

Reviewer Report

Title: Genome sequencing of deep-sea hydrothermal vent snails reveals adaptations to extreme environments

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Reviewer name: Reuben William Nowell, Ph.D.

Reviewer Comments to Author:

The manuscript of Zeng et al seems to describe a well-put together genome for one species of deep-sea snail, with an additional 'draft' genome for another species. It is clear and well-written, with most of the methods described sufficiently. My main criticism is that I found some of the discussions regarding the adaptative significance and/or putative "function" of various TE content and gene-family expansion results quite speculative, given that the comparative results are often observational with no hypothesis testing or statistical framework. That may well be beyond the remit of the paper, but the language could be more careful in places to reflect the putative nature of any hypothesised effects. Nonetheless I have no doubt that the genomes themselves will be useful additions to the community for future work on mollusc and animal evolution.

Minor comments:

- Typo line 38: "impedes"
- Line 158: is there a reference or two for this? I would assume that most TEs are simply selfish genetic elements that do not serve a "function" per se but exist only for their own purpose, i.e. to copy themselves independently of the host genome
- Line 158-160: but most TE content differences are probably driven by stochastic forces (i.e. drift) rather than deterministic forces such as adaptation, and here we have only 2 data points. The language used for this statement is careful, but I wonder if it is too far to extrapolate that some differences in TE content may be adaptive
- Line 196: I don't know what the authors mean by this statement
- Section on Ka/Ks values: there is no impression given about the statistical significance of the differences observed between Ka/Ks in any given lineage, or what the distribution of error looks like for these point estimates. Perhaps a more refined PAML analysis could resolve this? It is also not written how Ka/Ks values were calculated
- Typo line 214: CAFE not CAFÄ%
- Line 329: "region-specific feature shared between lineages" - not sure what is meant by this?
- Line 350: it seems speculative - surely both immune response and biomineralization are "vital" for all snails, not particularly deep-sea ones?
- Line 454: reference for GLEAN is missing
- Line 469: references for Solar and Hcluster are missing, and what is a H-score?
- Figure 2a: it's a weird looking tree that, in fact, looks a bit like a snail itself! Are the widths of the blobs representative of the error around the divergence times or topological support?

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