

ISWAVLD 2⁽¹⁾23

International Symposium of the World Association of Veterinary Laboratory Diagnosticians

29 JUNE-1 JULY 2023 Congress Centre

Lyon

Towards the veterinary diagnostics of the future

Main topic : Omics and big data, metagenomics: Open ended diagnosis

Contribution of whole genome sequencing of Mycobacterium bovis strains for epidemiological monitoring and surveillance of bovine tuberculosis in France

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Introduction

In recent years, the advent of whole genome sequencing (WGS) has opened up new perspectives in terms of disease monitoring and surveillance. In the case of bovine tuberculosis (bTB), this new technology makes it possible to access to the entire genetic information of Mycobacterium bovis and overcomes the limitations of old typing methods (spoligotyping and MIRU-VNTR), particularly in endemic areas where the same genotype (a spoligotype combined with 8 loci MIRU-VNTR profile) circulates.

Methods

We selected strains of M. bovis isolated from cattle (limited to 3 strains per infected herd) and all those available from different wildlife species (badger, wild boar, fox, deer). We studied different endemic areas currently affected by bTB in France: Côte d'Or (between 2009 and 2014), Dordogne-Haute-Vienne (between 2001 and 2017), Pyrénées-Atlantiques and Landes (between 2002 and 2018), Calvados and Orne (between 2014 and 2022), Charente (between 2019 and 2022).

Strains were sequenced using the Illumina technology. After a first step of data quality validation, the obtained data were analysed by mapping on a reference sequence. The most robust SNPs (strict criteria) were identified and employed for subsequent analyses. Maximum parsimony phylogenetic trees were constructed for each zone in order to establish a link between the strains and to enable epidemiological

monitoring. For some areas where the number of strains of each species is sufficient, modelling analyses (Beast) were carried out by combining SNPs with

For some areas where the number of strains of each species is sufficient, modelling analyses (Beast) were carried out by combining SNPs with epidemiological data in order to describe transmission patterns of M. bovis in these areas.

Results

WGS data allow a very fine discrimination of strains. In each area, phylogenetic trees have been used to establish links between bovine and wildlife strains. These initial results make it possible to identify groups and to distinguish between the relapse of the same strain or a new contamination in the same herd. Modelling studies carried out in Côte d'Or, Dordogne-Haute Vienne, Pyrénées-Atlantiques and Landes revealed different transmission patterns in the different study areas. These studies also made it possible to determine the rate of evolution and the date at which the most recent common ancestor of the strains studied would have circulated.

Conclusions

The introduction of WGS for bTB monitoring and surveillance offers great prospects. WGS data provide very useful information on the links between strains and thus contribute to epidemiological investigations in the field. Furthermore, the results of modeling studies have shown a diversity in transmission patterns depending on the studied area. All these results encourage us to work at very local levels in order to better understand the transmission of the disease in each area and potentially provide measures to better control bTB in each context.