

**TITLE:** GENOMIC TAXONOMY AS AN ESSENTIAL TOOL IN STUDIES INCLUDING INCONSISTENT IDENTIFICATIONS OF *Corynebacterium* SPECIES

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**ABSTRACT:**

Currently, the genus *Corynebacterium* comprises 132 species with some species having close phenotypic relationships. *Corynebacterium* spp. is widespread in the environment, animals, and humans. Several species are recognized as human pathogens, and some are of veterinary or of biotechnological interest. In recent decades, thousands of Bacteria and Archaea genomes have been sequenced, significantly increasing knowledge about the tree of life. Bacterial diversity also launched new tasks in various areas, including taxonomy. Recently, with the use of taxonomy genomic, several species could not only be described but also reclassified based on complete genome analyses. In this study, we demonstrated the importance of using genomic taxonomy to confirm species recovered from public repositories that were used for comparative analysis in a parallel project. Thus, eighteen complete genomes of *Corynebacterium amycolatum* deposited in GenBank were analyzed taxonomically to confirm species, including type strain DSM 6922 that were used for performed taxonomy genomic analyzes. Alignment techniques of 16S rRNA and *rpoB* genes were used to verify the related species by the CLUSTALX2 software. From data obtained in the alignment, phylogenetic studies were carried out with tree constructions for the respective genes and multilocus sequence analysis from the concatenation of seven housekeeping genes (*atpA-dnaE-dnaK-fusA-leuA-odhA-rpoB*). The trees were built using the MEGA X software. Additionally, mean nucleotide and amino acid analysis along with digital DNA-DNA hybridization were also performed. Finally, the construction of the supertree based on the complete genome was done using the online platform Type (Strain) Genome Server (TYGS). Of all the seventeen genomes analyzed, based on the results obtained by the taxonomic studies, only five genomes were compatibly reaching the values suggested as cutoff points for the species delineation when compared to the type strain *Corynebacterium amycolatum* DSM 6922. Twelve genomes were not listed as belonging to no *Corynebacterium* species previously described, suggesting that they belong to at least three new species that remain under investigation by our group. Finally, genomic taxonomy helps to design new taxa, especially when there is a close phenotypic relationship in *Corynebacterium* spp. Therefore, genome analysis should be necessary before conducting experimental research, especially concerning *Corynebacterium* spp.

**Keywords:** *Corynebacterium* spp., genomic taxonomy, MALDI-TOF, molecular assays, phenotypic diagnosis

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