



GROWTH CAPACITY AND DEGRADATION GENES IN THE *Burkholderia* GENUS.

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Keywords: *Burkholderia*, Plant-beneficial-environmental, Biodegradation

Introduction. The *Burkholderia* genus comprises over 60 species, which have been isolated from a wide variety of ecosystems. Phylogenetic analysis showed that *Burkholderia* includes mainly two large groups¹, the pathogens and a group known as the “plant-beneficial-environmental (PBE) *Burkholderia* cluster”². Some of these species have been proposed to carry biotechnological applications, such as recalcitrant xenobiotic compounds biodegradation³. This study assessed the xenobiotic compound-biodegradation capacity of most diazotrophic *Burkholderia* from the PBE cluster.

Methods. The capability of *Burkholderia* to grow on several xenobiotic compounds was tested on BSE medium³ containing 4.23mM from each compound. Several set of primers, for amplification of degradative genes, were tested in *Burkholderia*. The amplicons were cloned, sequenced and analyzed in the NCBI databases. The strains with the highest xenobiotic consumption were analyzed by HPLC.

Results. The analysis revealed that the nodulating species *B. mimosarum* and *B. nodosa*, *B. unamae*, *Burkholderia* BKR-type plant associated species and *B. sacchari* were able to grow on monocyclic aromatic compounds, such as phenol (Fig. 1).

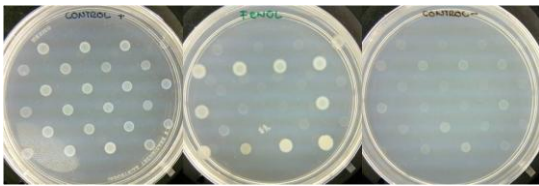


Fig. 1 Growth of *Burkholderias* in a 7-day Petri plate test with presence of phenol.

The nodulating strains *B. mimosarum*, *B. nodosa*, and *B. sabiae*, and the plant-associated *B. kururiensis*, *B. caribensis*, *B. graminis*, *B. terrae*, *B. unamae* and *B. xenovorans* were positive for the amplification of: A) toluene monooxygenase, B) phenol monooxygenase⁴ C) subfamily 1 of α -

subunits of hydroxylase component of multi-component mono-oxygenases⁵ D) biphenyl/toluene dioxygenase⁶ (Fig. 2)

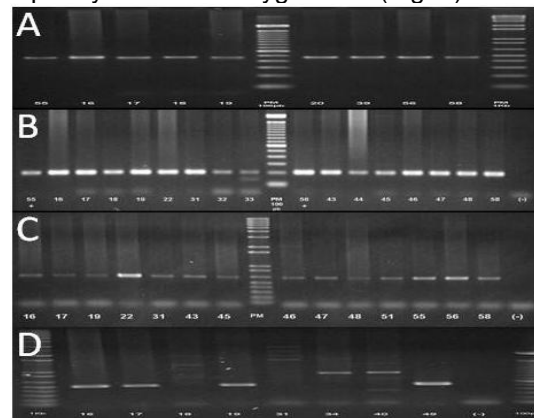


Fig. 2 Amplification of degradative genes in species of *Burkholderia*. with oligos A) toluene monooxygenase, B) phenol monooxygenase C) subfamily 1 of α -subunits of hydroxylase component of multi-component mono-oxygenases D) biphenyl/toluene dioxygenase.

Conclusions. Diazotrophic and nodulating bacteria of *B. nodosa*, *B. mimosarum*, *B. unamae*, and *Burkholderia* BKR-type species were capable to grow and consume several preferably monocyclic aromatic compounds as a carbon source.

Acknowledgements. The authors are grateful to CONACyT for the scholarship granted (No. 171087).

References.

1. Estrada P, Vinuesa P, Martinez L, Hirsch A, Caballero J. (2013). *Curr Microbiol.*
2. Suarez Z, Caballero J, Coutinho B, Mendonca L, James E, Venturi V. (2012). *Microb. Ecol.* 63:249-266
3. Estrada P, Bustillos R, Caballero J. (2001). *Appl. Environ. Microbiol.* 67:2790-2798
4. Baldwin B, Nakatsu H, Nies L. (2003). *Appl. Environ. Microbiol.* 69:3350-3358
5. Hendrickx B, Junca H, Vosahlova J, Lindner A, Rüegg I. (2006). *J. of Microbiol Methods* 250-265.
6. Witzig R, Junca H, Hecht H Pieper D. (2006). *Appl. Environ. Microbiol.* 72:3504-3514