



QuercusMap Guide

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Version 2.2

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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 screenshot shows the QuercusMap login interface. On the left, a green menu contains the following items: Genotype, Phenotype, Pedigree, CMap, and Administration. The main content area is titled 'Home' and contains the text 'Please, identificate you :'. Below this, there are two input fields: '*Login : ' and '*Password : '. A note below the password field states: 'If you are entitled, you can choose the database, else you are automatically directed to TEST database'. There are two radio buttons: 'TEST database: ' and 'REAL database: '. A 'validate' button is located below the radio buttons. At the bottom, there is a footer with the text 'Powered By INRA Pierroton laboratory Tested with Mozilla FireFox'. Annotations include: a green circle around the menu with an arrow pointing to it labeled 'Menu'; a green circle around the top right logos (INRA and PostgreSQL) with an arrow pointing to it labeled 'Links'; a yellow oval around the login field with an arrow pointing to it labeled 'Tape your login'; a yellow oval around the password field with an arrow pointing to it labeled 'Tape your password'; and a green circle around the radio buttons with an arrow pointing to it labeled 'Temporary choice'.

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.

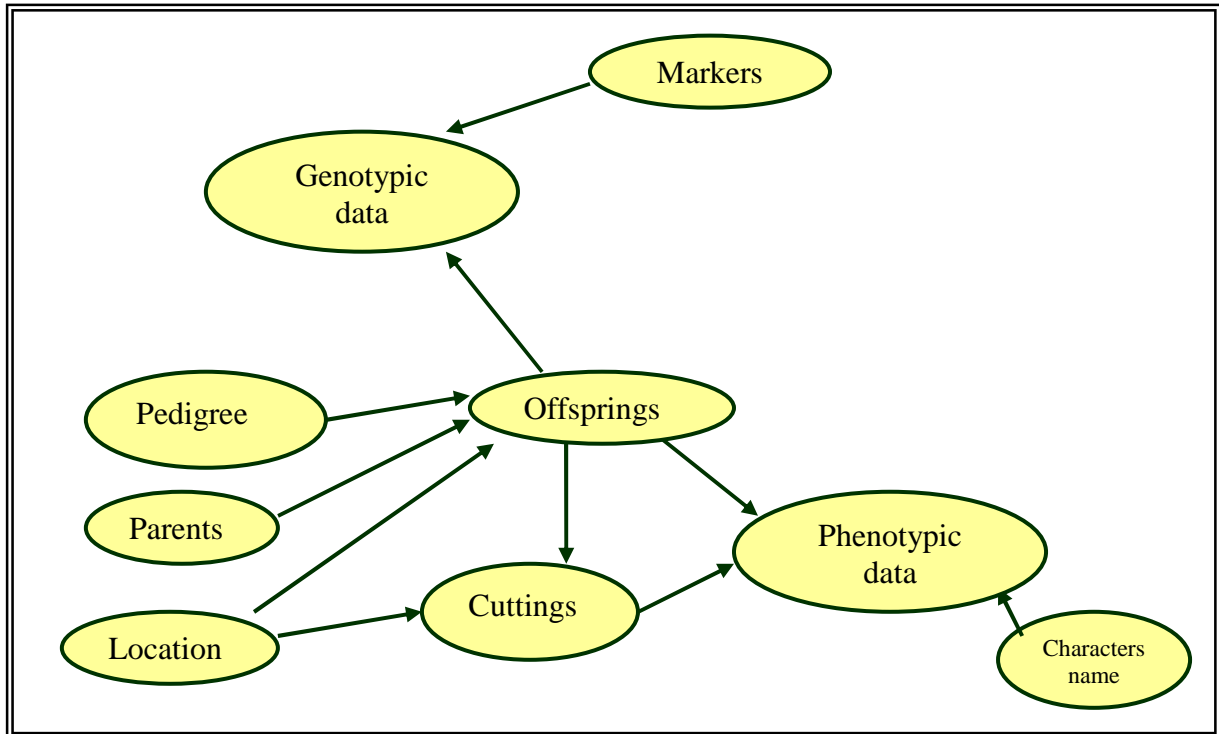
By default, you are connected on test database.

*** 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 offspring:

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:

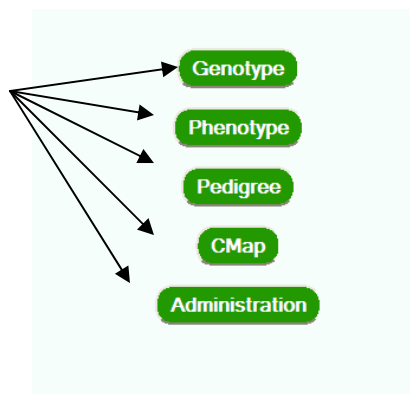
The ortets and the marker have to already exist in the database.

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

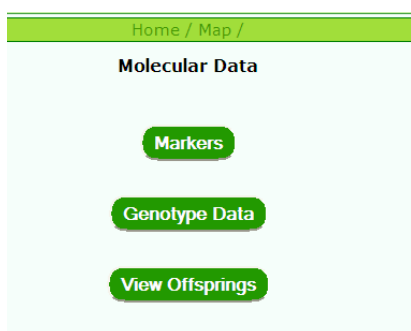
To insert location, pedigree, markers type, first parent, category of phenology, users you have for the moment to contact the administrator.

3- Principals parts

The data base is composed of 5 main parts:



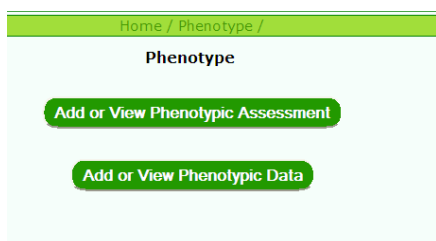
a) Molecular data, "Genotype":



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.

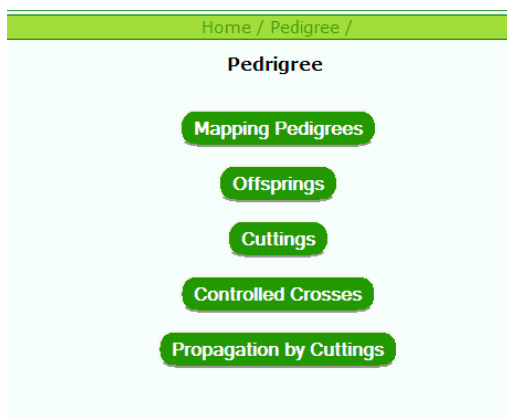
b) Phenotypics data, "Phenotype":



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.

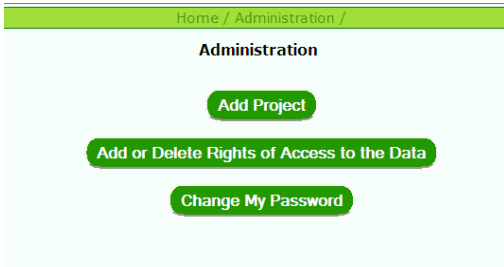
- "Mapping Pedigrees": overall information about all the pedigrees integrated in the database: number of offsprings, number of cuttings ...
- "Offsprings": add, modify or check data about a given ortet (offspring of a given pedigree)
- "Cuttings": add, modify or check data about cuttings of a given ortet.
- "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.

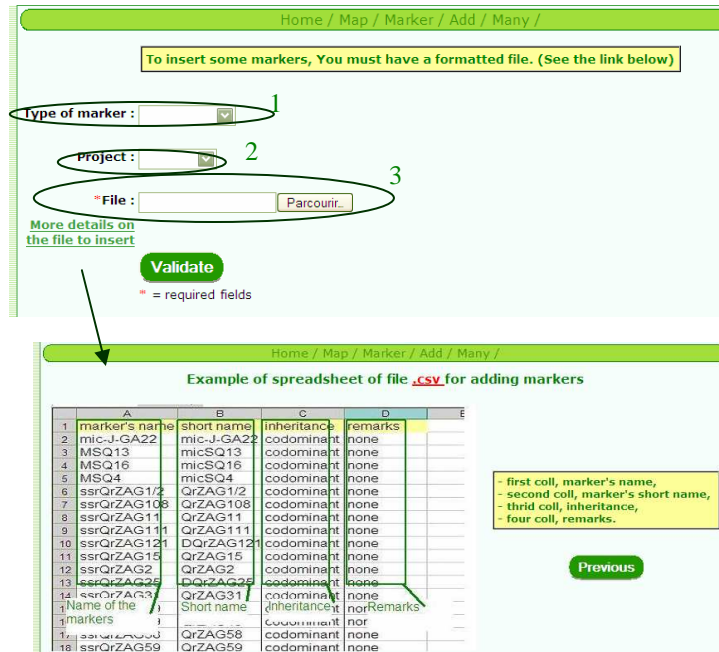
③ You have to select the project associated to this marker (Evoltree or older project).

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:**

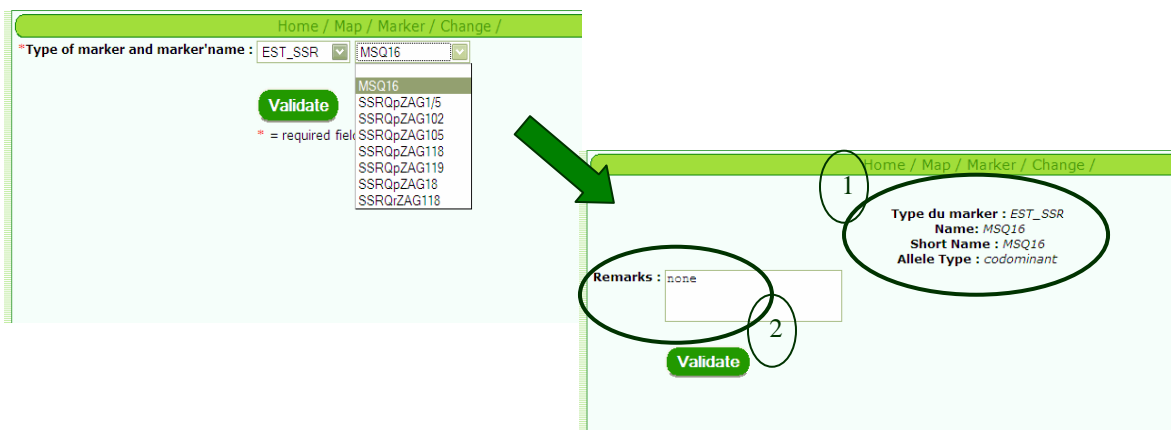


1 = you have to select the type of marker concerned by this insertion.
 2 = you have to select the project associated to this data
 3 = you have to select the file who contains the data to insert in the database.

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.

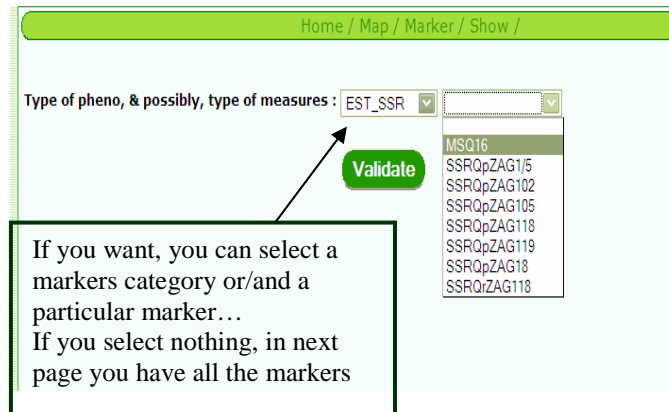
b) Change markers



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

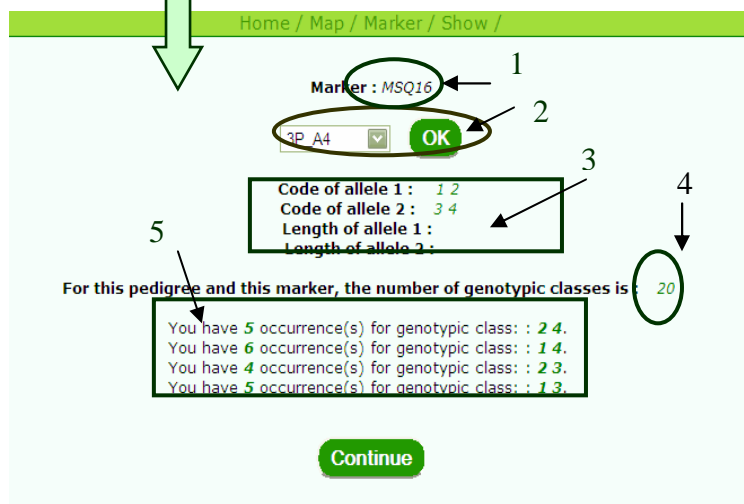


Home / Map / Marker / Show /

1 | 2 >

Type	Name	X-deux	Allele Type	Remarks	Creation
SSR	mic-J-GA22		codominant		2000-01-01
SSR	MSQ13		codominant		2000-01-01
SSR	MSQ13*		codominant		2000-01-01
SSR	MSQ16		codominant		2000-01-01
SSR	Q4		codominant	remarque 8/11	2000-01-01

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:

Example of spreadsheet of file .csv for adding genotypic data

You have to respect the numbers of lines and the position of yours informations to succeed your insertion.

Format With allele code :

A	D	E	F	G	H	I
1 pas de commentaires						
2	11P	QS21	10	11	12	13
3 ssrQpZAG110	-1	23	-2	-3	ND	-2
4 ssrQpZAG102	13	24	12	14	12	34
5 ssrQrZAG108	24	13	ND	ND	21	41
6 ssrQrZAG11	14	23	ND	12	43	42
7 MSQ16	11	23	12	12	ND	12

To include new genotypic, use the following scoring system:
 - "-" for unknow allele
 - "ND" for no data (No Data)

- 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).

- "-" for no data

Format With allele Length :

1	ceci est un fichier teste concernant les mesures a rentrer dans la base de données									
2	3 lignes de Pedigree sont a avoir									
3	avant de commencer a inserer ces données (en abscisse, les numeros des genotypes									
4	11P_QS29									
5		10	Orset	11		12		13		14
6	ssrOpZAG1E	-	-	102	29	102	41	102	41	303
7	ssrOpZAG10i	-	-	29	102	29	102	41	102	41
8	ssrOpZAG10i	102	29	102	29	41	29	41	29	-
9	ssrOpZAG11i	9	29	9	303	-	-	9	29	9
10	ssrOpZAG11i	102	29	102	41	102	29	303	41	303
11	ssrOpZAG10E	-	-	-	-	29	102	41	102	29
12	eggOpZAG11	-	-	102	29	41	303	41	303	41
13	MSQ_Markers	9	29	9	29	-	-	-	-	9

- first coll, mother length allele,
- second coll, father length allele,
- "9" for unknown allele length,
- "-" for missing data.

Previous

b) Change genotypic data

* **Marker :** MSQ16

* **Pedigree :** 3P_A4

* **Offspring :** 308

Validate

* = required fields

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.

Reminder

Marker : MSQ16
Pedigree : 3P_A4
Offspring : 308

Code of allele 1:

Length of allele 1:

Code of allele 2:

Length of allele 2:

Date:

Remarks:

Validate

You can modify all information but be careful to be coherent.

c) Show genotypic data

Home / Map / Genotype Datas / Show /

You can choose one or several fields !

Select one or several markers :

- MSQ16
- SSRQpZAG15
- SSRQpZAG102
- SSRQpZAG105
- SSRQpZAG118
- SSRQpZAG119
- SSRQpZAG123
- SSRQpZAG18
- SSRQrZAG118
- SSRQrZAG132

Pedigree : All

Offspring :

Date exact : / /

Validate

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.

Home / Map / Genotype Datas / Show /

Marker	Pedigree, Offspring	Code of allele 1	Length of allele 1	Code of allele 2	Length of allele 2	Users	Date	Remarks
MSQ16	3P_A4 ,14	-		3		Mélina Millox , Pia	2008-01-16	pas de commentaires
MSQ16	3P_A4 ,15	-		2		Mélina Millox , Pia	2008-01-16	pas de commentaires
MSQ16	Pedoncule ,3P	-		1		Mélina Millox , Pia	2008-01-16	pas de commentaires

You can export this table in excel and Joinmap format

Excel

JoinMap

Continue

4.3 View Offsprings

You can select one or more fields.

Pedigree :

Offspring :

Validate

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

Home / Map / View Ortets / Show /

1 | 2 | 3 | 4 | 5 » [37]

Cross :	Name :	Creation date :	Oaks alive : (offsprings + cuttings)	Oaks dead : (offsprings + cuttings)
3P_A4	100	2008-01-15	1 + 0	0 + 0
3P_A4	101	2008-01-15	1 + 0	0 + 0
3P_A4	102	2008-01-15	1 + 0	0 + 0
3P_A4	103	2008-01-15	1 + 0	0 + 0
3P_A4	104	2008-01-15	1 + 0	0 + 0
3P_A4	105	2008-01-15	1 + 0	0 + 0
3P_A4	106	2008-01-15	1 + 0	0 + 0
3P_A4	107	2008-01-15	1 + 0	0 + 0
3P_A4	108	2008-01-15	1 + 0	0 + 0
3P_A4	109	2008-01-15	1 + 0	0 + 0

Export **Continue**

Pagination

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:

Home / Phenotype / Assessment / Add / Character /

*Phenotypic assessment :

*Phenotypic character :

* Acronym :

*Unit of measure :

Validate

* = required fields

You have to select a phenotypic assessment.

Describe your new character (name, acronym and units)

b) View Existing Characters

Home / Phenotype / Assessment / Show /

Name :	Details :	More details :
Bud Phenology		
Growth And Biomass	Thèse Caro Saintagne	These Caro.pdf
Leaf Morphology	Thèse Caro Saintagne	These Caro.pdf
Ontogeny	Thèse Caro Saintagne	These Caro.pdf
Responce To CO2	Thèse Xavier Torti	These Xaviere.pdf
Response To Hypoxia	Thèse Julien Parelle	These Julien.pdf
Water Metabolism		

Export
Continue

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.

Home / Phenotype / Assessment / Show /

Character phenotypic : Growth And Biomass
 Details : Thèse Caro Saintagne

Name :	Acronym :	Units :
Total height at the end of the third growing season	Ht	none
Mean flush length	Lmoy	none
Total height increment during the 3rd growing season	Ltot	none
Number of flushes	Nuc	none

Previous
Continue

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 :

Home / Phenotype / Datas / Add /

*Plantation :

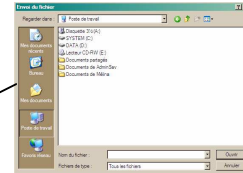
Please check the format of the files and the orthography of your fields !

*File :

[More details on the file to insert](#)

*Project :

* = required fields



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

Home / Phenotype / Datas / Add /

Presentation of type of file .csv to insert new phenotypics datas.

Lines who contains some comments										
Description des mesures :				Assessment						
empty line				Character (acronym)	Leaf Morphok	Leaf Morphok	Growth And	EGrowth And	Biomass	
	X	Y	Bloc	Ident	LL	NL	LMev	Et	Date	
6	1	1	151	220	0	1	2	2		
7	1	2	151	213	0	0	1	2		
8	1			209	0	1	1	1		
9	1			245	0	1	1	2		
10	1	5	50	195	1	1	1	1		
11	1	6	50	168	1	1	1	1		
12	1	7	32	285	0	2	2	2		
13	1	8	32	328	2	2	2	2		
14	1	9	32	120	1	2	2	3		
15	1	10	25	119	0	1	1	2		
16	1	11	25	102	0	0	1	2		

b) Show existing phenotypic data:

Home / Phenotype / Datas / Show /

*Phenotypic assessment or/and character :

*Pedigree :

You can choose One or More fields to restrict the results.

Plantation :

Date :

Offspring :

* = required fields

You have to select this data.

You may further select the plantation

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

Home / Phenotype / Datas / Show /

Phenotypic character : Leaf Morphology , Staining

1 | 2 | 3 | 4 | 5 > [23]

Date :	Oak :	Value :	Site :	geographical position
2006-11-09	11P_QS29 _ 203	2	Bourran2	86, 16, 4
2006-11-09	11P_QS29 _ 189	3	Bourran2	45, 5, 12
2006-11-09	11P_QS29 _ 352	2	Bourran2	100, 18, 2
2006-11-09	11P_QS29 _ 234	2	Bourran2	183, 24, 93
2006-11-09	11P_QS29 _ 249	2	Bourran2	68, 10, 59
2006-11-09	11P_QS29 _ 216	3	Bourran2	139, 26, 89
2006-11-09	11P_QS29 _ 133	2	Bourran2	135, 20, 17
2006-11-09	11P_QS29 _ 104	2	Bourran2	145, 10, 103
2006-11-09	11P_QS29 _ 351	1	Bourran2	137, 2, 90
2006-11-09	11P_QS29 _ 102	2	Bourran2	174, 15, 37
2006-11-09	11P_QS29 _ 279	3	Bourran2	125, 17, 27

[...scroll all the data...]

Export Continue

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

6- Pedigree

6.1. Mapping Pedigrees:

Home / Pedigree / Mapping Pedigrees /

Name	Author	Parental species	Number of offsprings	Number of cuttings	Remarks
3P_A4	Kremer Antoine	_chene pedoncule	363	0	no remarks
11P_Qs29	Kremer Antoine	_chene sessile _chene pedoncule	266	1	no remarks
A4_3P	Kremer Antoine		265	0	none

Export Continue

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.

Summary of existing data.

Offspring : 102 Pedigree : Qs28_Qs21
 Code of the mother : Qs28 Origin of the mother : Sessile
 Code of the father : Qs21 Origin of the father : Sessile

Geographical coordinate of the offspring

*Plantation :

*Block :

*Abscissa :

*Ordinate :

Remarks :

Parenthood checked

Validate

* = required fields

You have to indicate the exact location of the tree

You can add some remarks or confirming the verification of kinship.

* "Add many offsprings":

Home / Pedigree / Offsprings / Add / Add Many /

You can only insert some trees in the same plantation in a file who have a format defined.

* Plantation :

Remarks :

* File : Parcourir...

More details on the file to insert.

Validate

* = required fields

You have to select a date, by default it is the date of today, and the site, to insert the file and if needed to include some comments.

1	fichier créé par luy										
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 croisen	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

Home / Pedigree / Offsprings / Change /

Search the offspring to modify:

Pedigree :

* Offspring :

Validate

* = required fields

You have to select the offspring to modify.

Home / Pedigree / Offsprings / Change / reminder

Offspring : 307
 Pedigree : 3P_A4
 Date of the plantation : 2008-01-01
 Parenthood checked : non

Plantation : Parc_a_pied_mere
 Block : 0
 Abscissa : 3
 Ordinate : 20

Date of the death :

Remarks :

Validate

You can:
 - register the death date
 - insert or modify remarks

c) View Offspring:

Home / Pedigree / Offsprings / Show /

You have to select one or more fields:

If you want, you can select a subset of offsprings (by codes, spatial location etc...). Otherwise, all the ortets will be show.

Pedigree :
 Offspring :
 Plantation :

Geographicals coordinate:
 Block :
 Abscissa :
 Ordinate :

Statute :
 Alive :
 Dead :

Year of plantation :

Offspring identification

Concerning the ortet localisation if the offspring was vegetatively

Concerning the ortet statute

Home / Pedigree / Offsprings / Show /

Offspring	Pedigree	Plantation	Date of plantation	Date of death	block, X, Y	Rq	Nb copies
306	3P_A4	Parc_a_pied_mere	2008-01-01		0, 3, 28		0

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:

Home / Pedigree / Cuttings / Add / Add one /

*Pedigree :

*Offspring :

*Date of the plantation :

Geographical coordinate of the cutting

*Plantation :

*Block :

*Abscissa :

*Ordinate :

Remarks :

Validate

* = required fields

You have to specify the ortet that was vegetatively propagated .and indicate the date of creation.

You have to indicate the location of the cutting. Eventually you can insert some remarks.

* Add several cuttings:

Home / Pedigree / Cuttings / Add / Add many /

You can insert only cuttings in the same location contains in a file with a format already defined.

*Date of plantation :

*Plantation :

Remarks :

File : **Parcourir...**

Validate

* = required fields

More details on the file to insert.

You have to indicate the creation date, the site, the file and eventually the remarks.

Home / Pedigree / Cuttings / Add / Add Many /

Presentation of the file type (.csv) to insert news cuttings in the database:

4 lines of comments + :

	A	B	C	D	E	F
1	commentaire 1			fichier creee par albert dupond le 01/01/1999		
2	commentaire 2			derniere mise a jour le 01/01/2007		
3	commentaire 3			dispositif : Bourran1		
4	commentaire 4			remarques : biblbib		
5						
6	Block	X	Y	Identification	Code croisement	
7	16	1	1		322 3P_A4	
8	16	2	1		296 3P_A4	
9	16	3	1		305 3P_A4	
10	16	4	1		117 3P_A4	

Previous

b) "Modify cuttings"

Home / Pedigree / Cuttings / Change /

Search the cutting to modify :

* Pedigree : 11P_Qs29

* Offspring : 1

Geographical coordinate of the cutting:

* Plantation : Bourran1

* Block : 1

* Abscissa : 1

* Ordinate : 1

Validate

* = required fields

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

Home / Pedigree / Cuttings / Change /

Offspring : 1 Plantation: Bourran1

Pedigree: 11P_Qs29 Block: 1

Date of creation: 2008-01-21 Abscissa : 1

Parenthood checked : oui Ordinate : 1

Date of death :

Remarks : none

Validate

c) "View cuttings":

Home / Pedigree / Cuttings / Show /

Pedigree :

Offspring :

Plantation :

Geographicals coordinates of the cutting :

Block :

Abscissa :

Ordinate :

Statute :

Alive

Dead

Year of plantation:

Validate

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.

Home / Pedigree / Cuttings / Show /

Offspring	Pedigree	Plantation	Date of plantation	Date of death	block, X, Y	Remark	# of the copy
1	11P_Qs29	Bourran1	2008-01-21	2008-01-26	1, 1, 1	none	1
2	11P_Qs29	Bourran1	2008-01-07		1, 1, 2	none	1
3	11P_Qs29	Bourran1	2008-01-03		1, 1, 3	none	1

Excel **Continue**

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...

Pedigree	Female	Male	Date	Acorns	Aborted Acorns	Remarks
11P_Qs29	11P	Qs29	2008-01-17	25	20	none
3P_A4	3P	A4	2008-01-21	35	5	none

Excel

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.

	A	B	C	D	E
1	no remark				
2	test				
3	write by				
4	M.M.				
5	pedigree	id	cuttings	rooted cutting	remarks
6	3P_A4	200	12	10	no
7	3P_A4	210	12	11	no
8	3P_A4	221	15	5	no
9	3P_A4	156	12	10	no
10	3P_A4	202	12	11	no
11	3P_A4	102	15	5	no
12	3P_A4	256	12	1	no
13	3P_A4	290	12	1	no

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...

Offspring	Cuttings	Rooted cuttings	Date	Remarks
3P_A4_14	35	30	2008-01-21	none
3P_A4_308	12	8	2007-12-03	none

7- Administration

7.1. Add Project

Home / Administration / Project /

Names of existing projects

Cassidy	Evoltree	OakFlow
---------	----------	---------

*New Project Name :

validate

* = required field

A table shows us the project already existing in the database. You have just to type 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":

You have to select which datas you want shared :

*Phenotypic Assessment & Character :

AND / OR

Project :

AND / OR

Pedigree :

You have to select how many time you want shared :

Date until which the data are accessible :

Shared To :

* Laboratory :
 P1a . UMR 1202 Biogeco . Pierroton . France
 P1b . UR 629 . Avignon . France
 P1c . UMR 1137 . Champenoux . France
 P1d . UR 588 . Olivet cedex . France

validate

* = required fields

Some fields restrictive: for one or all phenotypic assessments and characters, one or all project, one or all pedigree.

If you want you can add a deadline. For example, I want to give access to my data only up to march 2006. The data create after this date will not available.

List of laboratory you want to share the data. You can choose one or many or all laboratory.

* "On Measure":

You have to select which datas you want shared :

Type of marker :

AND / OR

Marker :

AND / OR

Pedigree :

AND / OR

Project :

You have to select how many time you want shared :

Date until which the data are accessible :

Shared To :

* Laboratory :

Some fields restrictive: for one or all marker's type, one or all marker, one or all project, and one or all pedigree.

If you want you can add a deadline. For example, I want to give access to my data only up to march 2006. The data create after this date will not available.

List of laboratory you want to share the data. You can choose one or many or all laboratory.

* "On Marker":

You have to select which datas you want shared :

Type of marker :

AND / OR

Marker :

AND / OR

Project :

You have to select how many time you want shared :

Date until which the data are accessible :

Shared To :

* Laboratory :

Some fields restrictive: for one or all marker's type, one or all marker, one or all project

If you want you can add a deadline. For example, I want to give access to my data only up to march 2006. The data create after this date will not available.

List of laboratory you want to share the data. You can choose one or many or all laboratory.

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

* "On Pheno":

Home / Administration / Right / Delete /

Delete :	Date limited :	assessment :	character :	pedigree :	project :	lab share :
<input checked="" type="checkbox"/>	-	Leaf Morphology	All	11P_Q529	Evoltree	P1c
<input checked="" type="checkbox"/>	-	Leaf Morphology	All	11P_Q529	Evoltree	P1f
<input type="checkbox"/>	-	Leaf Morphology	All	11P_Q529	Evoltree	P2a
<input type="checkbox"/>	-	Leaf Morphology	All	11P_Q529	Evoltree	P2b
<input type="checkbox"/>	-	Leaf Morphology	All	11P_Q529	Evoltree	P2c
<input type="checkbox"/>	-	Leaf Morphology	All	11P_Q529	Evoltree	P1b

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[delete](#)

You have to select the line you want to delete and validate.

* "On Measure":

Home / Administration / Right / Delete /

Delete :	Date limited :	Type of marker :	Marker :	pedigree :	project :	lab share :
<input type="checkbox"/>	-	All	All	Pedoncule	Cassidy	P1e
<input type="checkbox"/>	-	All	All	Pedoncule	Cassidy	P1f
<input type="checkbox"/>	-	All	All	Pedoncule	Cassidy	P1d

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[delete](#)

Same things, you have to select the lines you want to delete and validate. Only

information in the table changes.

* "On Marker":

Home / Administration / Right / Delete /

Delete :	Date limited :	Type of marker :	Marker :	project :	lab share :
<input checked="" type="checkbox"/>	-	SSR	All	All	P1c
<input checked="" type="checkbox"/>	-	SSR	All	All	P1d
<input type="checkbox"/>	-	SSR	All	All	P1b

[delete](#)

Same things.

7.3. Change My Password

Home / Administration / PassWord /

*Please seize the current password :

*Please seize the new password :

*Checking of the seizure :

* = required fields

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.

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