

## Reviewer Report

**Title: Chromosome-level genome assembly reveals the unique genome evolution of swimming crab (*Portunus trituberculatus*)**

**Version: Original Submission**    **Date: 10/4/2019**

**Reviewer name: Joseph F. Ryan**

### Reviewer Comments to Author:

This paper describes a high-quality genome assembly of *Portunus trituberculatus*, one of the most widely fished species of crab in the world. The paper is written clearly and succinctly. The figures look excellent are clear and informative. I downloaded the genome and found an expected Hox cluster, which is in line with this being a high quality data set. The authors do not describe the Hox cluster and this is fine, but they should consider since it would not have to be that extensive of an analysis and a description plus Hox complex figure would increase the interest in the paper (it could also be a follow-up study). Nevertheless, this is a wonderful genomic resource, an excellent analysis, and if the authors address the reproducibility issues in my next paragraph, I would say that this is a model genome data note.

The methods appear thorough, however repeating these analyses in full would be impossible without guessing at some parameter settings etc. In order to make the work repeatable, please include ALL command lines in a supplemental document. There is an excellent example in the supplement linked here:

<https://academic.oup.com/mbe/article/35/2/486/4644721#113627427>

Line 34: "only limited transcriptome data currently available"

--This is untrue as there is a draft genome assembly available in GenBank:

<https://www.ncbi.nlm.nih.gov/nuccore/VSR000000000.1>

This available draft should be acknowledged in the manuscript (even though the assembly in this current study is far superior).

Line 70: "genomic research on the swimming crab has only been conducted at the transcriptome level[14-16], with the whole genome not yet described.

--Likewise, this line should be updated to mention this draft genome.

Line 84: "Muscle RNA was also extracted using TRIzol (Invitrogen) according to the manufacturer's instructions"

-- Should clarify whether the same animal used was used for extraction of RNA as the genome. Indeed it should also be noted if the same animal was used for all genomic sequencing.

Line 297 (and line 300): "greater survival pressures on these two species"

--I wouldn't attribute faster evolutionary rates to "survival pressures." Evolutionary rate has more to do with generation time (shorter=greater) and population size (larger=greater). The evolutionary rate makes sense in relation to both of these factors. Differences in survival pressures are heavily influenced by competition in large populations.

Table 2: It seems as if the "Summary" row represents the percentage for "Complete BUSCO (C)." The

label "Summary" does not make sense in this context. I would rename to "Summary (percentage Complete Busco)" or "percentage Complete Busco"

I love Figure 1! Beautiful creature!

Figure 2 and 3 legends should include more information. For example, what program was used to generate figure. What is the underlying data from, etc.

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