Reviewer Report

Title: A High-Quality Genome Assembly from a Single, Field-collected Spotted Lanternfly (Lycorma delicatula) using the PacBio Sequel II System

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Reviewer name: Shanlin Liu

Reviewer Comments to Author:

The authors present us a genome assembly for Spotted Lanternfly using the new sequencing platform Pacbio Sequel II. The genome quality is okay but requires further improvements.
Firstly, the authors may want to estimate its genome size using either a K-mer based analysis or flow cytometry. Although the BUSCO results showed good coverage of the coding regions, we can hardly conclude whether the assembly is redundant or not, especially for genome analysis regarding paralogous genes, such as gene expansion and contraction.
Then, those improvements claimed by the authors in the current study, such as sample collection, single individual based DNA extraction and sequencing, stem from the upgrade of the sequencer, "Pacbio Sequel II" which can generate eight million long reads per flow cell, rather than the half a million long reads of its previous version. Plus, the biomass of a single individual will considerably influence the DNA yield and then alter those improvements proposed by the authors. You may want to tone down them in your manuscript.
Additionally, as a data note publication without scientific hypothesis being resolved, the authors may want to release a high-quality genome assembly with cutting-edge techniques, such as Bionano, Hi-C. And RNA-Seq should also be included to improve the annotation quality.

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