Reviewer Report

Title: **Genome of the small hive beetle (Aethina tumida, Coleoptera: Nitidulidae), a worldwide parasite of social bee colonies, provides insights into detoxification and herbivory**

Version: **Original Submission** **Date:** 5/30/2018

Reviewer name: **Christopher Cunningham**

Reviewer Comments to Author:

Positive Comments

This looks like a professionally assembled and annotated genome. It fills in an important blank space within the genomic resources of beetles.

Major Comments

1. At is not "basal" to anything. It can help you infer what the LCA might have looked like, but it has had an equal amount of evolution compared with Phytophaga.

2. No evidence is given for metabolic plasticity, just increased copy number of some metabolic genes. Not the same thing.

3. Why so few shared ortho-groups? Even restricted to SC BUSCO genes, I would still expect several hundred. Dm has the lowest # of SC at ~1050, but only a 1/5 are SC across all species. Seems odd given BUSCO is SC and complete in 90% of species with the clade of interest, by definition. Just struck me as especially low.

4. Loss and duplication of core genes from small hive beetle genome section. This seems like a lot to read into the lack of something. Only 11 species were analyzed. Either I missed what is being said or this is a sweeping analysis of very few "samples."

5. GH's, Gr's, Nav's, Ace's, GST's, CP450's, etc sections. They are full of a huge amount of information that is not useful to the central message of the sections. Lots of speculation without that leading to specific hypotheses or broader meaning. It was not clear to me why every observed pattern was explained in such detail. Three examples: Line 265-274 can be deleted without any meaning being lost. Much of the information in the opening paragraphs of each sections are not revisited or used in further paragraphs. Line 346, why would that be informative? Not saying it would not be, but I see no particular reason that it would be. Line 453 paragraph, so much to read into so little evidence, only two of the analyzed species were non-beetles.

Minor Comments

Abstract. The results have nothing to do with what is discussed with the background section.

Abstract. The reader should be given some indication of gene compliment completeness before the manuscript speaks about gene copy numbers.

Line 59. Awkward sentence about behaviour.

Line 78. Unclear why this paragraph is sandwiched in between two At life history paragraphs.

Line 107. Endnote field code errors. And a few other places throughout.

Line 107. Genera should be completely spelled out if it is the first word of a sentence.

Line 113. 343.3 million base pairs is not the number given in Table 1.

Line 124 How was DNA extracted? Just realized this is not the methods section. Possibly tell reader details can be found below?

Line 142. Why was such as old tool, TopHat2, used? There is a whole generation of better tools; HISAT2, STAR, GSNAP (the updated version). TopHat2 consistently underperforms other tools, especially with default parameters (Baruzzo et al., 2017, Nature Methods).

Line 150. "The size of the ATUMI genome assembly is similar to that of the red flour beetle (165.9 Mbp)." Your assemble is over double that, reported as 343 Mb.

Line 164. 2444 needs a comma to be consistent with other number in manuscript.

Line 202. Recalcitrance. Great word.

Line 564. I assume default parameters were used with all programs when not stated. Nice thing to say to remove doubt for all software used.

Figure 6 legend. In the title, ATUMI is not bolded.

Methods

Are the methods appropriate to the aims of the study, are they well described, and are necessary controls included? Choose an item.

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