Reviewer Report

Title: Chromosomeâ€�level genome of the globe skimmer dragonfly (Pantala flavescens)

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Reviewer name: Panagiotis Ioannidis

Reviewer Comments to Author:

This paper describes the sequencing, assembly and annotation of a dragonfly (P. flavescens) genome. Very importantly, the assembly is at chromosome level, making it extremely useful for anyone who wants to run reliable comparative genomics analyses. Effectively, the authors have produced a reference palaeopteran genome. In addition to generating this very useful genomic resource, the authors have run a couple of analyses such as the study of the effective population size along evolutionary time, and a phylogenomic analysis.
I did note that the BUSCO score of the gene set is less than that of the genome assembly. The truth is that the difference is small; only 0.7%. Nevertheless, this means that the gene prediction pipeline doesn't work very well. If BUSCO was able to find 98.8% of conserved genes, then a usually more "sophisticated" gene prediction pipeline should be able to find at least the same number of genes (if not more). Quite often these genes could be missed because they're marked as repeats by RepeatModeler. For this reason, manual inspection of the "unknown" repeats is encouraged in order to exclude "normal" genes that look like repeats (e.g. duplicated genes). For the purposes of this Data Note and since the difference is small, I believe that it might not be necessary for the authors to improve the predicted gene set. If they decide to do so, then that would be great for anyone who would use their data in the future.
Regarding the methodology and results on the effective population size, I'm not an expert and therefore I cannot judge their correctness. As for the phylogenomic analysis, it was properly done and the results obtained are correct.
Last, while I was able to have a look at the deposited raw reads (PacBio and Illumina) in SRA, I wasn't able to see the deposited assembly and gene set. I know that it is possible to generate "reviewer links" for SRA submissions, but I'm not sure if it is also the case for submitted genome assemblies and gene sets. If it is possible, could the authors generate such a link?
Some minor corrections:

- Methods -> Evolutionary analysis: In the beginning of the section, where you mention the species you used, Zootermopsis is mentioned twice.
- Table S1: in the last column of the table, all numbers are "Gbp", not "G". The same is true for the numbers mentioned in the last column of Table 1; they should be "Mbp" and "Kbp".
- Table S2: I presume that the second column refers to homology-based prediction. If true, then please change the title of the column to "Homology", because "Homo" is confusing.
- Table S3: "Counts" doesn't adequately describe the numbers in this column. Maybe something like "Number of genes with significant similarity" would be more appropriate.

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