

# MLVABank 5.0 tutorial version 1.6



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## Welcome to MLVAbank for Microbes Genotyping

The version **[5.0 beta]** has been put online. [More informations on the MLVA wiki!](#)

The previous version **[3.0 beta]** can still be accessed at [version3](#).

Version 5 should be better in all respects, so we strongly encourage version 3 users to export their version 3 databases and import them back into version 5.

### Aim of the site

The aim of this site is to facilitate microbes (including pathogenic bacteria) genotyping essentially for epidemiological purposes. Typing is sequence-based. Data from a variety of assays can be managed, including polymorphic tandem repeat typing (MLVA), multiple locus sequence typing (MLST), single nucleotide polymorphisms (SNPs), and spoligotyping assays based upon clustered regularly interspersed palindromic repeats (CRISPRs).

General information on the way to create and manage databases can be found in [the MLVA wiki!](#) More specific informations on individual databases and associated assays can be found on dedicated support websites (links to articles, protocols, primer information).

Importantly, two sets of databases can be made after registration. The first set is called the "aggregated databases". Aggregated database are cooperative projects in which a number of databases maintained by different teams are queried simultaneously. It is a virtual consortium of databases.

The second set is composed of non aggregated databases.

Databases can be public or private.

We hope you will find this tool of use for your work and the making of communities.

Version 5 was created by [Christophe Tourtere](#) owing to financial support from Direction Générale de l'Armement (DGA), Agence Nationale de Sécurité Sanitaire (ANSES) and Agence Nationale de la Recherche (ANR). Previous version 3 was developed in 2007 by Nicolas Bouteiller.



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## ***1.1 Introduction and FAQ***

The aim of this site is to facilitate microbes (including pathogenic bacteria) genotyping essentially for epidemiological purposes. Typing is sequence-based. Data from a variety of assays can be managed, including polymorphic tandem repeat typing (MLVA), multiple locus sequence typing (MLST), single nucleotide polymorphisms (SNPs), and spoligotyping assays based upon clustered regularly interspersed palindromic repeats (CRISPRs).

Some complementary information on the way to create and manage databases can be found in [the MLVA wiki!](#) More specific information on individual databases and associated assays can be found on dedicated support websites (links to articles, protocols, primer information).

## ***1.2 What is a Database in MLVABank?***

A database in MLVABank is an interactive representation of typing data. After import from a comma-separated values (CSV) file, the data can be edited: modification or deletion of strain data, creation, renaming, deletion of columns, new CRISPR spacers, etc. MLVABank can support any numerical data as produced for instance by MLVA, MLST, SNP, "Spoligotyping" and "CRISPR" assays. A database can be queried or viewed. It can be shared with other registered users or even made public.

## ***1.3 What is a cooperative Database?***

A cooperative database is a conglomerate of independently managed databases. It may be useful to manage different projects, curated independently. The databases can be created by the same laboratory, but also by different laboratories in different countries. Cooperative databases can thus help strengthen a community of genotypers.

A minimum set of common rules have to be agreed in order for the aggregation to work. For this some coordination is needed. A cooperative database is created with a first database. Then additional database will be added to this cooperative database, but they need to contain the same headings, fields names, experiment names. It is recommended to practice with simple test files. Also, the internal communication tool may be convenient.

## ***1.4 What is a Query?***

A query is a method for comparing strains in database. A database is selected, then an assay and markers are chosen, before submitting data from one isolate. The result lists the closest strains present in the database. A dendrogram can be drawn, or a Newick format tree can be exported for drawing in dedicated software. If the database contains geographic localization information, the best matches can be geolocalised.

## ***1.5 What is a View?***

A View is a method to display all strains present in a database. Columns can be hidden. Lines can be sorted according to column content. The database creator or administrator may have made accessible a pdf file with extra general information on the database.

## ***1.6 What is a CSV file?***

A CSV file (comma-separated values) stores tabular data in a plain-text form. Each record contains a number of fields, separated by a comma ("," or ";").

## 2 Creating an account

### 2.1 Differences between visitor and user

Visitors can query and view public databases (including public cooperative databases). A logged-in user can create, modify, query, view and manage databases, including sharing them with other users, or making them public. A user has access to the “In Silico Genotyping” and the “Columns preferences” functionalities. Registration is free.

### 2.2 Home page overview

1. **[Home]**: Link to return to the MLVAbank home page.
2. **[Log on]**: link to login for registered users, or to create an account.
3. **[Cooperative Box]**: list of public cooperative databases.
4. **[Public Database Box]**: list of public databases.
5. **[Query]**: run a query (alternatively, double-click on the database name).
6. **[View]**: view a database.
7. **[Details]**: view and select the components of ancooperative database.
8. **[See List...]**: list all non-hidden databases.
9. **[Orsay Lab]**: Orsay-lab home page.
10. **[ClustrMaps®]**: link to overview of visits to mlva.u-psud.fr.

### 2.3 Creating an account and login

#### 2.3.1 Creating an account

To subscribe on the site, click "log on" then "get a login"

Fill the form and "subscribe!".

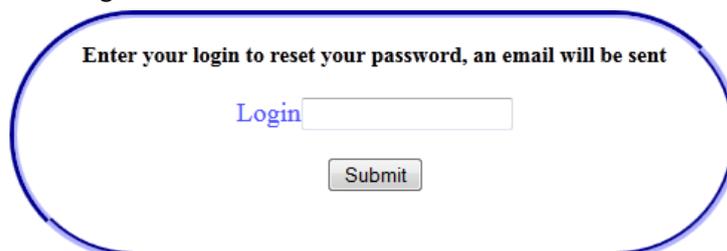
An email will be sent with login information.



The image shows a subscription form titled "Subscription" in blue. The form contains the following fields: First Name, Last Name, University, Institution or Laboratory, Country (a dropdown menu with "France" selected), Preferred Language (a dropdown menu with "english" selected), Login, E mail, Password, and Confirm your Password. The Password field has a strength indicator below it with three segments labeled "weak", "medium", and "strong". A "Subscribe!" button is located at the bottom center of the form.

### ***2.3.2 Resetting password***

To reset password, click "Log on" then "Reset it"



The image shows a form for resetting a password. It features a blue header that reads "Enter your login to reset your password, an email will be sent". Below the header is a text input field with the word "Login" in blue text to its left. A "Submit" button is positioned below the input field.

Enter login and an email will be sent to the associated e-mail address with a temporary password.

### ***2.3.3 Changing Profile and personal information***

To change personal settings fill the form and click "Apply changes".



To change the password click "Change password" and enter the new password in both fields.

To delete an account click "Delete your account". Databases created with this account will be erased, and groups created will be redistributed.

## 2.4 Managing Groups

### 2.4.1 Creating a group

**Create a group**

Enter the name of your group

*Select the users you want to add to the group*

first name	Last name	
First Name	Last Name	<input checked="" type="checkbox"/>
First Name 2	Last Name 2	<input type="checkbox"/>
First Name 3	Last Name 3	<input type="checkbox"/>

To create a group, find a name and check group members.

### 2.4.2 Leave a group or see members

**Manage Group**

**Your groups**

Group 1	Detail	Quit
Group 2	Detail	You are the manager you can't quit
Group 2	Detail	Quit

**Manage your own groups**

Select the user : User 1

Click on "detail" to see the other members of a group. The manager and the other group members will be shown.

Click "Quit" to be removed from a group. Group managers need to transfer the management to another user before quitting.

### 2.4.3 Managing groups

#### 2.4.3.1 Adding a member to a group

To add a member, select a user in the list and "Add"; multiple users can be added at once. Next, click on the second "Add" button to invite them.

#### 2.4.3.2 Showing members

To see member of a group click "Show Members".

#### 2.4.3.3 Excluding one member

After "show members", some members can be removed by clicking on "Exclude".

#### 2.4.3.4 Deleting the group

Clicking "Delete the group".

#### 2.4.3.5 Changing the manager

Select one group and a user. Then "Submit".

**Change group manager**

*To change owner of your groupe: Select your groupe and the next manager*

Groupe:

Next manager:

## 3 Managing Databases

Databases

### 3.1 Select a database

The screenshot shows a web interface for managing databases. At the top, there is a 'Link to: [In silico genotyping](#)' and a 'Manual available here' button. The main title is 'Simple Databases' with '+' and '-' icons. Below the title are three tabs: 'Own databases', 'Shared databases', and 'Public databases'. The 'Own databases' tab is active, showing a table with three database entries:

Database Name	Strains	Disabled	Panels	View	Query
Database Name 1 <small>Created by: Somebody Creation date: 2245-04-18 13:18:09</small>	384	0	1		
Database Name 2 <small>Created by: Another customer Creation date: 2013-02-31 09:29:54</small>	45	0	2		
Databasse Name 3 <small>Created by: ... Creation date: 2014-08-21 13:46:18</small>	713	0	0		

Below this table is a section for 'Cooperative Databases' with a scrollable list of three entries:

Cooperative Name	Databases	Panels	View	Query
Cooperative Name 1 <small>Created by: Mario Brothers Creation date: 1983-07-14 15:44:02</small>	1	3		
Cooperative Name 2 <small>Created by: Pr Tournesol Creation date: 2010-12-21 15:42:09</small>	1	4		
Cooperative Name 3 <small>Created by: ... Creation date: ...</small>	2	1		

At the bottom of the interface is a 'Home' button.

A database needs to be selected in order to make a query or modify it. Click “Database”, choose a simple or a cooperative database to click on the name or directly click on View or Query.

### 3.2 Database

#### 3.2.1 Create a database

To create a new database, click “+” on the left of “Simple Database”

The screenshot shows a form titled 'Import your database'. It contains the following fields and elements:

- A text input field with the placeholder text: 'What is the complete name you want to give to your database.'
- A text input field with the placeholder text: 'Please, select the CVS file which contains the informations of the database (The CVS file can be obtained by saving excel file in CSV file.)'
- Two bullet points with links:
  - [Example of a CSV file for Brucella \(separator '\t'\)](#)
  - [Example of a CSV file for Brucella \(separator '\n'\)](#)
- A file selection button labeled 'Parcourir...' and an 'Upload' button.

Choose a name for the database and select the corresponding CSV data file.

### Database Informations

Choose the column containing a unique identifier (key)

key ①

Choose the column which contains information on geographical position of the strain (information **MUST** be in the format "town, zipcode, country").  
The duration of the import depends on the number of different locations.

No column contains geographical data ②

Choose the column which contains the octal representation of Spoligotyping

No column contains octal data ③

---

### Manage Columns ④

[Click the button to select all rows below]

Name of the column	contains information	contains data for MLVA	contains data for MLST	contains data for SNP	contains data for Spoligotyping	contains data for CRISPR	do not import
key	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input checked="" type="checkbox"/>
strain	<input type="checkbox"/>	<input checked="" style="background-color: yellow;" type="checkbox"/> MLVA	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>
host	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>
isolated_in	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>
Biovar	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>
publication	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>
Contact	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>
group	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>
Bruce06-1322	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>
Bruce08-1134	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>
Bruce11-211	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>

1. Indicate which column is the « key » (by default, the first column will be taken as such).
2. Option: indicate which column (if any) contains the geographic location data.
3. Option: indicate which column (if any) contains the octal representation of spoligotyping.
4. Manage Columns:

Each column present in the data file must be defined as « information », « data » of some kind, or «unused» (do not import). Columns for which “do not import” (default option) is checked will not be imported in the database.

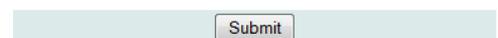
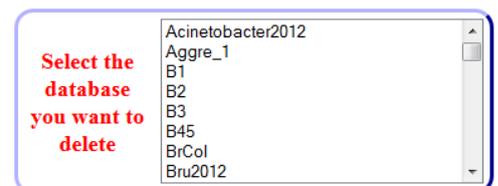
- a. Indicate which columns contain information worth importing in the database.
- b. Indicate columns corresponding to MLVA or other typing data.
- c. Tip for fast selection: click on the buttons to select all rows below.

Activate **“SEND”** at the bottom of the screen. Let the import proceed (it may take a few minutes, especially if a “geographic location” column has been defined, and depending on the size of your database). **The database has been created.**

As metadata it is possible to include columns with URLs or e-mail address using the format "nameoflink (http://www.adress.com)" or "Name ([address@address.com](mailto:address@address.com))" (<> can also be used instead of ()).

### 3.2.2 Deleting a database

To erase a database, click “-” in the left of “Simple Database” then choose one of them and “Submit”. All permissions, panels etc... will be permanently erased.



### 3.2.3 Modifying a database



**List of metadata and markers of "Name Database" database**

[Be careful when changing columns.]

Metadata	MLVA	MLST	SNP	Spoligotyping
Strain_ID <input type="button" value="Delete this column"/>	ETRA-2165 <input type="button" value="Delete this column"/>	mst1 <input type="button" value="Delete this column"/>	snp1 <input type="button" value="Delete this column"/>	s1 <input type="button" value="Delete this column"/>
Country <input type="button" value="Delete this column"/>	ETRB-2461 <input type="button" value="Delete this column"/>	mst2 <input type="button" value="Delete this column"/>	snp2 <input type="button" value="Delete this column"/>	s2 <input type="button" value="Delete this column"/>
group_spoligo <input type="button" value="Delete this column"/>	ETRC-0577 <input type="button" value="Delete this column"/>	mst3 <input type="button" value="Delete this column"/>	snp3 <input type="button" value="Delete this column"/>	s3 <input type="button" value="Delete this column"/>
	ETRD-0580 <input type="button" value="Delete this column"/>	mst4 <input type="button" value="Delete this column"/>	snp4 <input type="button" value="Delete this column"/>	s4 <input type="button" value="Delete this column"/>
	ETRE-3192 <input type="button" value="Delete this column"/>	mst5 <input type="button" value="Delete this column"/>	snp5 <input type="button" value="Delete this column"/>	s5 <input type="button" value="Delete this column"/>
	MIRU02-0154 <input type="button" value="Delete this column"/>	mst6 <input type="button" value="Delete this column"/>	snp6 <input type="button" value="Delete this column"/>	s6 <input type="button" value="Delete this column"/>
	MIRU10-0960 <input type="button" value="Delete this column"/>	mst7 <input type="button" value="Delete this column"/>	snp7 <input type="button" value="Delete this column"/>	s7 <input type="button" value="Delete this column"/>
	MIRU16-1644 <input type="button" value="Delete this column"/>		snp8 <input type="button" value="Delete this column"/>	s8 <input type="button" value="Delete this column"/>
	MIRU20-2050 <input type="button" value="Delete this column"/>		snp9 <input type="button" value="Delete this column"/>	s9 <input type="button" value="Delete this column"/>
	MIRU23-2531 <input type="button" value="Delete this column"/>		snp10 <input type="button" value="Delete this column"/>	s10 <input type="button" value="Delete this column"/>
	MIRU24-2687 <input type="button" value="Delete this column"/>		snp11 <input type="button" value="Delete this column"/>	s11 <input type="button" value="Delete this column"/>
	MIRU26-2996 <input type="button" value="Delete this column"/>		snp12 <input type="button" value="Delete this column"/>	s12 <input type="button" value="Delete this column"/>
	MIRU27-3006 <input type="button" value="Delete this column"/>		snp13 <input type="button" value="Delete this column"/>	s13 <input type="button" value="Delete this column"/>

Metadata

Metadata   
  MLVA   
  MLST   
  SNP   
  Spoligotyping

Strain\_ID

To modify a database click on "Database"=>"Other"=>"Manage Database".

#### 3.2.3.1 Adding columns

To add a column select the type of this column (Metadata, MLVA...) then write the name and "Add".

#### 3.2.3.2 Deleting columns

Click "Delete this column" to erase it. All information will be permanently erased.

#### 3.2.3.3 Renaming columns

To rename a column select the type of the column then choose the name in the list. Write the new name then "Rename" button.

#### 3.2.3.4 Rename the database

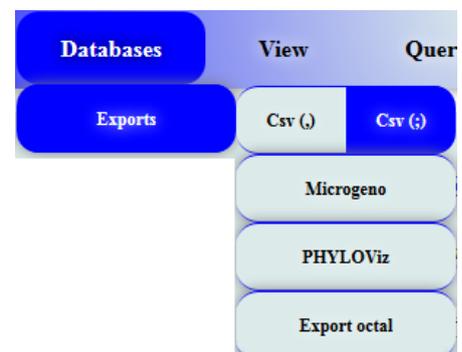
To rename the database, click on the name in the title, choose a new name and valid.

### 3.2.4 Export

A database can be exported in CSV format by clicking "Databases" =>"Exports".

Select the export output:

- CSV(:) : If French excel
- CSV(,) : If other excel
- MicroGeno: to import database in [microgeno.org](http://microgeno.org)
- PHYLOViz: to use [www.phyloviz.net](http://www.phyloviz.net)
- Octal: to export spoligotyping in octal



Export a database with some panels set the file with panels' informations and for each panels the genotypes of strains.

### 3.2.5 Define support web page

**Database information**

These informations will be displayed when querying your database.

Creator of the database	ctourterel
Web site	
Description	

Type	First Link	Second Link
Mlva	Title	
	Link	
Mlst	Title	
	Link	
Snp	Title	
	Link	
Spoligo	Title	
	Link	

**Submit**

It is possible to link out the database to an independent website providing support information. The upper part of the “Define support web page” contains three fields:

1. Creator: to indicate the owner of the database.
2. Website: a link to the external webpage for example.
3. Description field: e.g. a short description of the database or other comments.

The lower part allows to define one or two additional links, associated with each genotyping method.

### 3.3 Cooperative Database

**Create a new cooperative database** ①

Name:

Select the first base : choose the first base to add this

**Your cooperative databases** ②

Cooperative database 1 Select bases : choose a base to add  Add

Cooperative database 2 Select bases : choose a base to add  Add

Cooperative database 3 Select bases : choose a base to add  Add

③

**Cooperative databases other users are sharing with you**

Cooperative from other Select bases : choose a base to add  Add    
   ④

Cooperative from another other Select bases : choose a base to add  Add

#### 3.3.1 Create (1)

The creation of a database is required in order to be able to create a cooperative database. Choose a name and select a first database which will contribute to this cooperative database and submit.

#### 3.3.2 Manage (2)

The cooperative databases of the logged user are listed here.

##### 3.3.2.1 Show databases

Click “Show bases” to list the databases currently contributing to the corresponding cooperative database.

##### 3.3.2.2 Add and remove databases

To add a new database to a cooperative database, select one database in the list and “Add”.

If this database is not yet compatible in terms of field names, marker, etc. a popup window indicates some requirements for harmonization with the cooperative database matrix.

1. Add some columns to the cooperative database or delete columns of the database.
2. The cooperative database matrix or the database to be added may not have the same genotyping methods. The only solution is to create another database with the same genotyping methods, even if no data is provided.

To remove a database after “Show bases” click on “Take off” to take off this base of the cooperative database. The database itself will not be affected.

These Databases are not compatible:

[MLVA] Modification:

[Managager of Cooperative must add]:

bruce06\_BRU1322  
 bruce08\_BRU1134  
 bruce11\_BRU211  
 bruce12\_BRU73  
 bruce42\_BRU424  
 bruce43\_BRU379  
 bruce45\_BRU233  
 bruce55\_BRU2066  
 bruce04\_BRU1543  
 bruce07\_BRU1250  
 bruce09\_BRU588  
 bruce16\_BRU548  
 bruce18\_BRU339  
 bruce21\_BRU329  
 bruce30\_BRU1505

You don't have Spoligo genotyping

### 3.3.2.3 Edit the support web page

Indicate or modify the support website coordinates and some additional information. These information are shown in “View” or “Query”.

### 3.3.2.4 Export skeleton

Export the skeleton of a cooperative database (convenient way to create a new compatible database).

### 3.3.2.5 Generate Tree

Generate dendrogram tree (maximum 200 strains)

## **3.3.3 Delete**

A cooperative database can be deleted with the button “Drop this cooperative”. The contributing databases will not be affected.

## **3.3.4 Sharing a cooperative database**

### 3.3.4.1 The reasons for sharing

A cooperative database needs to be shared to make it visible by other selected users, or to allow users to contribute their own databases. See the page “[Sharing databases](#)”.

### 3.3.4.2 Adding a database to a cooperative database

This part works as “Add and remove databases” above.

### 3.3.4.3 Changing the ownership of a cooperative database (3)

To change the manager of a cooperative database select the cooperative database and a user then “Submit”.



The screenshot shows a web form titled "Change aggregated database owner". Below the title is a subtitle: "To change owner of your aggregated database: Select your base and the next owner". The form contains two dropdown menus: "Aggregated Databases: Select one aggregated database" and "Next owner: Select one user". At the bottom of the form is a blue "Submit" button.

### 3.3.4.4 Making a cooperative database publicly accessible

Cooperative databases (including all data of contributing databases) can be made public, i.e. visible by anyone. To publish one such database please contact the administrators by email or internal message to the group “AdminGp”.

### 3.3.4.5 Shared databases (4)

Cooperative databases to which the logged user has been granted access are listed. The framework of the database can be exported (skeleton) using either the comma or semi-colon separator. Databases can be added, if the right to do so has been given.

### 3.3.4.6 Export the data

To allow user to download your data from a cooperative click “Show Bases” and click “Enable export”.

## 3.4 Panel

### 3.4.1 Create

Create a new panel, select the markers you want to have in your panel  
A default panel is already created with all the markers

Enter the name of this panel : newpanel

MLVA

- Abaum-3406
- Abaum-3530
- Abaum-3002
- Abaum-2240
- Abaum-1988
- Abaum-0826
- Abaum-0017
- Abaum-0845
- Abaum-2396
- Abaum-3468

Panels of loci can be defined in order to easily select markers during a query. Markers constituting the panel are selected and subsequently ordered.

Click "Create a panel", choose a panel name. The first click on a marker will select the type of genotyping assay for this panel.

Markers are included or removed using the "X" button or double click. Green is for "included".

The arrows will move a marker up or down.

After a panel has been created, a genotype library will be automatically calculated. Panels can also be defined

in the initial CSV data file. After the header line, include one line per panel as described below:

1. In the first column type "panel"
2. In the second column indicate the name of the panel
3. Check by "X" each marker to be included in the panel.
4. If genotypes have already been defined for this panel, include a column using the panel name as column header. Indicate genotype numbers in this column.

In the CSV file if there is a problem with genotypes after the creation (such as different genotype numbers assigned to identical genotypes, or the opposite), an error message will be provided.

### 3.4.2 Deleting a panel

To delete a panel, "Remove a panel" in the left menu and select a panel. Click "Submit" to remove this panel. When a panel, is removed, all associated genotypes are also permanently erased.

### 3.4.3 Modifying a panel

The "Modify a panel" page is identical to the panel creation page. Adding or removing one marker will permanently erase the previous genotype library to generate a new one.

Databases

Panels

Create

Edit

Remove

Enter the name of this panel : newpanel

MLVA

- Abaum-3406
- Abaum-3530
- Abaum-3002
- Abaum-2240
- Abaum-1988
- Abaum-0826
- Abaum-0017
- Abaum-0845
- Abaum-2396
- Abaum-3468

submit erase the form

Select the panel you want to remove this database

Panel : select the panel to be removed

submit

MLVA Panels

MLVA Panels

SNP Panels

CRISPR Panels

## 3.5 Strains

### 3.5.1 Adding strains

To import data from new strains, two options are proposed: adding strains one by one or using a CSV file to add automatically multiple strains. When importing from a CSV file, the user can decide to overwrite preexisting data in case of entries with identical keys.

The interface shows a 'Databases' menu with 'Strain & Genotype' selected. On the right, there are buttons for 'Add strains', 'Edit strains', 'Delete/Hide', and 'Manage Genotype'. The main area is split into two panels:

- Left Panel: 'Fill the form to add one strain to the database'**
  - Section: **Metadata (Strain Information)**
  - Fields: key, Strain\_ID, Year, genus, species, publication, contact, isolated\_in.
- Right Panel: 'Or you can add some strain with a csv document'**
  - Text: 'Please, select the CVS file which contains the informations of the database (The CVS file can be obtained by saving excel file in CSV file.)'
  - Link: 'Example of a CSV file for Brucella'
  - Section: 'In case you have the same name of Strain:'
  - Options:  Prompt before Overwrite,  Overwrite All
  - Button: 'Parcourir...'
  - Button: 'Add Strains'

### 3.5.2 Editing strains

To modify strains in a database, select a number of strains in the list and click "Modify".

Strains associated data can be edited by clicking on a value.

To edit multiple values: select the type of data and one column, use the "find and replace" tool.

After modifications click on "Confirm Modification?" to validate changes.

#### 3.5.2.1 Deleting strains

To delete strains, select them, check the data and "confirm deletion".

The interface shows a 'Select strains for modification' window with a list of strain IDs: 2006LeFleche#001, 2006LeFleche#002, 2006LeFleche#013, 2006LeFleche#014, 2006LeFleche#017, 2007AIDahouk#057, 2007AIDahouk#058, 2007AIDahouk#059, 2007AIDahouk#060, 2007AIDahouk#061. A 'Modify' button is at the bottom.

Below the list is a search tool:

- Choose data: Metadata
- Find: [ ] in column: Strain and replace by: [ ]
- No approximate search:
- Modify button

The main area contains two tables:

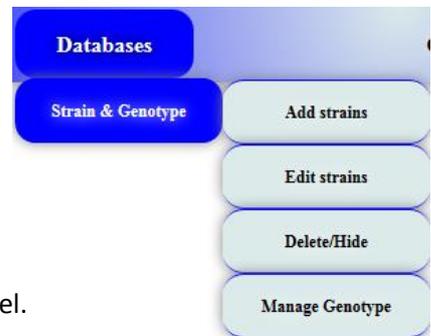
**Metadata Detail:**

Key	strain	host	isolated_in	Bovar	publication	Contact	group
2006LeFleche#001	REF 16M	goat	United States	B. melitensis 1	Le Fleche2006 (http://www.ncbi.nlm.nih.gov/pubmed/16469109)	Gilles Vergnaud (gilles.vergnaud@u-psud.fr)	57.0902400
2006LeFleche#002	REF 544	cattle	England	B. abortus 1	Le Fleche2006 (http://www.ncbi.nlm.nih.gov/pubmed/16469109)	Gilles Vergnaud (gilles.vergnaud@u-psud.fr)	52.3555177
2006LeFleche#013	REF Thomsen	swine	Denmark	B. suis 2	Le Fleche2006 (http://www.ncbi.nlm.nih.gov/pubmed/16469109)	Gilles Vergnaud (gilles.vergnaud@u-psud.fr)	56.2639200
2006LeFleche#014	REF 686	swine	United States	B. suis 3	Le Fleche2006 (http://www.ncbi.nlm.nih.gov/pubmed/16469109)	Gilles Vergnaud (gilles.vergnaud@u-psud.fr)	37.0902400
2006LeFleche#017	REF Porpoise	porpoise	Scotland	B. ceti	Le Fleche2006 (http://www.ncbi.nlm.nih.gov/pubmed/16469109)	Gilles Vergnaud (gilles.vergnaud@u-psud.fr)	56.4906712
2007AIDahouk#057	BR 17	human	Berlin, Germany	B. melitensis 1	AI Dahouk2007 (http://www.ncbi.nlm.nih.gov/pubmed/17261338)	Gilles Vergnaud (gilles.vergnaud@u-psud.fr)	52.5191710

**MLVA Detail:**

	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B
K	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
2006LeFleche#001	3	4	2	13	4	2	3	3	5	36	6	2	5	8	3	6				
2006LeFleche#002	4	5	4	12	2	2	3	3	5	42	8	3	5	3	4	5				
2006LeFleche#013	2	4	8	14	6	1	5	2	6	44	9	9	9	18	2	4				
2006LeFleche#014	2	3	4	11	3	1	5	2	4	38	9	7	5	10	4	5				
2006LeFleche#017	2	5	8	7	3	2	3	1	4	44	9	6	4	3	5	6				
2007AIDahouk#057	3	4	3	13	5	3	3	3	4	36	5	2	5	3	4	5				

Buttons: 'Validate modification?', 'Cancel'



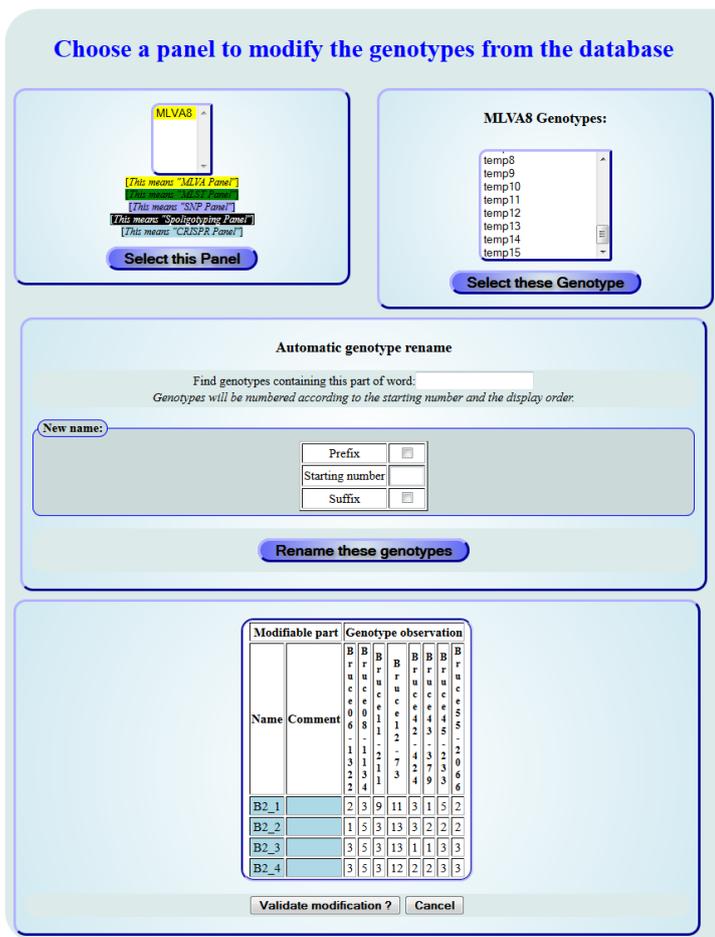
### 3.6 Genotyping

#### 3.6.1 *Generating genotype numbers*

A library of genotype numbers is automatically generated for each panel.

Genotype numbers can also be imported automatically during the creation of the database (see above, "Panel" paragraph).

#### 3.6.2 *Managing genotypes*



Automatically generated genotype numbers are identified by the "temp" prefix.

Click on "Manage Genotype" in the left menu, select a panel to see the list of genotypes for this panel.

Choose one or more genotype(s) and click on the button to see.

Click on the name or the comment to edit, then "Validate modification?" to save.

The "Automatic genotype rename" allows to rename each genotype with the part of word. Prefix and suffix are editable as well as the starting number.

### 3.7 Managing CRISPR data

**Fill the form to add one CRISPR Spacer**

**Spacer Information**

Key

Annotated Spacer

Sequence

**Or you can add some spacer with a csv document**

Please, select the CVS file which contains the informations of the database  
(The CVS file can be obtained by saving excel file in CSV file.)

• [Example of a CSV file for CRISPR Database](#)

**In case you have the same name of Strain:**  
 Prompt before Overwrite  
 Overwrite All

#### 3.7.1 Creating a CRISPR database

When using CRISPR data, a CRISPRtionary can be defined to associate spacer sequences to spacer Ids. As with the strain adding procedure, two import options are proposed, one by one or using a CSV file.

#### 3.7.2 Browsing the CRISPR database

**List of CRISPR Spacer**

© Key ACGT  Search

\* Sequence

Key	Annotated Spacer	Sequence
a12	Pourcel2005:12	C G G T C A T T C C C G A G T A T G A T T G T C G A T A C G T T A G
a15	Pourcel2005:15	A C G T C A A A G C T C G G C T T C
a20	Pourcel2005:20	A G A G G C A A C C A T A A T G G
a23	Pourcel2005:23	T T C T G A A G C T C T C G T A T T
a29	Cui2008:3	A C G G A C T T A C T T C T C T A A C
a33	Cui2008:7	T A C A T C T A T A C G T T T A G
a37	Cui2008:11	T C G T C A A T T T C C G G C G G T
a37*	Cui2008:12	T C G T C A A T T G A A T T C G G G A C G T T C C G G C G G T
a37**	Cui2008:13	T C G T C A A T T G A A T T C G G G A C G T T C C G G C G
a38	Cui2008:14	G T G C A G C T T T A A A C G T G T T G A G G T T G C G C T G A
a52	Cui2008:27	T G A G T C T G C A A C A C G T T G A A T A A A T T C C T G A C
a83	Nairobi:1	C A T A A G A A T C T C A G C T T C T T A C G T T G A T T G T
b5	Pourcel2005:39	A A C G A A C C C A C G T A G A A T T G C C A T T A C C G C C G G
b6	Pourcel2005:40	T G G A G T G G C G A G T T A G A G A G T A A A C G T A G G A A
b8	Pourcel2005:42	T T A A C G T A G C C A G G C G T G T G G A C A T A G C C T A G T
b10	Pourcel2005:44	A G T G A C T A A C A C G T C A C A A A T G T C G C G T T C T
b18	Cui2008:55	T G G A C G T T A T C G A A G C T A A A G A A T T T G C T G G C
b22	Cui2008:59	T G G G A C G C T T T A C A G T C T G C A C G T C T C T G A G T
b26	Cui2008:63	G A T A G C A T G G A C G T C A A G G C A C C T G C T G G C T A T
e8	Cui2008:77	T A A C G T C G T T A A T T C T A G C C A A T C G C C A T T T

**List of strain with this sequence:**

Number of strains: 5

- CFR467
- CFR479
- CFR517
- CFR519
- CFR562

Browsing the CRISPRtionary to see spacer sequences. To search key or sequence, select the search and fill the text area.

Click on sequence to see the strains containing this spacer.

#### Choose the data you want to modify or delete

a1  
a10  
a11  
a12  
a13  
a14  
a15  
a16  
a17  
a18

---

**Key:** Annotated Spacer

a13 Pourcel2005:13

---

**Sequence**

T T A T C C G T G A C C G A C T C A A A T A C A C G C T G G A A C G

---

#### 3.7.3 Modifying or deleting some CRISPR spacers

“Manage the CRISPR database” allows to edit the name, the annotation and the sequence for spacers.

Click on the element to modify it.

## 3.8 Updating Information

### 3.8.1 *Tree drawing*

### Update Trees

**Tree informations:**

Which informations do you want to see in the dendrogram ?

- Key
- strain
- host
- isolated\_in
- Biovar
- publication
- Contact
- group

**MLVA Tree:**

A dendrogram can be generated for a database containing up to 1000 strains. Select additional information to add in the dendrogram and click “Create Tree”.

After you can update this tree or draw it.

The tree can be accessed when viewing the database.

## 4 Viewing and querying databases

The "View" part allows to show every strains of a database or a cooperative. Lines can be sorted according to column content using the "arrow" button.

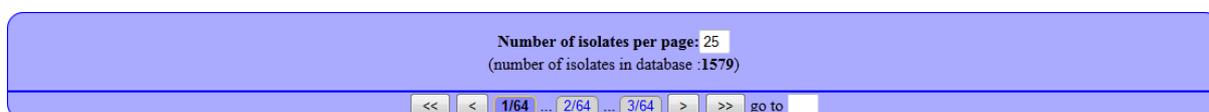
The "Query" part allows to compare a user submitted genotype to the database.

### 4.1 Table Manipulation

#### 4.1.1 Hiding columns

Columns can be hidden by clicking on their name. To restore the columns click on the leftmost column header, "Key". If there are some panels, select one to hide some markers.

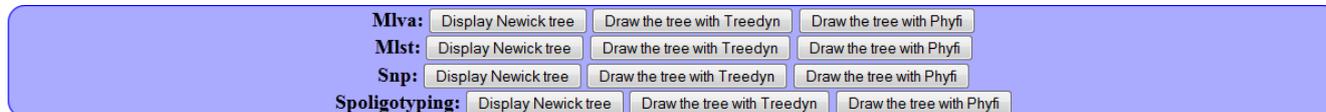
#### 4.1.2 Navigation



This menu allows the browsing of the database by selecting the number of line to show per page, clicking on the page or choose your page in the "go to" area.

To display other information in this menu, pass the cursor over this menu.

### 4.2 Newick tree



This menu provides the Newick tree calculated with "Update Informations" part.

### 4.3 Geographic location



This menu displays a link to see the geographic location from all strains if a geographic field and geographic information were provided.

To see the geographic location button, pass the cursor over the page menu.

### 4.4 Marker Selection and display of genotyping data in a query

To make a query choose some markers by:

- Selecting a panel (a predefined and ordered set of loci)
- or
- Checking markers

The "Display Part" of this page mean "display MLVA data" or other genotyping method. This auto-check when a marker or a panel are selected.

After the selection "Submit" this form.

## 4.5 Marker values and parameters

### 4.5.1 Parameters

The user can define a number of parameters during a query:

- Choose the maximum number of strains (200 max)
- Choose the maximum distance

### 4.5.2 Type of display

There are two display modes for the query

- Default: display the strains including strains with an identical genotype.
- No doublets: Display a single genotype, a list of the strains with an identical genotype is provided by clicking on the key.

### 4.5.3 Markers values

A sample genotype is indicated, corresponding to the first strain in the data file. Click on it, it will be pasted in the query window. Copy Paste in the first case some values fill the form correctly. To change values on spoligotyping value, click on the representation or change the number.

## 4.6

Currently selected:  
>> [Name of database] <<

**Enter character values**  
Genotypes must be entered in copy number, in the following order, with spaces to separate markers.

You have selected the following markers :

MLVA

- Bruce06-1322
- Bruce08-1134
- Bruce11-211
- Bruce12-73
- Bruce42-424
- Bruce43-379
- Bruce45-233

• Choose maximum number of strains to show

• Choose maximum distance

**Display type:**

Do not display duplicate genotypes

Default (Display all)

**Calculate with MLVA**

Enter the value for each *mlva* marker or paste in the first column to fill the rest

For instance, this is the profile corresponding to the 2006LeFliche#001 strain (B1) for the chosen markers:  
3 4 2 13 4 2 3 3

B	B	B	B	B	B	B
r	r	r	r	r	r	r
u	u	u	u	u	u	u
c	c	c	c	c	c	c
e	e	e	e	e	e	e
0	0	e	e	e	e	e
0	8	1	1	4	4	5
-	-	-	-	-	-	-
1	1	2	-	-	-	2
3	1	2	7	4	3	0
2	3	1	3	2	7	3
2	4	1	4	3	3	6

## Results

The results page of a query can be customized as follows:

### 4.6.1 Hiding columns

Clicking on columns headers will hide them. Clicking on the "Key" column header will restore all columns (see also "column preferences" available to logged users).

### 4.6.2 Genotype

Selecting a panel shows the strains genotype, click on "Genotype" to switch the display. If the strains were not genotyped for this panel there is no change. Comments or genotype values are shown when moving the cursor on the genotype.

To restore all values, click on "Genotype".

Nearest neighbors in the [B1] databases  
[Click the buttons to hide columns and click on 'Key' to view all] End means different results

Key <small>Show all columns</small>	Strain	publication	group	lon	lat	MLVA															
						B0	B1	B2	B3	B4	B5	B6	B7	B8	B9	B10	B11	B12			
Queried Strain						0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2006LeFlèche#001	REF 18M	Le Flèche2006	Americas	-95.7128910	37.0902400	3	4	2	13	4	2	3	3	3	3	3	3	3	3	3	3
2007AIDahouk#060	BFR 20	Al Dahouk2007	??	69.3451160	30.3753210	3	5	3	13	3	2	3	3	3	3	3	3	3	3	3	3
2007AIDahouk#057	BFR 17	Al Dahouk2007	Americas	13.4060912	52.5191710	3	4	3	13	5	3	3	3	3	3	3	3	3	3	3	3
2009Her#003	KRef03	Her2009	B.abortus	32.2902750	1.3733330	3	5	4	11	2	2	3	3	3	3	3	3	3	3	3	3
2007AIDahouk#061	BFR 27	Al Dahouk2007	Africa			2	5	3	13	4	2	3	3	3	3	3	3	3	3	3	3
2009Her#005	KRef05	Her2009	B.abortus	-1.1743197	52.3555177	3	5	3	12	2	2	3	3	3	3	3	3	3	3	3	3
2010Valdezate#001	#9700017	Valdezate2010	East mediterranean	-3.7908450	37.7678260	1	5	3	13	2	2	3	3	3	3	3	3	3	3	3	3
2010Valdezate#002	#9900120	Valdezate2010	East mediterranean	-4.7793835	37.8881751	1	5	3	13	2	2	3	3	3	3	3	3	3	3	3	3
2010Valdezate#003	#9900124	Valdezate2010	East mediterranean	-4.7793835	37.8881751	1	5	3	13	2	2	3	3	3	3	3	3	3	3	3	3
2010Valdezate#004	#9900125	Valdezate2010	East mediterranean	-4.7793835	37.8881751	1	5	3	13	2	2	3	3	3	3	3	3	3	3	3	3
2007AIDahouk#059	BFR 19	Al Dahouk2007	East mediterranean	8.4660395	49.4874592	1	5	3	13	3	2	3	3	3	3	3	3	3	3	3	3
2006LeFlèche#002	REF 544	Le Flèche2006	B.abortus	-1.1743197	52.3555177	4	5	4	12	2	2	3	3	3	3	3	3	3	3	3	3
2009Her#001	KRef01	Her2009	B.abortus	-1.1743197	52.3555177	4	5	4	12	2	2	3	3	3	3	3	3	3	3	3	3
2007AIDahouk#058	BFR 18	Al Dahouk2007	East mediterranean	35.2433220	38.9637450	1	5	3	13	3	3	3	3	3	3	3	3	3	3	3	3
2009Her#002	KRef02	Her2009	B.abortus	-1.1743197	52.3555177	4	5	4	12	2	1	3	3	3	3	3	3	3	3	3	3
2009Her#004	KRef04	Her2009	B.abortus	-1.1743197	52.3555177	4	5	4	12	2	2	3	3	3	3	3	3	3	3	3	3
2006LeFlèche#013	REF Thomsen	Le Flèche2006	B.suis biovar 2	9.5017850	56.2639200	2	4	8	14	6	1	5	2	2	2	2	2	2	2	2	2
2006LeFlèche#017	REF Porpoise	Le Flèche2006	B.ceti	-4.2026458	56.4906712	2	5	8	7	3	2	5	1	1	1	1	1	1	1	1	1
2006LeFlèche#014	REF 686	Le Flèche2006	B.suis biovar 3	-95.7128910	37.0902400	2	3	4	11	3	1	5	2	2	2	2	2	2	2	2	2

### 4.6.3 CRISPR

Nearest neighbors in the [Name of database] databases  
[Click the buttons to hide columns and click on 'Key' to view all] End means different results

Key <small>Show all columns</small>	Strain	Focus	biovar	contact	genus	lon	lat	CRISPR		
								Y P a	Y P b	Y P c
Queried Strain								<a href="#">a1</a> <a href="#">a2</a> <a href="#">a3</a> <a href="#">a4</a> <a href="#">a5</a> <a href="#">a13</a> <a href="#">a14</a>	<a href="#">b1</a> <a href="#">b9</a> <a href="#">b2</a> <a href="#">b10</a> <a href="#">b11</a> <a href="#">b12</a>	<a href="#">c1</a> <a href="#">c2</a> <a href="#">c3</a> <a href="#">c5</a> <a href="#">c6</a>
1	18	#4	caucasica	<a href="mailto:gilles.veronaud@u-psud.fr">gilles.veronaud@u-psud.fr</a>	Yersinia	-82.9071230	32.1574351	<a href="#">a1</a> <a href="#">a2</a> <a href="#">a3</a> <a href="#">a4</a> <a href="#">a5</a> TTATCCGTGACCGACTCAAATACACGCTGGAAGC <a href="#">a14</a>	<a href="#">b1</a> <a href="#">b9</a> <a href="#">b2</a> <a href="#">b10</a> <a href="#">b11</a> <a href="#">b12</a>	<a href="#">c1</a> <a href="#">c2</a> <a href="#">c3</a> <a href="#">c5</a> <a href="#">c6</a>
2	10		Orientalis	<a href="mailto:gilles.veronaud@u-psud.fr">gilles.veronaud@u-psud.fr</a>	Yersinia			<a href="#">a1</a> <a href="#">a2</a> <a href="#">a3</a> <a href="#">a4</a> <a href="#">a5</a> <a href="#">a6</a> <a href="#">a7</a> <a href="#">a8</a>	<a href="#">b1</a> <a href="#">b2</a> <a href="#">b3</a> <a href="#">b4</a> <a href="#">b5</a>	<a href="#">c1</a> <a href="#">c2</a> <a href="#">c3</a>
3	10		Orientalis	<a href="mailto:gilles.veronaud@u-psud.fr">gilles.veronaud@u-psud.fr</a>	Yersinia	37.9061930	-0.0235590	<a href="#">a1</a> <a href="#">a2</a> <a href="#">a3</a> <a href="#">a4</a> <a href="#">a5</a> <a href="#">a6</a> <a href="#">a7</a> <a href="#">a8</a>	<a href="#">b1</a> <a href="#">b2</a> <a href="#">b3</a> <a href="#">b4</a> <a href="#">b5</a>	<a href="#">c1</a> <a href="#">c2</a> <a href="#">c3</a>

The CRISPR handling is different, the number of "Shared Spacer" is used as a distance, instead of the categorical coefficient. The blue spacer mean present in the query. Click on a spacer to show available associated data ("Managing CRISPR data"). To hide the sequence double-click on it.

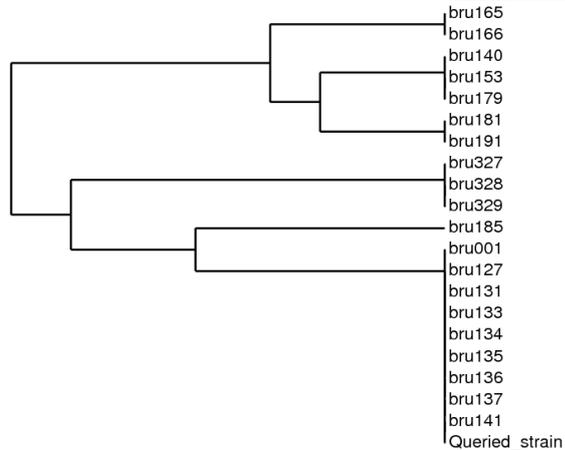
### 4.6.4 Display the list of strains with an identical genotype

If the "Do not display duplicate genotypes" option was selected, click on the italicized strain name to show other strains with the same genotype.

- Tree drawing
- Access geographic view
- Access the matrix of distances
- Export matrix of distances to MEGA format

## 4.7 Tree Drawing

To generate a Newick tree click on “Tree drawing” in the menu, choose relevant metadata and “Submit”. Now the tree is generated and can be displayed with “Treedyn” or “Phyfi”.



## 4.8 Accessing geographic view

If the database has some geographic location, it can be shown with “Access geographic view”, after selection of metadata and "submit".

## 4.9 Accessing the matrix of distances and Export matrix of distances to MEGA format

Click on the link.

# 5 Geolocalisation

## 5.1 Create a geolocalisation

Choose the column which contains information on geographical position of the strain (information **MUST** be in the format “town, zipcode, country”). The duration of the import depends on the number of different locations.  
 No column contains geographical data ▾

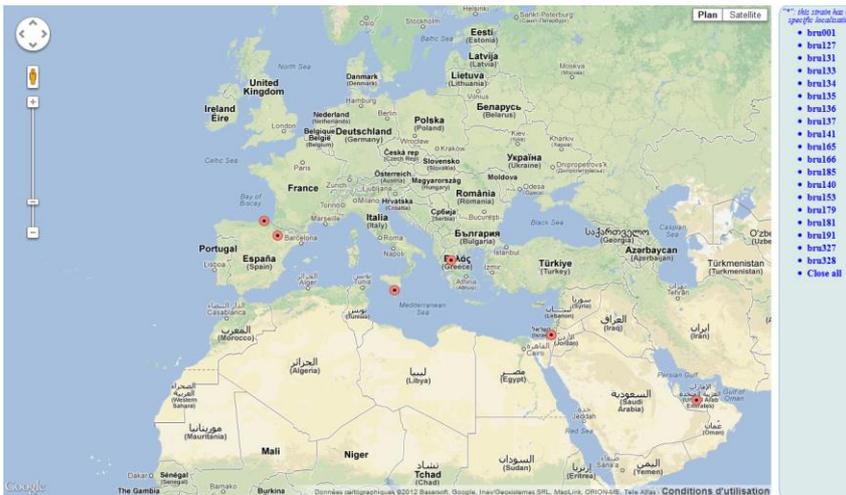
During the import of a new database(using “[Create](#)”) select the column which contains information on geographical position. Select this column in the second field.

If longitude and latitude information is available for some isolates, it needs to be provided in two columns called “lon” and “lat” respectively. When present, longitude and latitude data will be used rather than the information provided in the geolocalisation field, and a “\*” will be inserted before the name of city or country to reflect this.

## 5.2 Editing a geolocalisation

While “Editing strains”, longitude and latitude will be automatically recalculated and updated if the geographical information field is modified (here “isolated\_in”).

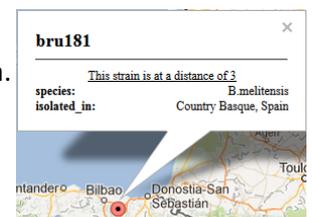
## 5.3 Accessing the geolocalisation



Access the geolocalisation from “View” or “Query”, select relevant metadata fields, “Submit” and the map appears.

Metadata Detail:		
cle	host	isolated_in
bru005	cattle	England
bru006	cattle	England
bru008	cattle	England
bru009	goat	Italia

The Right menu is the list of strains, click on to bring up the details of the metadata.



## 6 MailBox

This tool may be useful to communicate with other members of the site.

### 6.1 Inbox

The inbox display discussions with other registered users. The color code is red for unread messages and brown otherwise. Click on “X” button to stop following this discussion. In the absence of followers, all associated messages will be erased.

The “Communication” menu indicates how many messages are unread.

Mail 4	2012-08-22 09:54:46	Somebody	X
Mail 3	2012-08-21 18:12:09	Somebody	X
Mail 2	2012-08-10 15:02:13	Sender 1	X
Mail 1	2012-08-09 09:54:44	Sender 1	X

## 6.2 Composing or answering a message

To compose a message, first select users or group in the list and add them in the field “Users or group chosen” with the “Add” button.

Find a title to the discussion in “Subject”.

Write the message and “SEND” it (click next to the button to check the fields and then click on “SEND”).

An email will be send to all those selected.



The screenshot shows a form titled "Send a new private message". It includes two dropdown menus: "Select the user:" with "Again Bob" selected and "Select the group:" with "AdminGp" selected. Both have "Add" buttons. Below these are input fields for "Users or group chosen:" and "Subject:". A large text area for "Message body" is at the bottom, with a "SEND" button to its right.

To answer, open the message from inbox. A post can be deleted with the button, followers can be added to this discussion.



The screenshot shows a discussion page titled "Name of this discussion". It features a "List of users to this topic" with "Sender", "Other guy", and "You". Below is a list of messages:

<b>Sender</b> 2012-07-31 16:17:42	Text from the sender to every people for this topic
<b>Your login</b> 2012-07-31 16:18:04 <a href="#">Delete this post</a>	Response
<b>Sender</b> 2012-08-22 10:07:00	Another text...

Below the messages is an "Add followers:" section with a dropdown menu showing "Name of user" and an "Add" button. A "Submit" button is also present. At the bottom, there is a "Reply:" section with a text input field and a "Reply" button.

## 6.3 Sentbox

The Sentbox is a historic of sent messages, they can be read by clicking on the discussion title.

## 7 Sharing databases

### 7.1 Sharing a database with other users

Databases, including “cooperative” databases, can be shared with other users. Select users or groups in the list, choose one kind of database then the list of permission appears for simple database:

- Only see: the shared database can be queried or viewed.
- Panels: Allow this user to create new panels into the database and generate new genotype lists.
- Strains: the user can add strains data.
- All: Allows this user to add, modify, remove strains, information, panels etc...

“Cooperative” list of permission:

- Only see: the user can query or view the database.
- Add or remove: the user is allowed to add a database into the cooperative database.

### 7.2 Making a database public

**Make database public**

Select one database :

- Base 1
- Base 2
- Base 3
- Base 4

Submit

A database can be made visible by all with this menu. Select the database in the list and “Submit” and your database will be publish sometime after.

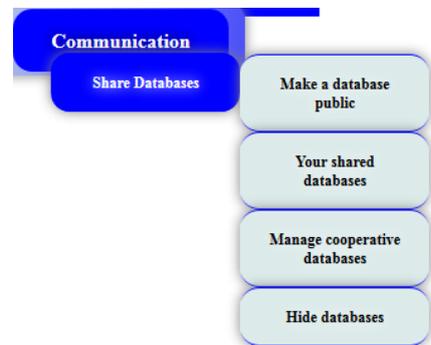
To make public a cooperative database see “Making a cooperative”

### 7.3 Shared databases

On this page all shared databases are listed.

### 7.4 Hidden databases

A hidden database will not be listed in “See list of private and no hidden databases”.



**Share your database with other users**

Select the user :  Add

Select the group :  Add

Users or group chosen:

Select one database :

- Base 1
- Base 2
- Base 3
- Base 4
- Base 5
- Base 6
- Base 7
- Base 8

Select cooperative database :

- Coop 1
- Coop 2
- Coop 3
- Coop 4

What power do you want to give to this user :  
Can only see the database and make queries inside

Submit

**These are your shared databases**

Databases you are sharing with other users

Base 1	User 2	Power of the sharer	Delete
Base 2	User 6	Can add panels to the database	X
Base 6	User 8	Can make all modifications to the database	X
Base 90	cpourcel	Can make all modifications to the database	X
Base 32	User 13	Can make all modifications to the database	X

Databases other users are sharing with you

Database	Owner	Your power
Base shared 1	Owner 1	Can add or remove database to the cooperative database
Base shared 2	Owner 2	Can make all modifications to the database
Base shared 3	Owner 3	Can make all modifications to the database
Base shared 4	Owner 4	Can only see the database and make queries inside
Base shared 5	Owner 5	Can make all modifications to the database
Base shared 6	Owner 6	Can make all modifications to the database

Your Public Databases  
not including your cooperative databases

Database	Info	Delete
Public base 1		X
Public base 2		X
Public base 3		X
Public base 4		X
Public base 5		X



### 8.3 Adding and Removing MLVA Primers Data

To add new personal primers, select a family or specify another. Copy paste primers and click “add”.

Primers must look like: name\_repeat-unit-size\_pcr-product-size\_associated-repeat-copy-number

“Mtub01\_18bp\_328bp\_10U GAGAAACAGGAGGGCGTTG TATTACGACGACCGCTATGC”

To delete primers, select family and primers, click on delete.

### 8.4 SNP specification

Upload the FASTA file of the reference strain, and copy paste the position list. The position list use a name for the column, an identification word to find in which plasmid or chromosome we must search. This word must be in the first FASTA and the reference FASTA. The last number it's the SNP position in the reference FASTA.

The size of sequence to find the FASTA is editable.

### 8.5 Submit a form

Before submitting the form, there are some modifiable configurations:

- Rounded to round correctly the copy number, by default
  1.  $[0,0.25[ = 0$
  2.  $[0.25,0.75] = 0.5$
  3.  $]0.75,1] = 1$
- Display copy number or/and size in base pair (and select how display the size).
- And keep the locus name or just the short name.

## 9 Columns Preferences

This menu is used to customise the appearance of a database. Fields can be masked or reordered. These preferences are user-specific.

To specify order and display metadata in a database.

Select a database, click on line to move up or down, display or hide, and save preference.

