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Genetic features of strains of *Mycobacterium avium* subsp. *paratuberculosis* circulating in the West of France deciphered by Whole-Genome Sequencing

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Background & Objective

Paratuberculosis is a chronic infection of the intestine, mainly the ileum, caused by *Mycobacterium avium* subsp. *paratuberculosis* (Map) in cattle and other ruminants. This enzootic disease is present worldwide and has a strong impact on the dairy cattle industry.

For this species, the typing tools do not make it possible to investigate the genetic diversity of the strains. These limitations can be overcome by the application of Whole Genome Sequencing (WGS), particularly for clonal populations such as Map. WGS analyses can provide comprehensive genetic information, including information on genome evolution, discrimination of closely related strains and virulence determinants.

The purpose of the present study was to undertake a whole-genome analysis of Map strains isolated from herds in western France. This allowed us to identify accurate phylogenetic relationships between isolates and further, establish correlations between genomic traits and epidemiological data within a population of well documented-strains.

Figure 1. Material and methods

