Jan 14, 2020

Dear Robert VanBuren,

Thank you for handling our revision of the manuscript previously entitled "A new *de novo* assembly of sweet cherry (*Prunus avium*) improves genome coverage and completeness". Reviewers' comments are very valuable and helpful for improving the quality and readability of the manuscript. Following their suggestions, we corrected and revised the manuscript. Please find our detailed responses (regular font) to the reviewers' comments (blue font in underlined) below and modified paragraphs in the paper (tracked changes).

For your comments:

- 1. More details are needed on the methods for assembling and anchoring the genome.

  Response: We appreciate your comments. More details were added to describe the methods for assembling (Line: 114-118) and anchoring the genome (Line: 125-139).

- 2. It would be useful to compare the reference genome presented here to the first sweet cherry genome sequence reported by Shirasawa et al., 2017. Simple comparative genomics analyses and a comparison of gene content differences would help strengthen this manuscript and validate the findings.

  Response: Two paragraphs have been added to analyze the whole sequence synteny and gene content difference between Tieton and Shirasawa genome assemblies and annotations (Line: 180-189, 279-296). Figure 3 and Table 7 were added in the revised manuscript.

- 3. There are a number of grammatical issues and the manuscript needs some heavy editing.

  Response: The revised manuscript was carefully edited by the PeerJ language editing service department.

For Reviewer 1

- Basic reporting
  This paper reports the whole-genome sequence of sweet cherry, for which the authors used 10X Genomics Chromium technology.
  Since the assembly presented in this paper is not dramatically improved in compare to the previous report, I recommend to delete "improves genome coverage and completeness" from the title.

Response: Thanks for your suggestion. We changed the title to "A *de novo* assembly of the sweet cherry (*Prunus avium* cv. Tieton) genome using linked-read sequencing technology"

- Experimental design
  The authors used 10X Genomics Chromium reads to estimate the size of the sweet cherry genome (299.17 Mb) and to evaluate the assembly quality (99.02%). However, as the authors have already pointed out, it might be due to bias in the Chromium library missing 38 Mb. I strongly recommend the authors to analyze again with whole-genome shotgun reads obtained from a PCR-free method, e.g., TruSeq DNA PCR-Free Sample.

Response: We re-analyzed the genome size of Tieton based on 37-nt k-mer length rather than 17-nt and got the estimation of 341.38 Mb, which is very close to the genome size of 338 Mb estimated from the flow cytometry. The genome size, heterozygosity and repeat content values of Tieton genome were corrected in Line: 201-206.

- Validity of the findings
  The text is totally descriptive and lacks any insights into biological aspects in sweet cherry.

Response: Our manuscript focuses on the sequencing method and assembly of sweet cherry genome using linked reads technology. To our knowledge, this is the first report of a genome assembly of *Prunus* plant using the 10X Genomics Chromium technology. We tried our best to improve the biological aspects in sweet cherry in the entire manuscript.

- Comments for the Author
  Please consider the comments to improve this manuscript.

Response: Thanks for your valuable and helpful comments. We improved the the quality and readability of the manuscript following your comments.

For Reviewer 2

- Basic reporting
  The paper: A new de novo assembly of sweet cherry (Prunus avium) improves genome coverage and completeness by the authors: Jiawei Wang, Weizhen Liu, Dongzi Zhu, Xiang Zhou, Po Hong, Hongjun Zhao, Yue Tan, Xin Chen, Xiaojuan Zong, Li Xu, Lisi Zhang, Hairong Wei and Qingzhong Liu prsent data for a new sweet cherry sequencing using the "Tieton" variety. I belive that the authors need to improve the introduction of the manuscript. There are few paper that should be considered, for instance: 1) Prunus genetics and applications after denovo genome

sequencing: achievements and prospects by Aranzana et al. Horticulture Research (2019)6 :58; Also is important to add info about organel sequencing: The complete mitochondrial genome sequence of sweet cherry (Prunus avium cv. 'summit') by Yang et aL., MITOCHONDRIAL DNA PART B 2019, VOL. 4, NO. 1, 1996–1997 AMONG OTHERS. The figures and tables need to be adreess in a more wide aspect.

Response: We followed the reviewer's suggestion to improve the introduction of the manuscript in Line 61-70. The two references were added, and figures and tables were improved.

- Experimental design

The paper present a new sweet cherry genome sequencing using two powerful tools that allow to improve the sequencing, however no much information is given for those methods: linked-read sequencing technology and the Supernova genome assembler. These techniques are very important for genome sequencing in plants and should be highlighted.

The research question is well defined but I stated previously it need to considerer more publication on the field.

Response: The linked-read sequencing technology and the Supernova genome assembler were highlighted in the introduction (Line:73-80), methods (Line:110-114), and results (Line: 210). In addition, we used the new title of the manuscript to highlight the linked reads sequencing technology.

- Validity of the findings

The results are good however they should discuss and compare their results with the previous sweet cherry sequencing (Shirasawa et al., 2017). This will allow to present more robust conclusions for this sequencing. Most of the genome sequencing papers in these do a deep genome sequencing with the same species or relates, for instance: peach; sweet cherry and apple.

Response: The sequence synteny and gene content difference were compared between Tieton and Shirasawa genome assemblies and gene annotations in Line 279-296.

Another concern is why the do not use the supplementary data through the manuscript?

Response: We carefully checked the order of supplementary data in the main text and used the supplementary data through the manuscript.

- Comments for the Author

The English need some improvement in the manuscript and supplementary data.

Response: We improved the English in the manuscript and supplementary data with the help provided by the PeerJ language editing service department.

Thank you very much for considering our manuscript for potential publication. I'm looking forward to hearing from you soon.

Sincerely,

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