

FT3-05. Exploring the genome of *Mycobacterium brumae*, a species of bacterium with therapeutic potential

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Mycobacterium brumae is a fast-growing, non-pathogenic *Mycobacterium* species, originally isolated from environmental and human samples in Barcelona, Spain (1). Previous studies have shown that the implementation of non-pathogenic mycobacteria, such as *Mycobacterium bovis* BCG can improve the treatment against high-risk non- muscle invasive bladder cancer (BC) by intravesical administration. *M. brumae* has beenshown to be non-pathogenic (2) and its phenotype and immunogenic effect have been well characterized. However, the knowledge of its underlying genetic composition is stillincomplete. In this study we have sequenced the genome by means of PACBIO of the *M. brumae* strain CR-270 obtaining the most complete assembly to date. We describe its genetic content by showing evolutionary relationships between different mycobacteriaand we compare its virulence gene content with other virulent mycobacteria such as H37Rv reference strain. Furthermore, we describe the genetic variability of *M. brumae* by comparative genomics using obtained Illumina sequences. Our results contribute to increase the knowledge about the genetic bases that explain the non-pathogenic phenotype of this bacterium with therapeutic potential.

- 1. Luquin M, Ausina V, E MALEELL, Belda F, Prats G, Daffe M. Nonphotochromogenic Mycobacterium. Int J Syst Bacteriol. 1993;43(3):405–13.
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