Reviewer Report

Title: A chromosomal-level genome assembly for the giant African snail Achatina fulica

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Reviewer name: Takeshi Takeuchi, Ph.D

Reviewer Comments to Author:

In this study the authors sequenced the genome of the giant African snail Achatina fulica using short and long read technologies as well as a Hi-C scaffolding method, and succeeded to develop chromosomal-level genome assembly. I think the data will contribute to our understanding of the biology of the species.

At the same time I found description of methods is not sufficient in the present manuscript, therefore it should be revised before publication.

In the Introduction the authors mentioned that it is important to study the biology of A. chatina because the species is one of the most threatening invasive species, and is the intermediate host of Angiostrongylus. However, I could not find how the present chromosomal-level genome assembly is useful to address these issues. I would like to request the authors to discuss the point more specifically. This will emphasize the importance of the study.

The information about transcriptome is absent despite the data might be used for gene model prediction (lines 206-207). The authors should describe in detail about the transciptome. For example, from which tissues was RNA extracted? How was the quality of the RNA? How was the stats of RNA-Seq (number of reads, average length, etc.)? In addition, mapping rate of the transcriptome to the genome assembly and gene models will be informative to evaluate the completeness of the assembly and model prediction, respectively.

Lines 178-180

High rate of heterozygosity (>1%) have been reported in bivalve genomes (oysters, scallops, etc.) but not the case in gastropods.

Fig. 3

I would suggest to show the genome assembly comparison data in a table, not in a scatter plot.

In general, scatter plot is used to see the correlation between two variables. This figure is not adequate to compare genome assemblies because 1)correlation between contig and scaffold N50s is not meaningful 2) most of the dots are put at the lower left and indistinguishable.

In addition, references should be cited when the authors used these genome data in the study.

Lines 232-235, Fig. 5

What kinds of fossil record were used for molecular clock calibration? Honestly speaking, I cannot believe the result (Fig.5), showing Spiralia diverged from Ecdysozoa 831 Mya (200 million years before the Ediacaran Period).

Version information of all software used are needed.

Level of Interest

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