



TITLE Comparative genomics of non-tuberculous mycobacteria: ecological and clinical implications

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The species classified as non-tuberculous mycobacteria (NTM), or rapid growing mycobacteria (RGM), are widely distributed in the environment and some of them are considered as emerging opportunistic pathogens. Nosocomial infections caused by NTM are usually difficult to treat due to their resistance to antibiotics or other external factors. The next-generation sequencing (NGS) technologies are opening new frontiers to different fields, and clinical microbiology is not an exception. The main objectives of this work imply the genome sequencing of NTM isolates (especially type strains), the identification of gene families, functional characterization, comparative analysis applying several clustering algorithms and the description of the core-pangenome of NTM. Briefly, the results obtained showed different rates of genome evolution and exclusive genes for each species (pangenomes). Interestingly, the pangenome analysis of NTM has revealed also the presence of toxin-antitoxins (TA) systems in several of the strains compared. Curiously, most of the TA systems discovered in NTM are also present in *M. tuberculosis*. Furthermore, a brand-new TA system has been discovered. The toxic potential of the proposed toxins and its neutralization with the hypothetical antitoxins have been tested *in vitro*.

Altogether, contributes to improve the NTM evolution knowledge, as well as to gain a better understanding of the mechanisms underlying their ability to adapt to different ecological niches; i.e., the resistome, the toxin-antitoxin systems or their ability to form biofilms. All these aspects affect the human's lifestyle. Definitively, the new NGS based information may lead to important breakthroughs, both in biotechnology and clinical microbiology.