

# How to use SITVITBovis

This is a user manual helping researchers how to easily navigate, to interrogate, and to analyze their data through the SITVITBovis database.

**Keywords:** *Mycobacterium bovis*, bovine tuberculosis, Database, Spoligotyping, Mycobacterial Interspersed Repetitive Units-Variable Number of Tandem Repeats (MIRU-VNTRs) typing, Evolution, Phylogeny, Demographics, Statistics, Epidemiology.

## Homepage

Homepage briefly introduces the SITVITBovis database which is dedicated to study genotyping markers (phylogenetical information based on Spoligotyping and MIRU-VNTRs typing) of *Mycobacterium bovis* (*M. bovis*) isolates. SITVITBovis also allows to get demographic (sex, age, origin of patients), drug resistance information, and statistical correlations between the different variables. The main functionalities of the Website are shown in figures below.

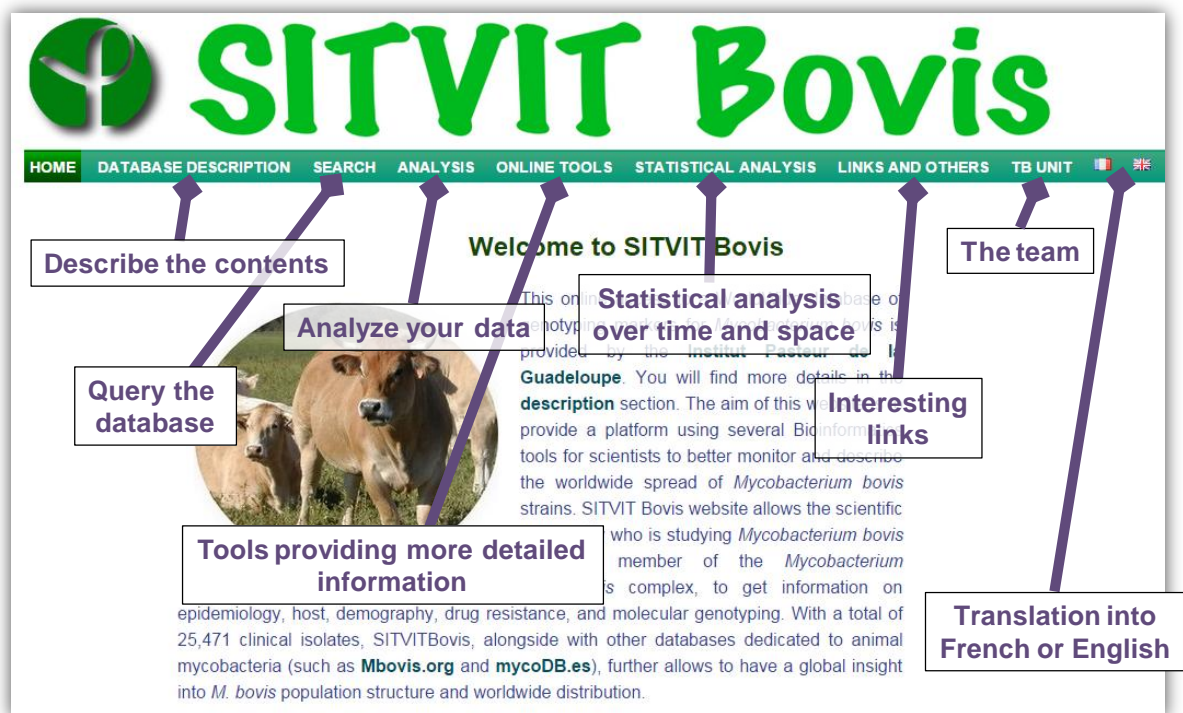
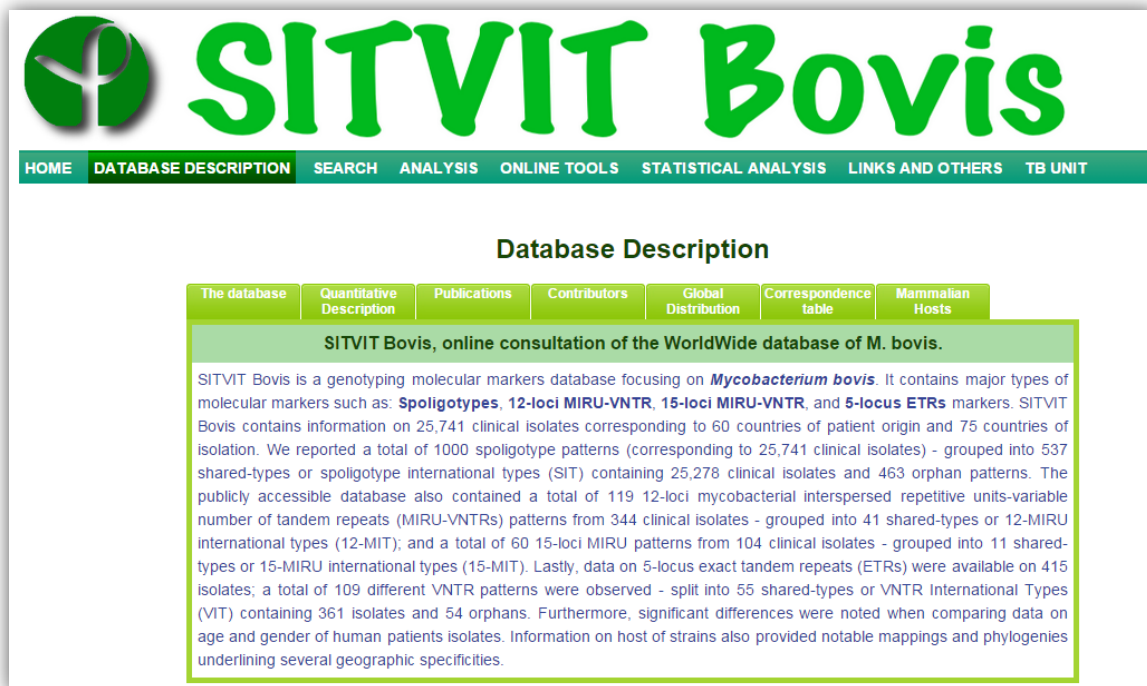


Figure 1: Homepage and brief description of main functionalities.

Users can easily navigate from one webpage to another. Please note that only the first page (titled 'Home') is translatable into French or English (**Figure 1**). The language of the other pages is English, however.

## Description

This section describes the main contents of the database (**Figure 2**).



The screenshot shows the SITVIT Bovis website interface. At the top, there is a logo on the left and the title 'SITVIT Bovis' in large green letters. Below the title is a navigation menu with the following items: HOME, DATABASE DESCRIPTION (highlighted), SEARCH, ANALYSIS, ONLINE TOOLS, STATISTICAL ANALYSIS, LINKS AND OTHERS, and TB UNIT. The main content area is titled 'Database Description' and contains a table with seven columns: 'The database', 'Quantitative Description', 'Publications', 'Contributors', 'Global Distribution', 'Correspondence table', and 'Mammalian Hosts'. The 'The database' column is selected, showing a detailed description of the database's contents, including the number of clinical isolates, spoligotype patterns, and various molecular markers.

The database	Quantitative Description	Publications	Contributors	Global Distribution	Correspondence table	Mammalian Hosts
<b>SITVIT Bovis, online consultation of the WorldWide database of <i>M. bovis</i>.</b>						
<p>SITVIT Bovis is a genotyping molecular markers database focusing on <i>Mycobacterium bovis</i>. It contains major types of molecular markers such as: <b>Spoligotypes</b>, <b>12-loci MIRU-VNTR</b>, <b>15-loci MIRU-VNTR</b>, and <b>5-locus ETRs</b> markers. SITVIT Bovis contains information on 25,741 clinical isolates corresponding to 60 countries of patient origin and 75 countries of isolation. We reported a total of 1000 spoligotype patterns (corresponding to 25,741 clinical isolates) - grouped into 537 shared-types or spoligotype international types (SIT) containing 25,278 clinical isolates and 463 orphan patterns. The publicly accessible database also contained a total of 119 12-loci mycobacterial interspersed repetitive units-variable number of tandem repeats (MIRU-VNTRs) patterns from 344 clinical isolates - grouped into 41 shared-types or 12-MIRU international types (12-MIT); and a total of 60 15-loci MIRU patterns from 104 clinical isolates - grouped into 11 shared-types or 15-MIRU international types (15-MIT). Lastly, data on 5-locus exact tandem repeats (ETRs) were available on 415 isolates; a total of 109 different VNTR patterns were observed - split into 55 shared-types or VNTR International Types (VIT) containing 361 isolates and 54 orphans. Furthermore, significant differences were noted when comparing data on age and gender of human patients isolates. Information on host of strains also provided notable mappings and phylogenies underlining several geographic specificities.</p>						

**Figure 2: Description of main contents of SITVITBovis.**

### Utility of the different thumbnails

*The database*: this part gives general information about genotyping molecular markers contained in the database.

*Quantitative description*: a quantitative description of molecular markers used is also provided.

*Publications*: list of publications which are in relation to the subject.

*Contributors*: a list of contributors is available upon request.

*Global Distribution*: Map showing the global distribution of *M. bovis* isolates in SITVITBovis.

*Correspondence table*: list of all spoligotyping patterns contained in SITVITBovis.

*Mammalian Hosts*: list of all mammalian hosts represented in the database.

## Search

This section allows users to query SITVITBovis database according to several criteria (such as Spoligotype, 12-loci MIRU, SIT, SB-number, 12-MIT, Lineage, Isolation Country, Drug resistance, Host, etc....) used alone or in combination each other. Note that you can use regular expression or REGEXP ([http://en.wikipedia.org/wiki/Regular\\_expression](http://en.wikipedia.org/wiki/Regular_expression)) in each field except fields "Drug resistance", and "Sex" (for which you can select directly the value).

The DHTMLX columns (see website: <http://dhtmlx.com/>) can be extended, and there is a scroll bar facilitating the navigation (**Figure 3**). The total number of isolates corresponding to the query is visible at the right bottom. The results can be exported as an Excel file.

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You can use REGEXP in each field. For more details see [HERE](#)

Fill your search criteria

IsoNumber	<input type="text"/>	Strain Name	<input type="text"/>	Spoligotype	<input type="text"/>	SIT	<input type="text"/>	SB number (Mbovis.org)	SB0120
5-locus ETRs (VNTR)	<input type="text"/>	12-loci MIRU	<input type="text"/>	15-loci MIRU	<input type="text"/>	VIT	<input type="text"/>	12-MIT	<input type="text"/>
15-MIT	<input type="text"/>	Lineage	<input type="text"/>	Origin Country	<input type="text"/>	Isolation Country	<input type="text"/>	Year	<input type="text"/>
Host	<input type="text"/>	Drug Resistance	<input type="text"/>	Sex	<input type="text"/>	Age	<input type="text"/>	Investigator	<input type="text"/>

Submit

ID	Strain	Nb	Spoligotype	MIRU12	MIRU15	VNTR	SIT	SB	12MIT	15MIT	VIT	Lineage	Origin	Isolation Country	Year	Drug R	Sex	Age	Host	Investigator
FXX030	173	1	6767377777			482		SB0120				BOV_1 ?	FR		0	?	?	?	?	Mauge
FXX030	181	1	6767377777			482		SB0120				BOV_1 ?	FR		0	?	?	?	?	Ma
PRT020		1	6767377777			482		SB0120				BOV_1 ?	FR		0	?	?	?	?	David S
JAM012	11058	1	6767377777			482		SB0120				BOV_1 ?	FR	06	0	?	?	?	human	Babool
JAM012	05504	1	6767377777			482		SB0120				BOV_1 ?	FR	08	1	?	?	0.7	human	Babool
SUR012		1	6767377777			482		SB0120				BOV_1 ?	SU	2	0	?	?	?	human	Babool
RUS012		1	6767377777			482		SB0120				BOV_1 ?	RU	2	0	?	?	?	?	Mokrou
DNK021		1	6767377777			482		SB0120				BOV_1 DNK	DN	1993	0	?	?	?	human	Lilleba
DNK021		1	6767377777			482		SB0120				BOV_1 DNK	DN	1993	0	?	?	?	human	Lilleba
DNK021		1	6767377777			482		SB0120				BOV_1 DNK	DN	1993	0	?	?	?	human	Lilleba
DNK021		1	6767377777			482		SB0120				BOV_1 DNK	DN	1993	0	?	?	?	human	Lilleba
DNK021		1	6767377777			482		SB0120				BOV_1 DNK	DN	1994	0	?	?	?	human	Lilleba
DNK021		1	6767377777			482		SB0120				BOV_1 DNK	DN	1995	0	?	?	?	human	Lilleba
DNK021		1	6767377777			482		SB0120				BOV_1 DNK	DN	1996	0	?	?	?	human	Lilleba
DNK021		1	6767377777			482		SB0120				BOV_1 DNK	DN	1997	0	?	?	?	human	Lilleba
DNK021		1	6767377777			482		SB0120				BOV_1 DNK	DN	1997	0	?	?	?	human	Lilleba
DNK021		1	6767377777			482		SB0120				BOV_1 VNM	DN	1997	0	?	?	?	human	Lilleba

Figure 3: Snapshot of 'Search' tool taking the example of strains isolated belonging to SB0120.

## Brief description of main search fields

- *IsoNumber (ID)*: code allowing the identification of each isolate contained in the database. The code is generated thanks to the following information: country of isolation, laboratory code, year of isolation, code of drug-resistance, and strain name.
- *Spoligotype*: octal code containing **15 digits** (e.g. 000000000003771).
- *12-loci MIRU*: **12 digits** representing the MIRUs 2-4-10-16-20-23-24-26-27-31-39- and 40.
- *15-loci MIRU*: **15 digits** representing MIRU 4, 10, 16, 26, 31, and 40, ETR-A, ETR-C, QUB-11b, QUB-26, QUB-4156, Mtub04, Mtub21, Mtub30, and Mtub39.
- *5-locus ETRs (VNTR)*: **5 digits** representing Exact Tandem Repeats (ETRs) A, B, C, D, E.
- *SIT*: an integer representing the shared-types in the database.
- *SB number*: a code provided by the database Mbovis.org (<http://www.mbovis.org/>)
- *12-MIT*: an integer identifying the 12-loci MIRU shared types.
- *15-MIT*: an integer identifying the 15-loci MIRU shared types.
- *VIT*: an integer identifying the 5-locus ETRs shared types.
- *Lineage*: phylogenetical lineage as described in SITVITBovis database (BOV, BOV\_1, BOV\_2, BOV\_3, BOV\_4-CAPRAE).
- *Isolation Country*: the country in which strains were isolated (note that Country information must be written as country name not as a code: e.g. you must write Mexico instead of MEX).
- *Origin Country*: the country of origin of patients. As the '*Isolation Country*' field, the country of origin must be written as country name.
- *Year*: the year of isolation of the strain

- *Drug resistance*: code between 0 and 4 indicating the kind of resistance (see <http://www.pasteur-guadeloupe.fr:8081/SITVIT2/submit.jsp>).
- *Sex*: this field corresponds to the patient's sex (either 'F' for female or 'M' for male).
- *Age*: this field corresponds to the patient's age (as an integer).
- *Host*: this field corresponds to the host ('Human', 'Cattle' or other animals; see Description section).
- *Investigator*: the name of the Contributor who has submitted isolates to the database.

## **Analysis**

This section allows you to analyze your own data, following the example file provided (freely downloadable; **Table 1**). Note that you can let a cell empty when the information is not available. Your datafile must also include the same headings as presented in **Table 1**. Make sure to prepare your analysis file as shown in the example, and do not let spaces between the characters used for molecular markers (Spoligotype43, MIRU12, MIRU15, and VNTR).

**Table 1: Example excel file for analysis of data**

STRAIN	SPOLIGOTYPE43	MIRU12	MIRU15	VNTR	COMMENTS
SITVITBovis001	67677377777600	222324253322	223532553500122	55623	France
SITVITBovis002	67677377777600	222324253322	223532553500122	55623	Russia
SITVITBovis003	67677377777600	222324253322	223532553500122	55623	Argentina
SITVITBovis004	67677367777600	222324253322	223532553500122	55623	Mexico
SITVITBovis005	67677367777600	222324253322	223532553500122	55623	Guadeloupe

Once you have followed the instructions to design and upload your file, the results of your analysis will be displayed on the webpage (**Figure 4**). This analysis tool allows you to identify your strains and see whether they already exist in the SITVITBovis database (if this is the case, your strains will be identified by International-Types or SB numbers). You can also export the results as an excel document.

**SITVIT Bovis**

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Analyze your data file

Download and fill this **Excel File** with your data, then upload it to search for similar profiles in SITVIT Bovis. If you are using a recent version of Microsoft Excel, please convert your file to Excel 2003 or XLS format.

**You can download an example**

Make sure that you are strictly respecting the good format for all Spoligotype and MIRU-VNTRs markers.

If you entered your spoligotype patterns at the binary format (o/n), it will be automatically converted into the octal format and vice versa. Note that the order of loci for MIRU-VNTRs are as follows:

- 5-locus Exact Tandem Repeats (ETRs) or VNTR order: A, B, C, D, and E.  
24-26-27-31-39- and 40.
- and 40, ETR-A, ETR-C, QUB-11b, QUB-26, QUB-4156, Mtub04, Mtub21, Mtub30, and Mtub39.

Furthermore, the MIRU-VNTRs loci labeled by letters A, B, C ... indicate the number of copies.

Correspondance nomenclature between designations of MIRUs/ETRs/Spoligotypes and VNTRs loci is available as an **Excel File** or as a **PNG figure**.

Although 24-loci MIRU\_VNTRs were not taken into account in this database, we strongly encourage contributors to submit their data with all 24-loci MIRU-VNTRs scheme, referring to "**SITVIT2 Submit page**".

Chisissez un fichier: Aucun fichier choisi

**Results of your analysis**

Analysis of your File

Strain	Spoligotype43	SIT	SB-number	Lineage	Miru12	12-MIT	Miru15	15-MIT	VNTR	VIT	Comments
1 SITVITBovis001	67677377777600	482	SB0120	BOV_1	222324253322	5	223532553500122	219	55623	206	France
2 SITVITBovis002	67677377777600	482	SB0120	BOV_1	222324253322	5	223532553500122	219	55623	206	Russia
3 SITVITBovis003	67677377777600	482	SB0120	BOV_1	222324253322	5	223532553500122	219	55623	206	Argentina
4 SITVITBovis004	67677367777600	481	SB0121	BOV_1	222324253322	5	223532553500122	219	55623	206	Mexico
5 SITVITBovis005	67677367777600	481	SB0121	BOV_1	222324253322	5	223532553500122	219	55623	206	Guadeloupe

Not defined (ND) statement indicates that a spoligotype or MIRU pattern does not exist in our database (i.e. this profile could be either null, an orphan, or a new pattern not yet reported in our database).

Figure 4: Snapshot of the 'Analysis' tool in SITVITBovis database.

## Online Tools

This webpage (**Figure 5**) allows users to get information on distribution/mapping of isolates in function of several characteristics. The distributions could be visualized at various scales/levels (worldwide, UN-subregion, or at the country level).

This section contains other 'sub-thumbnails' permitting the following functionalities:

- *Geographic Distribution*: provides a global visualization of isolates recorded in SITVITBovis.
- *Genotyping Markers*: provides a set of tools allowing to visualize data related to genotyping markers.
- *Lineages*: provides information and distribution of phylogenetical lineages in SITVITBovis.
- *Hosts*: provides information and distribution of isolates in function of the host organism.
- *M. bovis BCG strains*: provides a map on *M. bovis* BCG isolates recorded in the database.
- *Phylogenetic Analysis*: provides a set of phylogenetical analyses (MSTs and spoligoforests).
- *Maps*: provides several geographic maps representing the genotypes present in SITVITBovis.
- *12-loci MIRULogos*: provides a set of MIRULogos (performed with WebLogo application; <http://weblogo.berkeley.edu/logo.cgi>), based on *M. bovis* sublineages having 12-loci MIRU-VNTRs data in this database.

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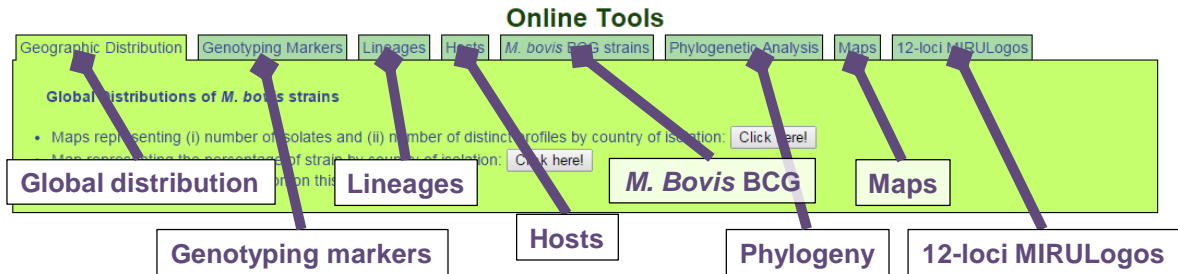


Figure 5: Snapshot of the 'Online Tools'.

## Statistical Analysis

This section allows users to get an overview on the distribution/evolution of isolates over time and space in function of the host information, by UN-subregion or by country (**Figure 6**).

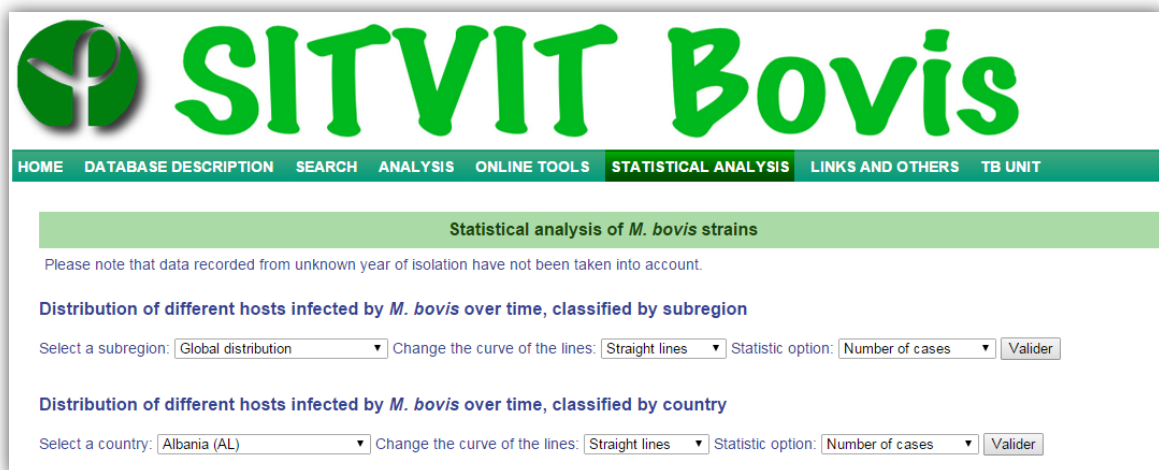


Figure 6: Snapshot of webpage 'Statistical Analysis'.

## Links and Others

This section contains various supplemental information and interesting links of softwares or web tools.

## TB Unit

This webpage briefly introduces the team working at the lab: "Unité de la Tuberculose et des Mycobactéries, Institut Pasteur de la Guadeloupe".