SHiNeMaS

(**S**eeds **Hi**story and **Ne**twork Management **S**ystem)

v1.1

User Guide
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A Introduction

In 2005, a collaboration started between the French National Institute for Agricultural Research (INRA) and the farmer organization Réseau Semences Paysannes (RSP). The aim was: (1) to study on-farm management of crop diversity; (2) to develop population-varieties adapted to organic and low inputs agriculture in the context of a participatory plant breeding program involving farmers, NGOs' facilitators and researchers.

In this project, researchers needed to map the history of the population-varieties using the network formalism. In addition to the diffusion among farms, they wanted to document the other steps of life cycle of the seed lot like the reproduction, the selection, and the cross steps. Data characterizing the different seed lots were produced at each step like phenotyping and cultural practices data. All this information needed to be centralized and stored.

Thus, we developed SHiNeMaS (Seeds History and Network Management System) a database with its web interface, dedicated to the management of the history of seed lots and the associated data.

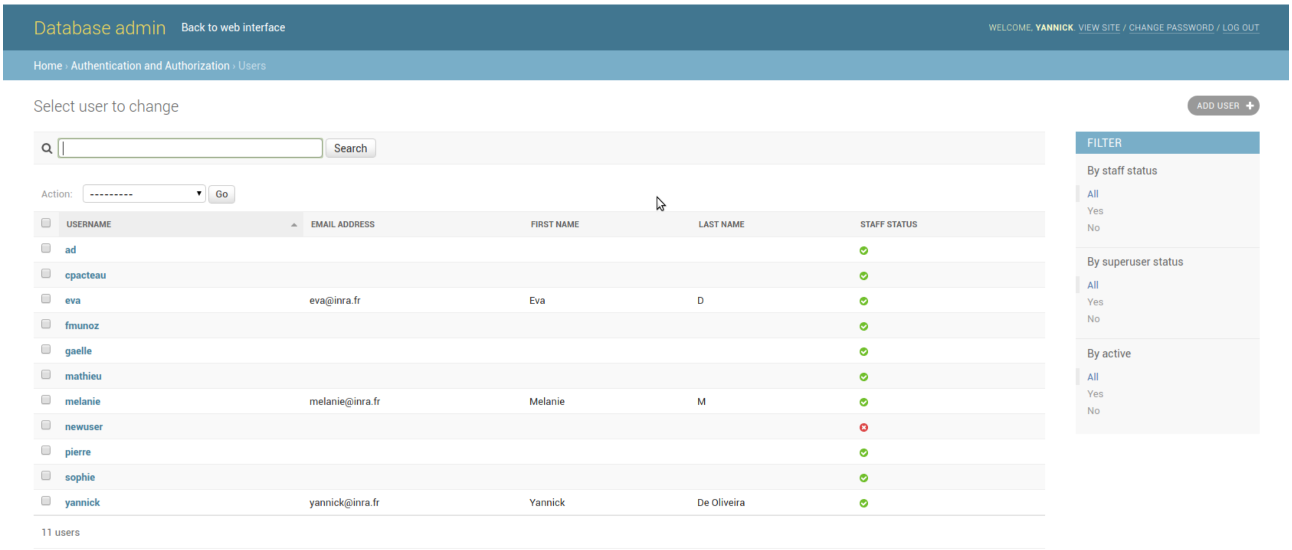
B Administration

B.1 Users management

B.1.a Create/Modify/Delete a user

To create users, go to the menu Admin data > Actors & Users > Users. This screen list all existing users (Figure 1).

To create a new user click on ‘Add User’, a first form (Figure 2) ask to fill the login and password of the new user. Click on ‘Save’ and finish to create the user filling useful information (First name, last name, email) with the second form. If a user is destined to be an administrator of the database, check the boxes ‘staff status’ and ‘superuser status’.



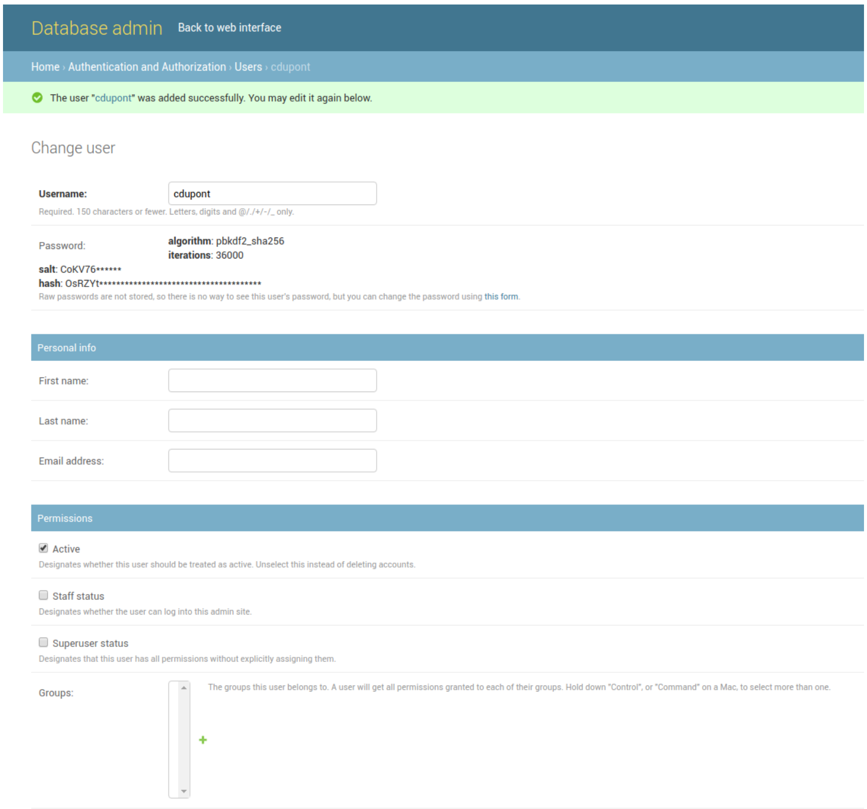
Select user to change

☐	USERNAME	EMAIL ADDRESS	FIRST NAME	LAST NAME	STAFF STATUS
☐	ad				✓
☐	cpacteau				✓
☐	eva	eva@inra.fr	Eva	D	✓
☐	fmunoz				✓
☐	gaelle				✓
☐	mathieu				✓
☐	melanie	melanie@inra.fr	Melanie	M	✓
☐	newuser				✗
☐	pierre				✓
☐	sophie				✓
☐	yannick	yannick@inra.fr	Yannick	De Oliveira	✓

11 users

Figure 1: User list

To edit a user, from the all users screen, click on the login. All information of a user can be updated with the form. Click on ‘Save’ to validate the changes. To reset the password of a user follow the link ‘this form’ in the ‘Password’ field set. To delete a user click on the ‘Delete’ button in the left down corner of the form and then confirm in the next screen that you really want to delete this user.



The user "cdupont" was added successfully. You may edit it again below.

Change user

Username: cdupont

Required. 150 characters or fewer. Letters, digits and @/./+/-/_ only.

Password: **algorithm**: pbkdf2_sha256 **iterations**: 36000 **salt**: CoKV76****** **hash**: OsRZYt**************************************

Raw passwords are not stored, so there is no way to see this user's password, but you can change the password using this form.

Personal info

First name:

Last name:

Email address:

Permissions

☑ Active

Designates whether this user should be treated as active. Unselect this instead of deleting accounts.

☐ Staff status

Designates whether the user can log into this admin site.

☐ Superuser status

Designates that this user has all permissions without explicitly assigning them.

Groups:

The groups this user belongs to. A user will get all permissions granted to each of their groups. Hold down "Control", or "Command" on a Mac, to select more than one.

Figure 2: New user creation form

B.1.b Users status

A user can have two status in SHiNeMaS : Administrator or read only. When creating/editing an admin user, it is import to check the two boxes ‘staff status’ and ‘superuser status’ (Figure 1) that the user has a full access to administrator features. The ‘superuser’ field enables create/modify/delete features on any data in the database. The ‘staff’ field gives access to the ‘admin’ screens of the SHiNeMaS web interface (link at the right top corner). The two boxes must be unchecked to create a read only user.

B.2 Projects and actors management

B.2.a Projects management

To manage projects go to the menu Admin data > Actors & Users > Projects. This screen displays a list of all projects in the database.

To create a new project, click on ‘Add project’, the form must be filled with a name and the starting date of this project. Click on the ‘Save’ button to validate it’s creation.

To edit a project, from the all project list screen, click on the name of a project. All information of a project can be edited with the next form. Click on ‘Save’ to validate modification.

To delete a project click on the ‘Delete’ button in the down left corner of the form and then confirm deletion in the next screen.

B.2.b Network actors (Person) management

The ‘person’ or actors of the network are physical people who produce data to store in the database without having necessarily a user access. To manage ‘people’ of SHiNeMaS go to the menu Admin data > Actors & Users > Persons. This screen displays all people already existing.

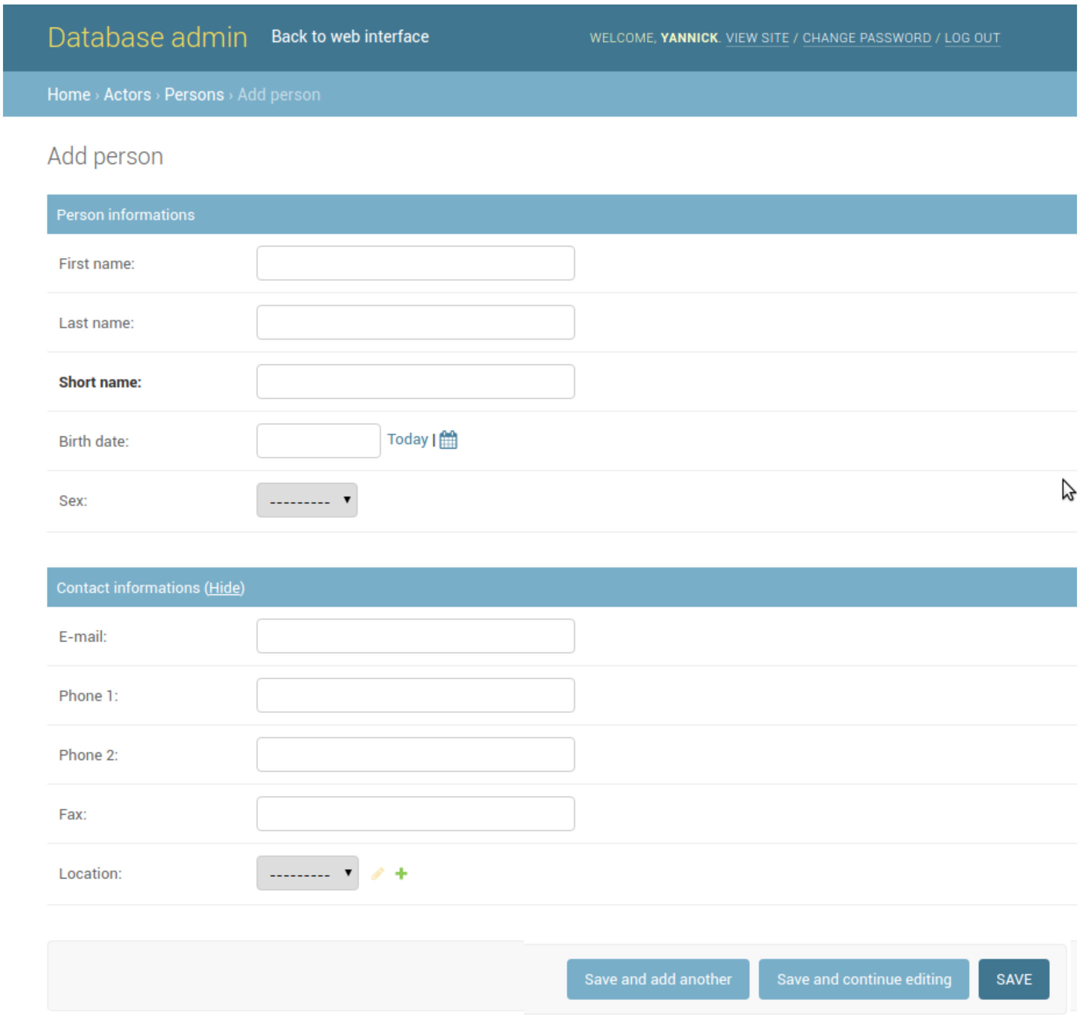


Figure 3: New person form

To create a new person click on ‘Add person’, the form (Figure 3) must be filled with a first name, a last name and a short name which will be used in many other screen of the app. By clicking on ‘Show’ a second part of the form is displayed in which contact information can be filled. Click on ‘Save’ to validate its creation.

To edit a person, from the people list screen, click on the short name. All information of a person can be edited from the form. Click on ‘Save’ to validate the modification.

To delete a person, click on the ‘Delete’ button in the down left corner and the confirm the deletion in the next screen.

B.2.c Location/farm (Location) management

To manage locations in the app go in the menu Admin data > Actors & Users > Locations. This screen shows all the existing locations.

To create a new location click on ‘Add location’. The form (Figure 4) must be filled with a name and other optional information as well as a short name (mandatory) for this location. This short name is import as it is used as described in « Rules about nomenclature of seeds lots» chapter. Click on ‘Save’ to validate its creation.

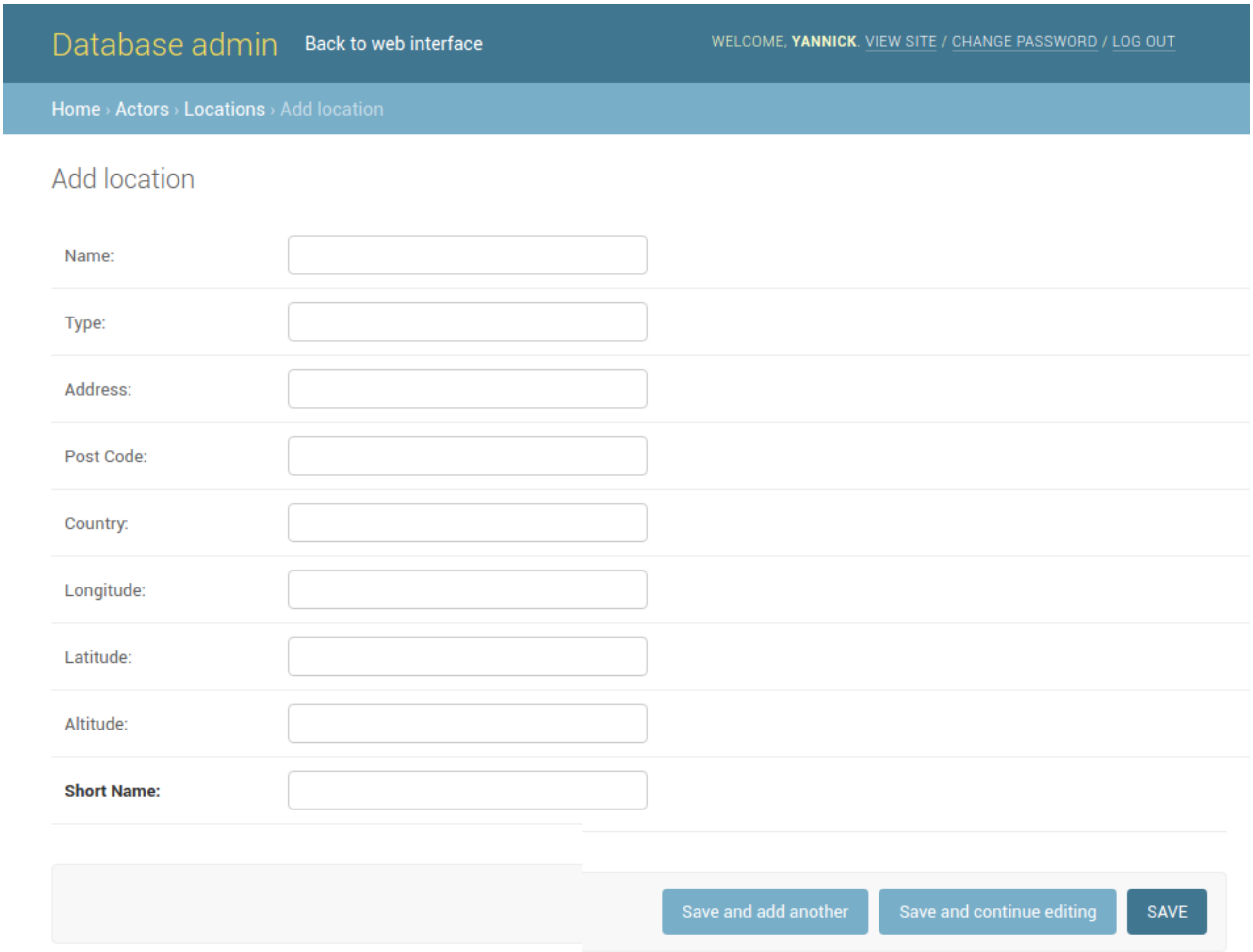


Figure 4: New location creation form

To edit a location, from the all locations screen, click on a location name. All information except the short name can be edited with the form. Click on ‘Save’ to validate the modification.

To delete a location click on the « Delete » button in the down left corner of the form and then confirm the deletion in the next screen.

B.3 Biological entities management

B.3.a Species management

To manage species in SHiNeMaS go to the menu Admin data > Biological Entities > Species. This screen displays all the existing species in the database.

To create a new species click on ‘Add species’. The form must be filled with a name (‘species’ field) as well as the Latin name and a description (optional) for this species. Click on ‘Save button to validate its creation.

To edit a species, from the all species screen, click on its name. All information of a species can be edited with the form. Click on the ‘Save’ button to validate the modification.

To delete a species, click on the ‘Delete’ button at the down left corner and then confirm deletion in the next screen.

B.3.b Germplasm type management

To manage germplasm type in SHiNeMaS go to the menu Admin data > Biological Entities >

Germplasm type. This screen displays all the existing germplasm type in the database.

To create a new germplasm type click on ‘Add germplasm_type’. The form must be filled with a name for this type as well as a description for this germplasm type. Click on ‘Save button to validate its creation.

To edit a germplasm type, from the all germplasm type screen, click on its name. All information of a germplasm type can be edited with the form. Click on the ‘Save’ button to validate the modification.

To delete a germplasm type, click on the ‘Delete’ button at the down left corner and then confirm deletion in the next screen.

B.3.c Germplasm management

To manage germplasm in SHiNeMaS go to the menu Admin data > Biological Entities > Germplasm. This screen displays all the existing germplasm in the database.

To create a new germplasm click on ‘Add germplasm’. The form must be filled with a name for this germplasm. It’s also possible to fill a germplasm type, a species (recommended) as well as the person who create this germplasm. Click on ‘Save button to validate its creation.

To edit a germplasm, from the all germplasm screen, click on its name. All information of a germplasm can be edited with the form except its name as it would impact all seeds lot names as described in « Rules about nomenclature of seeds lots» chapter. Click on the ‘Save’ button to validate the modification.

To delete a germplasm, click on the ‘Delete’ button at the down left corner and then confirm deletion in the next screen.

B.3.d Seeds lot management

To manage seeds lot go to the menu Admin data > Biological Entities > Seed lot.

It is not possible to create new seeds lot with admin web interfaces. New seeds lot are created through network events (see Seeds lot network management).

To edit a seeds lot, from the all seeds lot screen, click on its name. Only few information can be edited with this form. The name, the germplasm, creation date can’t be edited as it would have an impact on all the descendants of this seed lot. Generation information can be edited but information of the descendants and ascendants is not yet recalculated. It’s up to the user to be careful with this information. Click on the ‘Save’ button to validate the modification.

To delete a seeds lot, click on the ‘Delete’ button at the down left corner and then confirm deletion in the next screen.

B.4 Seeds lot network management

B.4.a Reproduction method management

To manage reproduction methods in SHiNeMaS go to the menu Admin data > Data Descriptors > Repro. method. This screen displays all the existing reproduction methods in the database.

To create a new reproduction method click on ‘Add reproduction_method’. The form must be filled with a name for this method as well as a description (optional) for this method. Click on ‘Save button to validate its creation.

To edit a reproduction method, from the all reproduction methods screen, click on its name. All information of a reproduction method can be edited with the form. Click on the ‘Save’ button to validate the modification.

To delete a reproduction method, click on the ‘Delete’ button at the down left corner and then confirm deletion in the next screen.

B.4.b Data methods management

To manage data methods in SHiNeMaS go to the menu Admin data > Data Descriptors > Data method. This screen displays all the existing data methods in the database.

To create a new data method click on ‘Add method’. The form must be filled with a name for this method as well as a description, a unit and some other information (optional) for this method. Click on ‘Save button to validate its creation.

To edit a data method, from the all data methods screen, click on its name. All information of a data method can be edited with the form. Click on the ‘Save’ button to validate the modification.

To delete a data method, click on the ‘Delete’ button at the down left corner and then confirm deletion in the next screen.

B.4.c File preparation

B.4.c.i Submitted file format

The submission files in SHiNeMaS are « tabulated » files and must fit with the following rules :

- Text file
- Column separator : tabulation
- Text delimiter : "

For example, a file open with a simple text editor, that will be submitted into SHiNeMaS must look like this :

```
"project"	"location"	"id_seed_lot"	"etiquette"	"event_year"	"split"	"quantity"
"PPB"	"FLM"	"Rouge-du-Roc_JFB_2004_0001"		2004	1	250
"PPB"	"FLM"	"Clomone_JFB_2004_0001"	2004	1	122
```

Each file type is described by mandatory fields (headers). It is possible to add additional columns regarding the method file (chapter B.4.c.ii). With this feature a user can customize variables definition.

B.4.c.ii Method file

Description

The method file contains the description of measures and the methods used to make these measures. Four fields described this file :

- **variable** : the name of the measured variable
- **type** : the type of the variable (variable types are described in the next chapter)
- **method_name** : the name of the method used to measure this variable.
- **correlation_group** : correlation groups used for this variable. Correlation groups usage is described in after the « variable type » chapter.

Variable type

Each data can have a different scope regarding the context. The scope affect how data are linked to the relations in a particular event. The table 1 described the variable types regarding their scope.

Type	*Scope*
Type 1	Whatever the event type, the data is linked to all the relations.
Type 2	In a breeding-cross the data is linked to the male relation
Type 3	In a breeding-cross the data is linked to the female relation
Type 4	In a reproduction, the data is linked only to the selection
Type 5	In a mixture, the data is linked to only one relation of the mixture
Type 6	In a reproduction, the data is linked to any relation that is not a selection
Type 7	The data is linked to the parent seeds lot
Type 8	The data is linked to the child seeds lot
Type 9	In a breeding-cross, the data is linked to the male seeds lot
Type 10	In a breeding-cross, they data is linked to the female seeds lot
Type 11	The data is an individual data

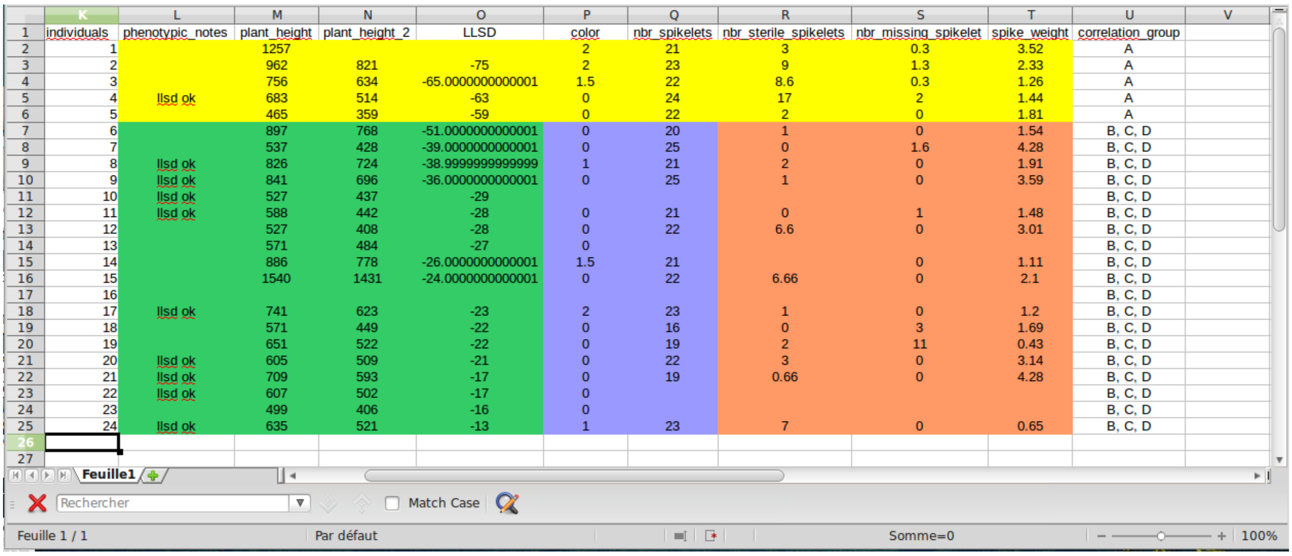
Table 1: Definition of the variable type and their scope

Correlation groups

Correlation groups are used for individual data. Let’s consider a data series (at a same date for example) on numerated individuals. For the next series (at another date) the user collect data on the same number of individuals. But two scenarios can occur :

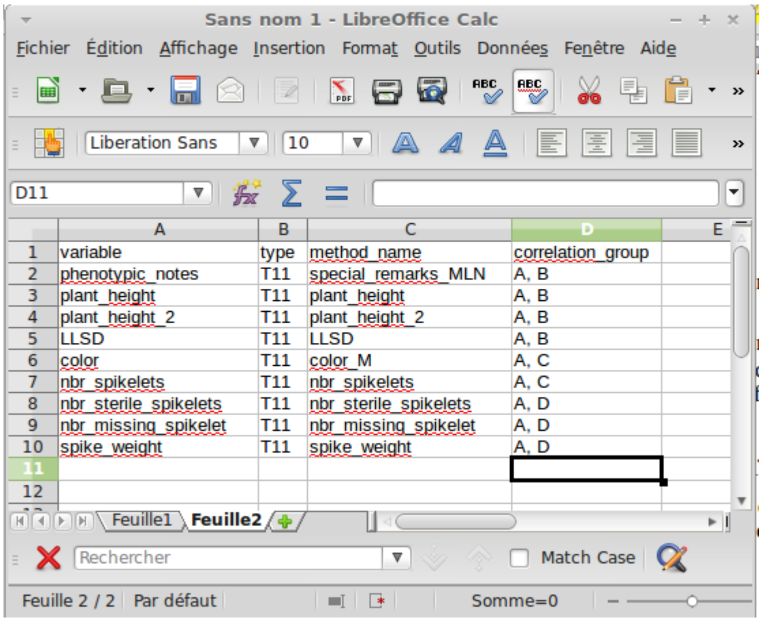
- The numerated individuals are not the same (You lost the numeration between the two series of data). In that case the data of the first series and the second series can’t be correlated as it’s haven’t be done on the same individuals. Example : Figure 5, on a single line, data in green, blue and orange aren’t correlated and belongs to 3 different groups B, C, and D
- The numerated individuals are the same. In that case all data can belong to the same correlation group. Example : Figure 5, the lines in yellow. The data belongs to the group A.

In the method file you should report in the **correlation_group** column all the correlation groups in which a variable is implied (Figure 6). For example, the variable ‘plant_height’ is implied in the correlation groups A (yellow) and B (green).



	K	L	M	N	O	P	Q	R	S	T	U	V
1	individuals	phenotypic_notes	plant_height	plant_height_2	LLSD	color	nbr_spikelets	nbr_sterile_spikelets	nbr_missing_spikelet	spike_weight	correlation_group	
2	1		1257			2	21	3	0.3	3.52	A	
3	2		962	821	-75	2	23	9	1.3	2.33	A	
4	3		756	634	-65.0000000000001	1.5	22	8.6	0.3	1.26	A	
5	4	llsd ok	683	514	-63	0	24	17	2	1.44	A	
6	5		465	359	-59	0	22	2	0	1.81	A	
7	6		897	768	-51.0000000000001	0	20	1	0	1.54	B, C, D	
8	7		537	428	-39.0000000000001	0	25	0	1.6	4.28	B, C, D	
9	8	llsd ok	826	724	-38.9999999999999	1	21	2	0	1.91	B, C, D	
10	9	llsd ok	841	696	-36.0000000000001	0	25	1	0	3.59	B, C, D	
11	10	llsd ok	527	437	-29						B, C, D	
12	11	llsd ok	588	442	-28	0	21	0	1	1.48	B, C, D	
13	12		527	408	-28	0	22	6.6	0	3.01	B, C, D	
14	13		571	484	-27	0					B, C, D	
15	14		886	778	-26.0000000000001	1.5	21		0	1.11	B, C, D	
16	15		1540	1431	-24.0000000000001	0	22	6.66	0	2.1	B, C, D	
17	16										B, C, D	
18	17	llsd ok	741	623	-23	2	23	1	0	1.2	B, C, D	
19	18		571	449	-22	0	16	0	3	1.69	B, C, D	
20	19		651	522	-22	0	19	2	11	0.43	B, C, D	
21	20	llsd ok	605	509	-21	0	22	3	0	3.14	B, C, D	
22	21	llsd ok	709	593	-17	0	19	0.66	0	4.28	B, C, D	
23	22	llsd ok	607	502	-17	0					B, C, D	
24	23		499	406	-16	0					B, C, D	
25	24	llsd ok	635	521	-13	1	23	7	0	0.65	B, C, D	
26												
27												

Figure 5: Individual data file – correlation groups



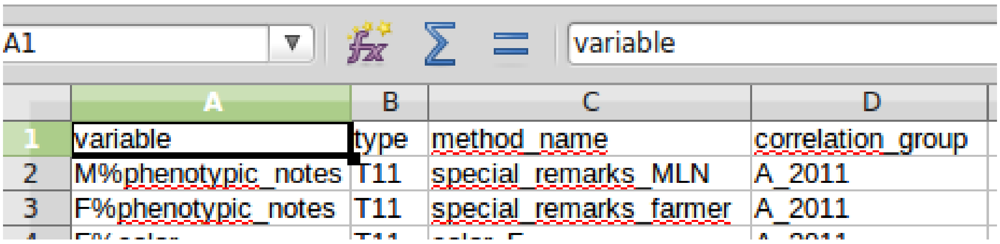
	A	B	C	D	E
1	variable	type	method_name	correlation_group	
2	phenotypic_notes	T11	special_remarks_MLN	A, B	
3	plant_height	T11	plant_height	A, B	
4	plant_height_2	T11	plant_height_2	A, B	
5	LLSD	T11	LLSD	A, B	
6	color	T11	color_M	A, C	
7	nbr_spikelets	T11	nbr_spikelets	A, C	
8	nbr_sterile_spikelets	T11	nbr_sterile_spikelets	A, D	
9	nbr_missing_spikelet	T11	nbr_missing_spikelet	A, D	
10	spike_weight	T11	spike_weight	A, D	
11					
12					

Figure 6: Fichier méthodes - groupes de corrélation

Particular case

It is possible to measure a same variable with two different method. To do the variable must be tagged with a prefix in the data file and in the method file. The following syntax is used (see Figure 7) :

prefix%variable_name



	A	B	C	D
1	variable	type	method_name	correlation_group
2	M%phenotypic_notes	T11	special_remarks_MLN	A_2011
3	F%phenotypic_notes	T11	special_remarks_farmer	A_2011

Figure 7: prefix usage to define a variable used with two methods

B.4.c.iii Rules about nomenclature of seeds lots

Case of already existing seed lots in the database

A nomenclature has been defined in SHiNeMaS in order to ensure the uniqueness of the data base seeds lots names. It bases on 3 indications : the name of the variety (VARIETE), the seed lot's creation year (ANNEE) and the location of this seed lot (LOCATION). We can imagine that one single variety has given several seed lots during one year on a single location. Therefore, a fourth indication is used : a four digits code (NUM) ensuring the uniqueness of a seeds lot.

Those indications are separated by an underscore ('_'). The use of this character is then forbidden to define a variety's name or the short name of a person.

A seeds lots' name is written as follows :

VARIETE_ANNEE_PERSON_NUM

Case of non already existing seeds lots in the database

This case happens when a seed lot enters the seeds history network although it has never appeared in the network before. In that case, the user has to indicate the following indications in the box corresponding to the seeds lot ID :

VARIETE_ANNEE_PERSON

The app will calculate automatically the four digits extension necessary to (1) ensure the uniqueness of the seeds lot's name and (2) respect the nomenclature defined in SHiNeMaS. If the variety VARIETE doesn't exist in the database, it would be created automatically.

It is important to indicate that it is possible to use the same structure VARIETE_ANNEE_PERSON several times in a single file. The app will consider that it refers to the same seeds lots used several times.

Selections' cases

When a selection is done (chapter B.4.c.viii) the seeds lot's name follows a specific nomenclature including the selection's name (SEL) :

VARIETE#SEL_ANNEE_PERSON_NUM

The '#' character (diez) is used to combine the variety's name to the selection's name. This character cannot be used in the variety's name. The expression VARIETE#SEL will be transferred to all the descending seeds lots when it is a reproduction or a spreading. If a new selection (NSEL) is done on a descending seeds lots, the expression SEL is then replaced by NSEL as follows :

VARIETE#NSEL_ANNEE_PERSON_NUM

As a mixture or a cross-breeding creates a new variety, the selection name's indication disappears and the seeds lot's name a classic nomenclature described in the first paragraph.

B.4.c.ivCross-breeding file

Objective

This file allows to create cross-breeding events between different varieties, as shown on Figure 8. A cross-breeding creates a new variety.

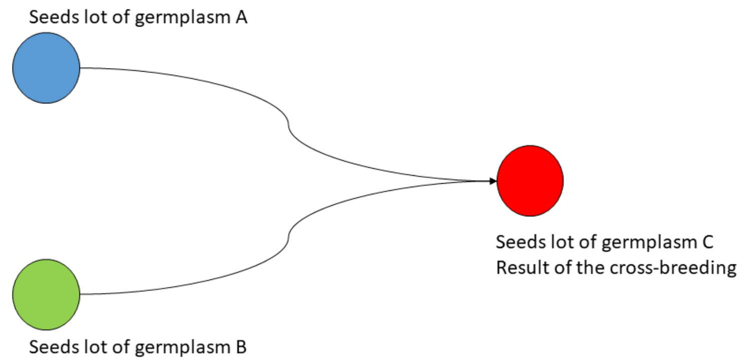


Figure 8: Cross-breeding picture

File structure

The breeding file describes the information necessary to create a cross-breeding event in the database. The fields needed to create a breeding are the following :

- **project** : Project in which the event has occurred

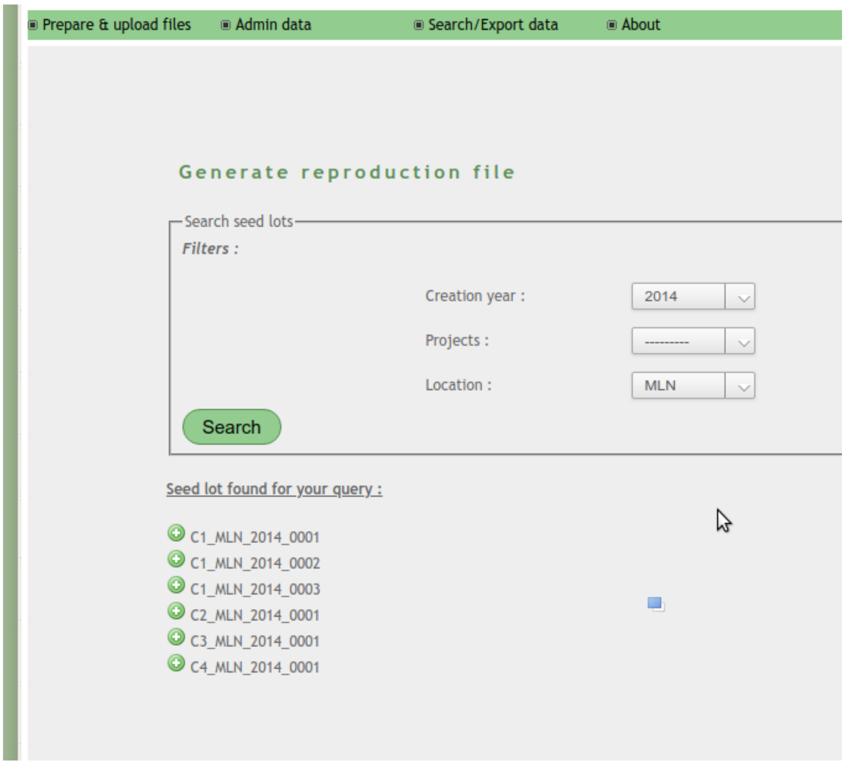
- **sown_year** : Parents seeds lots' sown year.
- **harvested_year** : Harvest year of the seed lot descended from the cross-breeding
- **quantity_harvested** : Quantity harvested after the cross-breeding. It is the initial quantity of the harvested seeds lot.
- **cross_year** : Year of the cross-breeding
- **cross_germplasm** : Name of the new created variety
- **number_crosses** : Number of cross-breeding done
- **kernel_number_F1** : Number of seeds obtained from the cross-breeding and used for the F1
- **male_seed_lot** : ID of the seeds lot used as a male
- **male_etiquette:** Label used for the male seed lot
- **male_split:** Indicates if the entire seed lot was used at cross-breeding: 0 for all and 1 otherwise
- **male_quantity:** Quantity of seeds from the seed lot used
- **male_block:** Block in which the seed lot has been sown
- **male_X:** X coordinate of the male seed lot
- **male_Y:** Y coordinate of the male seed lot
- **female_seed_lot:** Identifier of the seed lot used as female
- **female_etiquette**: Label used for the female seed lot
- **female_split:** Indicates if the entire female seed lot was used for the cross-breeding: 0 for all and 1 otherwise
- **female_quantity:** Quantity of the female seed lot used
- **female_block:** Block in which the female seed lot has been sown
- **female_X:** X coordinate of the female seed lot
- **female_Y:** Y coordinate of the female seed lot

Prepare a file

To prepare a cross-breeding file, go to the Prepare & Upload File> Prepare Files> Cross menu. This interface provides a “download template file” link to download a file filled with mandatory headers for cross-breeding.

A simplified search interface (Figure 9) suggests to search for seeds already filled in the database according to 3 criteria: year of creation, projects in which they are used, place on which they are stored.

A list is displayed with two icons ♂ ♀ that allow by a single click to add the seed lot to a list of lots that will be used as male or female (Figure 10). This list is visible by clicking on the icon 🟦 on the right of the results list. The lots are grouped by two (male / female). This action brings up a window that allows you to delete pairs of seed lots from the list or to complete the file preparation information.



Generate reproduction file

Search seed lots

Filters :

Creation year : 2014

Projects : ---------

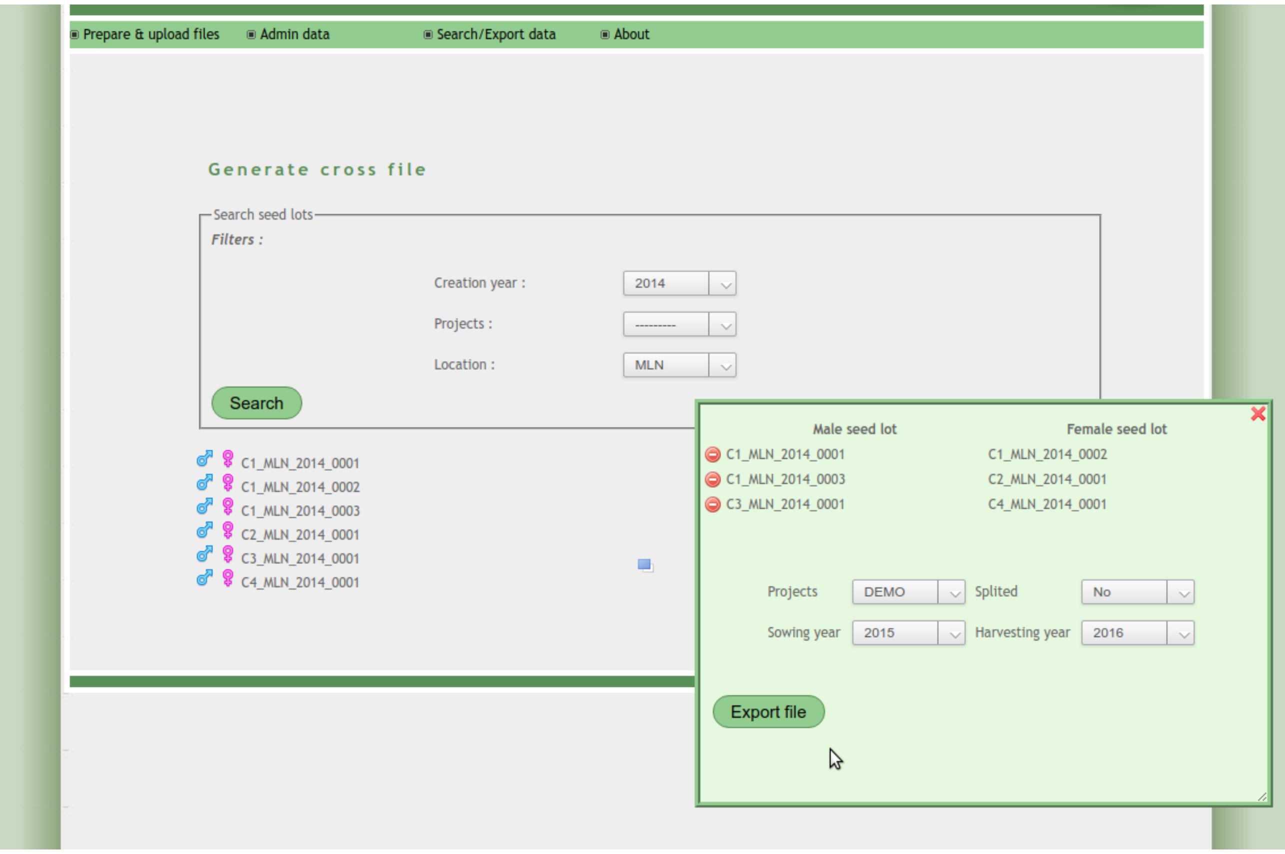
Location : MLN

Seed lot found for your query :

- C1_MLN_2014_0001
- C1_MLN_2014_0002
- C1_MLN_2014_0003
- C2_MLN_2014_0001
- C3_MLN_2014_0001
- C4_MLN_2014_0001

Figure 9: Simplified search form

Clicking on the 'Export File' button will download the pre-filled cross-breeding file. A user can also modify the search filters and restart it to complete his list of seed lots.



Generate cross file

Search seed lots

Filters :

Creation year : 2014

Projects : ---------

Location : MLN

- ♂ ♀ C1_MLN_2014_0001
- ♂ ♀ C1_MLN_2014_0002
- ♂ ♀ C1_MLN_2014_0003
- ♂ ♀ C2_MLN_2014_0001
- ♂ ♀ C3_MLN_2014_0001
- ♂ ♀ C4_MLN_2014_0001

Male seed lot	Female seed lot
C1_MLN_2014_0001	C1_MLN_2014_0002
C1_MLN_2014_0003	C2_MLN_2014_0001
C3_MLN_2014_0001	C4_MLN_2014_0001

Projects DEMO

Splited No

Sowing year 2015

Harvesting year 2016

Figure 10: Cross file preparation interface

B.4.c.v Diffusion file

Objective

This file is used to create diffusion events. A diffusion makes possible to send a seeds lot, entirely or partly, from a place A to a place B, as represented on Figure 11.

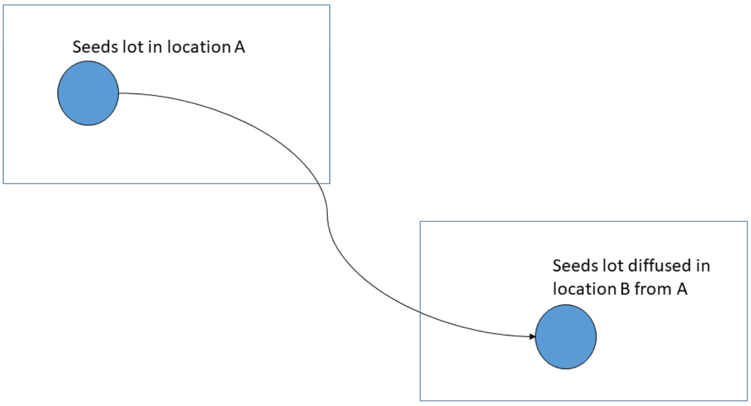


Figure 11: Diffusion picture

File structure

The diffusion file describes the information needed to create a diffusion event in the database. The fields required to create a diffusion are:

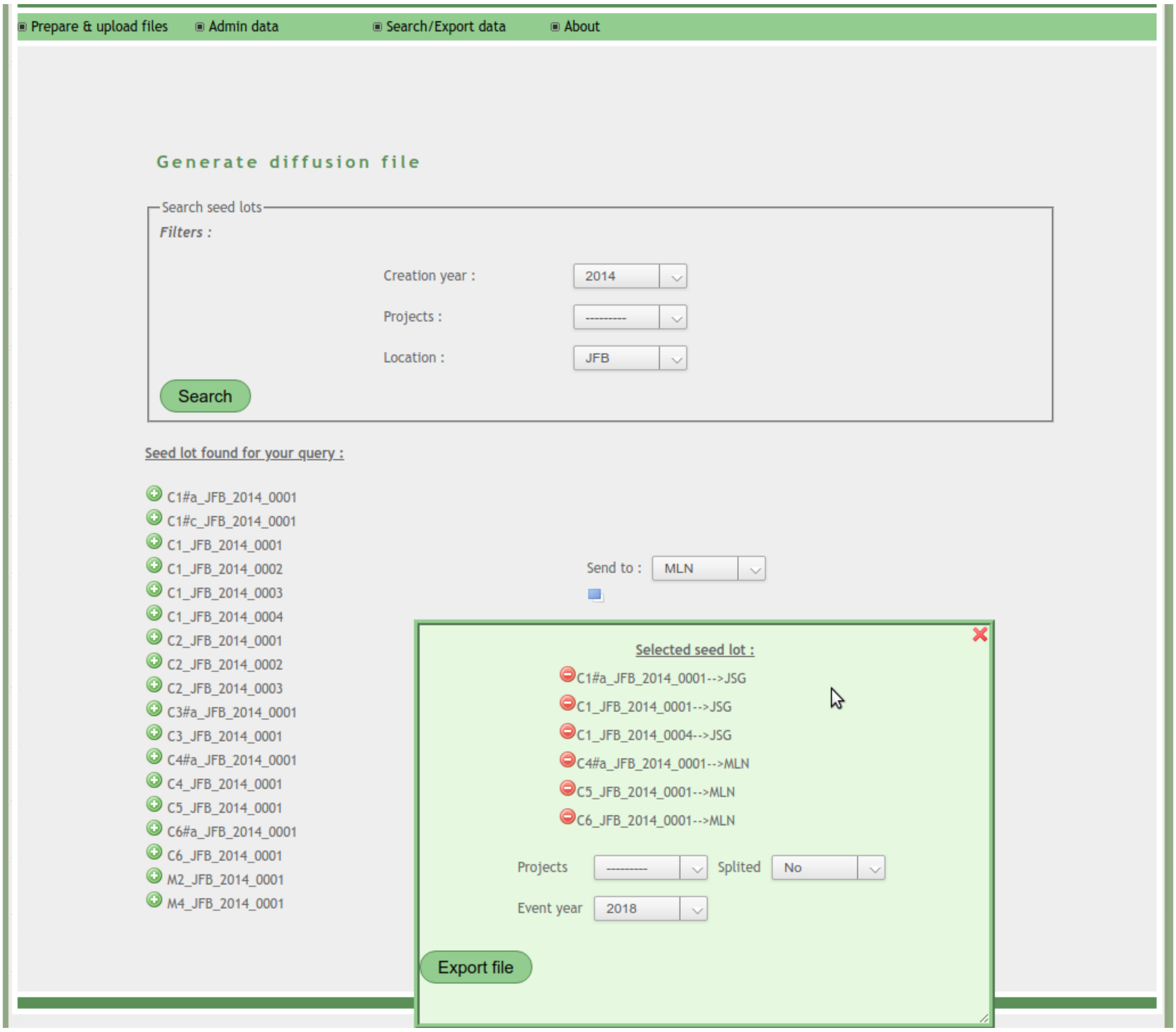
- **project** : Project in which the diffusion takes place
- **location** : Place where the seed lot is diffused
- **id_seed_lot** : Identifier of the "parent" sent seed lot
- **etiquette** : Label used for the parent seed lot
- **event_year** : Year of the diffusion
- **split** : Indicates if the entire "parent" seed lot has been diffused: 0 for all and 1 otherwise
- **quantity** : Quantity of seed lot released ("child" seed lot)

Prepare a file

To prepare a diffusion file, go to the menu Prepare & Upload File> Prepare Files> Diffusion. This interface provides a “download template file” link to download a file filled with mandatory headers for a diffusion event.

A simplified search interface (Figure 9) suggests to search for seeds already filled in the database according to 3 criteria: year of creation, projects in which they are used, place on which they are stored.

A list is displayed (Figure 12), you should select in a drop-down list the place of destination, then click on the ⊕ icon to add the seeds lots that will be used in a distribution relationship. The list is visible by clicking on the ❐ icon on the right of the results list. This action brings up a window that allows you either to erase seed lots from the list or to complete the file preparation information.



Generate diffusion file

Search seed lots

Filters :

Creation year : 2014

Projects : ---------

Location : JFB

Seed lot found for your query :

- C1#a_JFB_2014_0001
- C1#c_JFB_2014_0001
- C1_JFB_2014_0001
- C1_JFB_2014_0002
- C1_JFB_2014_0003
- C1_JFB_2014_0004
- C2_JFB_2014_0001
- C2_JFB_2014_0002
- C2_JFB_2014_0003
- C3#a_JFB_2014_0001
- C3_JFB_2014_0001
- C4#a_JFB_2014_0001
- C4_JFB_2014_0001
- C5_JFB_2014_0001
- C6#a_JFB_2014_0001
- C6_JFB_2014_0001
- M2_JFB_2014_0001
- M4_JFB_2014_0001

Send to : MLN

Selected seed lot :

- C1#a_JFB_2014_0001-->JSG
- C1_JFB_2014_0001-->JSG
- C1_JFB_2014_0004-->JSG
- C4#a_JFB_2014_0001-->MLN
- C5_JFB_2014_0001-->MLN
- C6_JFB_2014_0001-->MLN

Projects ---------

Splited No

Event year 2018

Figure 12: Diffusion file preparation interface

Clicking on the 'Export File' button will download the pre-filled diffusion file. A user can also modify the search filters and restart it to complete his list of seed lots.

B.4.c.vi Mixture file

Objective

This file is used to create mixture events as shown in Figure 13. A mixture consists in using at least two seeds lots and grouping them into a single seeds lot. There is no limit on the number of seed lots that can be mixed. However, all seed lots must come from the same place. A mixture leads to the creation of a new variety.

File structure

The mixture file describes the information needed to create a mixture event in the database. The mixture file has the particularity of describing a mixture event on several lines of the file. Each line describes a lot of seeds used in the mixture. The **germplasm** field, repeated on several lines, makes possible to group the seeds lots that are used in the same mixture. The fields needed to create a mixture are:

- **project** : Project in which the mixture has been done

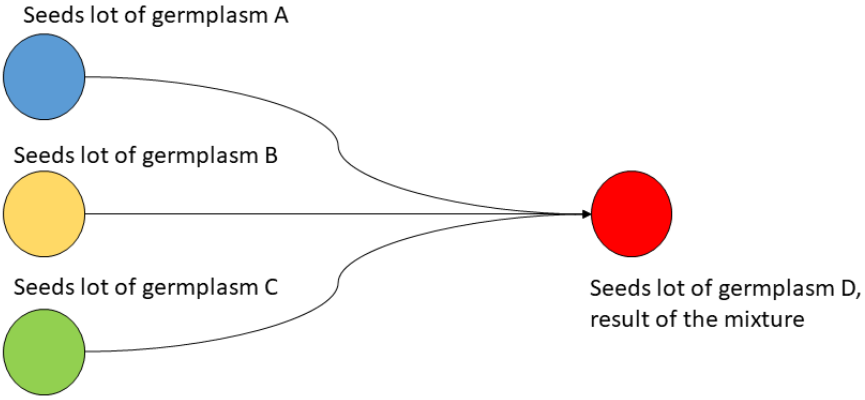


Figure 13: Mixture picture

- **id_seed_lot** : Identifier of the « parent » seeds lot mixed
- **etiquette** : Label used for the « parent » seeds lot
- **split** : Indicates if the entire seeds lot has been used for the mixture : 0 for all and 1 otherwise
- **quantity** : Quantity of the « parent » seeds lot mixed
- **germplasm** : Name of the created new variety
- **event_year** : Year of the mixture

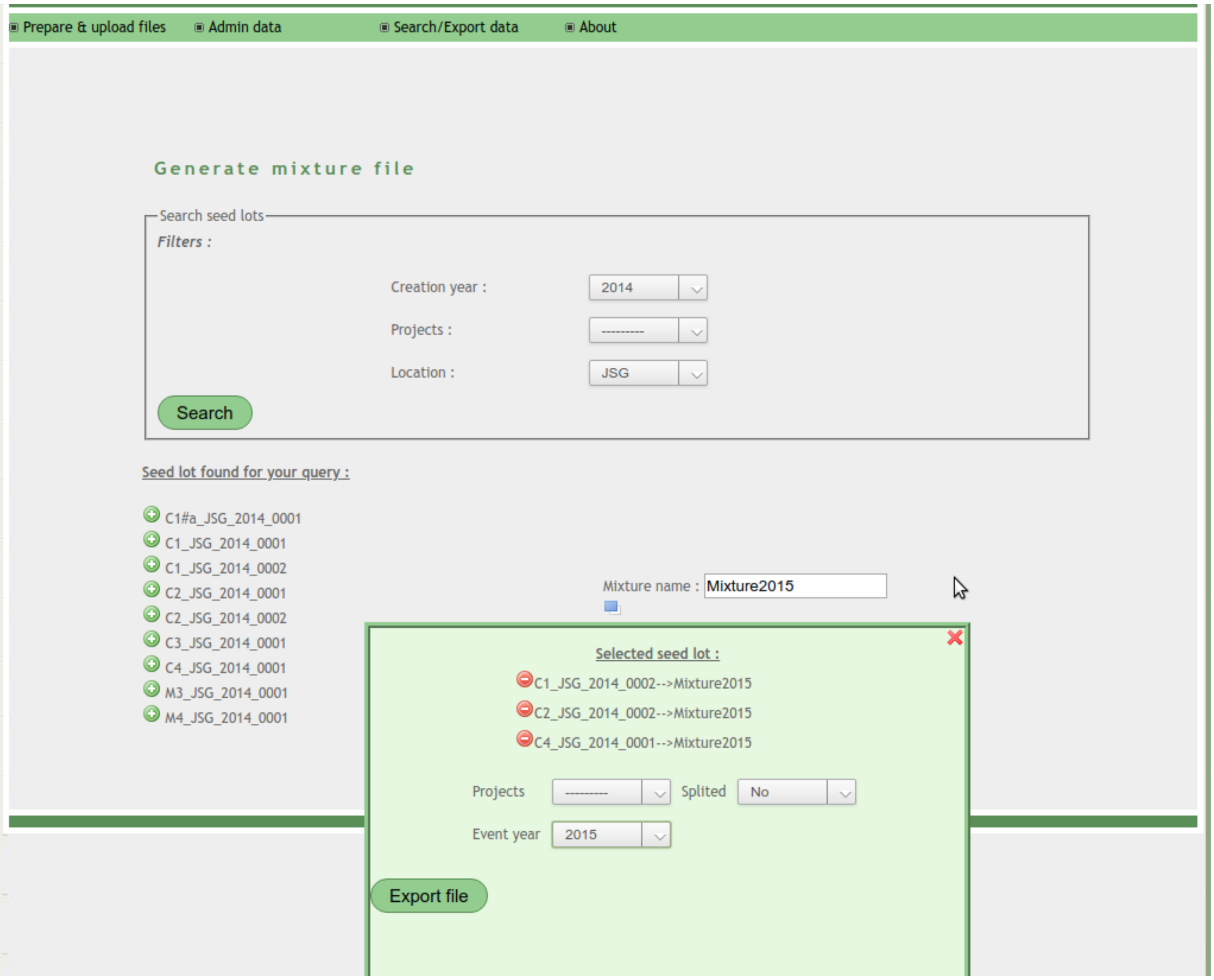
Prepare a file

To prepare a mixture file, go to the Prepare & Upload File> Prepare Files> Mixture menu. This interface provides a "download template file" link to download a file filled with mandatory headers for a mixture.

A simplified search interface (Figure 9) suggests to search for seeds already filled in the database according to 3 criteria: year of creation, projects in which they are used, place on which they are stored.

A list is displayed (Figure 14), you should indicate in a field text the name of the mixture and then click on the ⊕ icon to add the seeds lots that will be used in a mixing relationship. The list is visible by clicking on the ❐ icon on the right of the results list. This action brings up a window that allows you to either clear relationships from a mixture of seed lots or to complete the file preparation information.

Click on the 'Export File' button to download the pre-filled mixture file. A user can also modify the search filters and restart it to complete his list of seed lots.



Generate mixture file

Search seed lots

Filters :

Creation year : 2014

Projects : ---------

Location : JSG

Seed lot found for your query :

C1#a_JSG_2014_0001
C1_JSG_2014_0001
C1_JSG_2014_0002
C2_JSG_2014_0001
C2_JSG_2014_0002
C3_JSG_2014_0001
C4_JSG_2014_0001
M3_JSG_2014_0001
M4_JSG_2014_0001

Mixture name : Mixture2015

Selected seed lot :

C1_JSG_2014_0002-->Mixture2015
C2_JSG_2014_0002-->Mixture2015
C4_JSG_2014_0001-->Mixture2015

Projects ---------
Splited No
Event year 2015

Figure 14: Mixture file preparation interface

B.4.c.vii Reproduction file

Objective

This file makes it possible to create reproduction events as described on Figure 15. A reproduction takes place on a given place, at a given position, defined by its **block** and its **X** and **Y** coordinates.

A reproduction consists in sowing a seed lot at one or more locations and then harvesting the seed lot(s).

Figure 15: Reproduction picture

File structure

This file makes it possible to create reproduction events as described on Figure 4. A reproduction takes place on a given place, at a given position, defined by its block and its X and Y coordinates:

- **project** : Project in which the reproduction takes place
- **sown_year** : Sowing year of the parent seed lot
- **harvested_year** : Harvest year of seed lot "child"
- **id_seed_lot_sown** : ID of the « parent » sown seed lot
- **intra_selection_name :** Name of the selection
- **etiquette** : Label used for the « parent » seed lot
- **split** : Indicates if the entire « parent » seed lot has been sown : 0 for all, 1 otherwise
- **quantity_sown** : Quantity of the « parent » seed lot used
- **quantity_harvested** : quantity harvested for the « child » seed lot
- **block** : location block of the reproduction
- **X** : coordinate X
- **Y** : coordinate Y

Prepare files

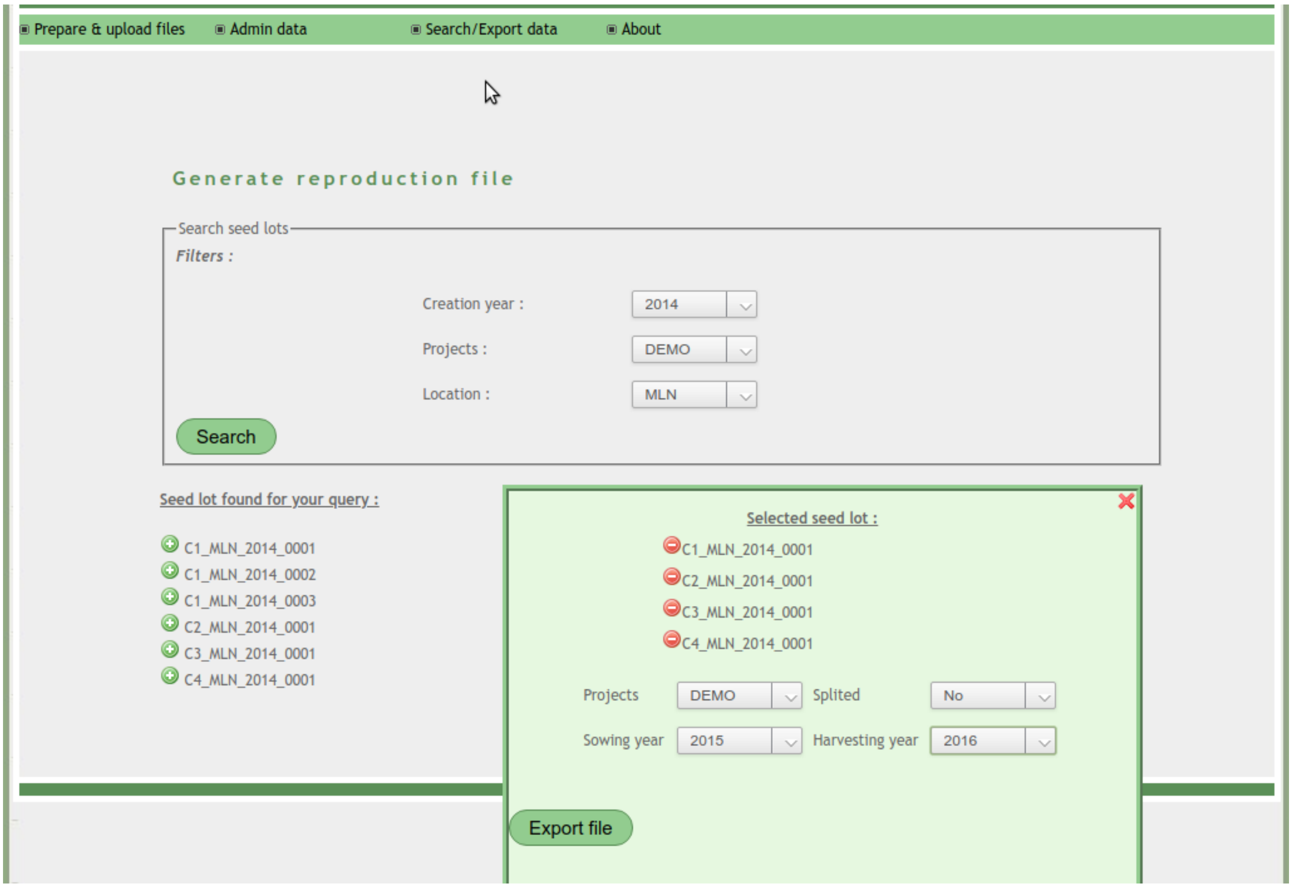
Two scenarios can occur to create a reproduction file. Either the file is submitted a first time (at sowing, for example). In this case the user will select a list of lots of seeds to be sown. In the second case the user will submit a file containing measurements on already existing reproductions (a sowing file already submitted). In this case the user will select reproductions from a list. Both interfaces provide a “download template file” link to download a file filled with mandatory headers for reproduction.

To prepare a sowing file

To prepare a reproduction file go to the menu Prepare & Upload File> Prepare Files> Reproduction.

A simplified search interface (Figure 9) suggests to search for seeds already filled in the database according to 3 criteria: year of creation, projects in which they are used, place on which they are stored.

A list is displayed (Figure 16) that allows you to click on the ⊕ icon to add the seed lots that will be used in a reproduction relationship. This list is visible by clicking on the ❐ icon on the right of the results list. This action brings up a window that allows you either to erase reproductions or to complete file preparation information.



Generate reproduction file

Search seed lots

Filters :

Creation year : 2014

Projects : DEMO

Location : MLN

Seed lot found for your query :

⊕ C1_MLN_2014_0001
⊕ C1_MLN_2014_0002
⊕ C1_MLN_2014_0003
⊕ C2_MLN_2014_0001
⊕ C3_MLN_2014_0001
⊕ C4_MLN_2014_0001

Selected seed lot :

⊖ C1_MLN_2014_0001
⊖ C2_MLN_2014_0001
⊖ C3_MLN_2014_0001
⊖ C4_MLN_2014_0001

Projects DEMO
Splited No
Sowing year 2015
Harvesting year 2016

Figure 16: Reproduction file preparation interface

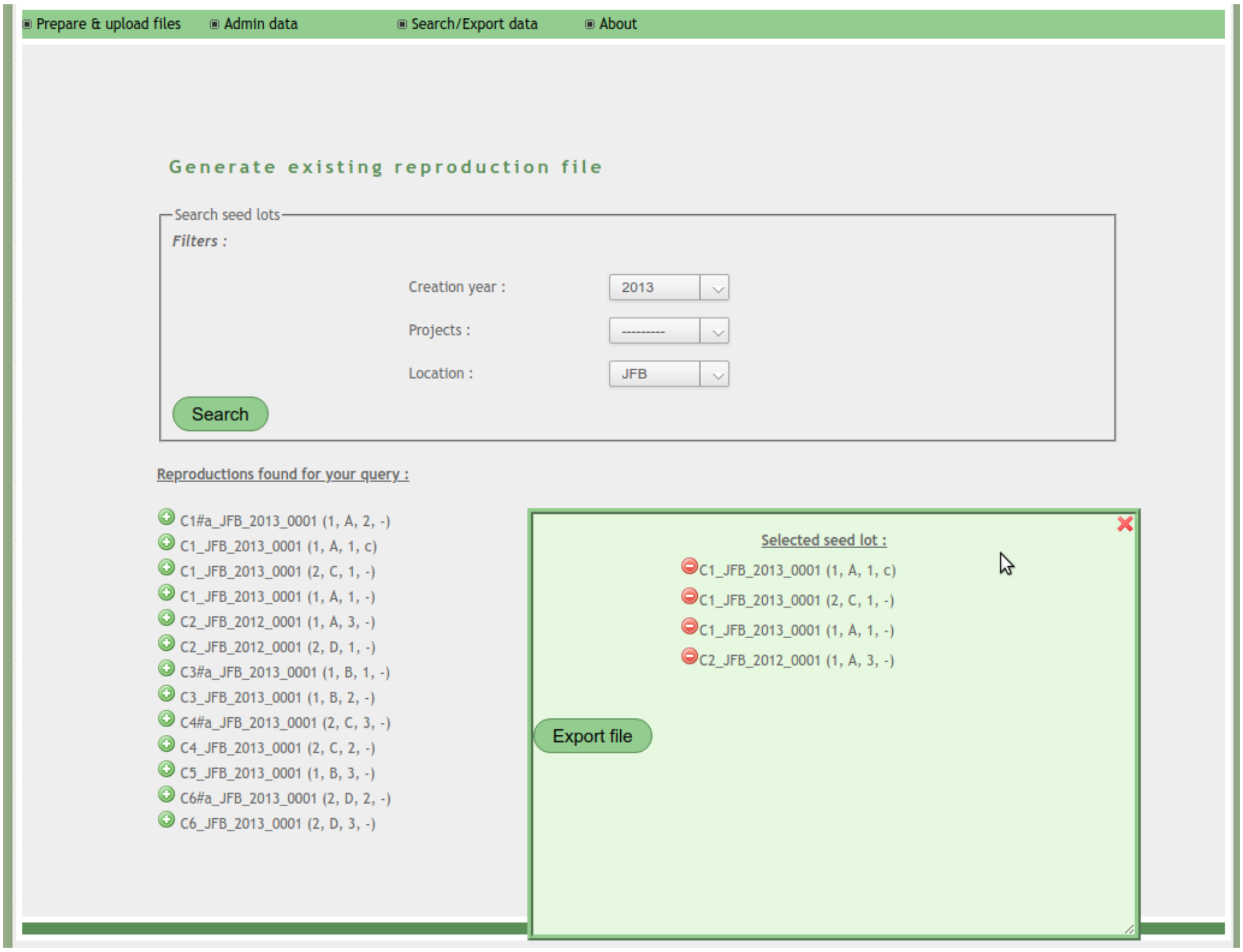
Clicking on the 'Export File' button will download the pre-filled reproduction file. A user can also modify the search filters and restart it to complete his list of seed lots.

Prepare an existing reproductions file

To prepare an existing reproductions file, go to the menu Prepare & Upload File> Prepare Files> Existing Reproduction.

A simplified search interface (Figure 9) suggests to search reproductions already existing in the database according to 3 criteria: year of creation of the seed lot seeded, projects related to the reproduction, place on which the reproduction takes place.

A list is displayed (Figure 17) which allows by a simple click on the ⊕ icon to add the reproductions to be exported in the file. The reproductions are here defined by the name of the seed lot sown and the location of the sowing. This list is visible by clicking on the ▭ icon on the right of the results list. This action brings up a window that allows you either to delete reproductions or to complete the file preparation information.



Generate existing reproduction file

Search seed lots

Filters :

Creation year : 2013
Projects : ---------
Location : JFB

Reproductions found for your query :

- C1#a_JFB_2013_0001 (1, A, 2, -)
- C1_JFB_2013_0001 (1, A, 1, c)
- C1_JFB_2013_0001 (2, C, 1, -)
- C1_JFB_2013_0001 (1, A, 1, -)
- C2_JFB_2012_0001 (1, A, 3, -)
- C2_JFB_2012_0001 (2, D, 1, -)
- C3#a_JFB_2013_0001 (1, B, 1, -)
- C3_JFB_2013_0001 (1, B, 2, -)
- C4#a_JFB_2013_0001 (2, C, 3, -)
- C4_JFB_2013_0001 (2, C, 2, -)
- C5_JFB_2013_0001 (1, B, 3, -)
- C6#a_JFB_2013_0001 (2, D, 2, -)
- C6_JFB_2013_0001 (2, D, 3, -)

Selected seed lot :

- C1_JFB_2013_0001 (1, A, 1, c)
- C1_JFB_2013_0001 (2, C, 1, -)
- C1_JFB_2013_0001 (1, A, 1, -)
- C2_JFB_2012_0001 (1, A, 3, -)

Figure 17: Existing reproduction file preparation interface

A click on the 'Export File' button will download the pre-filled reproduction file. A user can also modify the search filters and restart it to complete his list of reproductions.

B.4.c.viii Selection file

Objective

This file is used to create selection events as shown in Figure 18. A selection event is always associated with a reproduction. A selection can be made by an actor of the network.

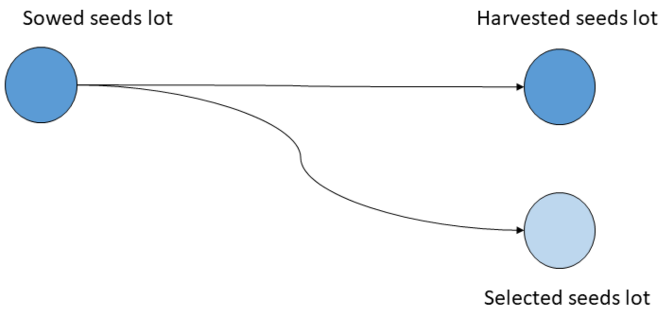


Figure 18: Selection picture

File structure

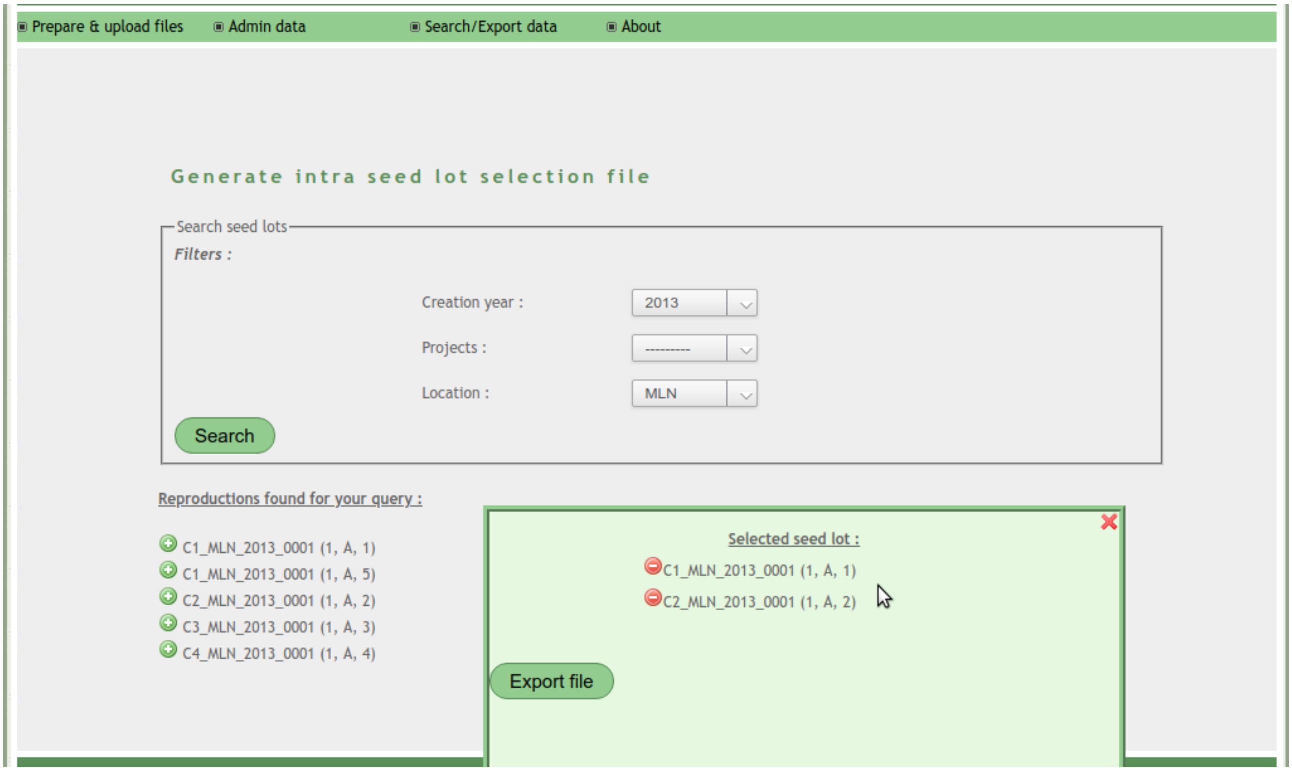
The selection file describes the information needed to create a selection event in the database. The fields required to create a selection are :

- **project** : Project in which the selection takes place
- **sown_year** : Sowing year of the « parent » seed lot
- **harvested_year** : Harvest year of seed lot « child »
- **id_seed_lot_sown** : Identifier of « parent » seed lots
- **etiquette** : Label used for the « parent » seed lot
- **block** : block where the reproduction take place
- **X** : X coordinate
- **Y** : Y coordinate
- **selection_person** : Short name informing the person who made the selection
- **selection_quantity_ini** : Quantity selected
- **selection_name** : Name given to this selection

Prepare a file

To prepare a selection file go to the menu Prepare & Upload File> Prepare Files> Intra seed lot selection. This interface provides a “download template file” link to download a file filled with mandatory headers for a selection event.

A simplified search interface (Figure 9) proposes to search reproductions already existing in the database according to 3 criteria: year of creation of the seed lot sown, projects related to the reproduction, place on which the reproduction takes place.
A list is displayed (Figure 19) which allows you to click on the ⊕ icon to add the reproductions to be exported to the file. The reproductions are here defined by the name of the seed lot sown and the location of the sowing. This list is visible by clicking on the ❐ icon on the right of the results list. This action brings up a window that allows you to either erase reproductions or complete file preparation information.



Generate intra seed lot selection file

Search seed lots

Filters :

Creation year : 2013

Projects : ---------

Location : MLN

Reproductions found for your query :

- C1_MLN_2013_0001 (1, A, 1)
- C1_MLN_2013_0001 (1, A, 5)
- C2_MLN_2013_0001 (1, A, 2)
- C3_MLN_2013_0001 (1, A, 3)
- C4_MLN_2013_0001 (1, A, 4)

Selected seed lot :

- C1_MLN_2013_0001 (1, A, 1)
- C2_MLN_2013_0001 (1, A, 2)

Figure 19: selection file preparation interface

Clicking on the 'Export File' button will download the pre-filled selection file. A user can also modify the search filters and restart it to complete his list of reproductions.

B.4.c.ix Individual data file

Objective

This file is used to enter individual data concerning reproductions or selections. Individual data is associated with numbered individuals.

File structure

The individual data file describes the information needed to insert individual data into the database. The fields required to insert this data are as follows:

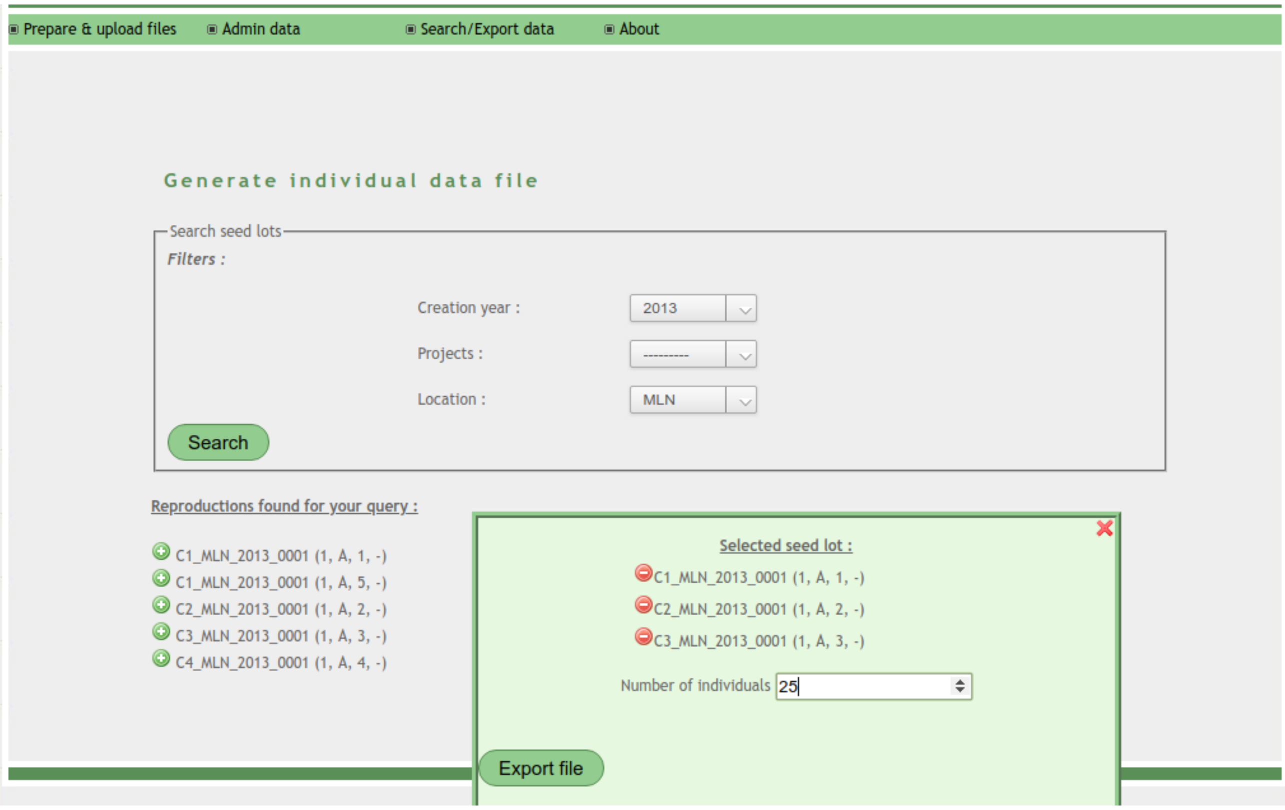
- **project** : Project in which the selection takes place
- **sown_year** : Sowing year of the « parent » seed lot
- **harvested_year** : Harvest year of seed lot « child »
- **id_seed_lot_sown** : Identifier of « parent » seed lots
- **intra_selection_name :** Name of selection if applicable
- **sown_etiquette** :Label used for the « parent » seed lot
- **id_seed_lot_harvested** : Identifier of the « child » seed lot harvested
- **harvested_etiquette** : Label used for the «child» seed lot
- **block** : block where the reproduction take place
- **X** : X coordinate
- **Y** : Y coordinate
- **individuals** : Number of the individual

Prepare a file

To prepare a file of individual data, go to the menu Prepare & Upload File> Prepare Files> Individual data. This interface provide a “download template file” link to download a file filled with mandatory headers for individual data.

A simplified search interface (Figure 9) proposes to search reproductions already existing in the database according to 3 criteria: year of creation of the seed lot sown, projects related to the reproduction, place on which the reproduction takes place.

A list is displayed (Figure 20) which allows you to click on the ⊕ icon to add the reproductions to be exported to the file.
The reproductions are here defined by the name of the seed lot sown and the location of the sowing. This list is visible by clicking on the 🗔 icon on the right of the results list. This action brings up a window that allows you to either erase reproductions or complete file preparation information.



Generate individual data file

Search seed lots

Filters :

Creation year : 2013

Projects : ---------

Location : MLN

Reproductions found for your query :

- ⊕ C1_MLN_2013_0001 (1, A, 1, -)
- ⊕ C1_MLN_2013_0001 (1, A, 5, -)
- ⊕ C2_MLN_2013_0001 (1, A, 2, -)
- ⊕ C3_MLN_2013_0001 (1, A, 3, -)
- ⊕ C4_MLN_2013_0001 (1, A, 4, -)

Selected seed lot :

- ⊖ C1_MLN_2013_0001 (1, A, 1, -)
- ⊖ C2_MLN_2013_0001 (1, A, 2, -)
- ⊖ C3_MLN_2013_0001 (1, A, 3, -)

Number of individuals 25

Figure 20: individual data file preparation interface

Click on the 'Export File' button to download the pre-filled individual data file. A user can also modify the search filters and restart it to complete his list of reproductions.

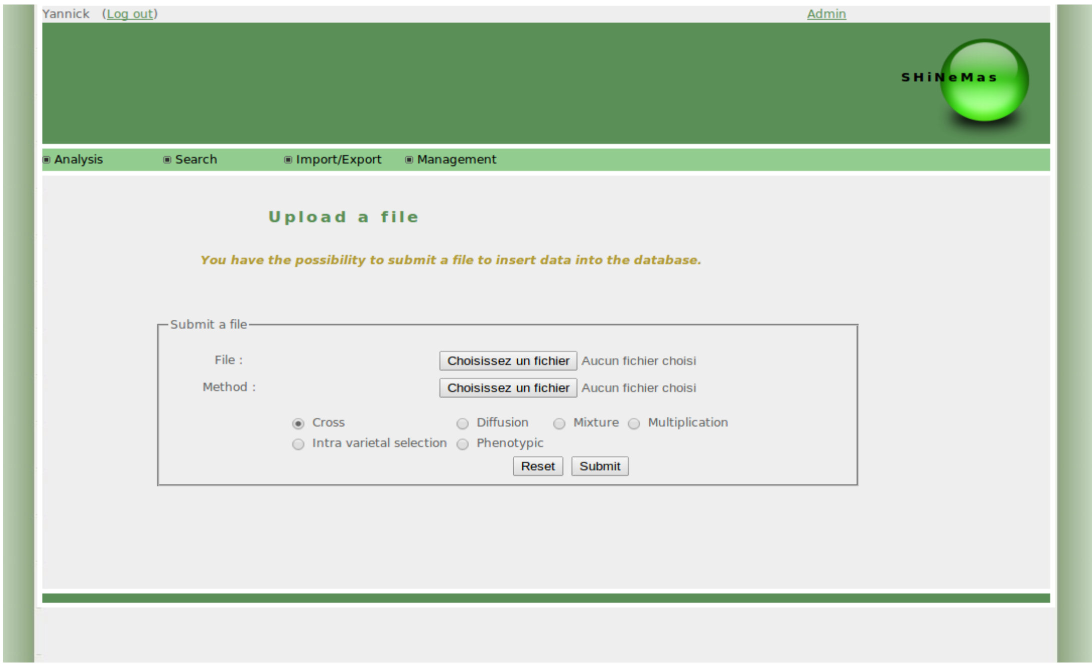
B.4.c.x Prohibited characters in the different SHiNeMaS fields

Information	*List of prohibited characters*
Germplasm names	#, _, space
Short name of person	#, _, space
Name of variables	%

Table 2: Summary of prohibited characters in the different SHiNeMaS fields

B.4.d Submission of the file

B.4.d.i File submission interface



Upload a file

You have the possibility to submit a file to insert data into the database.

Submit a file

File : Aucun fichier choisi

Method : Aucun fichier choisi

● Cross ○ Diffusion ○ Mixture ○ Multiplication
○ Intra varietal selection ○ Phenotypic

Figure 21: File submission interface

In Import / Export> Upload, choose a data file in the "File" field, a method file in the "Method" field. Select the correct file type from: Cross, Diffusion, Mixture, Multiplication, Intra varietal selection or Individual data. Click on "Submit".

B.4.d.ii Special treatments when submitting a file

Special treatments common to all files

- When the **project** field indicates a project that does not exist this one is automatically created by the application
- Seed lots that do not exist in the database are treated as described in chapter 'Case of non already existing seeds lots in the database'

Case of crosses

- In the case of a **number_crosses** equal to 0 the application generates a virtual seed lot named according to the nomenclature NOTCROSSED_NUM, NUM ensuring its uniqueness.
- In the case of a **kernel_number_F1** equal to 0 the application generates a virtual seed lot named according to the nomenclature NOTCROSSED_NUM, NUM ensuring its uniqueness.

Case of reproductions

- When reproduction is in progress at a given place (even location, X, Y) you can not sow a seed lot of the same species.
- However, you can add data to a current reproduction. The reproduction will be identified by the same seed lot sown at the same place.

Case of selections

- A selection is always associated with a reproduction (identified by the seed lot sown, and its place). However, if a selection event is filled in a file but no reproduction matches, the application will create a new reproduction.
- A selection name can only be used once for a germplasm

Case of individual data

- Reproductions declared in the individual data file must exist

B.4.e Submission reports

B.4.e.i Successful submission

A report is produced after each submission (Figure 22). This submission report summarizes information that was included into the database. This information is of different types and indicates:

```
⊟ Female seed lots created:
line 2: (female) Rouge-du-Roc_JFB_2010_0002 (5 g).
line 3: (female) Cloche_JFB_2010_0002 (5 g).
line 4: (female) Blé-du-Lot_JFB_2010_0004 (5 g).
line 6: (female) Touselle-Anone_JFB_2010_0004 (5 g).

(Total : 4)

⊟ Male seed lots created:
line 2: (male) Blé-du-Lot_JFB_2010_0003 (5 g).
line 5: (male) Touselle-Anone_JFB_2010_0003 (5 g).

(Total : 2)

⊟ Son seed lots created:
line 2: (son) C1_JFB_2011_0001 (300.0 g).
line 3: (son) C2_JFB_2011_0001 (100.0 g).
line 4: (son) C3_JFB_2011_0001 (200.0 g).
line 5: (son) C4_JFB_2011_0001 (100.0 g).
line 6: (son) C5_JFB_2011_0001 (300.0 g).
line 7: (son) C6_JFB_2011_0001 (250.0 g).

(Total : 6)

⊟ Relations created:
line 2: cross between Rouge-du-Roc_JFB_2010_0002 (female) & Blé-du-Lot_JFB_2010_0003 (male) --> C1_JFB_2011_0001 (son).
line 3: cross between Cloche_JFB_2010_0002 (female) & Rouge-du-Roc_JFB_2010_0002 (male) --> C2_JFB_2011_0001 (son).
line 4: cross between Blé-du-Lot_JFB_2010_0004 (female) & Cloche_JFB_2010_0002 (male) --> C3_JFB_2011_0001 (son).
line 5: cross between Blé-du-Lot_JFB_2010_0004 (female) & Touselle-Anone_JFB_2010_0003 (male) --> C4_JFB_2011_0001 (son).
line 6: cross between Touselle-Anone_JFB_2010_0004 (female) & Cloche_JFB_2010_0002 (male) --> C5_JFB_2011_0001 (son).
line 7: cross between Rouge-du-Roc_JFB_2010_0002 (female) & Touselle-Anone_JFB_2010_0003 (male) --> C6_JFB_2011_0001 (son).

(Total : 6)

⊟ The following seed lots created do not have quantity_ini:
line 2: (female) Rouge-du-Roc_JFB_2010_0002.
line 2: (male) Blé-du-Lot_JFB_2010_0003.
line 3: (female) Cloche_JFB_2010_0002.
line 4: (female) Blé-du-Lot_JFB_2010_0004.
line 5: (male) Touselle-Anone_JFB_2010_0003.
line 6: (female) Touselle-Anone_JFB_2010_0004.

(Total : 6)


Submission successfull
```

Figure 22: Report of a successful submission

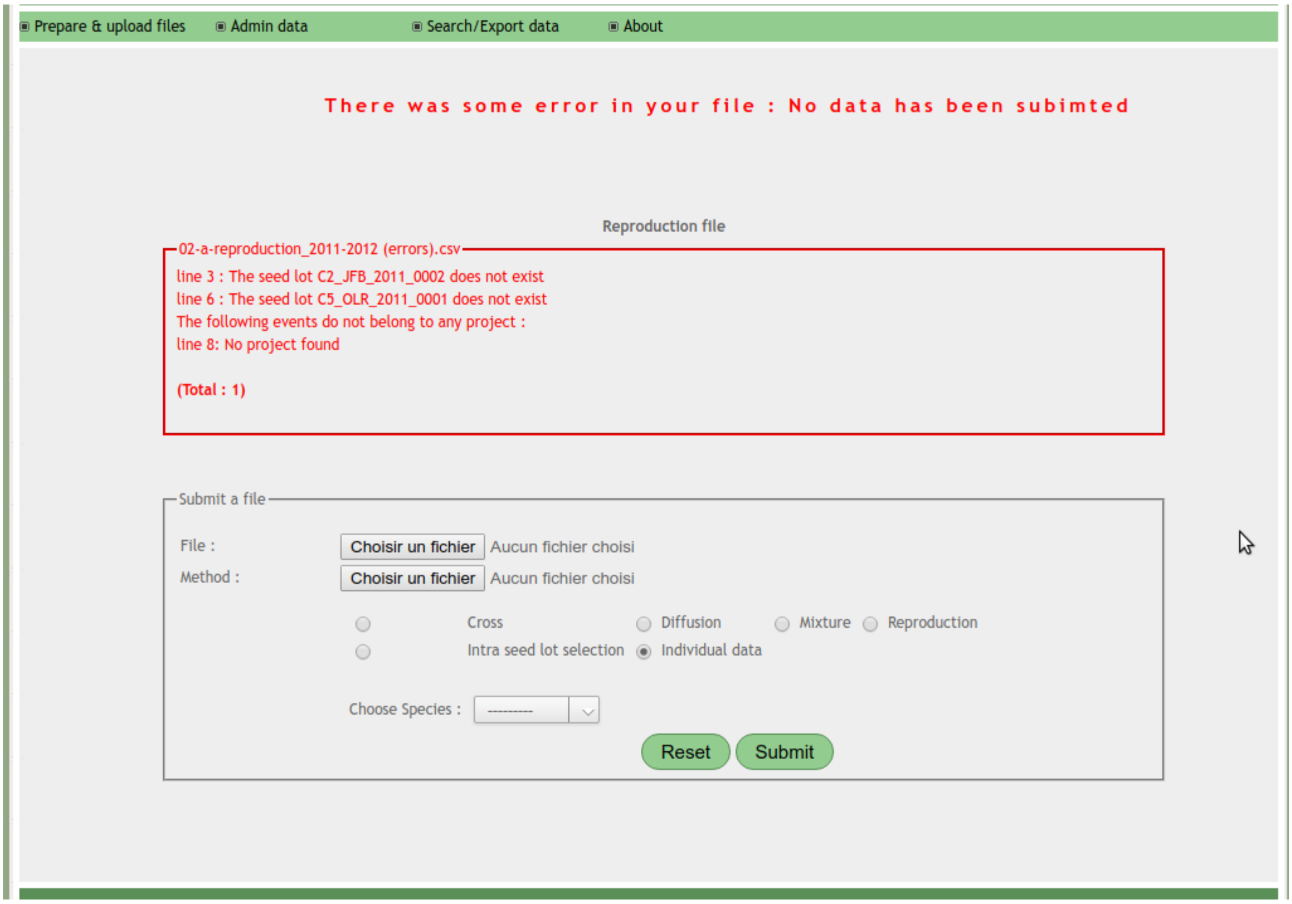
- New created variables
- New created varieties
- New created seed lots
- New created relation between seed lots

- On going replicates
- Seed lots without initial quantity
- Relations which quantities are not indicated
- Reproductions which coordinates are not indicated

It is also possible to perform some actions directly from the submission report. These actions are detailed in the next section (Post-submission processing)

B.4.e.ii Interpretation of the error message

In some cases, file submission can produce errors (Figure 23) that stop the submission process before the end. In this case, all on going operations are canceled and an error report is produced.



There was some error in your file : No data has been subimted

02-a-reproduction_2011-2012 (errors).csv
line 3 : The seed lot C2_JFB_2011_0002 does not exist
line 6 : The seed lot C5_OLR_2011_0001 does not exist
The following events do not belong to any project :
line 8: No project found

(Total : 1)

Figure 23: Errors report

These errors can be of different types :

- a variable was found in the method file or in the data file and not within the other.
- one line of the file was not associated to a project
- a method did not exists in the database
- a variety already existed in the database (in the case of crossing or mixture)
- The variety name contained a forbidden character
- One actor of the network no longer exist
- The seed lot name was not filled
- The seed lot name contained a forbidden character '#'
- The seed lot no longer exist in the database

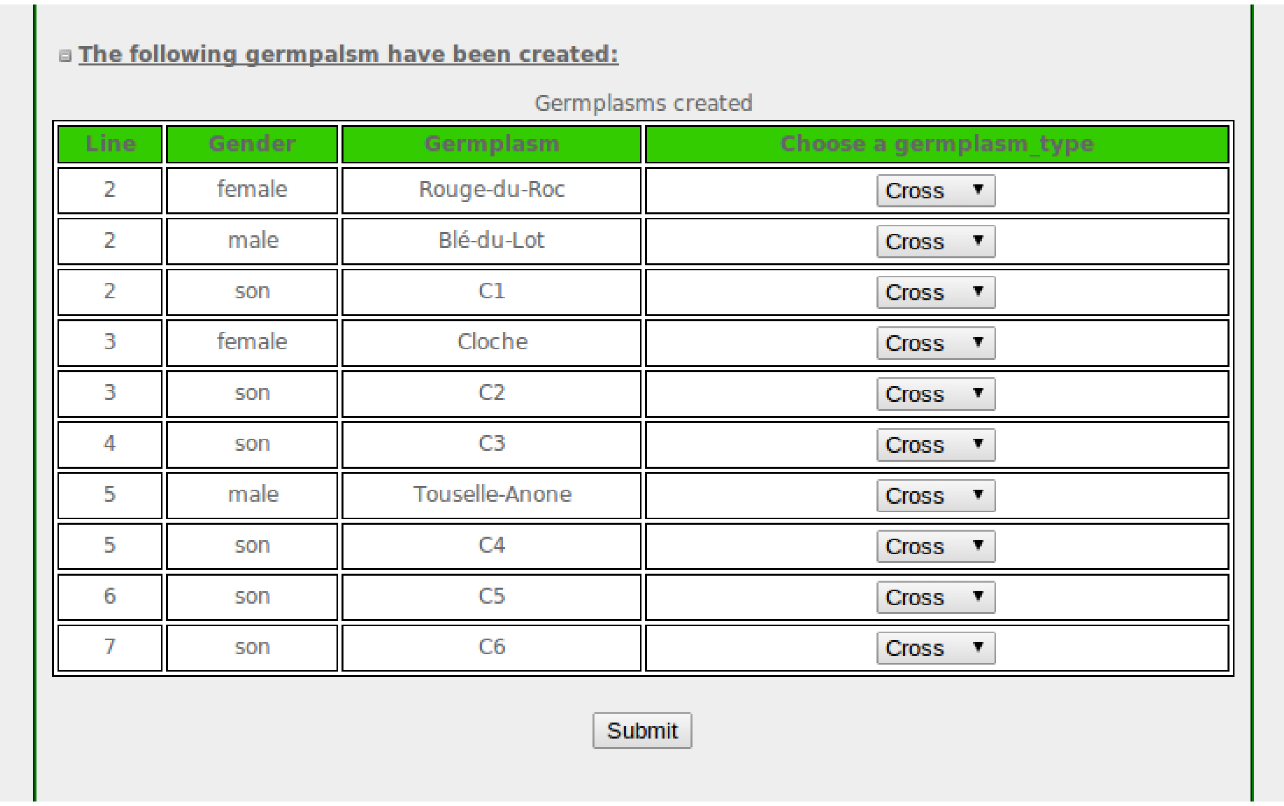
- No-valid value for a ‘split’ field (i.e. value different of 0 or 1)
- Seed lot nomenclature was not respected
- Some mandatory fields were empty
- Some correlation groups were inconsistent
- Some dates were inconsistent (for instance : sowing date after harvesting date)
- Some errors were detected for the locations of the reproductions

B.4.f Post-submission processing

B.4.f.i To associate a variety type

It is possible to associate a variety type for a variety newly created directly from the submission report. Variety types need to be created previously to the association (Germplasm type management). In the table Figure 24 the column 'Choose a germplasm type' allows to select which type of variety to be associated to the variety name cited in the column 'Germplasm'. Click on the 'Submit' button only after associating all the varieties types to the varieties.

It is always possible to modify the type of variety associated to a variety after this step. How to modify the type of the variety is explained in section Germplasm type management.



⊟ The following germpalsm have been created:

Germplasms created

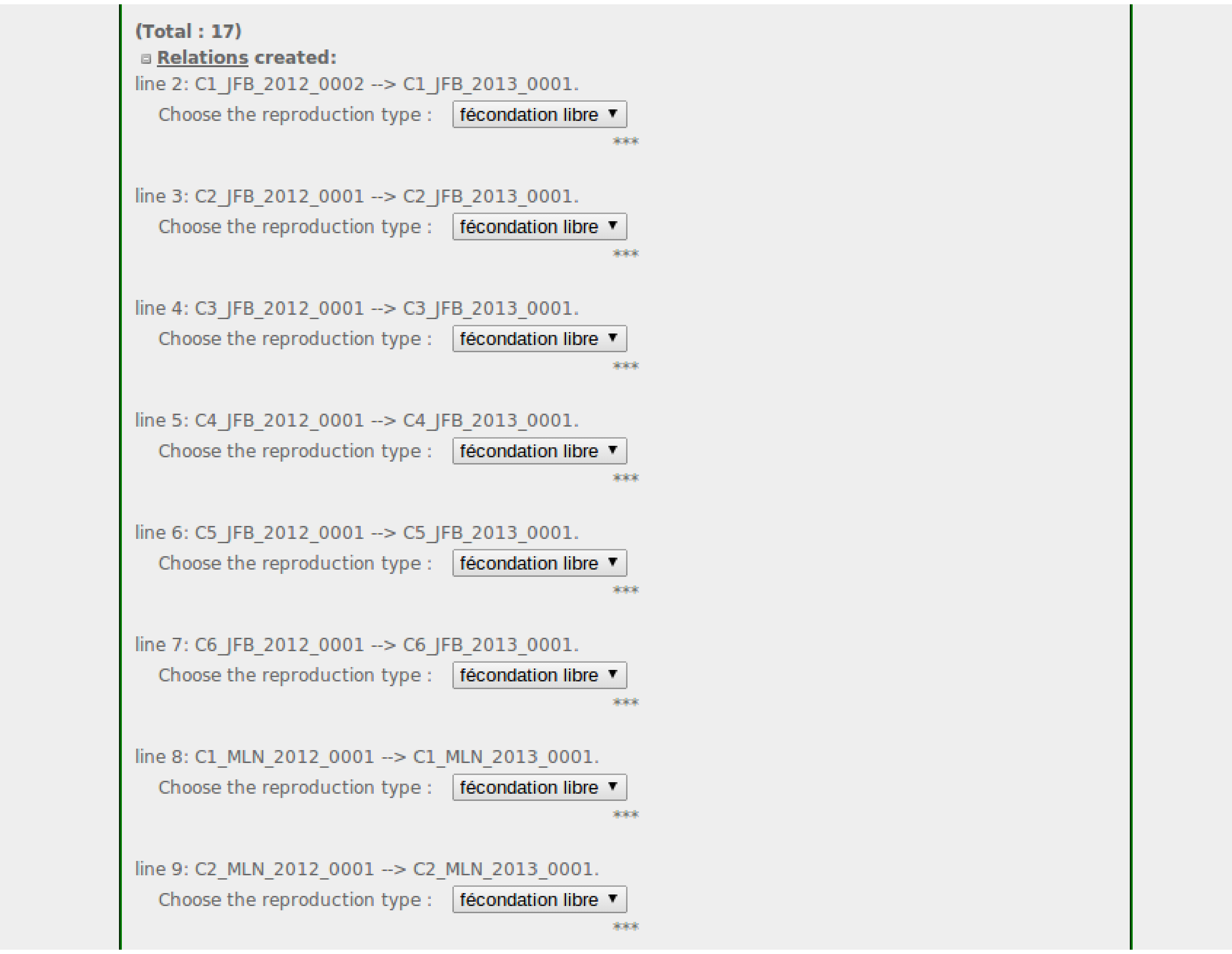
Line	Gender	Germplasm	Choose a germplasm_type
2	female	Rouge-du-Roc	Cross ▼
2	male	Blé-du-Lot	Cross ▼
2	son	C1	Cross ▼
3	female	Cloche	Cross ▼
3	son	C2	Cross ▼
4	son	C3	Cross ▼
5	male	Touselle-Anone	Cross ▼
5	son	C4	Cross ▼
6	son	C5	Cross ▼
7	son	C6	Cross ▼

Figure 24: Template allowing to associate a type of variety to a variety

B.4.f.ii To associate a reproduction type

It is possible to associate a reproduction type to an on going reproduction directly from the submission report. To be able to make such associations, reproduction types need to be created before the production of the submission report (Reproduction method management). In the example Figure 25 the line 'Choose the reproduction type' allows to select which type of reproduction is associated to the reproduction describes on the above line. Click on the 'Submit' button only after finished all the associations.

It is always possible to modify the type of reproduction associated to the reproduction.



(Total : 17)

⊟ **Relations created:**

line 2: C1_JFB_2012_0002 --> C1_JFB_2013_0001.
Choose the reproduction type : fécondation libre ▼
***

line 3: C2_JFB_2012_0001 --> C2_JFB_2013_0001.
Choose the reproduction type : fécondation libre ▼
***

line 4: C3_JFB_2012_0001 --> C3_JFB_2013_0001.
Choose the reproduction type : fécondation libre ▼
***

line 5: C4_JFB_2012_0001 --> C4_JFB_2013_0001.
Choose the reproduction type : fécondation libre ▼
***

line 6: C5_JFB_2012_0001 --> C5_JFB_2013_0001.
Choose the reproduction type : fécondation libre ▼
***

line 7: C6_JFB_2012_0001 --> C6_JFB_2013_0001.
Choose the reproduction type : fécondation libre ▼
***

line 8: C1_MLN_2012_0001 --> C1_MLN_2013_0001.
Choose the reproduction type : fécondation libre ▼
***

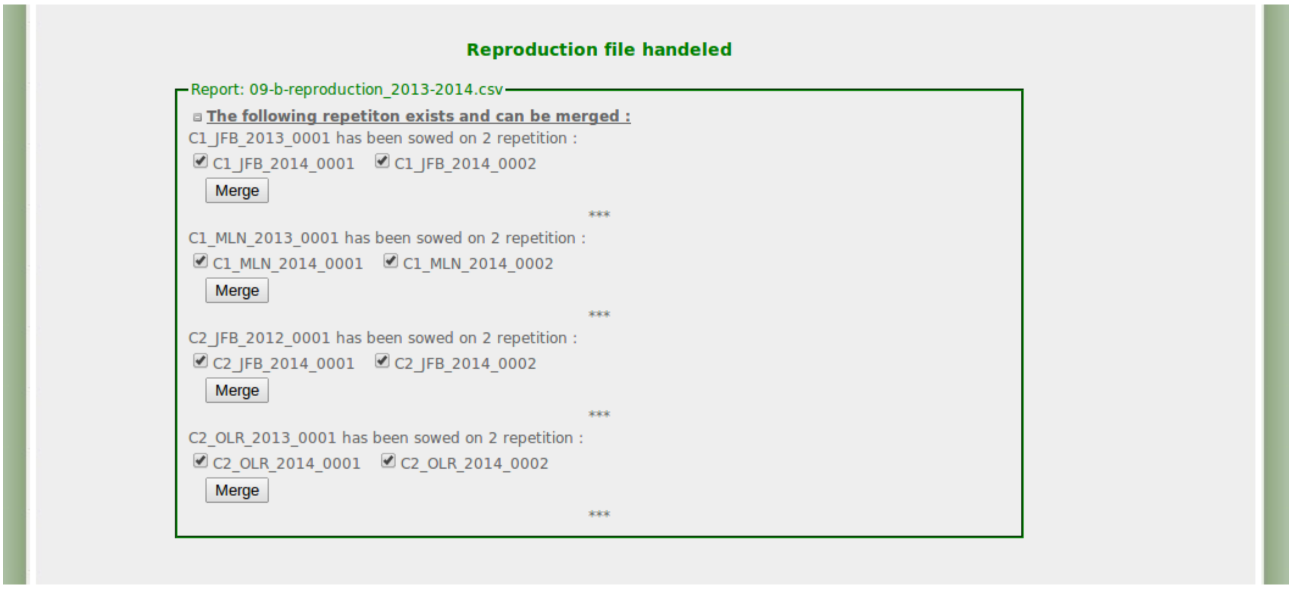
line 9: C2_MLN_2012_0001 --> C2_MLN_2013_0001.
Choose the reproduction type : fécondation libre ▼
***

Figure 25: Form to link a reproduction method to a running reproduction from the submission report

B.4.f.iii To merge seed lots coming from different replicates after a submission

It is also possible to merge on going seed lots coming from different replicates from the submission report. Each series of seed lots distributed in different replicates is separated by '***' (Figure 26). Seed lots that needs to be merged can be selected by checking proper boxes. After selecting the seed lots, clicking on the 'Merge' button. It is necessary to repeat this operation for each series of seed lots distributed in different replicates.

Merging seed lots coming from different replicates leads to create a new mixture event without creating a new variety (mixture excepted). Be careful, this operation is irreversible.


Reproduction file handeled

Report: 09-b-reproduction_2013-2014.csv

The following repetiton exists and can be merged :

C1_JFB_2013_0001 has been sowed on 2 repetition :

☑ C1_JFB_2014_0001 ☑ C1_JFB_2014_0002

***

C1_MLN_2013_0001 has been sowed on 2 repetition :

☑ C1_MLN_2014_0001 ☑ C1_MLN_2014_0002

***

C2_JFB_2012_0001 has been sowed on 2 repetition :

☑ C2_JFB_2014_0001 ☑ C2_JFB_2014_0002

***

C2_OLR_2013_0001 has been sowed on 2 repetition :

☑ C2_OLR_2014_0001 ☑ C2_OLR_2014_0002

***

Figure 26: Merge repetitions after a submission

It is always possible to perform this operation latter on if the user leaves the report submission before merging all the needed seed lots coming from different replicates (Event creation through administration interface).

B.4.g Edit raw data

From the menu Admin data > Seed lot relation > *Any relation type* > Edit raw data, a user can access to a simple autocompletion list where he can choose the relation containing the data to edit. As soon as the event card appears the user, if he is an administrator of the database, can click on a


Edit raw data

Variable :
poids_epis (T11)

Method :
poids_epis

Raw data :
3.09

Date :
2015-07-23

Comment :

> C4_CLM_2015_0001

Individual data

Individual	hauteur (T11)	poids_epis (T11)
1	179.0 (July 4, 2015, hauteur_tige)	3.09 (July 23, 2015, poids_epis)
2	139.5 (July 4, 2015, hauteur_tige)	1.63 (July 23, 2015, poids_epis)
3	122.2 (July 4, 2015, hauteur_tige)	1.85 (July 23, 2015, poids_epis)
4	124.8 (July 4, 2015, hauteur_tige)	3.03 (July 23, 2015, poids_epis)
5	120.4 (July 4, 2015, hauteur_tige)	4.12 (July 23, 2015, poids_epis)

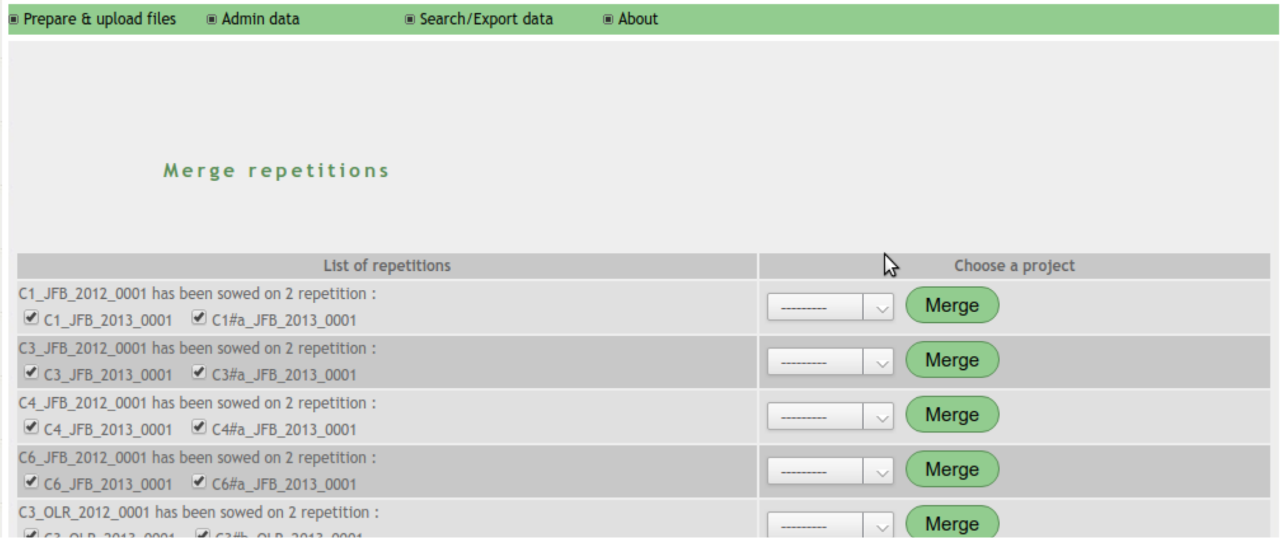
Figure 27: Form enabling data edition from a card

data and display a form in which the data can be edited (Figure 27). When a data is edited, the user can add a comment to explain why this edition, or keep the track of the previous value. Note that the date of the last update and the username is also track and displayed in the data table in the card when moving the mouse over the value.

B.4.h To merge seed lots coming from different replicates

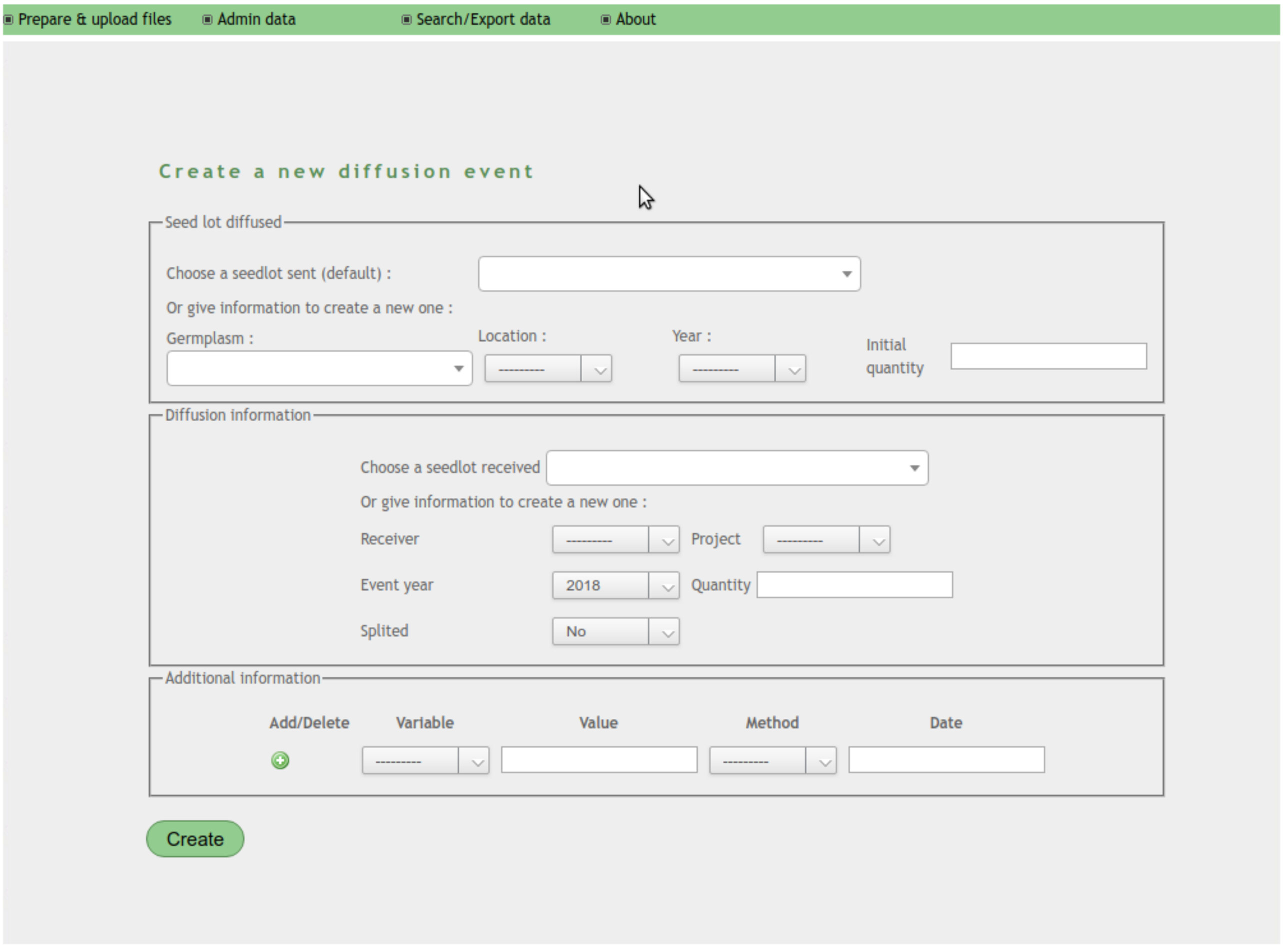
Seed lots coming from different replicates can be merged by the admin user later after the submission step of reproduction file. To process to such change, go to the menu :Admin data > Tools > Merge Reps. A screen (Figure 28) shows all the seed lots coming from different replicates that can be merged. It is possible to select/unselect seed lots to merge for each line. Select the corresponding project that need to be link to this event and click on the 'Merge' button. A message appears with the name of the new created seed lot when operation happens successfully.

B.4.i Event creation through administration interface



Merge repetitions

List of repetitions	Choose a project
C1_JFB_2012_0001 has been sowed on 2 repetition : ☑ C1_JFB_2013_0001 ☑ C1#a_JFB_2013_0001	---------
C3_JFB_2012_0001 has been sowed on 2 repetition : ☑ C3_JFB_2013_0001 ☑ C3#a_JFB_2013_0001	---------
C4_JFB_2012_0001 has been sowed on 2 repetition : ☑ C4_JFB_2013_0001 ☑ C4#a_JFB_2013_0001	---------
C6_JFB_2012_0001 has been sowed on 2 repetition : ☑ C6_JFB_2013_0001 ☑ C6#a_JFB_2013_0001	---------
C3_OLR_2012_0001 has been sowed on 2 repetition :	---------



Create a new diffusion event

Seed lot diffused
Choose a seedlot sent (default) :
Or give information to create a new one :
Germplasm :
Location : ---------
Year : ---------
Initial quantity

Diffusion information
Choose a seedlot received
Or give information to create a new one :
Receiver ---------
Project ---------
Event year 2018
Quantity
Splited No

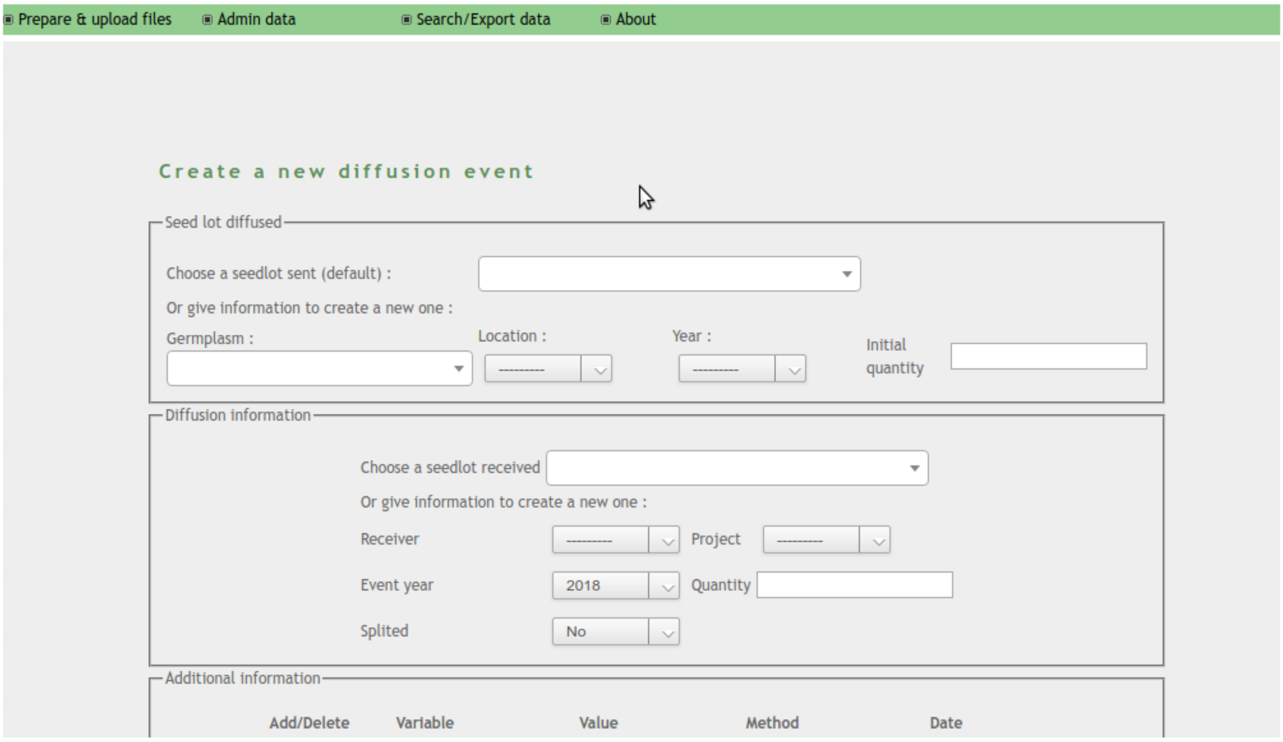
Additional information

Add/Delete	Variable	Value	Method	Date
⊕	---------		---------	

Figure 29: New diffusion creation form

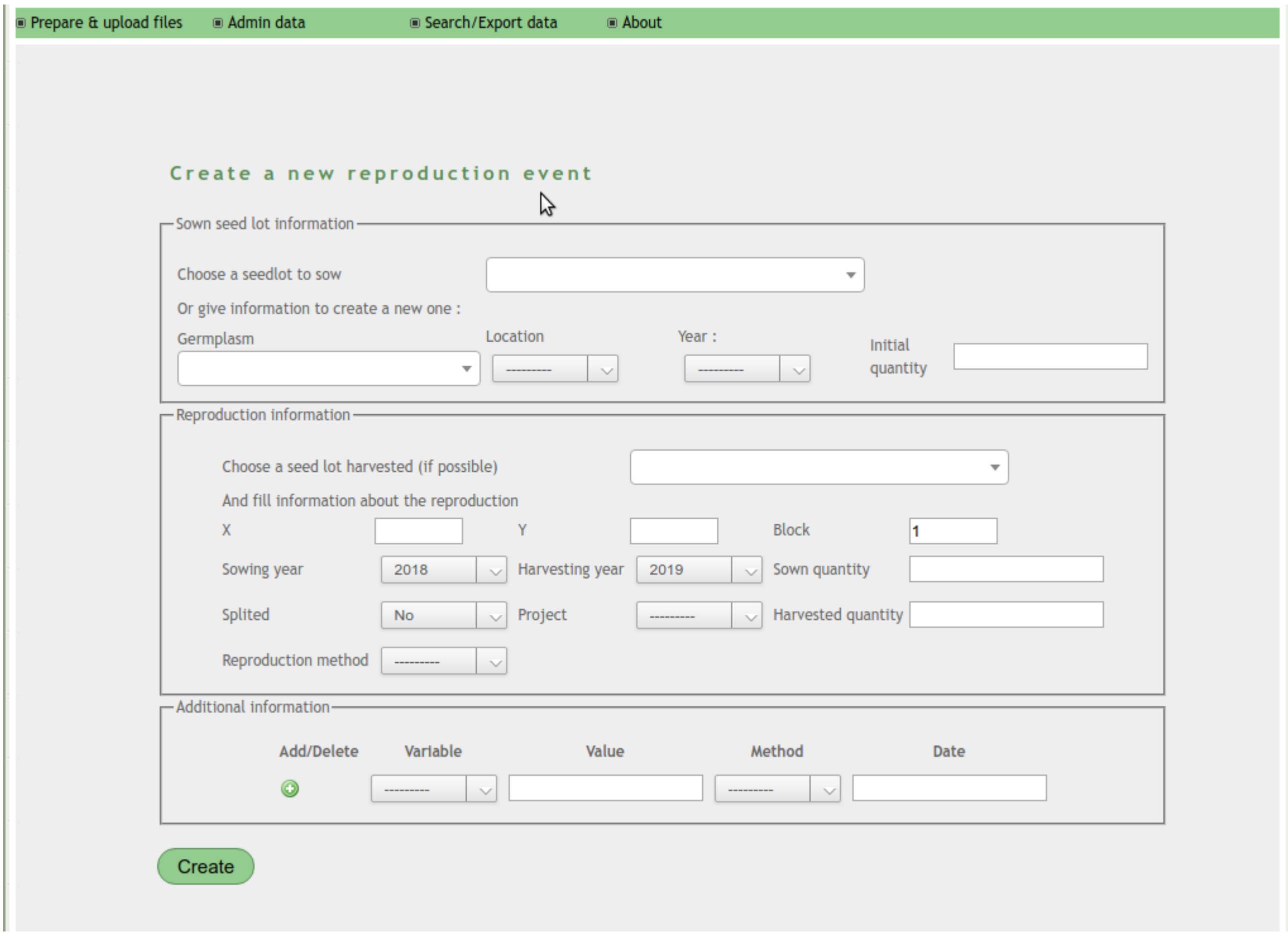
B.4.i.i Diffusion

To go to the menu: Admin data > Network > Diffusion > New, to create a diffusion event. Administrator interface is divided into three blocks of information (Figure 29). In the block ‘Seed lot diffused’, the user has to fill the diffused seed lot (to choose within a list of existing seed lots) or to provide information to create a new one. In the block ‘Diffusion information’, the user has to fill the targeted seed lot involved in the diffusion relation by selecting within the list of the existing seed lot or by creating a new one by filling the fields ‘receiver’ and ‘event_year’. The user has to fill the other fields of the block. The different rules to create a diffusion event by loading a file (Special treatments when submitting a file) also apply to this interface. Note that when the user



Event year 2018

Splited No



Block 1

Sowing year 2018

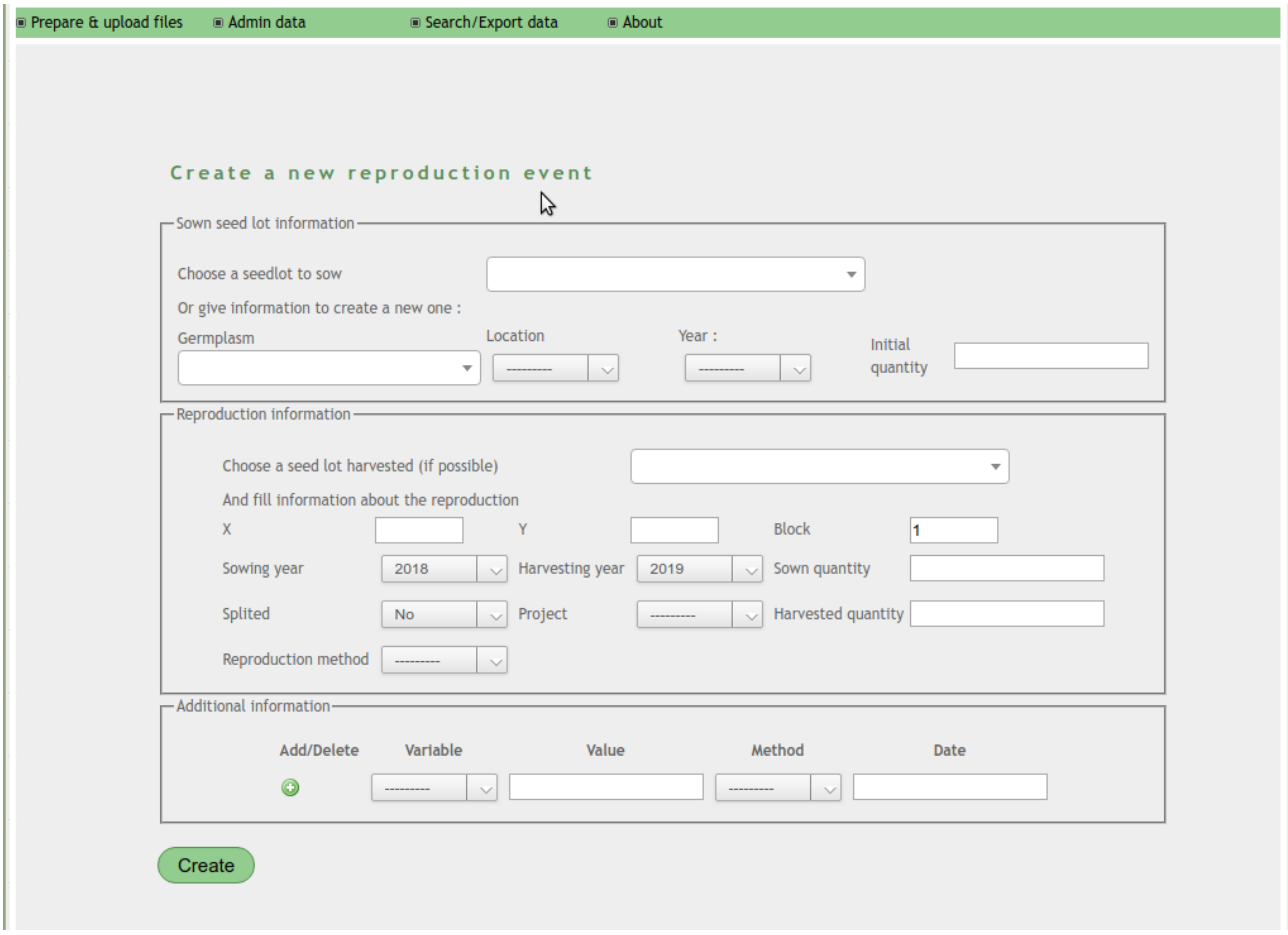
Harvesting year 2019

Splited No

Figure 30: Reproduction creation form

B.4.i.ii Reproduction

To go to the menu: Admin data > Network > Reproduction > New, to create a reproduction event. The administration interface (Figure 30) is divided into three blocks of information. In the block ‘Sown seed lot information’, the user has to fill the seed lot that was sown by choosing within a list of existing seed lots or by filling the required information to create a new one. In the block ‘Reproduction information’ the user has to fill the harvested seed lot by selecting the seed lot in the list coming from the reproduction relation or by creating a new one by filling the field ‘harvested_year’. The user has to fill the other fields of the block. The different rules to create a reproduction event by loading a file (Special treatments when submitting a file) also apply to this interface. Note that when the user select an existing seed lot in the block ‘Reproduction information’, this one cannot be created by any other relation. Otherwise, an error message will appears. Finally, in the block ‘Additional information’ the user can add data linked to this reproduction event. By clicking on the (+) button make additional lines appear. Then, to click on the ‘Create’ button to valid the event creation.



Create a new reproduction event

Sown seed lot information

Choose a seedlot to sow

Or give information to create a new one :

Germplasm

Location: ---------

Year : ---------

Initial quantity

Reproduction information

Choose a seed lot harvested (if possible)

And fill information about the reproduction

X

Y

Block: 1

Sowing year: 2018

Harvesting year: 2019

Sown quantity

Splited: No

Project: ---------

Harvested quantity

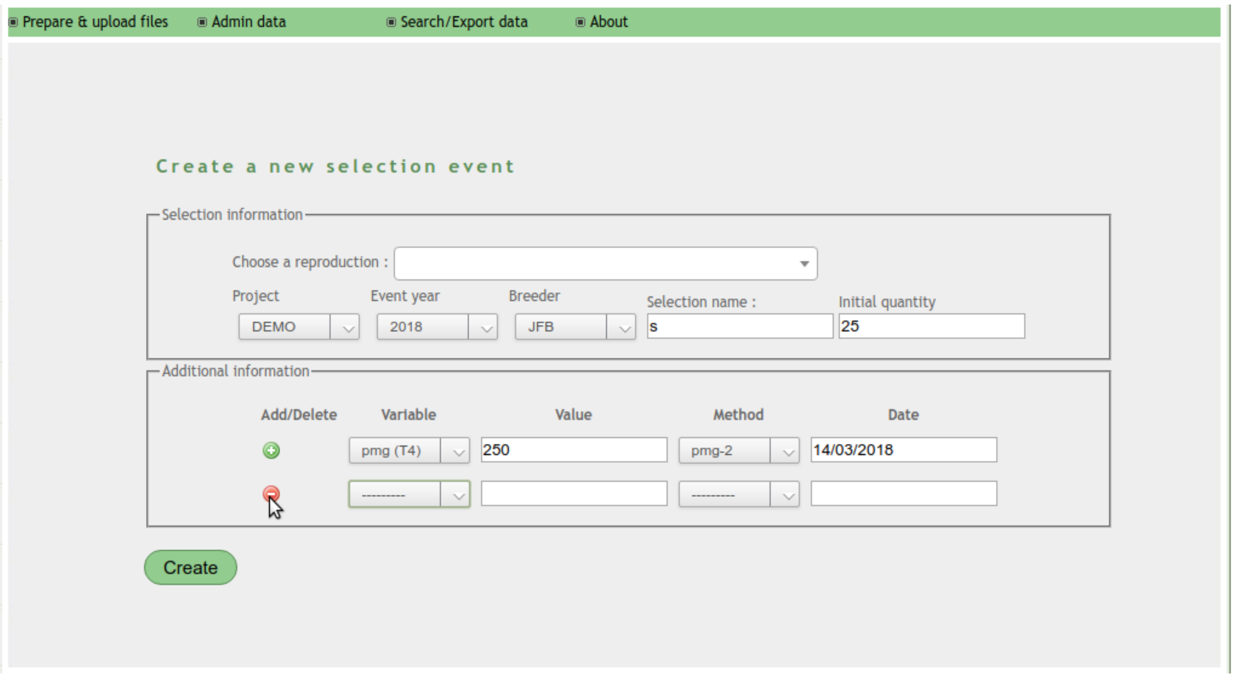
Reproduction method: ---------

Additional information

Add/Delete	Variable	Value	Method	Date
+	---------		---------	

Figure 30: Reproduction creation form

B.4.i.iii Selection



Choose a reproduction :

Project: DEMO
Event year: 2018
Breeder: JFB
Selection name : s
Initial quantity: 25

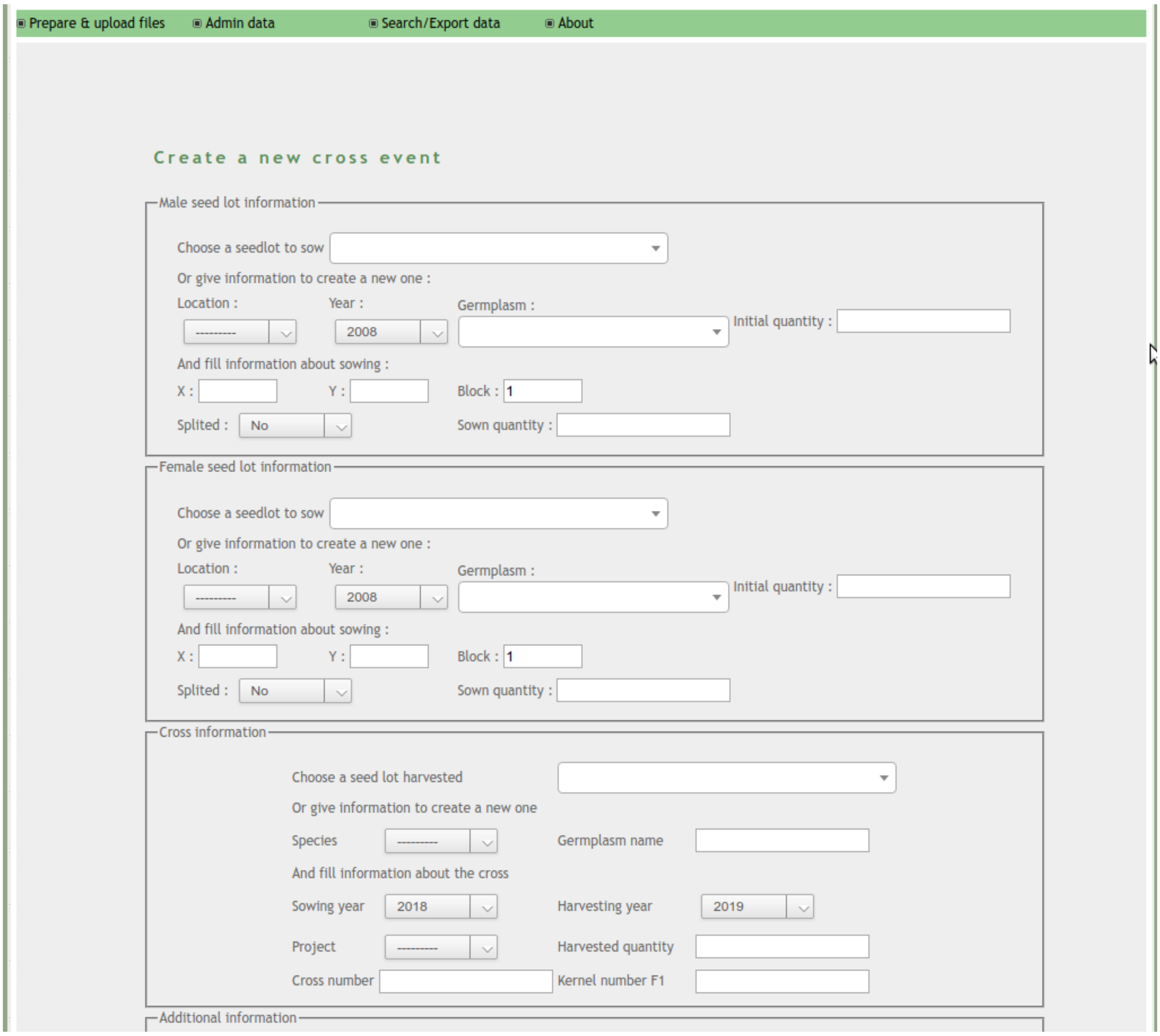
Variable	Value	Method	Date
pmg (T4)	250	pmg-2	14/03/2018
---------		---------	

Figure 31: Selection creation form

To go to the menu : Admin data > Network > Selection > New, to create a selection event . The administration interface (Figure 31) is divided into two blocks of information. In the block ‘Selection information’, the user has to fill an existing reproduction event by choosing it within a list. Then, to fill the other field of the block. The different rules to create a selection event by loading a file (Special treatments when submitting a file) also apply to this interface. Finally, in the block ‘Additional information’ the user can add data linked to this selection event. By clicking on the (+) button make additional lines appear. Then, to click on the ‘Create’ button to valid the event creation.

B.4.i.iv Cross

To go to the menu : Admin data > Network > Cross > New, to create a cross event. The administration interface (Figure 32) is divided into four blocks of information. In the block ‘Male seed lot information’, the user has to fill the male seed lot by choosing within a list of existing seed lots, or by providing information to create a new one by filling the fields ‘location’, ‘year’, and ‘germplasm’. Then, one has to fill information relative to the sowing of the male seed lot. In the block ‘Female seed lot information’, the user has to fill the female seed lot by choosing within a list of existing seed lots, or by providing information to create a new one by filling the fields ‘location’, ‘year’, and ‘germplasm’. Then, one has to fill sowing information of the female seed lot. In the block ‘Cross information’, the user has to fill the targeted seed lot of the cross relation by selecting it within a list, or by filling field ‘species’ and ‘germplasm’ to create a new one. Then, the user has to fill the other fields of the block. The different rules to create a cross event by loading a file (Special treatments when submitting a file) also apply to this interface.



Create a new cross event

Male seed lot information
Choose a seedlot to sow
Or give information to create a new one :
Location : ---------
Year : 2008
Germplasm :
Initial quantity :
And fill information about sowing :
X :
Y :
Block : 1
Splited : No
Sown quantity :

Female seed lot information
Choose a seedlot to sow
Or give information to create a new one :
Location : ---------
Year : 2008
Germplasm :
Initial quantity :
And fill information about sowing :
X :
Y :
Block : 1
Splited : No
Sown quantity :

Cross information
Choose a seed lot harvested
Or give information to create a new one
Species ---------
Germplasm name
And fill information about the cross
Sowing year 2018
Harvesting year 2019
Project ---------
Harvested quantity
Cross number
Kernel number F1

Additional information

Figure 32: New cross form

Note that when the user select an existing seed lot in the block ‘Cross information’, this one cannot be created by any other relation. Otherwise, an error message will appears. Finally, in the block ‘Additional information’ the user can add data linked to this cross event. By clicking on the button make additional lines appear. Then, to click on the ‘Create’ button to valid the event creation.

B.4.j Delete information

B.4.j.i Delete an event through the administration interface

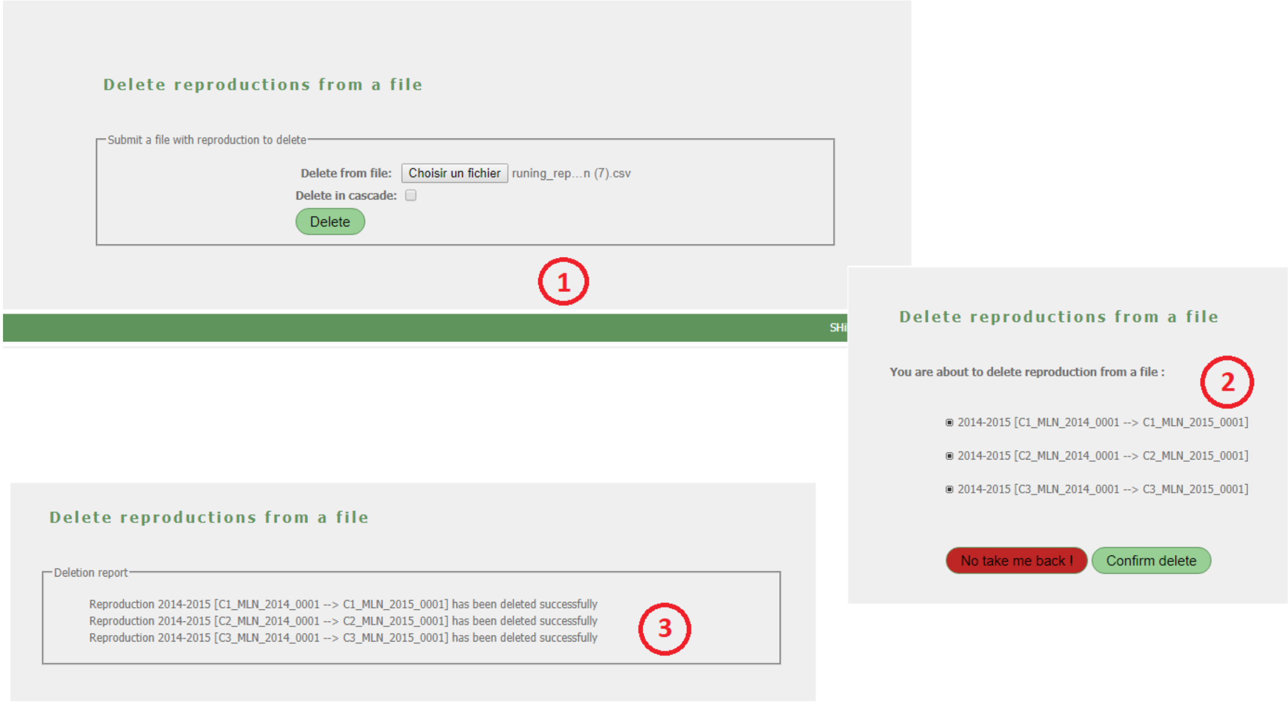
To go to the menu : Admin data > Network > « Event type » > Delete, to remove an event. The user can access to an administration interface which lists all the events of the event type selected by the user. On the right, filters help the user to limit this list. This page allows to select different events and to remove them through the ‘Delete selected « event »’ action. Nevertheless, this method is to avoid because deletion would be partial. To remove an event properly, it is advised to click on its name. The page of the event details appears and propose two kinds of deletion :

- The ‘Delete’ button helps the user to remove the considered event with all the associated data/measurements at the condition that these data are not associated themselves to another event. If the « child » seed lot is not used in any other relation, it is also removed.
- The ‘Delete in cascade’ button helps the user to remove the considered event with all the posterior events resulting of this event. On the same way, all the associated data/measurements will be removed at the condition that these data are not associated themselves to another event.

In the both cases, the user will be directed to a page that will ask him to confirm the deletion. To confirm the choice, to click on the ‘Yes I’m sure’ button. Otherwise, to click on the ‘No, take me back’ button.

B.4.j.ii Delete reproduction events from a file

From the menu Prepare & upload files > Delete from file > Reproduction, a user can delete a set of events by submitting a file. The first step (Figure 33) aims to sumbit a reproduction file. This file has the same format that the one described in the chapter Prepare an existing reproductions file. The deletion can be done in cascade or not as described in the chapter Delete an event through the administration interface. The second step read the file and inform the user of the reproductions that will be deleted. If the user accepts the reproductions are deleted and a report is displayed (step 3). The user can also go back to the submission form.



Delete reproductions from a file

Submit a file with reproduction to delete

Delete from file: runing_rep…n (7).csv

Delete in cascade: ☐

Delete reproductions from a file

You are about to delete reproduction from a file :

- 2014-2015 [C1_MLN_2014_0001 --> C1_MLN_2015_0001]
- 2014-2015 [C2_MLN_2014_0001 --> C2_MLN_2015_0001]
- 2014-2015 [C3_MLN_2014_0001 --> C3_MLN_2015_0001]

Delete reproductions from a file

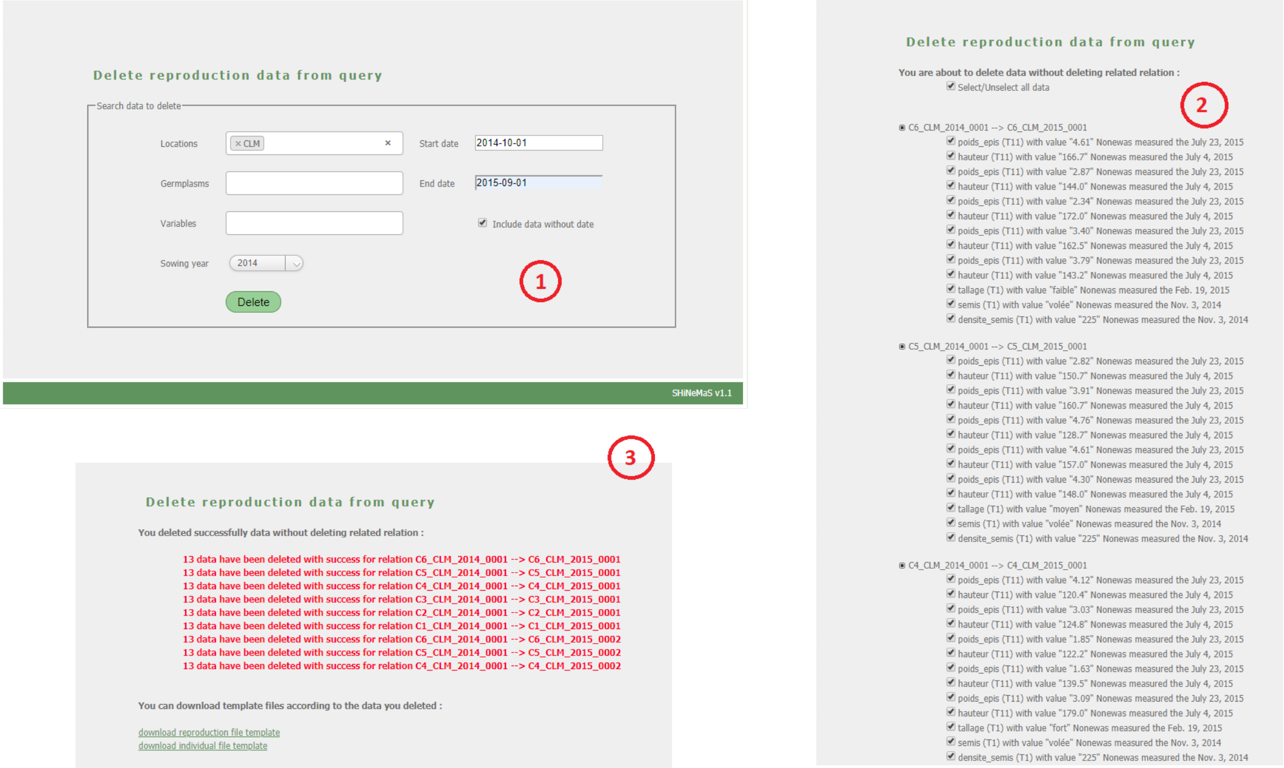
Deletion report

Reproduction 2014-2015 [C1_MLN_2014_0001 --> C1_MLN_2015_0001] has been deleted successfully
Reproduction 2014-2015 [C2_MLN_2014_0001 --> C2_MLN_2015_0001] has been deleted successfully
Reproduction 2014-2015 [C3_MLN_2014_0001 --> C3_MLN_2015_0001] has been deleted successfully

Figure 33: The 3 steps to delete reproduction events with a file

B.4.j.iii Delete raw data from a query

From the menu Admin > Seed lot relation > Reproduction > Delete raw data a user can delete a set of raw data without deleting related reproductions. Raw data can be selected with a form (Figure 34) filtering according to locations, germplasms, variables, a range of date (including also data without date), and the sowing year. The second step list all the raw data found as result of the query. The user can select/unselect each value before validation. As soon as the user has accepted his selection a report is displayed with the number of raw data deleted for each reproduction. Just below this report the user can download two templates files filed with the relations and the variables related to the raw data deleted.



Delete reproduction data from query

Search data to delete

Locations: × CLM

Start date: 2014-10-01

Germplasms:

End date: 2015-09-01

Variables:

☑ Include data without date

Sowing year: 2014

Delete reproduction data from query

You are about to delete data without deleting related relation :

☑ Select/Unselect all data

▣ C6_CLM_2014_0001 --> C6_CLM_2015_0001
- ☑ poids_epis (T11) with value "4.61" Nonewas measured the July 23, 2015
- ☑ hauteur (T11) with value "166.7" Nonewas measured the July 4, 2015
- ☑ poids_epis (T11) with value "2.87" Nonewas measured the July 23, 2015
- ☑ hauteur (T11) with value "144.0" Nonewas measured the July 4, 2015
- ☑ poids_epis (T11) with value "2.34" Nonewas measured the July 23, 2015
- ☑ hauteur (T11) with value "172.0" Nonewas measured the July 4, 2015
- ☑ poids_epis (T11) with value "3.40" Nonewas measured the July 23, 2015
- ☑ hauteur (T11) with value "162.5" Nonewas measured the July 4, 2015
- ☑ poids_epis (T11) with value "3.79" Nonewas measured the July 23, 2015
- ☑ hauteur (T11) with value "143.2" Nonewas measured the July 4, 2015
- ☑ tallage (T1) with value "faible" Nonewas measured the Feb. 19, 2015
- ☑ semis (T1) with value "volée" Nonewas measured the Nov. 3, 2014
- ☑ densite_semis (T1) with value "225" Nonewas measured the Nov. 3, 2014

▣ C5_CLM_2014_0001 --> C5_CLM_2015_0001
- ☑ poids_epis (T11) with value "2.82" Nonewas measured the July 23, 2015
- ☑ hauteur (T11) with value "150.7" Nonewas measured the July 4, 2015
- ☑ poids_epis (T11) with value "3.91" Nonewas measured the July 23, 2015
- ☑ hauteur (T11) with value "160.7" Nonewas measured the July 4, 2015
- ☑ poids_epis (T11) with value "4.76" Nonewas measured the July 23, 2015
- ☑ hauteur (T11) with value "128.7" Nonewas measured the July 4, 2015
- ☑ poids_epis (T11) with value "4.61" Nonewas measured the July 23, 2015
- ☑ hauteur (T11) with value "157.0" Nonewas measured the July 4, 2015
- ☑ poids_epis (T11) with value "4.30" Nonewas measured the July 23, 2015
- ☑ hauteur (T11) with value "148.0" Nonewas measured the July 4, 2015
- ☑ tallage (T1) with value "moyen" Nonewas measured the Feb. 19, 2015
- ☑ semis (T1) with value "volée" Nonewas measured the Nov. 3, 2014
- ☑ densite_semis (T1) with value "225" Nonewas measured the Nov. 3, 2014

▣ C4_CLM_2014_0001 --> C4_CLM_2015_0001
- ☑ poids_epis (T11) with value "4.12" Nonewas measured the July 23, 2015
- ☑ hauteur (T11) with value "120.4" Nonewas measured the July 4, 2015
- ☑ poids_epis (T11) with value "3.03" Nonewas measured the July 23, 2015
- ☑ hauteur (T11) with value "124.8" Nonewas measured the July 4, 2015
- ☑ poids_epis (T11) with value "1.85" Nonewas measured the July 23, 2015
- ☑ hauteur (T11) with value "122.2" Nonewas measured the July 4, 2015
- ☑ poids_epis (T11) with value "1.63" Nonewas measured the July 23, 2015
- ☑ hauteur (T11) with value "139.5" Nonewas measured the July 4, 2015
- ☑ poids_epis (T11) with value "3.09" Nonewas measured the July 23, 2015
- ☑ hauteur (T11) with value "179.0" Nonewas measured the July 4, 2015
- ☑ tallage (T1) with value "fort" Nonewas measured the Feb. 19, 2015
- ☑ semis (T1) with value "volée" Nonewas measured the Nov. 3, 2014
- ☑ densite_semis (T1) with value "225" Nonewas measured the Nov. 3, 2014

Delete reproduction data from query

You deleted successfully data without deleting related relation :

13 data have been deleted with success for relation C6_CLM_2014_0001 --> C6_CLM_2015_0001
13 data have been deleted with success for relation C5_CLM_2014_0001 --> C5_CLM_2015_0001
13 data have been deleted with success for relation C4_CLM_2014_0001 --> C4_CLM_2015_0001
13 data have been deleted with success for relation C3_CLM_2014_0001 --> C3_CLM_2015_0001
13 data have been deleted with success for relation C2_CLM_2014_0001 --> C2_CLM_2015_0001
13 data have been deleted with success for relation C1_CLM_2014_0001 --> C1_CLM_2015_0001
13 data have been deleted with success for relation C6_CLM_2014_0001 --> C6_CLM_2015_0002
13 data have been deleted with success for relation C5_CLM_2014_0001 --> C5_CLM_2015_0002
13 data have been deleted with success for relation C4_CLM_2014_0001 --> C4_CLM_2015_0002

You can download template files according to the data you deleted :

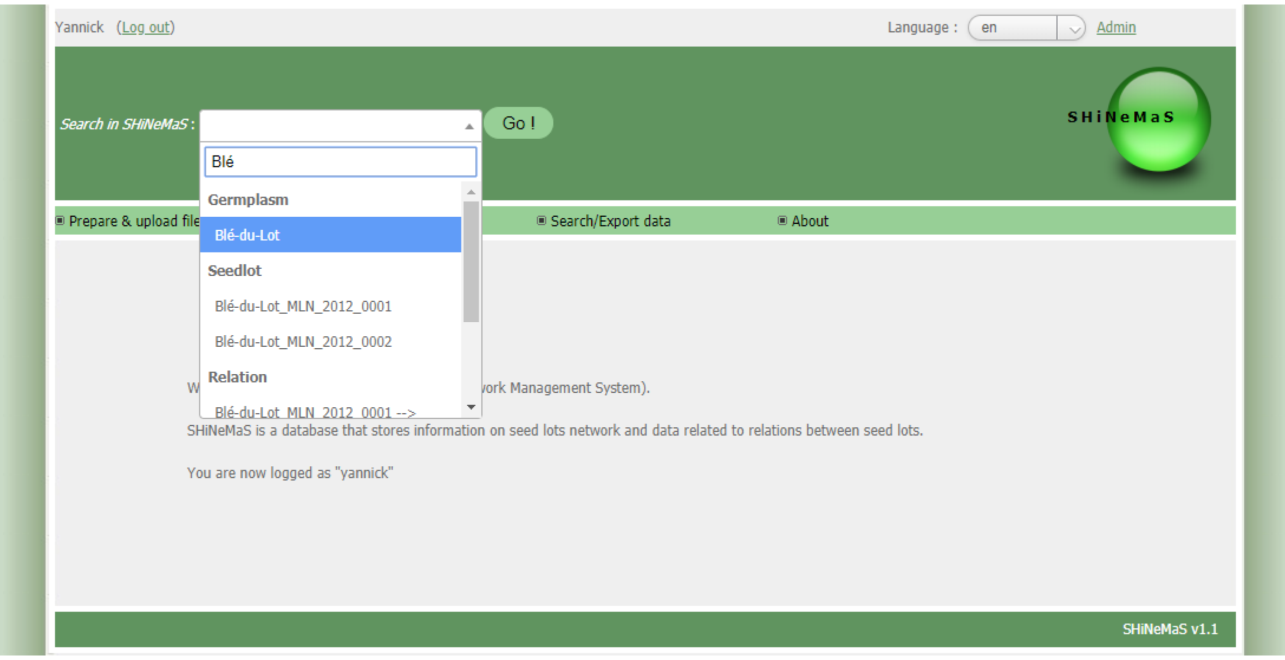
download reproduction file template
download individual file template

Figure 34: Steps to delete raw data of a reproduction event

C Consulting data

C.1 Global search toolbar

From any screen in SHiNeMaS a global search bar at the top of the web interface (Figure 35) provide a useful tool to search any kind of information (Germplasm, Seed lot or Relation) in the database. The search is done by auto-completion, meaning that a user starts to write a text in the bar and a restricted list is shown in the bar. As soon as an object is selected a click on the “Go” button forward to the corresponding card (see below the description of the cards).



Blé

Blé-du-Lot

Blé-du-Lot_MLN_2012_0001

Blé-du-Lot_MLN_2012_0002

Blé-du-Lot_MLN_2012_0001 -->

W… ork Management System).

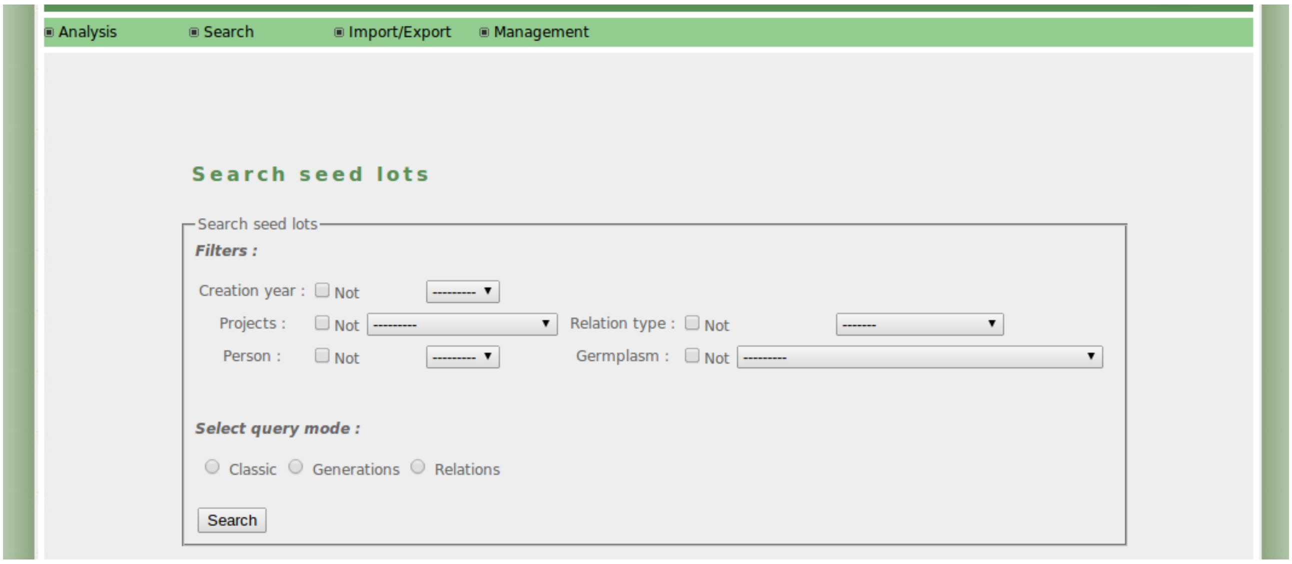
SHiNeMaS is a database that stores information on seed lots network and data related to relations between seed lots.

You are now logged as "yannick"

Figure 35: Global search toolbar

C.2 Advanced query

C.2.a Filters



Filters :

Creation year : ☐ Not ---------

Projects : ☐ Not ---------

Relation type : ☐ Not -------

Person : ☐ Not ---------

Germplasm : ☐ Not ---------

Select query mode :

○ Classic ○ Generations ○ Relations

Figure 36: Advanced query form

The Advanced query interface (Figure 36) makes possible to filter results according to some criteria :

- 'Creation year' : creation year of the seed lot. It can be harvesting year, reception year (in the case of a diffusion), mixture year etc.
- 'Projects' : projects in which the seed lot is used
- 'Person' : person owning this seed lot
- 'Relation type' : Filter on relation type which creates this seed lot (Diffusion, mixture, reproduction etc.)

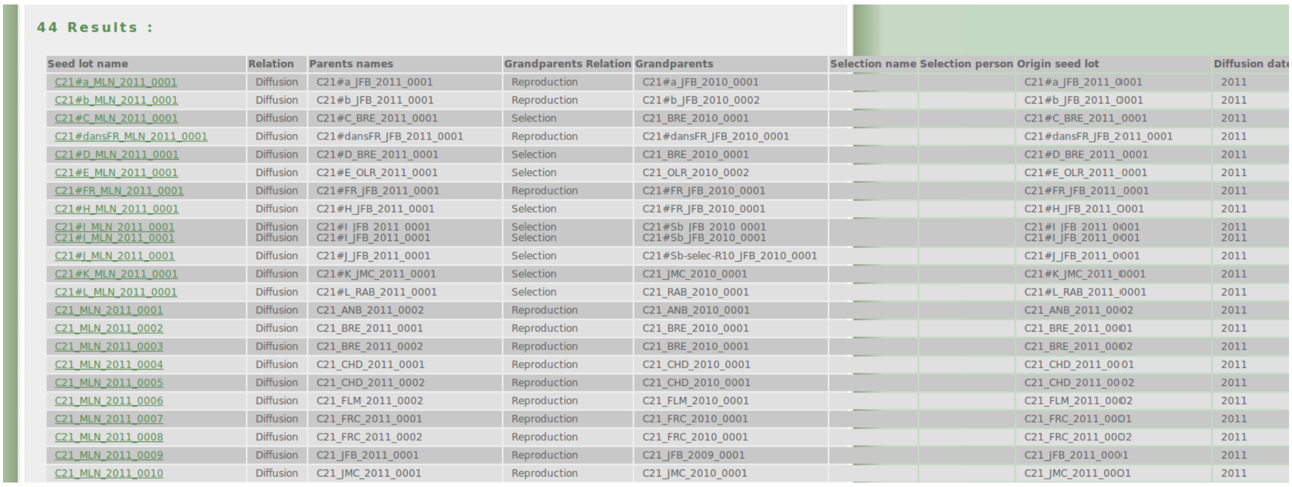
- 'Germplasm' : Filter on germplasm

Each filter offers a box 'Not' which allows to define an exclusion criteria (« All except »...). Click on the « Search » button to apply filters.

C.2.b Classic mode

The « Classic » query mode shows the list of seed lot from applied filters. Some additional information are available :

- **Seed lot name :** the name of the seed lot
- **Relation :** The relation type that produce this seed lot
- **Parent names :** The names of parents seed lot
- **Grandparents Relation :** The relation type that produce parents seed lot
- **Grandparents :** The names of grandparents seed lot
- **Selection name :** The selection name when the seed lot is produced from a selection
- **Selection person :** Person who made the selection when a seed lot is produced from a selection
- **Origin seed lot :** Location where the seed lot comes from
- **Diffusion date :** Year of the last diffusion of the seed lot



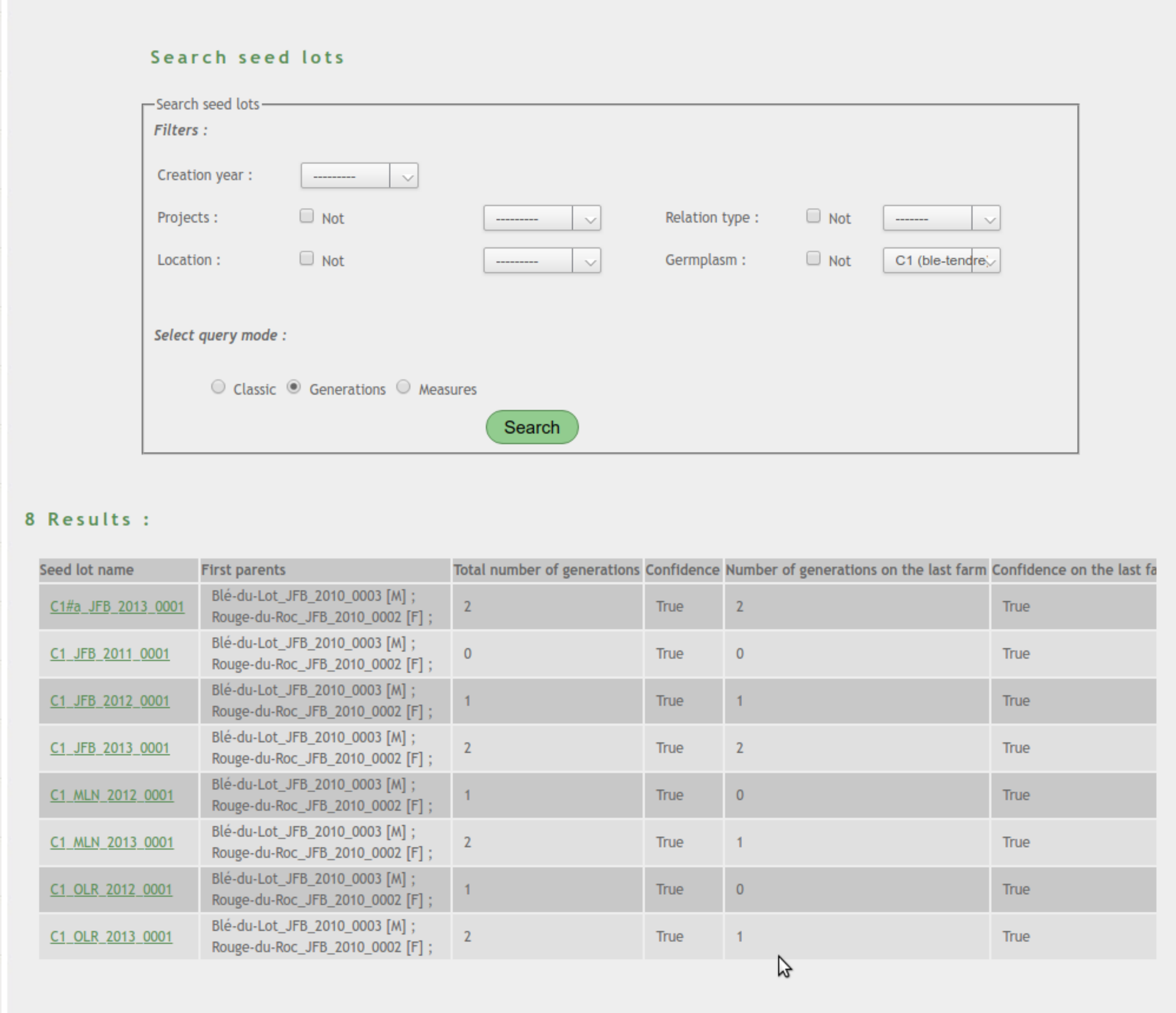
44 Results :

Seed lot name	Relation	Parents names	Grandparents Relation	Grandparents	Selection name	Selection person	Origin seed lot	Diffusion dat
C21#a_MLN_2011_0001	Diffusion	C21#a_JFB_2011_0001	Reproduction	C21#a_JFB_2010_0001			C21#a_JFB_2011_0001	2011
C21#b_MLN_2011_0001	Diffusion	C21#b_JFB_2011_0001	Reproduction	C21#b_JFB_2010_0002			C21#b_JFB_2011_0001	2011
C21#C_MLN_2011_0001	Diffusion	C21#C_BRE_2011_0001	Selection	C21_BRE_2010_0001			C21#C_BRE_2011_0001	2011
C21#dansFR_MLN_2011_0001	Diffusion	C21#dansFR_JFB_2011_0001	Reproduction	C21#dansFR_JFB_2010_0001			C21#dansFR_JFB_2011_0001	2011
C21#D_MLN_2011_0001	Diffusion	C21#D_BRE_2011_0001	Selection	C21_BRE_2010_0001			C21#D_BRE_2011_0001	2011
C21#E_MLN_2011_0001	Diffusion	C21#E_OLR_2011_0001	Selection	C21_OLR_2010_0002			C21#E_OLR_2011_0001	2011
C21#FR_MLN_2011_0001	Diffusion	C21#FR_JFB_2011_0001	Reproduction	C21#FR_JFB_2010_0001			C21#FR_JFB_2011_0001	2011
C21#H_MLN_2011_0001	Diffusion	C21#H_JFB_2011_0001	Selection	C21#FR_JFB_2010_0001			C21#H_JFB_2011_0001	2011
C21#I_MLN_2011_0001 C21#I_MLN_2011_0001	Diffusion Diffusion	C21#I_JFB_2011_0001 C21#I_JFB_2011_0001	Selection Selection	C21#Sb_JFB_2010_0001 C21#Sb_JFB_2010_0001			C21#I_JFB_2011_0001 C21#I_JFB_2011_0001	2011 2011
C21#J_MLN_2011_0001	Diffusion	C21#J_JFB_2011_0001	Selection	C21#Sb-selec-R10_JFB_2010_0001			C21#J_JFB_2011_0001	2011
C21#K_MLN_2011_0001	Diffusion	C21#K_JMC_2011_0001	Selection	C21_JMC_2010_0001			C21#K_JMC_2011_0001	2011
C21#L_MLN_2011_0001	Diffusion	C21#L_RAB_2011_0001	Selection	C21_RAB_2010_0001			C21#L_RAB_2011_0001	2011
C21_MLN_2011_0001	Diffusion	C21_ANB_2011_0002	Reproduction	C21_ANB_2010_0001			C21_ANB_2011_0002	2011
C21_MLN_2011_0002	Diffusion	C21_BRE_2011_0001	Reproduction	C21_BRE_2010_0001			C21_BRE_2011_0001	2011
C21_MLN_2011_0003	Diffusion	C21_BRE_2011_0002	Reproduction	C21_BRE_2010_0001			C21_BRE_2011_0002	2011
C21_MLN_2011_0004	Diffusion	C21_CHD_2011_0001	Reproduction	C21_CHD_2010_0001			C21_CHD_2011_0001	2011
C21_MLN_2011_0005	Diffusion	C21_CHD_2011_0002	Reproduction	C21_CHD_2010_0001			C21_CHD_2011_0002	2011
C21_MLN_2011_0006	Diffusion	C21_FLM_2011_0002	Reproduction	C21_FLM_2010_0001			C21_FLM_2011_0002	2011
C21_MLN_2011_0007	Diffusion	C21_FRC_2011_0001	Reproduction	C21_FRC_2010_0001			C21_FRC_2011_0001	2011
C21_MLN_2011_0008	Diffusion	C21_FRC_2011_0002	Reproduction	C21_FRC_2010_0001			C21_FRC_2011_0002	2011
C21_MLN_2011_0009	Diffusion	C21_JFB_2011_0001	Reproduction	C21_JFB_2009_0001			C21_JFB_2011_0001	2011
C21_MLN_2011_0010	Diffusion	C21_JMC_2011_0001	Reproduction	C21_JMC_2010_0001			C21_JMC_2011_0001	2011

Figure 37: « Classic » mode query result

C.2.c Generation mode

The « Generation » query mode (Figure 38) shows the list of seed lot according to selected filters. It also shows information about generation number (total and on a same location) :



Search seed lots

Filters :

Creation year : ---------

Projects : ☐ Not ---------

Relation type : ☐ Not -------

Location : ☐ Not ---------

Germplasm : ☐ Not C1 (ble-tendre)

Select query mode :

○ Classic ● Generations ○ Measures

8 Results :

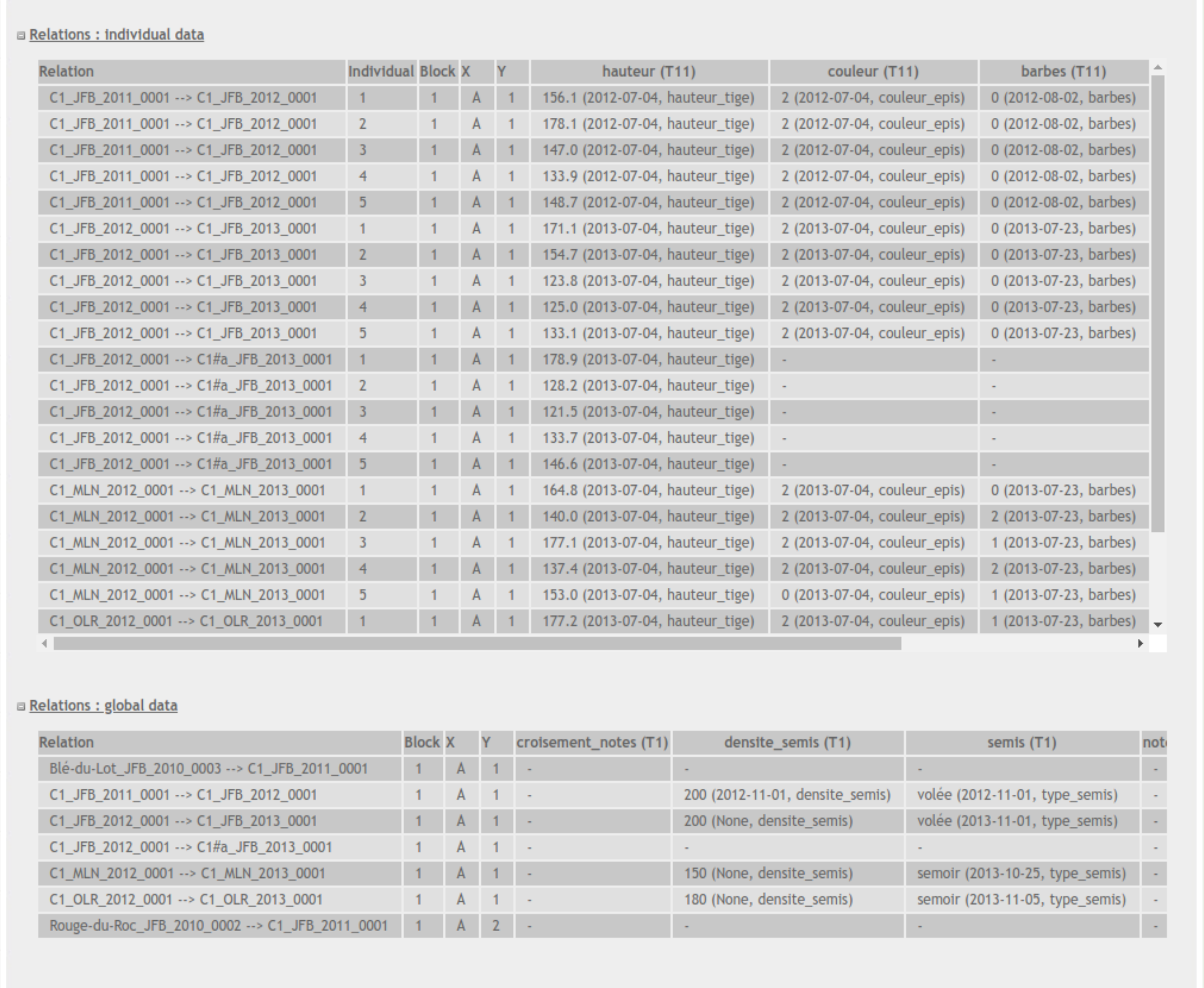
Seed lot name	First parents	Total number of generations	Confidence	Number of generations on the last farm	Confidence on the last fa
C1#a_JFB_2013_0001	Blé-du-Lot_JFB_2010_0003 [M] ; Rouge-du-Roc_JFB_2010_0002 [F] ;	2	True	2	True
C1_JFB_2011_0001	Blé-du-Lot_JFB_2010_0003 [M] ; Rouge-du-Roc_JFB_2010_0002 [F] ;	0	True	0	True
C1_JFB_2012_0001	Blé-du-Lot_JFB_2010_0003 [M] ; Rouge-du-Roc_JFB_2010_0002 [F] ;	1	True	1	True
C1_JFB_2013_0001	Blé-du-Lot_JFB_2010_0003 [M] ; Rouge-du-Roc_JFB_2010_0002 [F] ;	2	True	2	True
C1_MLN_2012_0001	Blé-du-Lot_JFB_2010_0003 [M] ; Rouge-du-Roc_JFB_2010_0002 [F] ;	1	True	0	True
C1_MLN_2013_0001	Blé-du-Lot_JFB_2010_0003 [M] ; Rouge-du-Roc_JFB_2010_0002 [F] ;	2	True	1	True
C1_OLR_2012_0001	Blé-du-Lot_JFB_2010_0003 [M] ; Rouge-du-Roc_JFB_2010_0002 [F] ;	1	True	0	True
C1_OLR_2013_0001	Blé-du-Lot_JFB_2010_0003 [M] ; Rouge-du-Roc_JFB_2010_0002 [F] ;	2	True	1	True

Figure 38: "Generation" mode query result

- **Seed lot name :** Seed lot name
- **First parents :** Name of the parents used for the cross from origins (when there was one)
- **Total number of generation :** Total number of multiplication needful to obtain this seed lot
- **Number of generation on the last farm :** Number of multiplication that happened on this location to obtain this seed lot
- **Confidence** : Confidence accorded to the number of generation. For example a seed lot which integrate spontaneously the network will have a default confidence at false
- **Confidence on last farm** : Confidence accorded to the number of generation on a same location.

C.2.d Measures mode

The «Measures» query mode shows collected data on a given time interval (Figure 39). User fill variables name in the form and the dates that define the time interval. The results are shown in 3 tables :



⊟ Relations : individual data

Relation	Individual	Block	X	Y	hauteur (T11)	couleur (T11)	barbes (T11)
C1_JFB_2011_0001 --> C1_JFB_2012_0001	1	1	A	1	156.1 (2012-07-04, hauteur_tige)	2 (2012-07-04, couleur_epis)	0 (2012-08-02, barbes)
C1_JFB_2011_0001 --> C1_JFB_2012_0001	2	1	A	1	178.1 (2012-07-04, hauteur_tige)	2 (2012-07-04, couleur_epis)	0 (2012-08-02, barbes)
C1_JFB_2011_0001 --> C1_JFB_2012_0001	3	1	A	1	147.0 (2012-07-04, hauteur_tige)	2 (2012-07-04, couleur_epis)	0 (2012-08-02, barbes)
C1_JFB_2011_0001 --> C1_JFB_2012_0001	4	1	A	1	133.9 (2012-07-04, hauteur_tige)	2 (2012-07-04, couleur_epis)	0 (2012-08-02, barbes)
C1_JFB_2011_0001 --> C1_JFB_2012_0001	5	1	A	1	148.7 (2012-07-04, hauteur_tige)	2 (2012-07-04, couleur_epis)	0 (2012-08-02, barbes)
C1_JFB_2012_0001 --> C1_JFB_2013_0001	1	1	A	1	171.1 (2013-07-04, hauteur_tige)	2 (2013-07-04, couleur_epis)	0 (2013-07-23, barbes)
C1_JFB_2012_0001 --> C1_JFB_2013_0001	2	1	A	1	154.7 (2013-07-04, hauteur_tige)	2 (2013-07-04, couleur_epis)	0 (2013-07-23, barbes)
C1_JFB_2012_0001 --> C1_JFB_2013_0001	3	1	A	1	123.8 (2013-07-04, hauteur_tige)	2 (2013-07-04, couleur_epis)	0 (2013-07-23, barbes)
C1_JFB_2012_0001 --> C1_JFB_2013_0001	4	1	A	1	125.0 (2013-07-04, hauteur_tige)	2 (2013-07-04, couleur_epis)	0 (2013-07-23, barbes)
C1_JFB_2012_0001 --> C1_JFB_2013_0001	5	1	A	1	133.1 (2013-07-04, hauteur_tige)	2 (2013-07-04, couleur_epis)	0 (2013-07-23, barbes)
C1_JFB_2012_0001 --> C1#a_JFB_2013_0001	1	1	A	1	178.9 (2013-07-04, hauteur_tige)	-	-
C1_JFB_2012_0001 --> C1#a_JFB_2013_0001	2	1	A	1	128.2 (2013-07-04, hauteur_tige)	-	-
C1_JFB_2012_0001 --> C1#a_JFB_2013_0001	3	1	A	1	121.5 (2013-07-04, hauteur_tige)	-	-
C1_JFB_2012_0001 --> C1#a_JFB_2013_0001	4	1	A	1	133.7 (2013-07-04, hauteur_tige)	-	-
C1_JFB_2012_0001 --> C1#a_JFB_2013_0001	5	1	A	1	146.6 (2013-07-04, hauteur_tige)	-	-
C1_MLN_2012_0001 --> C1_MLN_2013_0001	1	1	A	1	164.8 (2013-07-04, hauteur_tige)	2 (2013-07-04, couleur_epis)	0 (2013-07-23, barbes)
C1_MLN_2012_0001 --> C1_MLN_2013_0001	2	1	A	1	140.0 (2013-07-04, hauteur_tige)	2 (2013-07-04, couleur_epis)	2 (2013-07-23, barbes)
C1_MLN_2012_0001 --> C1_MLN_2013_0001	3	1	A	1	177.1 (2013-07-04, hauteur_tige)	2 (2013-07-04, couleur_epis)	1 (2013-07-23, barbes)
C1_MLN_2012_0001 --> C1_MLN_2013_0001	4	1	A	1	137.4 (2013-07-04, hauteur_tige)	2 (2013-07-04, couleur_epis)	2 (2013-07-23, barbes)
C1_MLN_2012_0001 --> C1_MLN_2013_0001	5	1	A	1	153.0 (2013-07-04, hauteur_tige)	0 (2013-07-04, couleur_epis)	1 (2013-07-23, barbes)
C1_OLR_2012_0001 --> C1_OLR_2013_0001	1	1	A	1	177.2 (2013-07-04, hauteur_tige)	2 (2013-07-04, couleur_epis)	1 (2013-07-23, barbes)

⊟ Relations : global data

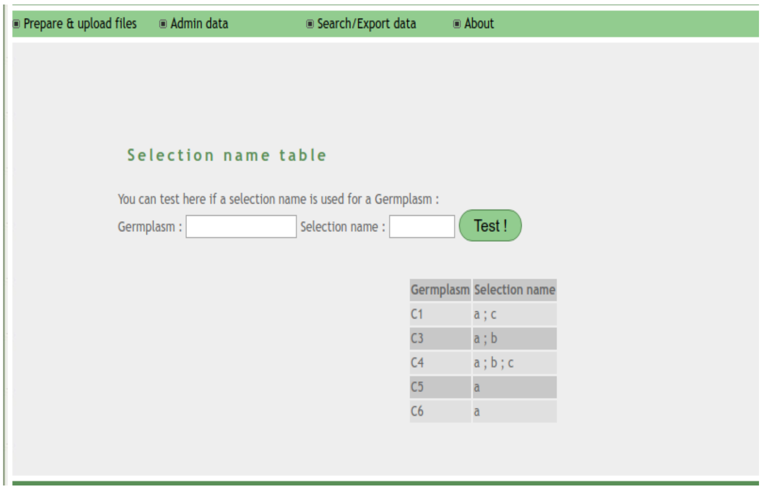
Relation	Block	X	Y	croisement_notes (T1)	densite_semis (T1)	semis (T1)	not
Blé-du-Lot_JFB_2010_0003 --> C1_JFB_2011_0001	1	A	1	-	-	-	-
C1_JFB_2011_0001 --> C1_JFB_2012_0001	1	A	1	-	200 (2012-11-01, densite_semis)	volée (2012-11-01, type_semis)	-
C1_JFB_2012_0001 --> C1_JFB_2013_0001	1	A	1	-	200 (None, densite_semis)	volée (2013-11-01, type_semis)	-
C1_JFB_2012_0001 --> C1#a_JFB_2013_0001	1	A	1	-	-	-	-
C1_MLN_2012_0001 --> C1_MLN_2013_0001	1	A	1	-	150 (None, densite_semis)	semoir (2013-10-25, type_semis)	-
C1_OLR_2012_0001 --> C1_OLR_2013_0001	1	A	1	-	180 (None, densite_semis)	semoir (2013-11-05, type_semis)	-
Rouge-du-Roc_JFB_2010_0002 --> C1_JFB_2011_0001	1	A	2	-	-	-	-

Figure 39: "Measure" mode query result

- **Seed lot data :** the table displays the seed lot name and data related to this seed lot.
- **Individual data related to the relations :** the table displays the name of the relation as well as coordinates in the field, individual number and data related to this individual.
- **Global data related to the relations** : the table displays the name of the relation as well as coordinates of the reproduction and data related to the plot.

C.3 Selection table

The selection table (Figure 40) displays a table with all the selection names used for a germplasm. You can find it in the « Admin data > Tools > Selection table » menu. When many selection already



Selection name table

You can test here if a selection name is used for a Germplasm :

Germplasm : Selection name :

Germplasm	Selection name
C1	a ; c
C3	a ; b
C4	a ; b ; c
C5	a
C6	a

Figure 40: Table des sélections

occurred, a form (germplasm and selection name) is available to test if the name is already used.

C.4 Seed lot card

Advanced query displays a list of seed lot (Advanced query). By clicking on the name of a seed lot, it is possible to view the seed lot card (Figure 41).

The card gives information ('seed lot information' frame) about the variety of the seed lot, its owner, its creation date (harvesting, diffusion, mixture etc.) as well as the project in which the seed lot is used.

History of the seed lot is also displayed, especially the event that created the seed lot and the events in which it is used ('seed lot history' frame).

Seed lot profil : C1_JFB_2012_0001

Seed lot informations

Name : **C1_JFB_2012_0001**

Species : ble-tendre

Germplasm : C1

Owner : **JFB**

Creation year : **2012**

Projects involved in : **DEMO,**

Seed lot history

Creation history :

C1_JFB_2011_0001 ⇒ **C1_JFB_2012_0001** in a Reproduction event

Use history :

C1_JFB_2012_0001 ⇒ C1_MLN_2012_0001

C1_JFB_2012_0001 ⇒ C1_OLR_2012_0001

C1_JFB_2012_0001 ⇒ C1#a_JFB_2013_0001

C1_JFB_2012_0001 ⇒ C1_JFB_2013_0001

Seed lot data

No data for this seed lot

Stock information

Seed lot still available ? **Yes**

Initial quantity : **700 g**

Quantity used :
50 g used in this relation : C1_JFB_2012_0001 --> C1_MLN_2012_0001
51 g used in this relation : C1_JFB_2012_0001 --> C1_OLR_2012_0001
51 g used in this relation : C1_JFB_2012_0001 --> C1#a_JFB_2013_0001
200 g used in this relation : C1_JFB_2012_0001 --> C1_JFB_2013_0001

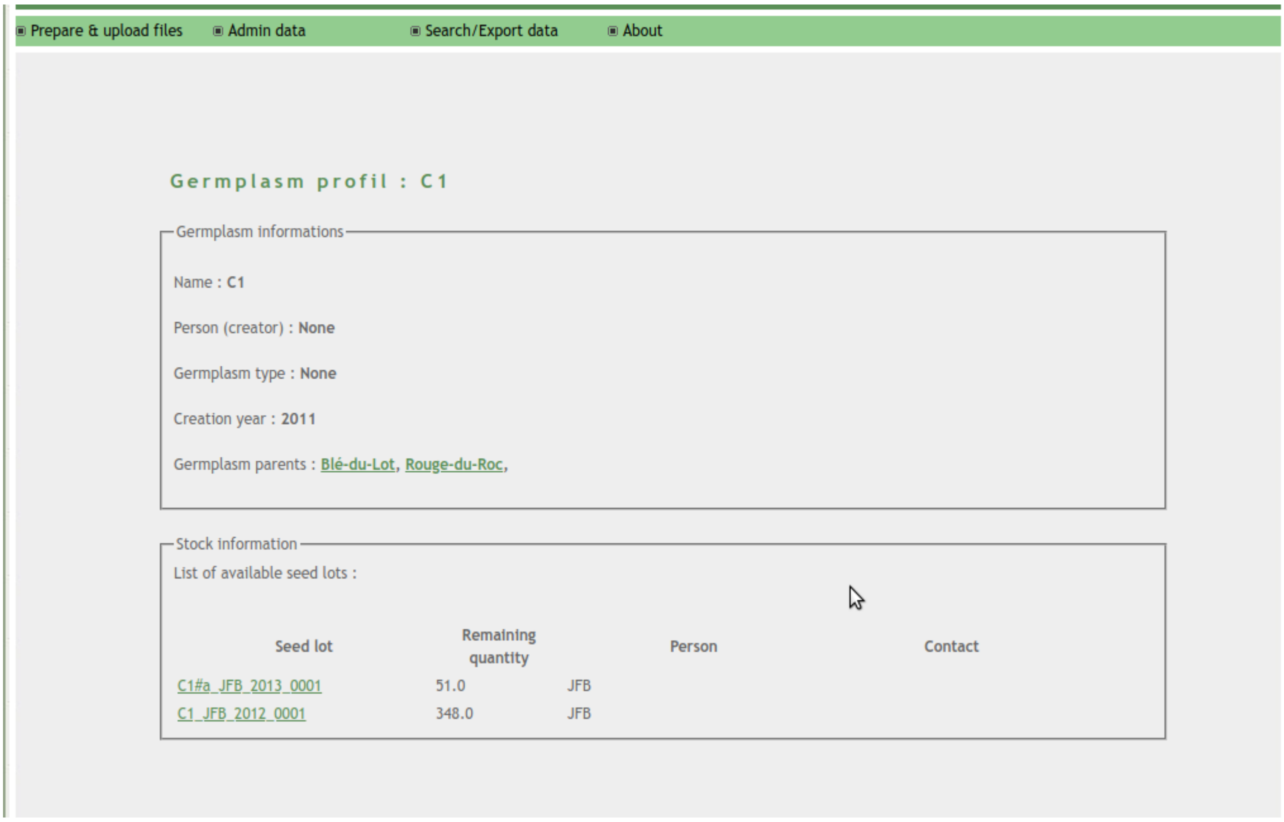
Remaining quantity : **348.0 g**

Figure 41: Seeds lot card

At last, the frame 'stock information', displays data about stock information if the seed lot.

C.5 Germplasm card

From a seed lot card (Seed lot card chapter) it is possible to click on the name of a variety to displays its card (Figure 42).



Germplasm profil : C1

Germplasm informations

Name : **C1**

Person (creator) : **None**

Germplasm type : **None**

Creation year : **2011**

Germplasm parents : Blé-du-Lot, Rouge-du-Roc,

Stock information

List of available seed lots :

Seed lot	Remaining quantity	Person	Contact
C1#a_JFB_2013_0001	51.0	JFB	
C1_JFB_2012_0001	348.0	JFB	

Figure 42: Germplasm card

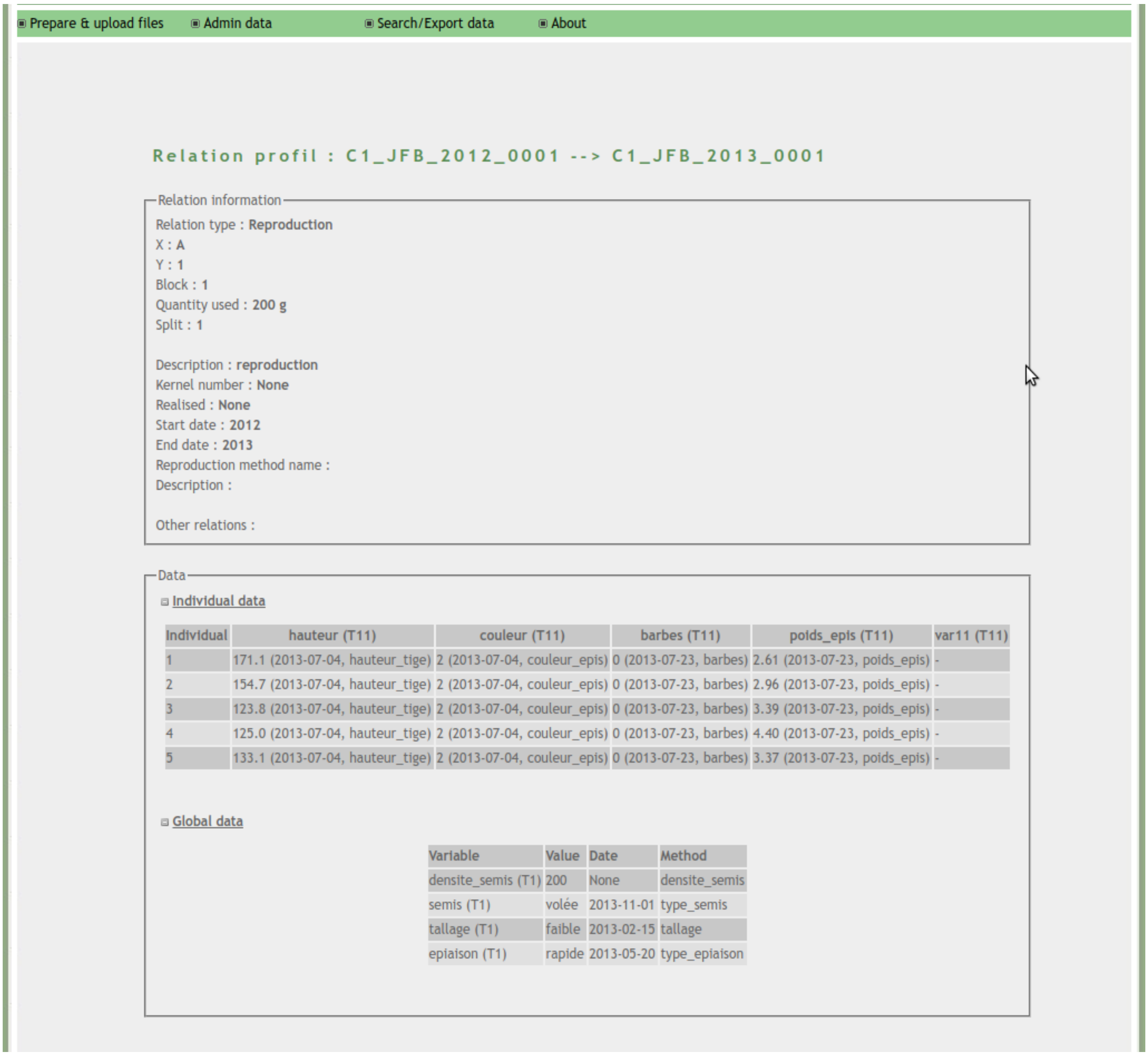
The 'Germplasm information' frame shows the name of the variety, the person who obtained this variety when information is available, as well as the type of the variety.

The 'Germplasm history' frame displays how the variety has been created especially when it is a cross or a mixture.

At last, the 'stock information' frame shows who owns seed lots of this variety. Contact information can be shown when it is possible.

C.6 Relation card

From a seed lot card (Seed lot card chapter) it is possible to click on the ‘relation’ icon ➡ to display its card (Figure 43).



Relation profil : C1_JFB_2012_0001 --> C1_JFB_2013_0001

Relation information

Relation type : **Reproduction**
X : **A**
Y : **1**
Block : **1**
Quantity used : **200 g**
Split : **1**

Description : **reproduction**
Kernel number : **None**
Realised : **None**
Start date : **2012**
End date : **2013**
Reproduction method name :
Description :

Other relations :

Data

Individual data

Individual	hauteur (T11)	couleur (T11)	barbes (T11)	poids_epis (T11)	var11 (T11)
1	171.1 (2013-07-04, hauteur_tige)	2 (2013-07-04, couleur_epis)	0 (2013-07-23, barbes)	2.61 (2013-07-23, poids_epis)	-
2	154.7 (2013-07-04, hauteur_tige)	2 (2013-07-04, couleur_epis)	0 (2013-07-23, barbes)	2.96 (2013-07-23, poids_epis)	-
3	123.8 (2013-07-04, hauteur_tige)	2 (2013-07-04, couleur_epis)	0 (2013-07-23, barbes)	3.39 (2013-07-23, poids_epis)	-
4	125.0 (2013-07-04, hauteur_tige)	2 (2013-07-04, couleur_epis)	0 (2013-07-23, barbes)	4.40 (2013-07-23, poids_epis)	-
5	133.1 (2013-07-04, hauteur_tige)	2 (2013-07-04, couleur_epis)	0 (2013-07-23, barbes)	3.37 (2013-07-23, poids_epis)	-

Global data

Variable	Value	Date	Method
densite_semis (T1)	200	None	densite_semis
semis (T1)	volée	2013-11-01	type_semis
tallage (T1)	faible	2013-02-15	tallage
epiaison (T1)	rapide	2013-05-20	type_epiaison

Figure 43: Relation card

The ‘Relation information’ frame displays the type of the relation, as well as all information related to this relation (date, coordinates when it is a cross or a reproduction, quantity used etc.)

The ‘Data’ frame displays all data collected in this relation.

C.7 Download data

From any card or from the advanced query result table it is possible to download the data table by clicking on the 💾 icon.

D Lexique

- Repetition: plots of the try that contains the same seed lot.
- Reproduction : A reproduction is the cycle of the plant, a seed grow to give new seeds.
- Selection : inside a seed lot, selection of individuals to create a new seed lot. It’s an

intravarietal selection.

- Variety : Set of plants that have close phenotypes.

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