

## Reviewer Report

**Title:** The genome sequence and transcriptome of *Potentilla micrantha* and their comparison to *Fragaria vesca* (the woodland strawberry)

**Version:** Original Submission    **Date:** 01 Aug 2017

**Reviewer name:** Manuel Spannagl

### Reviewer Comments to Author:

In this manuscript the authors report the genome sequencing, annotation and analysis of *P. micrantha* and compare transcriptome & genome data to the related *Fragaria* clade to investigate fleshy fruit development. I agree with the authors that this new resource represents a valuable tool to further and in-depth study fruit development and evolution in this clade and beyond. The analysis of exactly this, however, remains superficial in this study albeit the title promises more...this is my main point of criticism. The identification of the three differentially expressed orthologous clades seems sound from the methodology point of view but lacks any further evaluation or analysis. What about the promoter regions of these orthologs? Any explanation for the different expression profiles? I understand this is a genome and comparative genomics study but it would be nice to see some additional (e.g. experimental) evidence for the functional role of those genes except of their sequence homology to *Arabidopsis*. Also, do you find any additional (differentially expressed or not) genes potentially related to fruit development (e.g. known genes from *Fragaria*)? Until this is not included, you should at least tone down the title's promises...

Additional points to consider:

- a.) Figure numbering is incorrect between legends and actual figures.
- b.) Figure 3 (anchoring...fig 2 in the legend): I understand that this figure represents the anchoring of the scaffolds on the pseudochromosomes of *Fragaria* but I also feel that this figure is somewhat suggestive of an aspect that the authors cannot really assess. As the scaffolds are not ordered or oriented along a map (see pg. 18...and no attempts were made either according to authors) the authors can assess the micro-synteny but not the macro-synteny (this is also clearly mentioned in the methods). The ordering along the *Fragaria* pseudochromosomes in Figure 3 together with too general conclusions about syntenic conservation (see chapter "Scaffold anchoring and synteny..." and conclusions pg.12, ln 22) between *P. micrantha* and *Fragaria* give the impression about high conservation on the macro-synteny level, too (though possible, but not shown).
- c.) Annotation: there is no real evaluation of the gene prediction quality other than BLAST searches and BLAST2GO annotations. It would be nice to see a BUSCO evaluation or even a gene family clustering with related species...this would give a good proxy on gene prediction completeness and also quality. What about the ~9,000 *P. micrantha* genes not identified on the *F. vesca* pseudomolecules? Are they all true species-specific genes? Is there expression evidence for them in your data?
- d.) Gene expression during fruit development: with 1,556 DEGs in *P. micrantha* and 816 DEGs in *F. vesca* I was wondering about the overlap and differences between these two genes sets? This would be much more informative than the GO annotation statistics for these...in that context, I do not understand Fig.

S1. How are the different categories exactly defined and what should be the conclusion of it? I was also wondering about the comparability of the expression data generated in this study and the one by Kang et al. Although they should represent identical tissues etc., is there any statistical and/or technical evaluation available (e.g. PCA etc.)?

e.) Parts of the transposon analysis read extremely descriptive without major conclusions...this could be substantially shortened in my view.

f.) Hormonal treatment: this chapter seems very much isolated...what is the conclusion here and how does it relate to the rest of the analyses?

g.) Is there a reason for not showing the miR1511 data and analysis? This appears to be potentially interesting but cannot be assessed if just mentioned in the discussions...

### **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? No

### **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? There are no statistics in the manuscript.

### **Quality of Written English**

Please indicate the quality of language in the manuscript: Acceptable

### **Declaration of Competing Interests**

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

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