

## Reviewer Report

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

**Version:** Original Submission    **Date:** 9/4/2016

**Reviewer name:** Denis Tagu

### Reviewer Comments to Author:

I have reviewed this *Bemisia* genome paper with interest: this is a long time that the community is expecting the release of the genome of this Hemipteran pest, and I am satisfied to see that a consortium tackled the difficulty.

This is a regular genome paper whose aim I guess is to provide basic data of an annotated genome and a few analyses. There is thus an interest to publish it, if the community has access to a well-structured genome database of *B. tabacci*, so that the community will still improve annotation and provide new knowledge with other analyses. My first recommendation is thus to provide this access, more than from NCBI. I suggest the authors to contact the i5k community who developed a dedicated database for insects, with a nice interface allowing search, blast and web Apollo annotation (I am not member of this i5k database!).

As I said before, the general analyses are global, and centered on specific gene families such as detoxification (in relation to insecticide resistance and host plant interactions) and immune system (in relation to endosymbiont relationship). There are thus many other gene families that would deserve analyses but I understand that this might not be essential for the paper. But as the paper focuses on a small number of family genes, I would expect more biological experiments that would allow testing some of the hypotheses suggested by the authors. For instance, authors could provide some RNA expression data of candidate genes (e.g. P450) on different host plants or insecticides, or from different *Bemisia* populations with others insecticide resistance profiles. Or some experiments on the IMD pathways such as the one provided for the *A. pisum* paper. I don't say the authors should provide all these analyses, but at least put more biological data.

The hypothesis of HGT is also interesting, but it is known that final demonstration is complicated. So please revise a bit the text to lower the fact that this is an HGT. It could be, but this remains to be demonstrated.

Another trait of *Bemisia* is the transmission of plant viruses, as the authors several times mention it in the text. I would expect some gene family analysis of proteins that possibly play roles in virus transport (vesicle processes?).

The text needs strong English editing. Some parts are OK, but others are different to follow. I suggest the English-native co-authors carefully check all the manuscript, including figure and table legends.

Other minor points:

Does the strain that have been sequenced disseminate plant viruses?

Males are haploid. For Hymenoptera genome projects, males are usually used for sequencing in order to get rid off heterozygosity. I am not a specialist of whitefly biology, but why did not you use only male individuals for this genome project?

The authors used CEGMA for quality control of sequencing and assembly. I would suggest using BUSCO which proposed a larger set of conserved proteins for Insects or Arthropods. The authors will thus have a better assessment of their genome I guess.

The authors could check within the non-assembled reads whether some missing genes that are not present in the assembly might be there, or even other bacterial sequences/genomes.

Repetitive element analysis is a bit poor. No possibility to describe a bit more the different families of transposons?

The gene coverage section is short and difficult to follow (page 11 lines 10 and following).

In the text, comparison of insect-symbionts system is very difficult to follow too.

Conclusion (at least as it is today) is not necessary: too long and redundant with the text.

Figure 3: any possibility to put all the proteins present in the table within the figure/flow chart?

Figure 4: I guess that the arrows showing the transfer of metabolites are not demonstrated but suggested by this work? Please mention it.

Figure 5: please improve the legends that are not clear and incomplete (e.g. what are the green boxes in 5B?).

Figure S4, Table S3, Table S7, Table S9; not sure they are necessary

## **Methods**

Are the methods appropriate to the aims of the study, are they well described, and are necessary controls included? Yes

## **Conclusions**

Are the conclusions adequately supported by the data shown? Yes

## **Reporting Standards**

Does the manuscript adhere to the journal's guidelines on [minimum standards of reporting](#)? Yes

## **Statistics**

Are you able to assess all statistics in the manuscript, including the appropriateness of statistical tests used? No, and I do not feel adequately qualified to assess the statistics.

### **Quality of Written English**

Please indicate the quality of language in the manuscript: Not suitable for publication unless extensively edited

### **Declaration of Competing Interests**

Please complete a declaration of competing interests, considering the following questions:

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