

TITLE: TRANSCRIPTOME PROFILE OF THE BRAZILIAN SOIL BACTERIUM *Burkholderia catarinensis* IN RESPONSE TO A PHYTOPATHOGENIC FUNGUS AND WHEAT

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ABSTRACT:

Species from the *Burkholderia cepacia* complex (Bcc) can not only be found causing lung infections, but are also widely isolated from soils and commonly associated with the rhizosphere of economically important grasses as wheat, corn, and rice. The new Bcc species *Burkholderia catarinensis* was isolated from Brazilian grassland soils and showed plant growth promotion and biocontrol features. Despite the current restrictions imposed on the use of this genus for inoculation purposes, we are interested in understanding its ecological importance in agricultural systems. Thus, here we aim to study the transcriptome of *B. catarinensis* 89 when interacting with the phytopathogenic fungus *Drechslera tritici-repentis* or with wheat plants contaminated with this fungus. The experiment was performed in three 50 mL Falcon tubes for each condition: bacterium grown in 25% Hoagland solution with 0.2% glucose (OD₆₀₀= 0.35, control); the control solution with 10⁴ fungal conidiophores (fungus treatment); and three wheat plants per tube (5 days after germination) in contact with the fungus treatment solution (plant treatment). After 3h of incubation under light agitation, at 25 °C, these solutions were mixed with RNA protect®. Bacterial RNA was extracted using the RiboPure™ RNA Purification kit, which yielded nine high-quality libraries. Data was sequenced using the Ion Torrent Platform that generated high-quality reads and reliable statistical analysis. After processing the reads with Trimmomatic, Bowtie2, HTSeq-count, and DESeq2 tools, we found 347 bacterium genes differentially expressed in the condition with the fungus and 436 in the plant condition (considering a *p*_{adj}<0.1 and ±1.5 of log₂foldchange). Comparing to the control, we found 83 and 155 up-regulated genes and 179 and 291 down-regulated genes exclusively in the fungus and plant treatments, respectively. The Gene Ontology annotation revealed more functional categories repressed in the plant treatment. Overall, in this treatment, the bacterium increased membrane activities while lowering other metabolic and catabolic processes. In both treatments, genes related to transport, nitrogen metabolism, and ATP synthase were down-regulated, whereas those related to drug and stress resistance, and molybdopterin-related proteins were up-regulated. The functional investigation of these genes is currently underway and may contribute to the understanding of the interaction of this group of bacteria with other soil organisms.

Keywords: *Burkholderia catarinensis*, RNA-Seq, phytopathogenic fungus, wheat

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