Characterization of the conjugal transfer mechanism of *Mycobacterium avium* plasmid pMA100

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Abstract:

Mycobacterium avium and *Mycobacterium kansasii* are nontuberculous mycobacteria that can cause opportunistic human infections, especially in immunocompromised patients. In a previous project from our lab we detected a horizontal gene transfer (HGT) event between these two mycobacterial species, mediated by a novel plasmid that was named pMA100. Conjugal transfer mediated by pMA100 was reproduced in the laboratory using the *M. avium* strain 88.3 as donor and as receptors three different strains of *M. kansasii* and *M. bovis* BCG strain Moreau. To characterize the conjugal mechanism of pMA100 we sequenced the complete genome of *M. avium* 88.3 (carrying the pMA100 plasmid), using Roche 454 FLX e Titanium platforms. The genome of *M. avium* 104 (GenBank accession no. CP000479) was used to filter common sequences using the Newbler v. 2.5.3 program. A total of 14.650 reads not mapped in the genome of *M. avium* 104, thus exclusive of *M. avium* 88.3, was considered for plasmid assembly. The results were confirmed by mate-pair sequencing with the Illumina platform. Annotation was performed in the Sabia platform (www.sabia.lncc.br). The plasmid has 116.415 pb, GC content of 66,73% and 113 ORFs, of which 56 are hypothetical proteins. The plasmid has a genetic organization similar to that found in two other plasmids recently described in slow growing mycobacteria. The tree plasmids bear a cluster of genes that code for a complete type VII secretion system (T7SS), besides ORFs similar to genes from type IV secretion systems (T4SS) and the gene of exonuclease V. Exonuclease V and these proteins from the T4SS could have a role in the cleavage of DNA and transport to the T7SS during conjugal transfer. T7SS is responsible for protein secretion in mycobacteria but can also be used for DNA secretion. The confirmation of this mechanism of conjugal transfer will be the object of future projects of our laboratory.

Keywords: *Mycobacterium avium*, pMA100, sequencing

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