

# SSR Database User Manual



## SSR Database

[Home](#)

News  
 New version of SSR database is now available! If you have any problem you can contact us by clicking [here](#).  
 The tutorial is being written. Soon available.

### The Evoltree Project

Evoltree is a large EU-funded network of excellence launched in april 2006 to analyze the impacts of climate change on forest ecosystems from an evolutionary perspective.



**A BETTER UNDERSTANDING OF THE EVOLUTIONARY** history of forest trees can help us to predict how they might respond to climate change. Forests are complex ecosystems and subsequently forest research needs to apply different approaches to gain a better understanding of how they function. The European forest research community has carried out numerous important studies on forest biodiversity. However, many institutes maintain overlapping research infrastructures and often carry out similar studies without coordination.

**EVOLTREE WILL LAST FOUR YEARS** and will create a Network of Excellence to integrate European research infrastructures and resources to study the adaptive capacity of tree species using sophisticated methods, and to engage the scientific community into a dialogue with policy-makers and other stakeholders.

**THE EVOLTREE NETWORK INVOLVES 26 RESEARCH GROUPS** from 15 European countries that are working together to identify and study genes of adaptive significance in order to evaluate the contribution they make to the evolution of tree species and tree communities.

### The SSR Database

The SSR database allows to store the large quantity of microsatellites or single sequence repeats (SSRs) being developed within the Evoltree Network of Excellence, or developed by other partner's projects.



Properties	
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# I. Organization and technical information

## 1. Technical information

The web interface of the SSR Database has been developed in Ruby on Rails and tested on Mozilla Firefox. The database system management used is PostgreSQL (8.1.x).

## 2. SSR Database organization

### a. Authentication page

You must be connected to access to the database. Login and password are delivered by the database administrator on demand ([audrey@pierroton.inra.fr](mailto:audrey@pierroton.inra.fr)).

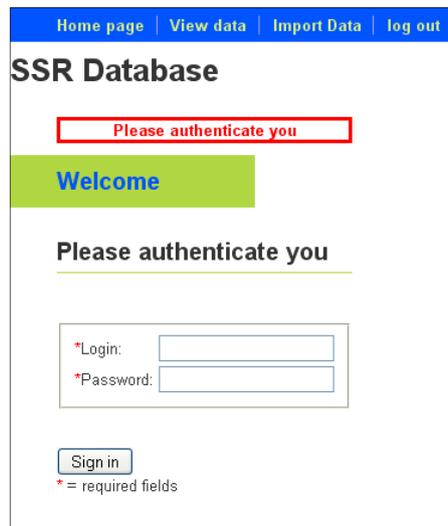


Figure 1 : login page

### b. Home page

The home page contains an abstract on the Evoltree Project, which involves the SSR database. A frame on the right announces the last modifications concerning the database. A link is also proposed to contact the database administrator in case.



Figure 2: home page

### c. Importation, Viewer, Logout

Those functions are accessible from the navigation bar.

## II. Functionalities

### 1. View data

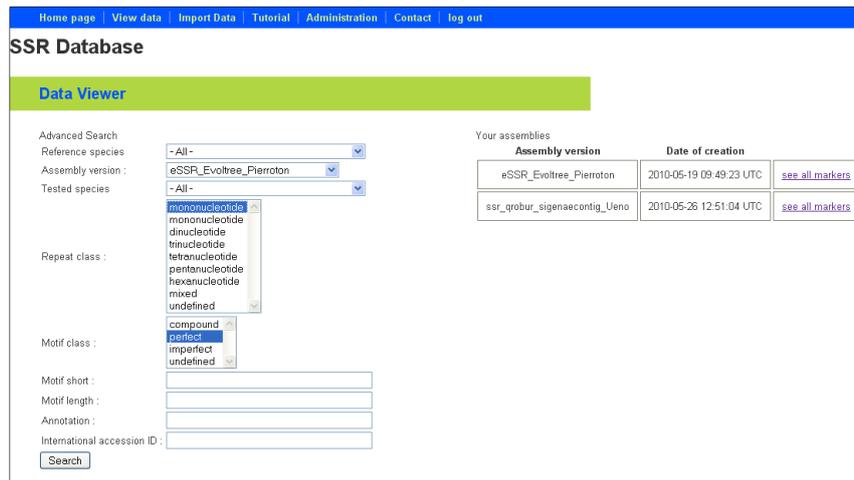


Figure 3 : The "Viewer"

The data displaying is accessible from the navigation bar. On this page (see Figure 3), the user can display all markers contained in an assembly which has been inserted by himself: those assemblies are listed in a table.

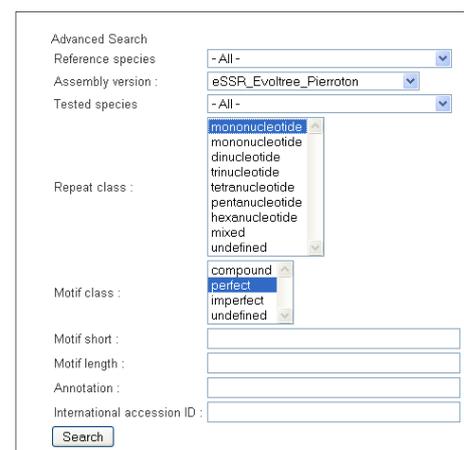
Your assemblies		
Assembly version	Date of creation	
assembly_version1	2010-01-20 14:58:22 UTC	<a href="#">see all markers</a>
assembly_version2	2010-01-25 10:52:03 UTC	<a href="#">see all markers</a>
assembly_version3	2010-01-27 15:26:18 UTC	<a href="#">see all markers</a>

Figure 5: assemblies display

Figure 4: Search form

The user can search on the entire database, in the existing assemblies with a search form. The following fields must be completed:

- *Referenced species*: the species on which the marker was developed
- *Tested species*: the species of interest. The search can be done for one species or for all the species.



- *Assembly version*: Assembly name.
- *Repeat class*: can be mono, di, tri, tetra, penta or hexanucleotides.
- *Motif class*: Motif can be compound, perfect or imperfect.

The display of the search results or of all markers of an assembly is the same: the markers are listed in a table with all disposable information.

Reference Species	Locus name	Locus short name	Reference sequence	International accession ID	Annotation	Repeat class	Number of repeats	Repeat start	Repeat end	Motif class	Motif string short	Motif string	Forward primer	Reverse primer
Populus tremula < Populus tremuloides	ai194501	ai194501		ai194501		undefined				undefined			CCACCCAAACCATGCCCTTTATC	GAATCCCT
Populus tremula < Populus tremuloides	ai194501	ai194501		ai194501		undefined				undefined			CCACCCAAACCATGCCCTTTATC	GAATCCCT
Populus tremula < Populus tremuloides	ai194501	ai194501		ai194501		undefined				undefined			CCACCCAAACCATGCCCTTTATC	GAATCCCT
Populus tremula < Populus tremuloides	ai194501	ai194501		ai194501		undefined				undefined			CCACCCAAACCATGCCCTTTATC	GAATCCCT
Populus tremula < Populus tremuloides	bi128189	bi128189		bi128189		undefined				undefined	AG/REV		GGTTGAGTAACTGATTOAAGAG	GAACACAGAT
Populus tremula < Populus tremuloides	bi128189	bi128189		bi128189		undefined				undefined	AG/REV		GGTTGAGTAACTGATTOAAGAG	GAACACAGAT
Populus tremula < Populus tremuloides	bi135774	bi135774		bi135774		undefined				undefined	AG		CCTTCTTTGAAACCTCACAAAC	TTGCAACC

Figure 6: marker's display

## 2. Exportation

The export is made at the level of the data's display. When the search result is displayed, a button "export" appears under the table (Figure 7). By clicking on it, you will be redirected to a page with a link to download the file (Figure 8).



Figure 7: export button



Figure 8: link to download

## 3. Data insertion

Data are imported in the database with an importation file in a CSV format (separator ";"). The access to the importation function is done by clicking on *Import Data* in the navigation bar. An excel template is disposable to downloading. It's important to save the importation file in the CSV format. The importation is done with a form. The name of the assembly must be filled in the field *Assembly version*.

Warning: this name is unique. To insert markers in an existing assembly, it's important to respect the spelling and the case. An automatic completion helps to fill this field.



Figure 9: Importation form

Then the file (CSV FILE!!) to import is selected, and it can be validated or not before importation by ticking the option: “*validate the file*”. This validation is fully recommended before the importation. Anyway, if the file is incorrect, the importation won't be done and this will be notified by a warning message (Figure 11).



Figure 10: correct file

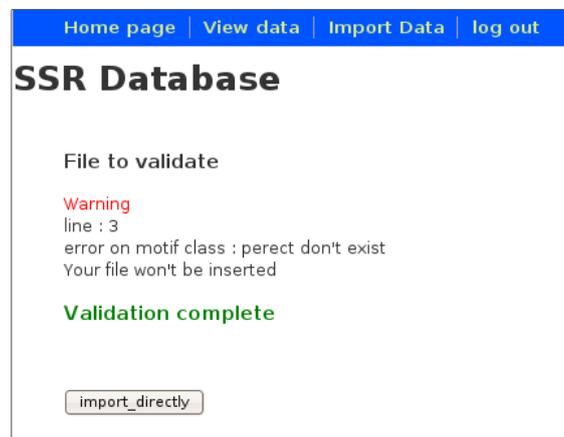


Figure 11: incorrect file



Figure 12: importation complete

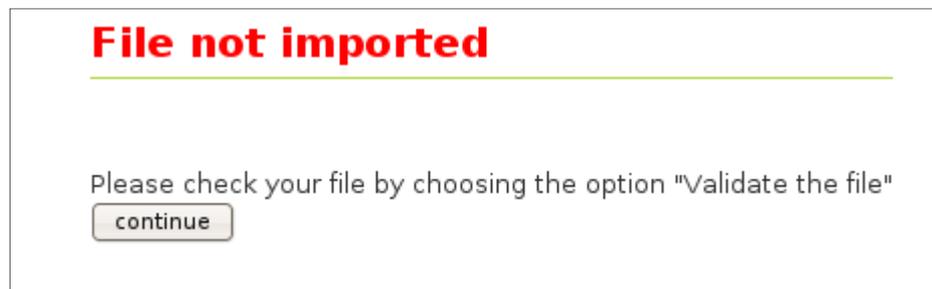


Figure 13: aborted importation

### III. FAQ

***The exportation failed while my files were validated:***

- Check if you filled the “species\_ref” column
- If you filled the “publication\_author” column, the “publication\_title” must be filled too
- The column separator is “;”
- The file must be a CSV file
- The first line of the template describes the columns; don’t keep it in your CSV file.

***Informations concerning tested populations have not been inserted:***

- Check if you filled the “population\_ident” and the “population\_type” columns.