

CHARACTERIZATION OF THE *rrn* OPERONS OF *MYCOBACTERIUM CELATUM* AND THEIR IMPLICATION IN MYCOBACTERIAL EVOLUTION

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Traditionally, slow growing mycobacteria are thought to possess one *rrn* operon per genome located downstream *murA* gene (*rrnA*) while fast growers possess two, one located *murA* gene (*rrnA*) and the other downstream *tyrS* gene (*rrnB*). However, three fast growers (*M. abscessus*, *M. chelonae* and *M. marinum*) have been identified to have only one operon (*rrnA*) and, some slow growers (*M. terrae* and *M. celatum*) have two, indicating that there is no correlation between the rate of growth and the number of *rrn* operons. The aim of this work is study the organization of the two *rrn* operons of *M. celatum* as representative of slow grower species that posses two operons per genome. As well as, propose a posible explanation of their phylogenetic relationship with several mycobacterial species. We have confirmed the presence of two heterologous *rrn* operons in the slow grower *M. celatum*, and shown that they correspond to the *rrnA*- and *rrnB*-type of operons. Nucleotide sequence analysis of the promoter, leader and, intergenic regions 1 and 2 (ITS-1 and ITS-2) showed that the operons are heterologous and complete. Primer Extension and 5' end RACE analysis have demonstrated that both operons are functional; *rrnA* operon possess two active promoter elements and *rrnB* possess only one. 16S rDNA sequences of *M. celatum* and several mycobacterial species were analyzed throughout mycobacterial evolution and based on the phylogenetical trees that we have obtained, we propose that mycobacterial species with one *rrn* operon per genome have lost the operon downstream *tyrS* and that this event occurred at least twice during mycobacterial evolution, one leading to the *M. chelonae* and *M. abscessus* single operon and the other, to the traditionally slow growers with one operon per genome.