TITLE: *IN SILICO* ANALYSIS OF GENES POTENTIALLY INVOLVED IN RESISTANCE TO ANTIMICROBIAL AGENTS OF *Corynebacterium amycolatum*

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ABSTRACT:

Corynebacterium amycolatum has emerged as pathogen of nosocomial and community-acquired infections, frequently expressing multiresistance profiles. Genomic features of *C. amycolatum* strains are rarely reported. Nowadays, as complete genome sequences are freely available, computational biology tools can be used to better understand multifactorial behavior of microorganisms. This study aimed to identify the presence of resistance genes through comparative genomic *in silico* analyzes of *C. amycolatum* genomes available in GenBank. At first, to confirm the identification of *C. amycolatum*, eighteen complete genome sequences were analyzed by genomic taxonomy: 16S rRNA and *rpo*B genes sequence analysis, mean nucleotide and amino acid identities, digital DNA-DNA hybridization and super tree construction. Taxonomic analyzes were performed using the type strain of *C. amycolatum* DSM 6922 included among these genomes. Subsequently, confirmed genomes were submitted to automated annotation by the PathoSystems Resource Integration Center (PATRIC) platform to detect the presence of resistance genes. Interestingly, from eighteen genomes available in GenBank annotated as *C. amycolatum,* only five were confirmed by genomic taxonomy analysis. Annotations obtained by the PATRIC platform identified a total of twenty-nine genes involved in antimicrobial resistance mechanisms, including antimicrobial agents targets in susceptible species (Alr, Ddl, , EF-G, EF-Tu, folA, Dfr*,* folP, gyrA, gyrB, Iso-tRNA, MurA, rho, rpoB, rpoC, S10p, S12p), cell wall charge altering proteins (Gdpd, PgsA), antimicrobial agents target replacement proteins (FabG, HtdX), and modulating expression of gene regulators of antimicrobial agents resistance (MtrA, MtrB, OxyR) for all genomes of *C. amycolatum*. Moreover, Erm(X) gene encoding macrolide resistance was found in three *C. amycolatum* genomes. The antimicrobial inactivating enzyme genes (APH (3') - Ia, APH (3' ') - Ib, APH (6) -Ic, APH (6) -Id) and gene Cmx that confers resistance to chloramphenicol by efflux pump were also found in two genomes. In conclusion, considering the ability of pathogens to acquire genes and consequently the impact of multiresistance in nosocomial environment, current data emphasizes the importance of clinical and laboratorial investigation, including antimicrobial susceptibility assays, especially when recovered from invasive infections, to improve the approach therapy in treatment of *Corynebacterium* spp. infections.

Keywords: *Corynebacterium amycolatum, in silico* analysis*,* multiresistance