

Reviewer Report

Title: A Chromosomal-Level Genome Assembly for the insect vector for Chagas disease, *Triatoma rubrofasciata*

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Reviewer name: Ben Mans

Reviewer Comments to Author:

The authors present a very high quality assembly of the genome for *Triatoma rubrofasciata* that was generated using Illumina X Ten, PacBio and Hi-C libraries. The final genome size reported was 680 Mbp with scaffold and contig N50 values that is superior to most other insect genomes reported to date. The completeness of the genome was estimated at 98% with very few duplicated regions. The genome consists of 12,695 protein coding genes of which 12,304 could be annotated. The gene models compare very well with other insect genomes with regard to gene, CDS, exon and intron length distribution. The data provided with the manuscript adequately cover all features of the study and is accessible in various databases. Some issues follow below.

Page 1, line 57: ... BUSCO genes ...

Page 3, lines 57-60: A plot of the read length distribution/ratio would be useful beyond reporting mean length.

Page 3, line 60: ... mean length of reads was 8.43 Kb.

Page 4, line 6: Is reference 8 the appropriate reference for the HTQC package, i.e. Yang et al., 2013?

Page 4, line 19-22: Independent estimation of the genome size using Kmer analysis is a nice confirmation that the PacBio assembly is correct. Can the Kmer graph be included?

Page 5, line 13: The references for LACHESIS [17] seem to be inappropriate. Reference Burton et al. 2013?

Page 5, line 35: It is not clear from Figure 3 how many insect genomes are compared since the majority is clustered too close to distinguish between them. Can the genomes be listed in the Figure legend?

Page 5, line 41: Not sure why sentence refers to difficulty of mollusk genome assembly? It seems as if parts of the manuscript were copied from another manuscript without updating key words or references?

Page 7, lines 1-8: The phylogenetic analysis needs more information. How was the nodes calibrated for the molecular clock analysis? Include specific fossil data used for calibration. It should be noted that the date estimates for the divergence of *Rhodnius/Triatoma* (51-96 MYA) is much older than other molecular clock estimates (Hwang and Weirauch, 2012). In fact the upper estimate is almost as old the estimate for the higher Reduviidae as a group. The authors should at least address these differences.

Level of Interest

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