Reviewer Report

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

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Reviewer Comments to Author:

The manuscript entitled "Genome sequencing of deep-sea hydrothermal vent snails reveals adaptations to extreme environments" presents a nice description of a good genome assembly (16 chromosomes representing ~80% of the genome) of the scaly foot snail (Chrysomallon squamiferum) and compare it to genomes of other molluscan species. Overall the paper is well written and presents a nice view of some unique adaptations by this deep-sea mollusc. One concern that I had is throughout the manuscript (starting at line 164 and onward) the authors describe comparing two mussels, two freshwater snails and two shallow-water snails to their genomes. However, these other molluscan species include C. gigas and P. fucata...which are both oysters and not mussels, and while two of the other molluscs included in the tree are in Gastropoda and considered snails, Lottia gigantea is a limpet and Aplysia californica is a sea slug. I would encourage the authors to describe all of these species more accurately, i.e., as limpet and sea slug, because these are very different from what people commonly think of when they hear "snail", represented by the more traditional Pomacea and Biomphalaria. Referring to all the "snails" as gastropods would be a more suitable term that captures the true diversity of this large group. But when discussing individual species, I would prefer to see the more accurate descriptions because limpets and sea slugs are different from traditional snails, and will have unique adaptations of their own related to their unique characteristics. Overall, the authors give a good general description of the results and present a reasonable discussion about some of the potential adaptations that they observed in the genome. One minor point - thioredoxins are much more likely play a role in repairing proteins that have been altered by oxidation (Lines 255-256), so to limit this expansion to innate immunity leaves out a lot of other possibilities. My other question was regarding the source of the genomic DNA. The authors describe using muscle samples for isolating DNA, but it is not clear if DNA from one individual was used for all sequencing or if pooling occurred?

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