

Reviewer Report

Title: *Trochodendron aralioides*, the first chromosome-level draft genome in Trochodendrales and a valuable resource for basal eudicot research

Version: Revision 1 **Date: 9/6/2019**

Reviewer name: Jun Chen

Reviewer Comments to Author:

The authors generally answered my questions together with changes in the text so I think this paper should be accepted for publication. However, I still have to clarify some issues:

1. An E-value cutoff = $1e-5$ for protein search means a piece (HSP) of shorter than 20 bp with low identity would pass. And I don't believe this did not change their results. There is no standard for the e-value cutoff as the authors argued and even if there were, I believe it would not be $1e-5$. I can make a much longer list of literatures using more stringent and serious cutoffs from different statistics. I am sorry to say that the so called "standard" used in the studies provided by authors is not so serious.

As an example for an randomly picked sequence blastp against NCBI:

Range 1: 145 to 168GenPeptGraphicsNext MatchPrevious Match

Alignment statistics for match #1

Score Expect Identities Positives Gaps

51.1 bits(113) 1e-05 16/24(67%) 17/24(70%) 0/24(0%)

Query 1 CGNETMKILLGAVEVLWAQQEQEW 24

CGNETM IL GA E LW +EQ W

Sbjct 145 CGNETMIILAGALEALWSAHEQNW 168

2. I am not sure if adding "de novo identified TEs" improved the estimation or just greatly overestimated the TE% due to e.g. very loose cutoff choice by the authors. It almost triple the size. Simply increase the TE family size cannot be called as "improved"

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