

POSTER - PHYLOGENY AND EVOLUTION

EXPLORING PHYLOGENOMIC FEATURES IN KLEBSIELLA SPECIES.

Douglas Vinícius Dias Carneiro (dougbuick@gmail.com)

Diego Lucas Neres Rodrigues (diego.neresr@gmail.com)

Juan Carlos Ariute (jcarlosariute@gmail.com)

Mateus Sudário Pereira (msudario25@gmail.com)

Agatha Lemos Rezende Cristeli De Araujo (agatha.lemos@vetufmg.edu.br)

Mariana Silva Batista (mariana.sbatista7@gmail.com)

Rodrigo Profeta (profeta.biotec@gmail.com)

Ana Maria Benko-Iseppon (ana.iseppon@gmail.com)

Flavia Figueira Aburjaile (faburjaile@gmail.com)

Klebsiella is a genus of gram-negative, non-motile, rod-shaped bacteria that belong to the family Enterobacteriaceae. They are commonly found in a variety of environments, including soil, water, plants, and the gastrointestinal tract of humans and animals. In plants, they are normally established as endophytes and are active in nitrogen fixation. The genus contains six species, with *K. pneumoniae* and *K. oxytoca* being the most clinically relevant. *K. michiganensis* is closely related to *K. oxytoca*, sharing similar characteristics, such as carrying its chromosomal β -lactamase (class A). Initially misclassified as *K. oxytoca*, *K. michiganensis* was first discovered in a Michigan home from a toothbrush holder, in which it has 99% nucleotide sequence

identity to the 16S rRNA gene sequence. Due to the proximity, misclassified strains were recorded. In Pernambuco, Brazil, a phytopathogen of cabbage was identified as *K. oxytoca* and showed a close relationship with strains of *K. michiganensis*. Due to results showing misclassification of strain CCRMKO592, as well as previous studies showing misclassification this work sought to analyze the taxogenomics of strain CCRMKO592 and compare its similarity to public data on *K. oxytoca* and *K. michiganensis*. For this study, all the complete genomes of the two species were downloaded from the NCBI database. The JSpeciesWS tool was used for prior identification of proximity to the CCRMKO592 strain from its database. Then, the average nucleotide identity (ANI) was calculated by the ANIm method, available in pyani. Phylogenomic trees were made using the OrthoFinder tool. Our work corroborates recent studies indicating that misclassification may have occurred between *K. oxytoca* and *K. michiganensis* strains, as all comparative analyses from the JSpeciesWS and ANI tool and phylogenomics revealed paraphyletic groups. Regarding the results, it can be stated that this study is extremely relevant because it presents problems related to the classification between the two species. Therefore, our study suggests further genomics analysis of the strains present in the NCBI database, for better classification and understanding of these species.