

Review of: "Complete genome sequence of *Bacillus velezensis* YYC, a bacterium isolated from the tomato rhizosphere"

Jose A. Castillo

Potential competing interests: The author(s) declared that no potential competing interests exist.

This is an interesting manuscript by Yan et al about the genomic sequence of a newly discovered *B. velezensis* strain with potential for biocontrol of important plant pathogens and for promoting plant growth.

This paper has the potential to be accepted, but minor corrections have to be taken before we can proceed with full acceptance. Here, I summarize these points:

B. velezensis YYC has induced systemic resistance against *Ralstonia solanacearum*. I wonder if only *R. solanacearum* has shown a reduction in pathogenesis, but also other pathogens. Most likely, other pathogens could also be restricted by *B. velezensis* YYC.

Why do the authors spell ri-bosome? There are two or three times that we can found "ri-bosome". Please correct.

How many housekeeping genes were used for alignments? Which ones? Why do the author use alignments and not a phylogenetic tree to show species identity and relatedness to other *Bacillus* species?

I would like to see a more detailed description of the cases (i.e. genes) involved in cross-kingdom quorum sensing.

There is no description of how the authors performed digital DNA-DNA hybridizations. What software did they use for this analysis? What conditions, parameters, etc were used for the analysis?