

Reviewer Report

Title: The genome of common long-arm octopus *Octopus minor*

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Reviewer Comments to Author:

In the present manuscript, the authors provide the genome of the common long-arm octopus *Octopus minor*. It has been reported that the genome of the California two-spot octopus *O. bimaculoides* has a high amount of repeat content and several gene family expansions related to its morphological novelty. *O. minor* is closely related to *O. bimaculoides*, belonging to the same genus. The authors compared gene families and repetitive elements of these two octopus genomes with other lophotrochozoans and concluded that these two octopus genomes seem to be evolved independently.

Overall, this is a significant contribution to the field of cephalopod genomics. In order to support their hypothesis, the authors should address the issue of phylogenetic analyses of major gene families and repeats before publication.

Major comments:

1. The manuscript is well-written and straightforward. However, I find that there is a lack of evidence to show which events are related to *Octopus* genus-specific events or those of species-specific. Since one major conclusion from gene family and repeat analyses is that *O. minor* and *O. bimaculoides* evolved independently, the authors should provide evidence to test their hypothesis. For example, one major finding in the *O. bimaculoides* genome is that gene family expansions of protocadherins and the C2H2 superfamily of zinc-finger genes. Given that we have an additional genome from the same genus, the authors should provide gene trees to show that if these gene family expansions are general to the genus *Octopus*, or there was a convergent evolution in which these gene family expanded independently.
2. Also, it is worth to check the genomic organization of these gene family expansions in two octopus genomes. Are they usually expanded in a tandemly duplicated manner on the same scaffold? Or are they distributed among different scaffolds?
3. Similar situation for the repetitive elements, although the authors showed that the repeat landscape is different between two octopus genomes, there is no information about which repeat expansions have happened at the genus-level and which are at the species-level. The authors should at least examine some representative repetitive elements in details by providing their phylogenetic analysis with repeat trees.
4. In addition, the authors mentioned that they did RNA-seq of 13 tissues, but there is no description of this dataset. Are there some gene family expansions related to tissue-specific expression? The authors should provide some results from their RNA-seq data.

Minor comments:

1. Introduction: Given that octopuses are members of lophotrochozoans and the authors also used a lot of lophotrochozoan genomes for comparisons, the authors should properly describe previous work related to this topic. I would suggest the authors add some description about the relationship of molluscs and other lophotrochozoans and cite major papers to give an overview for the rationale of phylogenetic and gene analyses.

References:

Takeuchi et al. (2012) Draft genome of the pearl oyster *Pinctada fucata*: a platform for understanding bivalve biology. *DNA Res* 19, 117-30.

Zhang et al. (2012) The oyster genome reveals stress adaptation and complexity of shell formation. *Nature* 490, 49-54.

Simakov et al. (2013) Insights into bilaterian evolution from three spiralian genomes. *Nature* 493, 526-31.

Luo et al. (2015) The *Lingula* genome provides insights into brachiopod evolution and the origin of phosphate biomineralization. *Nat Commun* 6, 8301.

2. Line 12: "bilaterian animal species" -> "bilaterian species". Bilaterians are bilaterally symmetric animals, so using "bilaterian animal" would be redundant.

3. Line 40: Most *O. minor* habitats are "mud and sand"...

4. Line 42: The following sentence is unrelated to the scientific study, especially for the later part: "As an important economic cephalopod in South Korea, fishermen normally catch *O. minor* by digging a hole in the mudflat with shovels."

5. The Results section (or Analyses) "Genome sequencing and annotation" looks like for the Methods section. Should that be called "Data description" in GigaScience format?

6. Line 61: The authors should describe the strategy and sequencing platform they used. It is mentioned in the RNA part at line 73 but not for DNA. Did authors use the same strategy here?

7. Line 64: What kinds of paired-end sequences were used?

8. Line 69: thirteen -> "13".

9. Line 72: Remove "TM".

10. Line 73: Pacbio -> "PacBio".

11. Line 124: *O. bimaculoides*.

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