Reviewer Report

Title: Evolution of complex genome architecture in gymnosperms

Version: Original Submission Date: 6/3/2022

Reviewer name: David Neale

Reviewer Comments to Author:

I agreed to review this paper based on what was stated in the title and abstract. This suggested the paper would be a comprehensive review and comparative analysis of all elements of currently published gymnosperm genome sequences. In fact, the paper is detailed discussion of just three aspects of these genome sequences; (1) repetitive sequences, (2) whole genome duplications and (3) intron length. There is absolutely no discussion of the coding gene content of these genomes.

 I suggest the authors and journal editors take one of two options. 1. Rename the title of this paper and rewrite the abstract and then have the paper reviewed by experts in 1-3 above. I am not such an expert.
Revise the paper so it includes all aspects of genome sequences, notably the gene space.

Also, the timeline of public release of conifer genome sequences given in this paper is totally wrong. The loblolly pine reference genome sequencing project was funded in 2010 and began in 2011. In early 2013, a draft assembly was released. The Norway spruce genome was published later that year, only half the genome actually sequenced and the assembly was of very poor quality.

Methods

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

Conclusions

Are the conclusions adequately supported by the data shown? Choose an item.

Reporting Standards

Does the manuscript adhere to the journal's guidelines on <u>minimum standards of reporting</u>? Choose an item.

Choose an item.

Statistics

Are you able to assess all statistics in the manuscript, including the appropriateness of statistical tests used? Choose an item.

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