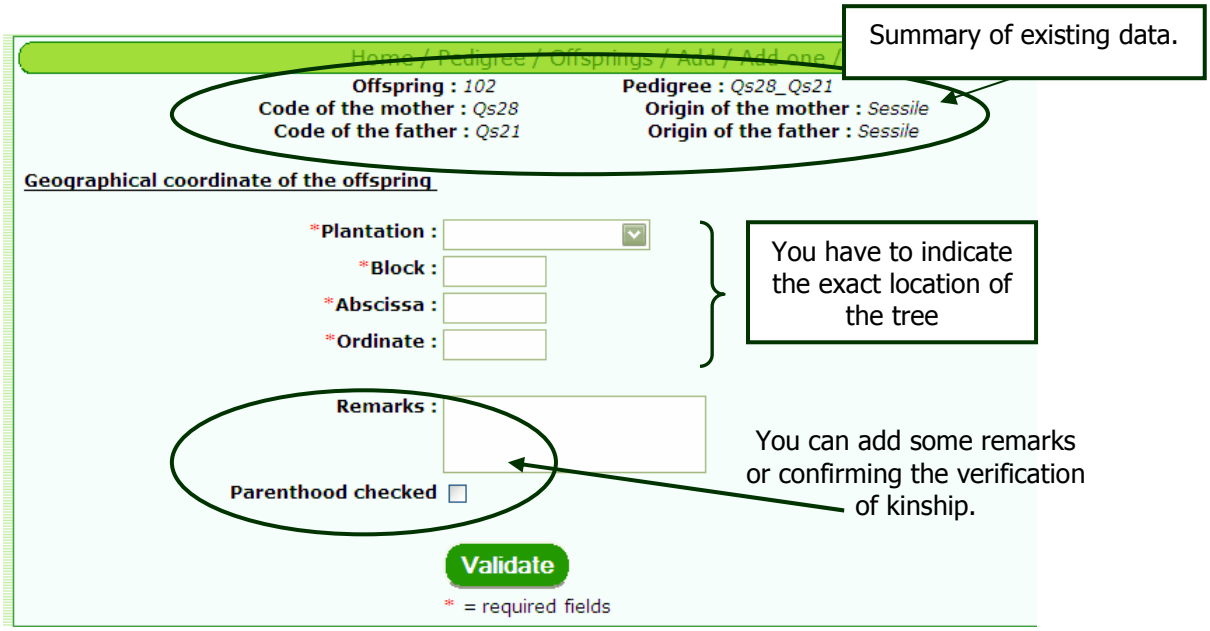
You can add offsprings one by one, or by inserting data from an excel file.

* "Add only one offspring":

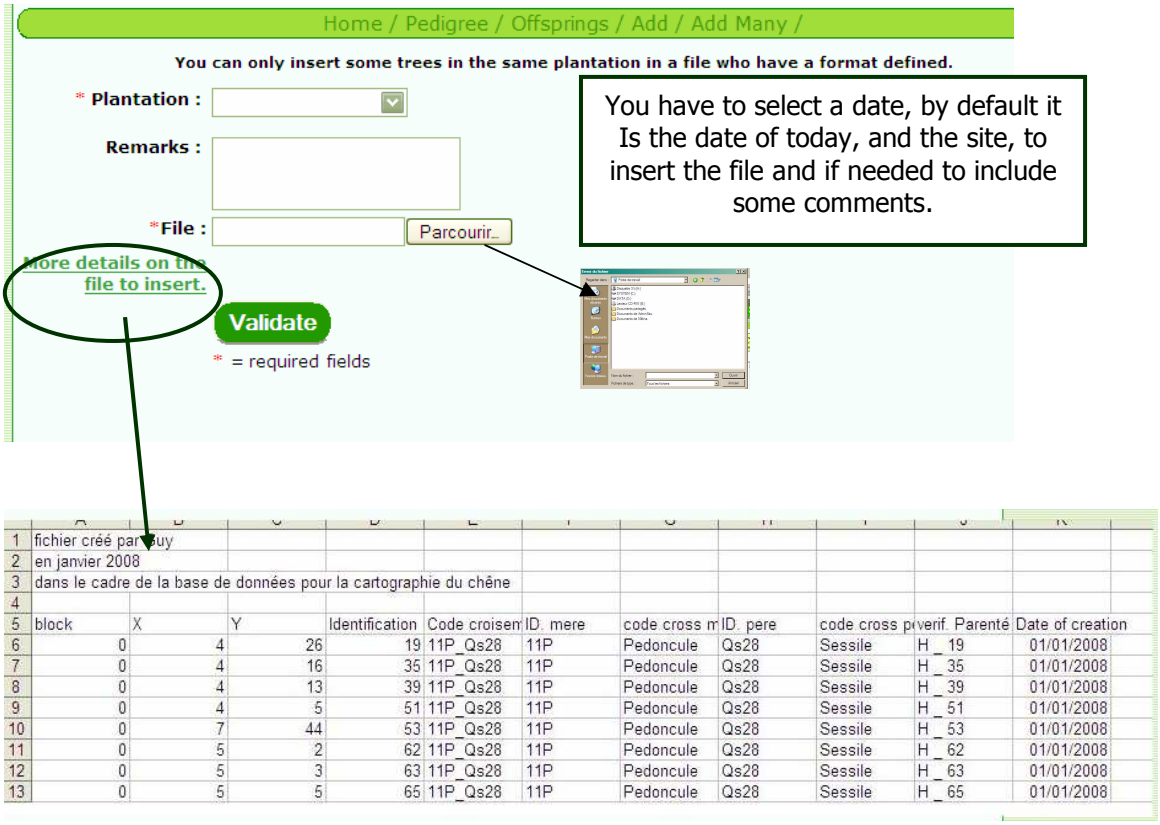


To add one offspring, you have to fill the following fields: code of the pedigree, code of the offspring, date of creation, code of the female and male parent, species of the female and male parent

In the case the offspring is installed in a stool bed to be further vegetatively propagated it becomes an ortet. The information about the spatial location in the stool bed plantation is stored on the following.

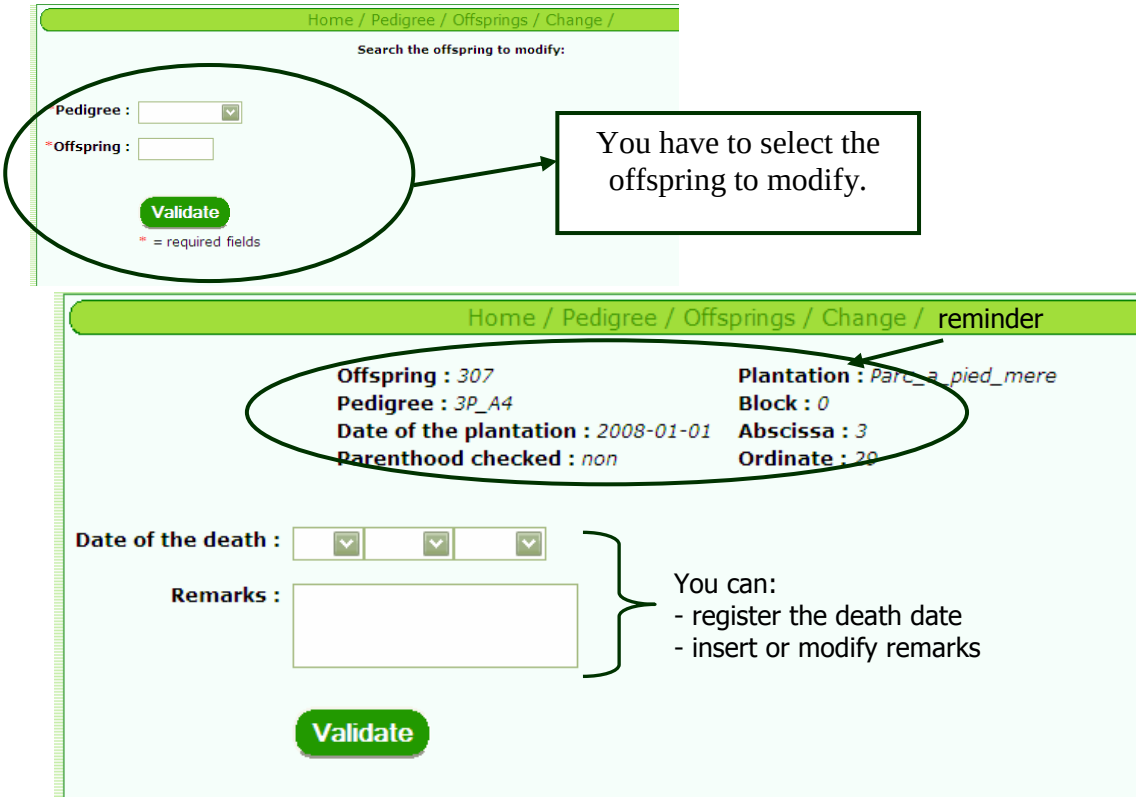


* "Add many offsprings":

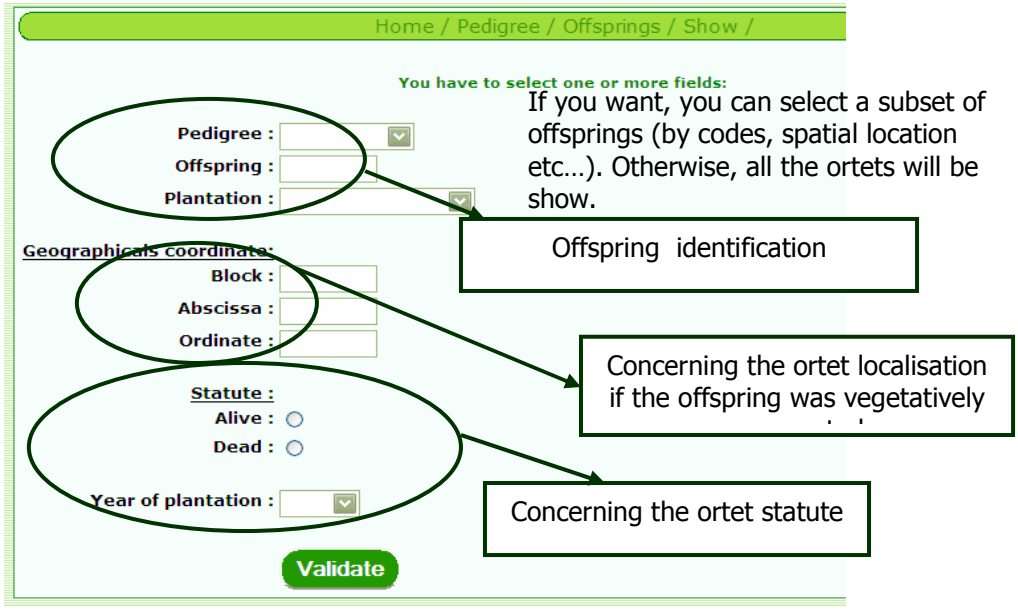


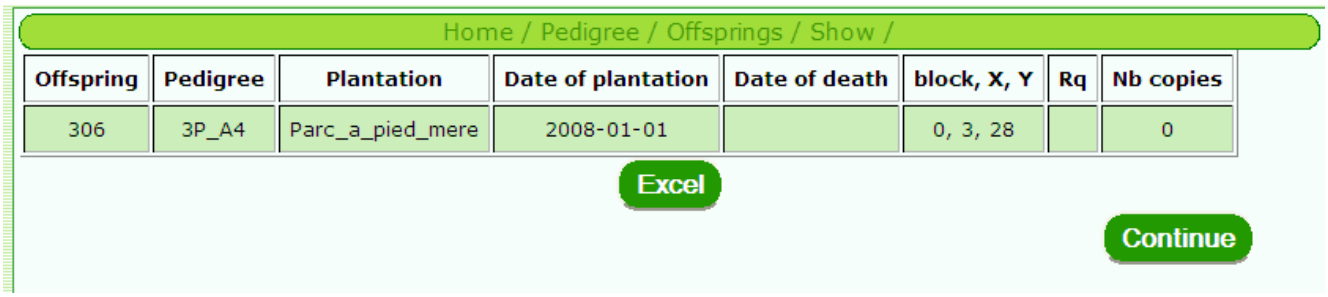
	A	B	C	D	E	F	G	H	I	J	K
1	fichier créé par Guy										
2	en janvier 2008										
3	dans le cadre de la base de données pour la cartographie du chêne										
4											
5	block	X	Y	Identification	Code croisem	ID. mere	code cross m	ID. pere	code cross p	verif. Parenté	Date of creation
6	0	4	26	19	11P_Qs28	11P	Pedoncule	Qs28	Sessile	H _ 19	01/01/2008
7	0	4	16	35	11P_Qs28	11P	Pedoncule	Qs28	Sessile	H _ 35	01/01/2008
8	0	4	13	39	11P_Qs28	11P	Pedoncule	Qs28	Sessile	H _ 39	01/01/2008
9	0	4	5	51	11P_Qs28	11P	Pedoncule	Qs28	Sessile	H _ 51	01/01/2008
10	0	7	44	53	11P_Qs28	11P	Pedoncule	Qs28	Sessile	H _ 53	01/01/2008
11	0	5	2	62	11P_Qs28	11P	Pedoncule	Qs28	Sessile	H _ 62	01/01/2008
12	0	5	3	63	11P_Qs28	11P	Pedoncule	Qs28	Sessile	H _ 63	01/01/2008
13	0	5	5	65	11P_Qs28	11P	Pedoncule	Qs28	Sessile	H _ 65	01/01/2008

b) Modify offsprings



c) <u>View Offspring:</u>





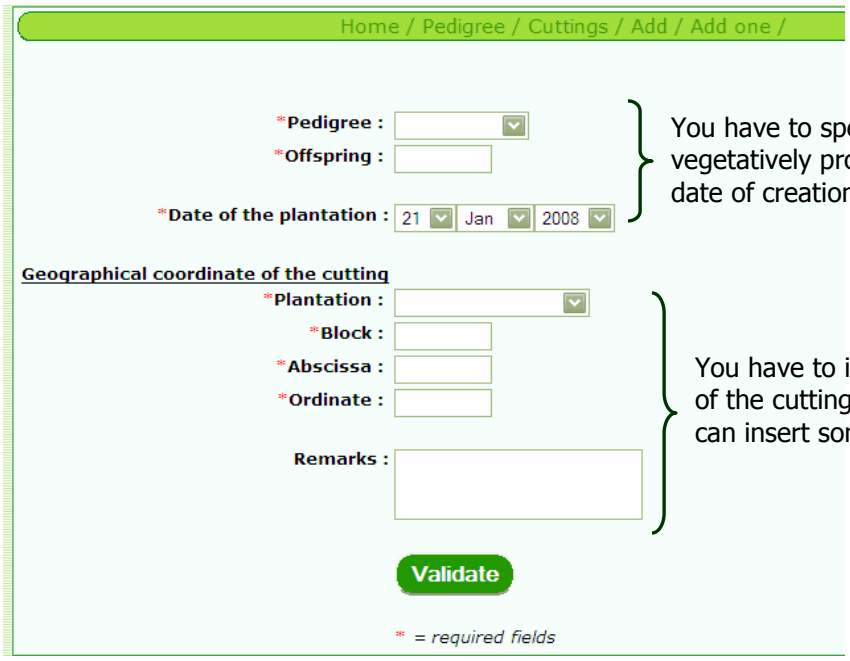
The table contains the information of the offsprings: date of creation, location of the ortets, number of vegetative copies that were produces so far ….

6.3. Cuttings:

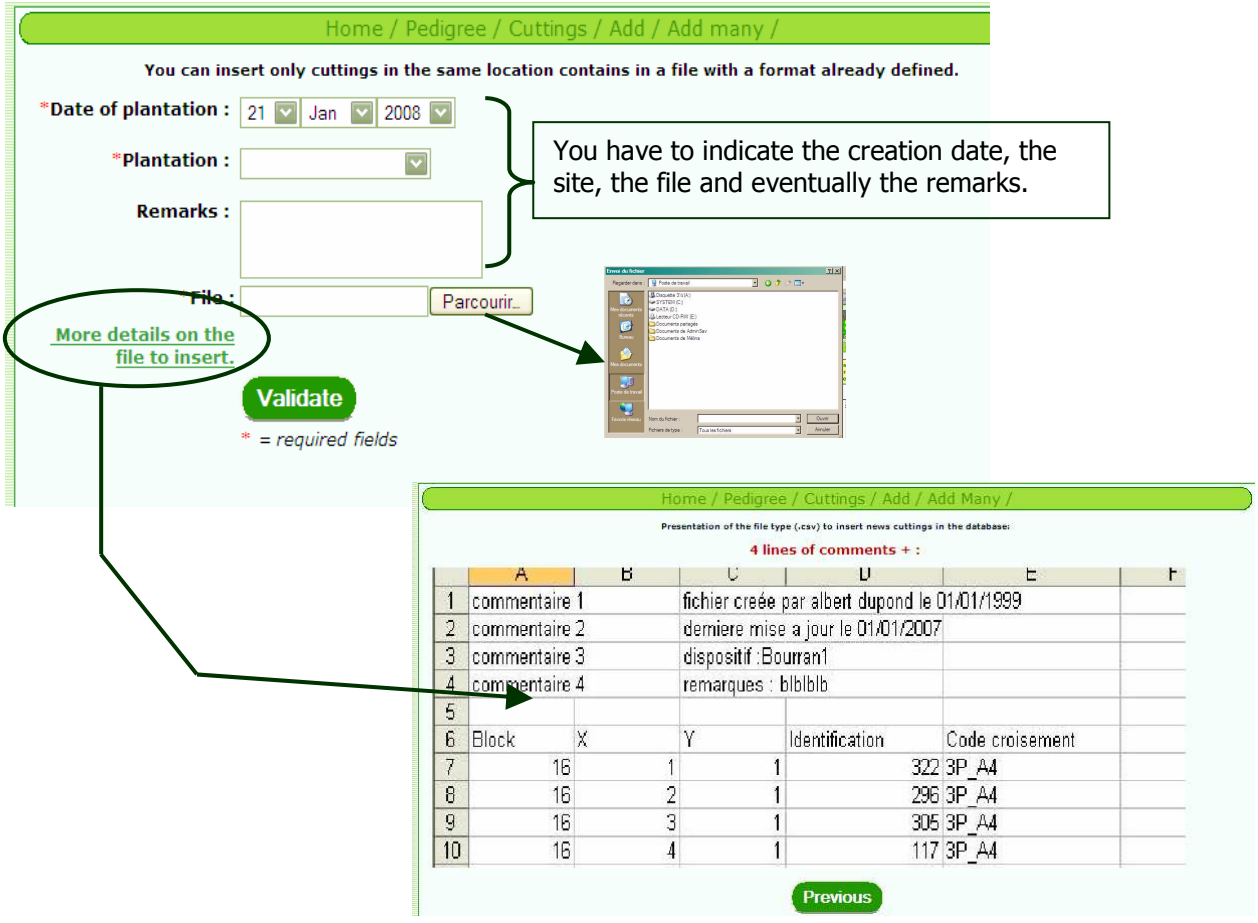
In this section, you can add new cuttings, modify information about existing cuttings or view data about the cuttings

a) "Add cuttings":

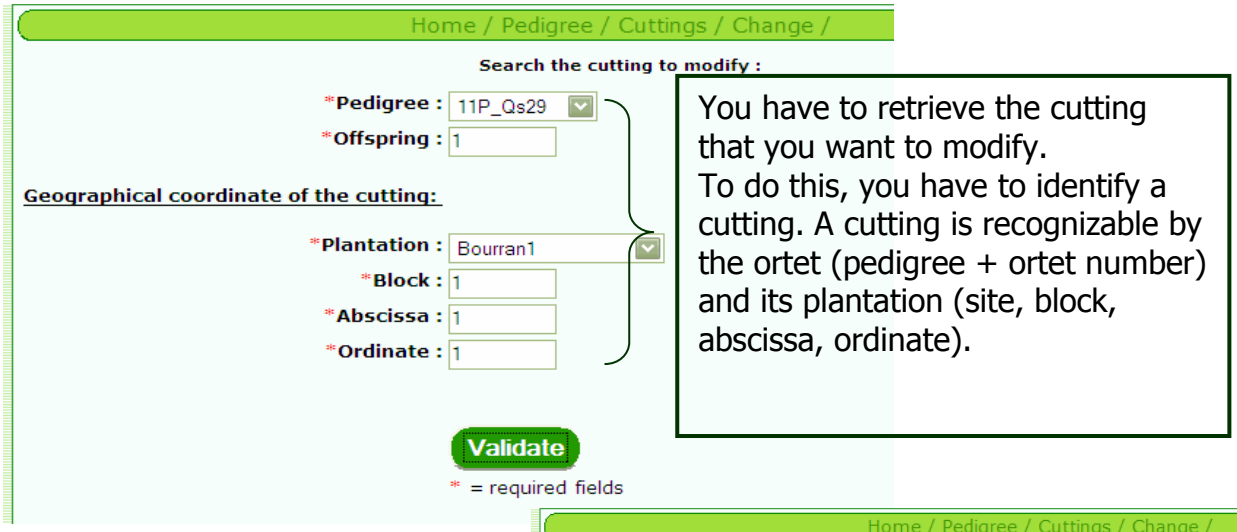
* Add only one cutting:



* Add several cuttings:



b) "Modify cuttings"

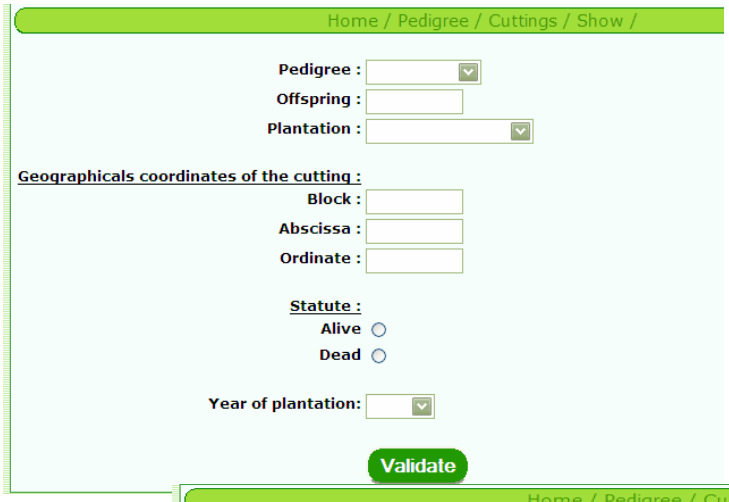


You have to retrieve the cutting that you want to modify.
To do this, you have to identify a cutting. A cutting is recognizable by the ortet (pedigree + ortet number) and its plantation (site, block, abscissa, ordinate).

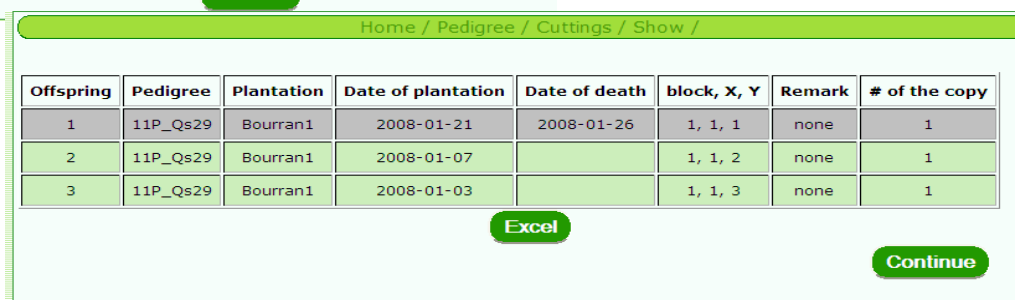
As for the modification of offspring, brief information of the cutting is shown on the screen.

You can only change the date of death or remarks about the cutting

c) "View cuttings":



If you do not fill any fields, all cuttings will be shown. Otherwise, you can select the pedigree or/and the ortet number or/and the site or/and the localisation information and/or the statute and/or the year of creation.

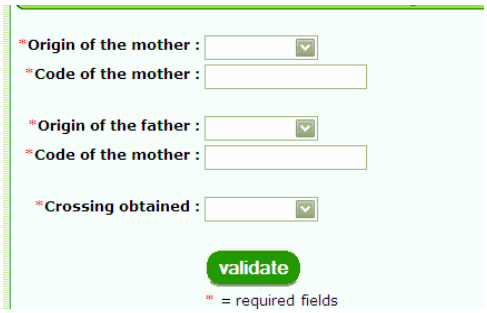


The line in grey indicates that the cutting is dead.
"# of the copy" indicates the serial number of vegetative propagation of the offspring.
You can also export this file in an excel format.

6.4. Controlled crosses:

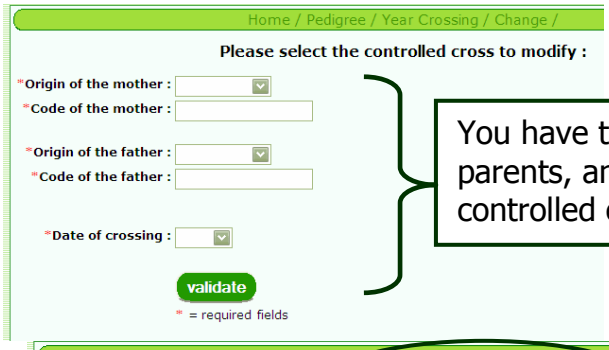
This section contains the information about the controlled crosses made to obtain the mapping pedigree, especially when the same cross was repeatedly made over years in order to increase the number of offsprings needed.
You can add a new cross, modify information about existing crosses or view data about the crosses.

a) "Add new controlled cross":



You have to indicate the code of the male and female parent. And provide the code of the cross obtained, which becomes the code of the new pedigree.
All this information are required fields (*).

b) "Modify a cross"

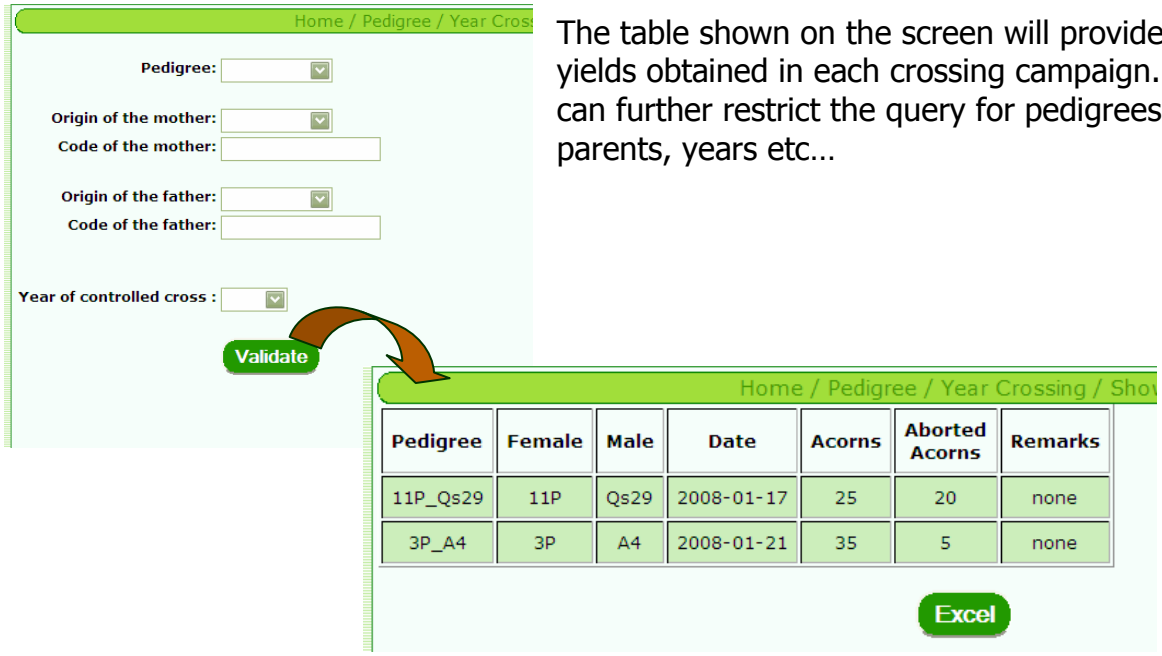


You have to indicate the code of parents, and the year of controlled cross.

Information about the cross

You can modify the number of acorns obtained, the number of aborted acorns, the remarks and the number of living offsprings obtained.

c) "View controlled crosses":

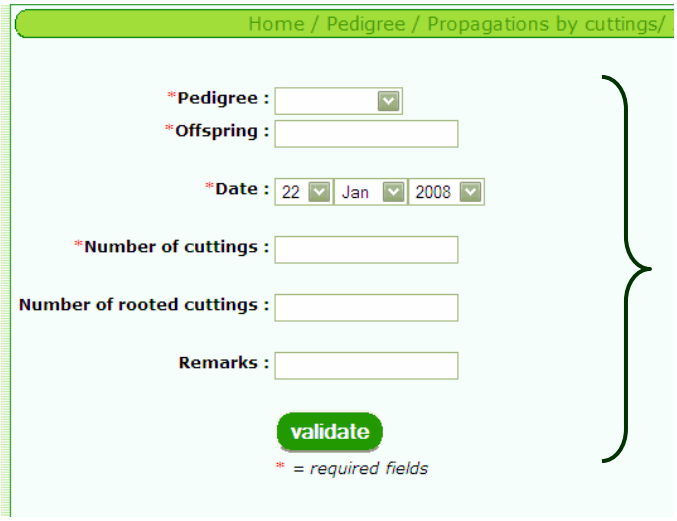


The table shown on the screen will provide the yields obtained in each crossing campaign. You can further restrict the query for pedigrees, parents, years etc…

6.5. Vegetative propagation

a) « Add vegetative propagation» :

* « For one ortet only» :

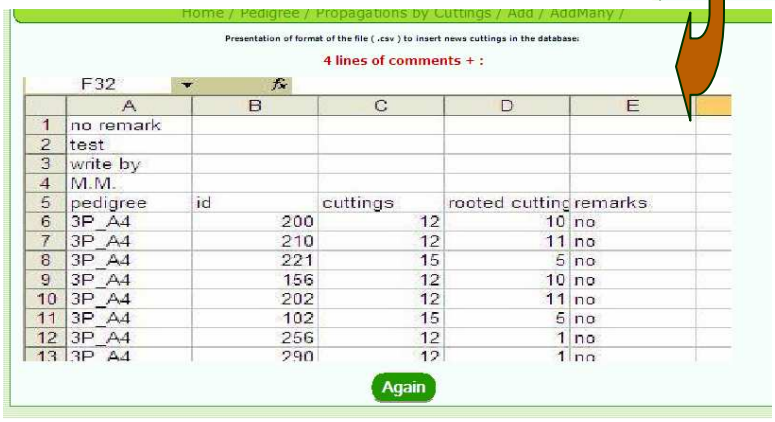


You have to indicate the identity (pedigree code + ortet code) of the ortet vegetatively propagated.

You have also to select the date and the number of cuttings obtained.
You can specify the number of cuttings who have rooted and the remarks.

* « Many cuttings »:

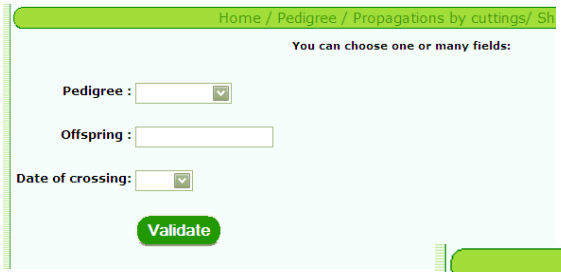
You have to select the date and the directory that contains the file to be inserted
As help info, you can click on the green link to view the required file format to be used for the insertion in the data base.



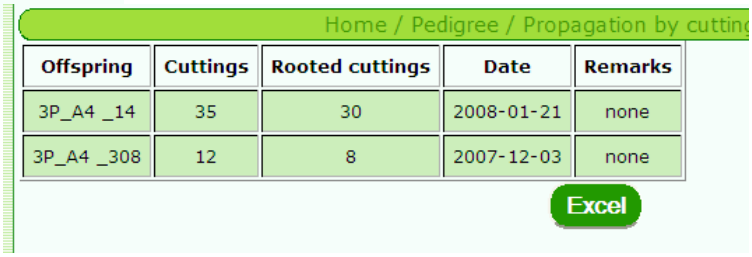
b) « Modify vegetative propagation » :

Indicate the code of the ortet, and of the pedigree. The only field that can be changed is the number of successful cuttings obtained

c) « View vegetative propagation »:

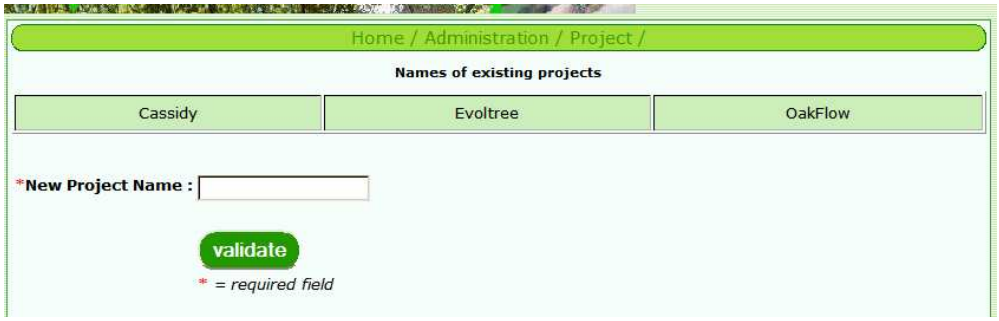


The table shown on the screen will provide the number of rooted cuttings obtained for each ortet. You can further restrict the query for pedigrees, parents, ortets, years etc…



7- Administration

7.1. Add Project



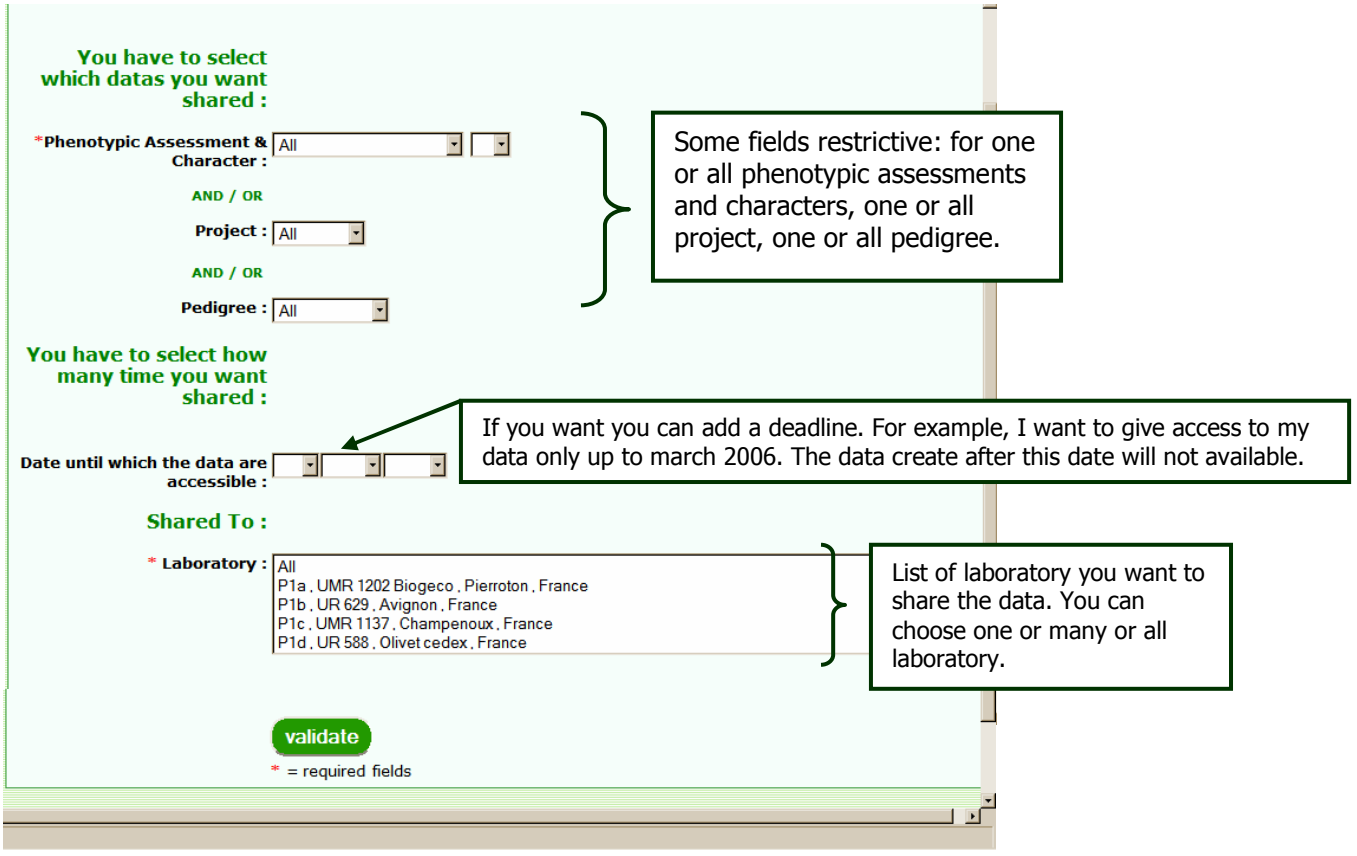
A table shows us the project already existing in the database.
You have just to tape your new project name and to validate.
Do care to the punctuation, the uppercase and the orthography!

7.2. Add or Delete rights of access to the database

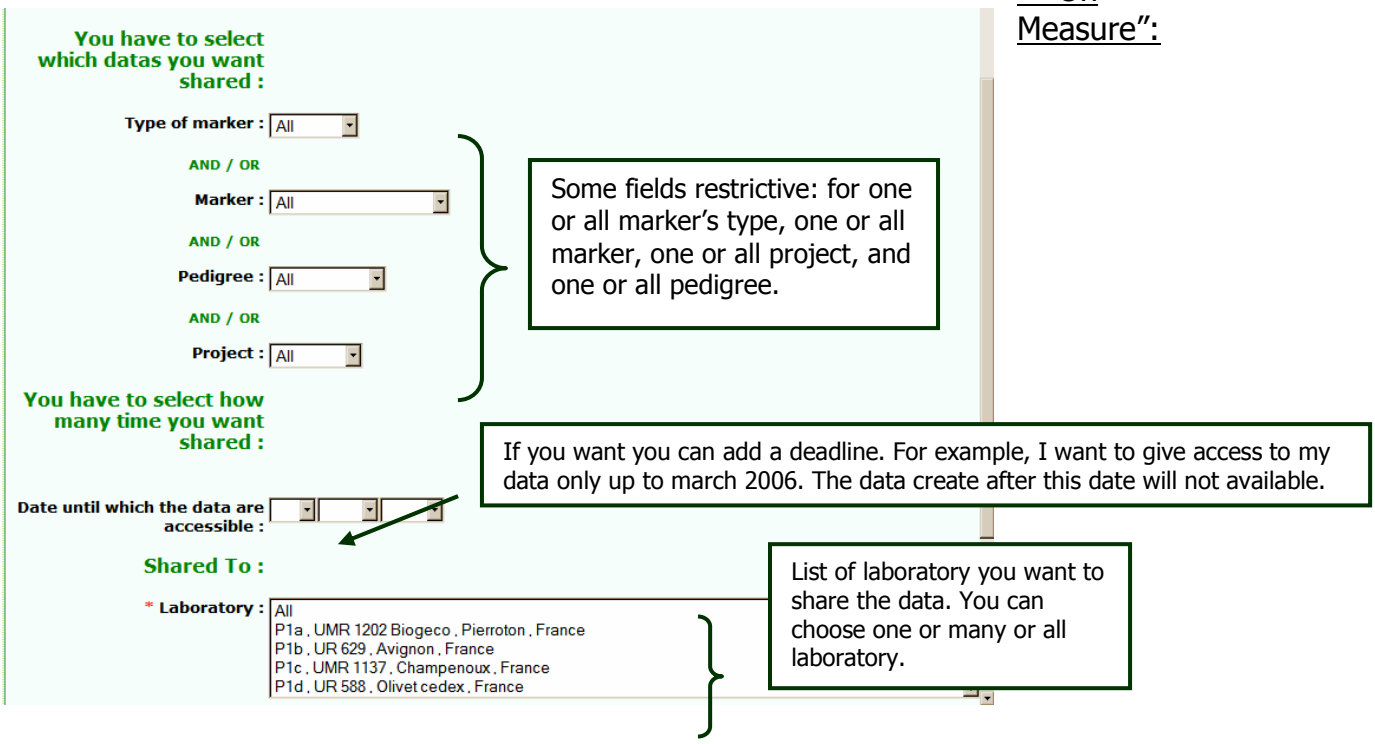
To manage the data, a system of right has been established. This system allows to specify some rights for the genetics data (measures and markers) and for the phenotypics data. You can notably specify some rights according the project or a deadline.
You have to do care to sequencing the rights correctly. For example, if you give rights to all assessment to one laboratory and after to

a) "Add news rights of access to my data":

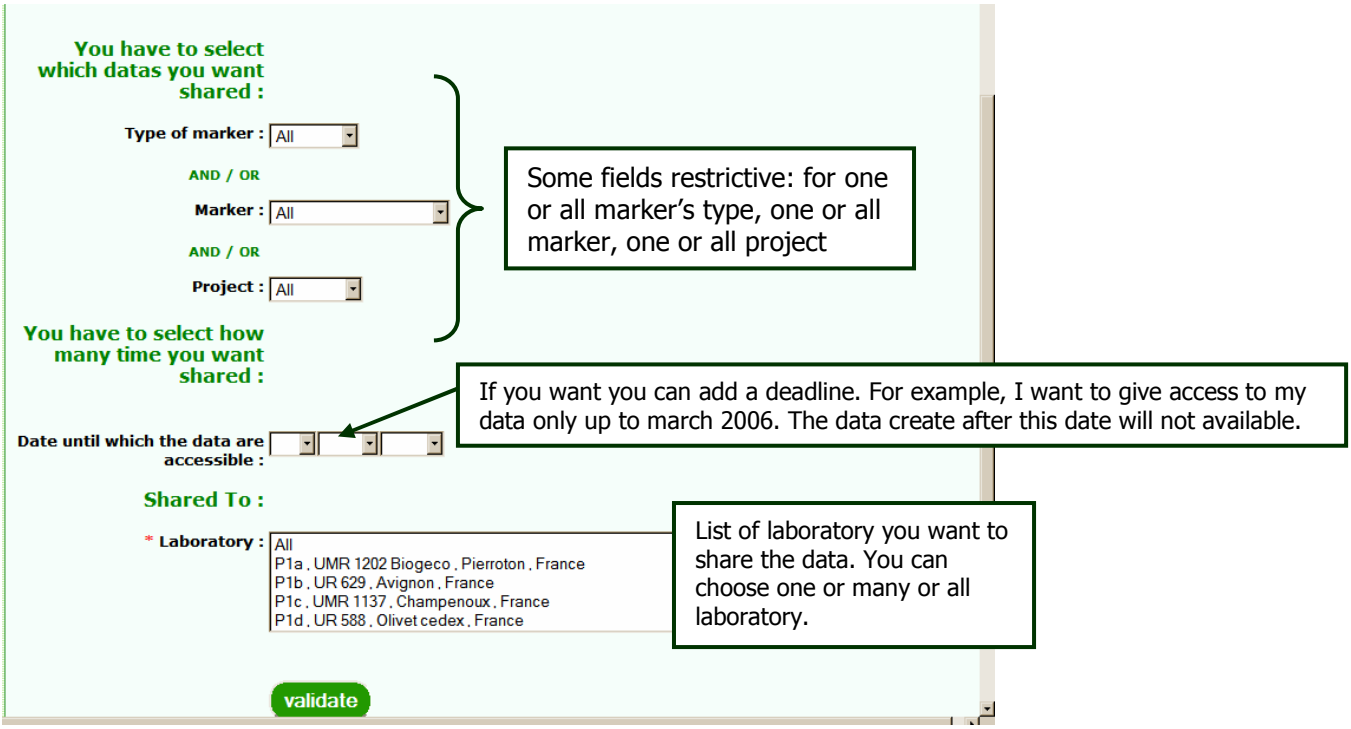
* "On Pheno":



* "On Measure":

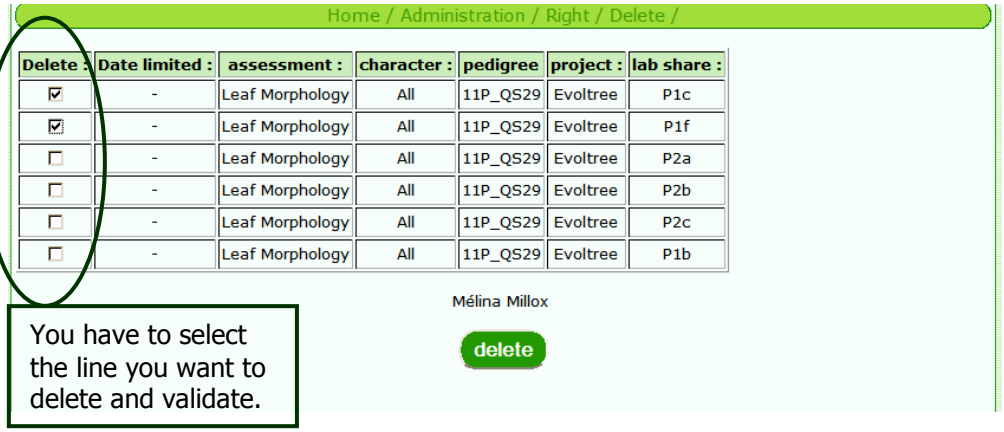


* "On Marker":

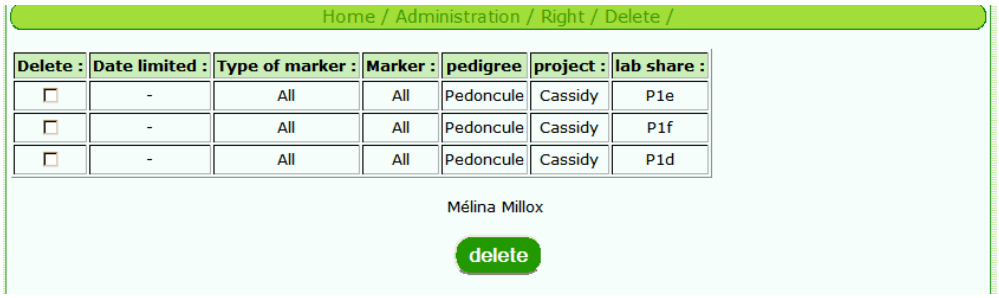


b) "Delete rights of access to my data":

* "On Pheno":



* "On Measure":

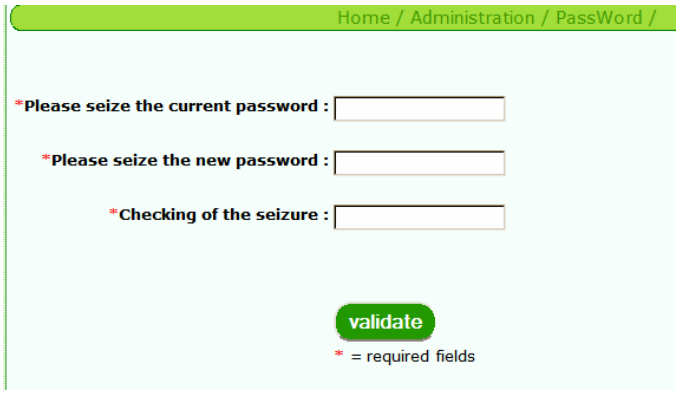


Same things, you have to select the lines you want to delete and validate. Only information in the table changes.

* "On Marker":

Same things.

7.3. Change My Password



You have just to tape your old password, your new password and your new password again to be sure that it's correctly tape the first time.
You have to do care to the PUNCTUATION & UPPERCASE & ORTHOGRAPHY & SPACE!
Don't forget your password, if it is, ask to the administrator to you return.

8- CMap

Not yet available.

9 – Other information

In Annexe A, you can see the conceptual model of the database.
You have to do care to the format of the file insert in the database (number and position of the rows and columns), to the punctuation, the uppercase and the orthography.

Conclusion

Some ameliorations of the software have been planned.
Any suggestion or remark, please contact mélina millox at Mélina.Millox@pierroton.inra.fr or Frederic Raspail at Frederic.Raspail@pierroton.inra.fr .

Annexe A : MCD