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Abstract Book

Glutamicibacter creatinolyticus strain LGCM 259 infection in a horse: first genetic characterization

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OBJECTIVES

Glutamicibacter creatinolyticus (formerly *Arthrobacter creatinolyticus*) belonged to the family Micrococcaceae. It plays a significant role in many ecosystems: soil, water, air, cheese, plant, and it was associated to urinary tract infections and bacteremia in humans [1]. Recently, *G. creatinolyticus* LGCM 259 (LGCM-259) was isolated from diffuse subcutaneous nodules adherent to muscular tissues from a mare in Italy. Since the identification is only possible using 16S rRNA and MALDI-TOF sequence analyses, this study was carried out to: -characterize LGCM-259 with a complete DNA sequence and annotation; -identify genes encoding virulence factors.

MATERIALS AND METHODS

By comparative analyses among four isolated species of different habitats, available in the NCBI database, chromosomal sequencing using Hiseq technology (Illumina, USA) was conducted. The genome of LGCM-259 was automatically annotated using PROKKA. A phylogenomic tree and the presence of virulence genes were generated by Phylogenomic Tree Tool in Pathosystems Resource Integration Center (version-3.5.17), and BLASTp against the Virulence Factor Database (VFDB), respectively.

RESULTS

LGCM-259 strain was sequenced and assembled in a circular chromosome, which exhibits a length of 3.3 Mb, with a G+C content of 66.4%, and a total of 2882 CDSs, 4 clusters of rRNAs (5S, 16S, and 23S), and 61 tRNA genes, respectively. The locus tag LGCM259_1698, LGCM259_0905 and LGCM259_1698 may be involved in multiple drug resistance to Rifampin, Elfamycin, and Fluoroquinolone (*rpoB*, *tufA*, *tufB*). The genome also displayed copper tolerance genes (*copZ*, *csor_1*, *cutC*, *aniA*, *pcoC*), resistance to heavy metals such as arsenic, cobalt-zinc-cadmium (*cobT*, *cobS*, *cadA*), and chrome composts which are serious environmental contaminants.

CONCLUSION

The LGCM 259 strain's genome was first characterized and its chromosome sequence has been deposited in the NCBI database under accession number CP034412. It affects animals and carries important bacterial virulence factors that are essential in cell viability and pathogenicity.

REFERENCES

[1] H.J. Busse, Int J Syst Evol Micr 66 (2016) 9–37.