Response to the reviewers on "SNP discovery by exome capture and resequencing in a pea genetic resource collection"

The authors want to thank the reviewers for the two suggestions. Our answers are below.

Reviews

Reviewed by anonymous reviewer, 31 May 2023 07:54

The authors have addressed all my suggestions, and I now recommend to accept the revised manuscript.

Reviewed by Rui Borges, 05 Jun 2023 09:34

During the initial round of revisions for Aubert's research article entitled "SNP discovery by exome capture and resequencing in a pea genetic resource collection," I expressed a significant concern regarding the phylogenetic analyses, accompanied by several minor concerns. I am pleased to report that all of these concerns have been effectively addressed. The authors employed a coalescence-based phylogenetic inference in conjunction with the standard substitution model, leading to the observation of variations in the clades, which were attributed to adixture leading to incomplete lineage sorting (ILS).

Nevertheless, I would like to propose two final suggestions.

1. Firstly, I would recommend the authors to incorporate clade support measures within their tree representations. While acknowledging that the authors are preparing a subsequent paper dedicated to comprehensive phylogenetic analyses, it is important to acknowledge that once a phylogenetic tree is published, it often becomes the foundation for subsequent analyses, even when certain clades may exhibit lower resolution. In light of the present study's indication of disparate outcomes between the two employed methods, likely due to ILS, providing measures of clade support derived from these methods becomes important. Such information would empower potential users of the analyses to assess the robustness of these discrepancies and make more informed decisions.

Clade support measures have been incorporated to Figure1.

2. Additionally, I suggest highlighting the specification of the two methods used, namely the standard substitution model and the coalescence-based approach, in line 143.

Text has been modified accordingly.

Overall, I express my satisfaction with the revisions implemented in this manuscript.

Rui Borges (Institute of Population Genetics, Vetmeduni Vienna)