Reviewer Report

Title: Genome of the ramshorn snail Biomphalaria straminea - an obligate intermediate host of schistosomiasis

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Reviewer name: Jacob Tennessen

Reviewer Comments to Author:

This paper describes a new genome assembly for the snail Biomphalaria straminea. Reported contiguity is much higher even than the existing assemblies for the model snail in the genus, B. glabrata. This assembly will be a useful resource for research on B. straminea and for studies of the genus as a whole, including B. glabrata and the African snail vectors which have the largest impact on human health. The descriptions of gene families and synteny are insightful. Inclusion of experimental data (drug and hormone treatment) is unusual for a genome paper but not inappropriate. However these results are somewhat buried in the paper; there is no indication in the abstract that there is any RNA data, even though the authors sequenced the entire transcriptome and conducted RT-qPCR on candidate genes. The authors may wish to emphasize this aspect of the paper more strongly. In general, there is a lack of genomic resources for mollusks given the importance of the phylum (see Davison & Davis

Minor comments:

Discussion of the African clade is confusing, as the authors don't explain that B. glabrata is neotropical but a phylogenetic sister to the African Biomphalaria, and no actual African snails were analyzed here. The point is simply that B. straminea and B. glabrata represent two major clades in the genus, and thus the conserved synteny between them suggests it is conserved across the genus. It would be good to cite Campbell again in this section or another phylogenetic study (e.g. DeJong et al. 2001 Mol Biol Evol). The statement "Perhaps more thorough sequencing of B. glabrata could determine if this is shared in the genus" is correct, but it would be even more useful to have genomes from additional Biomphalaria species, not just more B. glabrata.

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