



# A SNP-MLST Method to Decipher the Genetic Diversity of French Mycobacterium bovis Strains of Animal Origin CONTEXTE

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## ► To cite this version:

Lorraine Michelet, Thierry Cochard, Franck Biet, Maria Laura Boschioli. A SNP-MLST Method to Decipher the Genetic Diversity of French Mycobacterium bovis Strains of Animal Origin CONTEXTE. 7th International conference on Mycobacterium bovis, Jun 2022, Galway (National University of Ireland - Galway), Ireland. anses-03947502

**HAL Id: anses-03947502**

**<https://anses.hal.science/anses-03947502>**

Submitted on 19 Jan 2023

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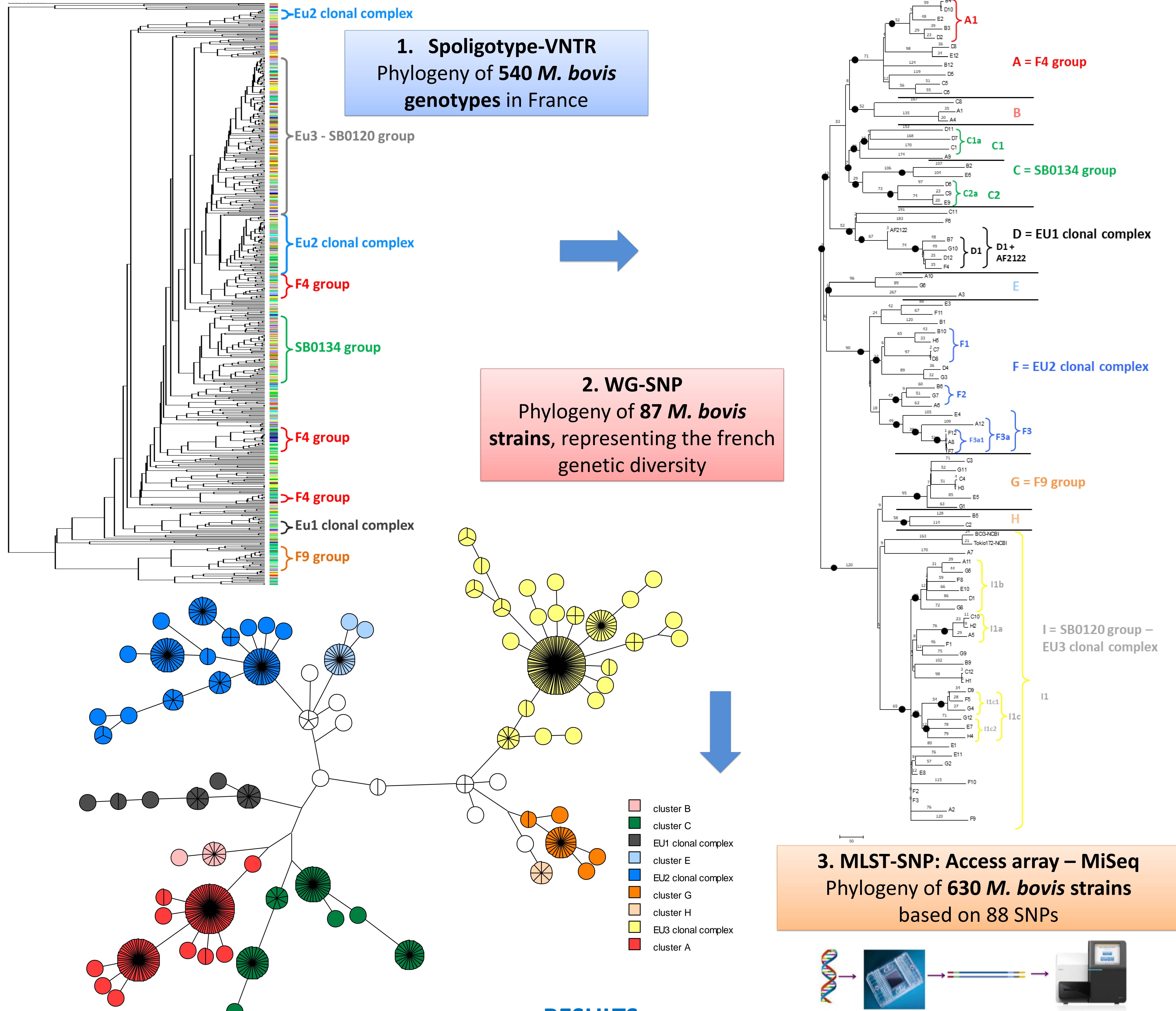
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## CONTEXTE

Like other members of the *Mycobacterium tuberculosis* complex (MTBC), *Mycobacterium bovis* is highly clonal. After having employed the mildly discriminative **spoligotyping** and **MLVA** methods but also the highly resolving – albeit still not used in routine- NGS approaches, the objective of our study was to develop an **easy and highly discriminative** genotyping method for characterising *M. bovis* strains: **MLST SNP**.



## RESULTS

- ⇒ panel of **630 strains** from the French TB National Reference Laboratory (NRL) collection (**1979-2018**) isolated from cattle (92%), wildlife (wildboars, badgers, deer) (4%) and others (4%)
- ⇒ **6 dominant clonal groups** were well identified : I – Eu3 CC (n = 170), C (n = 94), Eu2 CC(n = 115), Eu1 CC (n = 24), A (n = 131) and G (n = 30)
- ⇒ the remaining three groups also well confirmed in the overall analysis

## CONCLUSIONS

This **SNP-MLST method** is more resolutive than classical genotyping methods. It provides data to construct a robust phylogeny and give an **overview of the diversity evolution** avoiding WGS of a whole collection. Our data can be used to better understand the epidemiology of *M. bovis* in France by providing additional information on the different clonal groups, their variability and their maintenance over time.