Reviewer Report

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

Version: Original Submission **Date:** 8/6/2019

Reviewer name: Jun Chen

Reviewer Comments to Author:

The authors provide a high confident genome assembly of Trochodendron aralioides, which is a basal eudicot species next to Amborella and Winteracease. By providing the first high quality chromosome-level genome assembly of its kind, this study shall contribute greatly to the genome evolution research of eudicot plants. The assemble, annotation, and phylogentic/selection analysese are well performed with clear description. Therefore, I would suggest for publication in gigaScience.
Minor Issues:
1. For functional annotation, the evalue cutoff of 1E-5 seems too low for protein similarity search (BLASTP, Pfam, KEGG etc).
2. For the ortholog search I think all-against-all OrthoMCL may not perform well with diverged over hundreds millions years. The authors only specified that the longest transcript per locus was selected. I think it would be good to provide more details of the selected orthologs (the number of orthologs selected by OrthoMCL, the distribution of ortholog similarity, how many were used for ML tree inference, how many were used for positive selection analyses PAML, etc).
3. "we used Gblocks [48] to eliminate poorly aligned positions and divergent regions from the alignment ". Please specify what criteria were used for alignment quality control and divergent filtering. Do removing of the most divergent regions change the estimates? Please provide a distribution of Ka/Ks for the genome or 238 genes. I don't think the KEGG results for those 238 genes are significantly enriched for cell metabolism as the adjust p-values are quite high (0.28 or higher, Table S11).
4. what is the synonymous mutation rate and average Ka/Ks for the species? How these compared to other species, especially the ones in the basal position of eudicot?
5. Table 2 the last header should be "Combined TEs". It seems a big discrepancy between results of RepeatMasker (TE protein) to those of other two methods.

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