The authors of Comparative genomics and transcriptomic response to root exudates of six rice root associated *Burkholderia sensu lato* species present a very interesting dataset based on transcriptomes and genomes. The find a very individual response of the different strains and can show the importance of the ED-pathway and putrescine in the bacterial answer to the host.

Although I believe the study is well designed, some questions remain open and need clarification e.g. how many replicates were used. Additionally, some parts in the result section would fit better to the discussion. A combined Results & Discussion section would make that easier. See further comments below.

Abstract

Definition of Rhizosphere is broadly known and there is no need to explain it in an Abstract.

L25: it is not true that they are mostly studied for human opportunistic traits. Change to often. The Abstract in general should be more concise, focusing more on the why and what was done in the study without being lost in basic rhizosphere definitions.

L43-46 To this list references should be added

L88ff: please try to use the genus name and be more precise – only stating bacteria is not enough for making clear what bacterial strains/genus you isolated and compared

L103 ff Please explain how many strains you isolated and how many of these were new. Please also explain if ABIP444 is a new strain in this study

L122 “and” is missing after (Table 1); please also add how you validated their colonization in a few words

Results

102ff: to increase readability of this first section I would recommend to refer to a table with the coverage information and only mention the critical values (e.g. ABIP659)

Table 1: Please also add Chromosomes and Plasmids

Figure1: I would recommend to not add the accession number in the figure’s label but rather main factors for the tree construction

L150: please mention for the transcriptome how many replicates were sequenced

L153: rich minimal medium: please call it the same way in result and method section

L170: please add how many fold change down/upregulation you received

Discussion

L303 “one would have” is very colloquial

L367 The conclusion of why analysing 6 instead of 2 strains doesn’t make much sense here – did you plan to do only two or do you mean that other studies rely only on 2 strains?

Materials and Methods

Please also reference and describe the Loess method? Please explain what dpi is?

L377 Please describe how you collected the hydroponic media

L384ff: please include if the strains were deposited to a strain collection

L404: Where the roots washed before the pulverisation? If not, I would suggest mentioning in the discussion that you can’t divide between colonizers of the outside or inside of root

L410: Please mention the number of plants treated

L415: Pleas add references to R and the different packages; Please also add the. access date to homepages

L420: as described above? Please write abbreviations in brackets when used the first time and not the other way around.

L430: did you measure the quantity of the RNA also with other system e.g. Fluorescence? Did you check the successful DNA depletion?

L447: Which sequencing kit was used?

L450: Please reference to the results table to the sequencing results

What was your threshold p value for RNA Sequencing analysis / gene expression analysis

Please also make sure to mention how many replicates you sequenced, if technical or biological

DNA Extraction: Although referenced, please mention which kits/extraction method you used

Please add a reference to all tools you used– e.g. Cutadapt

Please give more details concerning your data analysis.

Figures: Please don’t use any abbreviation in the figure labels.