

## Reviewer Report

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

**Version:** Original Submission    **Date:** 15 Aug 2017

**Reviewer name:** Sook Jung

### Reviewer Comments to Author:

The paper titled "The genome sequence and transcriptome of *Potentilla micrantha* shed light on the origins of strawberry fruit development" reports the new genome and transcriptome data of *Potentilla micrantha*, a species that belongs to the genus *Potentilla* that is closely related to that of *Fragaria*. The work is important for the researchers who are interested in the mechanism of fruit development in *Fragaria*. However, I feel that some of the conclusions and claims made in the manuscript, including the title, cannot be justified by the data. Below are two main examples.

#### 1) Synteny analysis

The scaffolds have not assembled into a larger chromosome, so the macrosynteny conservation could not be evaluated as stated in the methods section. In the results section, however, authors state that "Comparison of the two genomes revealed a remarkable degree of synteny with *P. micrantha* scaffolds spanning the entirety of the *F. vesca* genome sequence". The authors need to clarify that the level of synteny detected is micro-level throughout the manuscript, not just in Methods section. The resolution of the Figure 3 (Figure 2?) is too low to see any letters but it looks like a couple of hundreds scaffolds were anchored to each *F. vesca* chromosome. There is no evidence that majority of these scaffolds aligned to one chromosome is in the same *P. micrantha* chromosome.

#### 2) RNA-seq data

The authors reported 1,556 differentially expressed genes between the four developmental stages in *P. micrantha*, and 816 in *F. vesca*. They did GO annotation on these genes but they didn't seem to have looked any further. Were there any difference in the profile of the differentially expressed genes in both species and that only in *F. vesca*?

In conclusion, a lot more work needs to be done (anchoring scaffolds to chromosomes to assess the level of macrosynteny and do a further analyses to develop at least some hypotheses on the genetic mechanism of the fruit development). On the other hand, I feel this work is worthwhile to be published as long as the title and text is appropriately edited to reflect the results accurately.

## 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? No, I do not feel adequately qualified to assess the statistics.

### **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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