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 want to keep their statements of those advantages on entomological genomics. Although I still consider all these advantages are derived from the upgrade of Pacbio SMRT sequencing system, I have no objection if the authors insist on it. This is not the issue I am most worried about. The authors obtained this genome using only long reads, as I mentioned in my comments the last round, this is an incomplete genome assembly. The authors also think this paper should be categorized as Data Note, however, it is well known that genome assembled using only the error-prone long reads tends to have lots of small-scale errors like InDels which will introduce frameshift and premature stop codons and affect the interpretation of translated regions. The authors can find more details in a paper recently published on NBT (https://doi.org/10.1038/s41587-018-0004-z), it mentioned that the human genome assembly generated using only the Pacbio long reads included the most errors compared to the other assembly, with thousands of protein-coding genes predicted to be disrupted by indels. Therefore, the authors may want to include shortgun reads to polish this genome and correct those potential and critical errors before its publication. In addition, you may want to include some transcriptome data as well to improve the genome annotation if you such dataset.

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