Genome-Guided strategy to access Burkholderia diversity from environment and its chemistry.

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Palavras Chave: *Burkholderia, Genome, Isolation Method, Chemical Prediction.*

Introduction

According to recent discoveries, the genus Burkholderia, being part of the phylum Proteobacteria, has been recognized to contain a substantial number of clusters encoding putatively novel natural products, but to date has not been well studied.[1] Since there are few efficient methods to isolate Burkholderia species from environmental sources, this project aims to develop a new isolation method using genomic, metagenomic and metabolic information to take advantage of unique properties of Burkholderia metabolism. This approach relies on examination of important metabolic properties, including antibiotic resistance, metal resistance, as well as the carbon and nitrogen metabolism profiles from Burkholderia and untargeted species in bacterial communities.

Thus, this strategy can generate the possibility to construct differential culture media to access this genus in diverse types of environmental samples. Ultimately, the objective of this research program is to examine environmental samples of the genus Burkholderia in order to discover next-generation antibiotics, guided by chemical predictions, with unique molecular architectures and biological modes of action for the treatment of drug resistant infections.

Results

All experiments have demonstrated that this method is reliable for specific isolation for the genus Burkholderia. The results presented 100% of efficacy when the method was complete (Table 1). Once there is the possibility of using bioinformatics tools guiding the secondary metabolites production, all the genomic predictions were created for future isolation and identification of compounds.[2] The structure's core and its amino acids; nrps sequences were found (Figure 1) and these results show all the sources of compounds that possibly can be produced by the biosynthetic gene clusters in Burkholderia species.

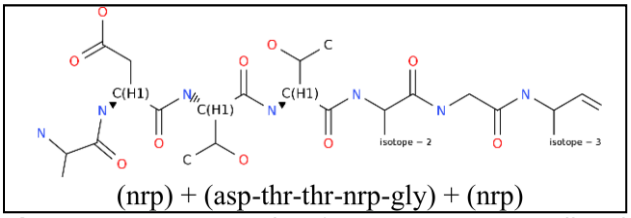

Figure 1. One example of core structure predicted for *Burkholderia sp. CCGE1003* from Nrps biosynthetic cluster and its subunits sequence.

Table 1. Species isolated by using the genome-guide method from one environmental spot.

SAMPLE NAME	*SPECIES*
RL14-064-BSI-A	*Burkholderia gladioli strain CACua-73 16S*
RL14-064-BSJ-A	*Burkholderia sp. FSGSA12 16S ribosomal*
RL14-065-BSA-A	*Burkholderia multivorans ATCC 17616*
RL14-065-BSB-A	*Burkholderia gladioli strain 2002721590*
RL14-065-BSC-A	*Burkholderia gladioli strain 2002721590*
RL14-065-BSD-A	*Burkholderia sp. FSGSA12 16S*

Conclusions

All the results demonstrated that this genome-guided method is efficient for isolating microorganisms of chemical interest.

Agradecimentos

We thank other members of Linington Lab; S. Lokey and W. Bray for biological screening facilities; The fellowship from CAPES-Brasil (Process number 8074135). Unifal-MG. This work was funded by NIH-TW006634.

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