

Reviewer Report

Title: "Genome sequencing of the sweetpotato whitefly Bemisia tabaci MED/Q"

Version: Revision 2 **Date:** 2/22/2017

Reviewer name: Denis Tagu

Reviewer Comments to Author:

Dear authors,

I am OK with the very last version of your paper now as a note.

I still apologize that the genome is badly available. We can of course download the data, but biologists will need a database to browse, search for annotated genes and so on and so forth. And again, i5K@NAL provides very easily this service. It's up to you to follow or not this advice, but integratinfg in i5k database will give more visibility to your genome.

Table 1 indicates differences in the two genomes that are mainly due, to my opinion, to the different approaches used for sequencing, assembling and annotating the genomes.

Now that those two strains have been sequenced, this opens new tracks for further studies on population genomics and phylogeograpghy, which is great.

All the best

Level of Interest

Please indicate how interesting you found the manuscript: An article of limited interest

Quality of Written English

Please indicate the quality of language in the manuscript: Acceptable

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