

## Reviewer Report

**Title:** The genome draft of coconut (*Cocos nucifera*)

**Version:** Original Submission    **Date:** 4/26/2017

**Reviewer name:** Sebastian Proost

### Reviewer Comments to Author:

The authors present a draft of the *Cocos nucifera* aka Coconut genome. Apart from economic importance of the species it should also be noted that the Areaceae provide an excellent outgroup for evolutionary studies of the Poaceae which include all major cereals. The manuscript mainly highlights the methods used to sequence the genome and assemble the reads (which has been done using current standards), but offers little more than that. MAJOR=====This manuscript is little more than a claim the coconut genome has been sequenced. Some traditional analyses one would expect from a genome paper are missing. Homologous gene families using a larger set of genomes would allow a gain-/loss analysis (check the *Zostera* (seagrass) genome paper Figure 1a for a recent example), some venn diagrams based on this showing how many genes are shared with close relative (e.g. *Elaeis*), other monocots (e.g. rice) and dicots (e.g. *Arabidopsis*) could also be generated based on this (e.g. orchid genome paper figure 1a). A synteny/collinearity analysis is usually included, often combined with a Ks analysis (see the Orchid genome paper Figure 2, *Zostera* genome paper Figure 2). MINOR=====No case study is included, I feel there should be at least one (though as the paper is submitted as a data note the journal might not require one). The authors are the first ones to have a glimpse at the genome of this species. I would make sense to check a few relevant gene families (coconuts are clearly very different from seeds of other monocots, so seed related gene families would be likely candidates for a more in depth study) For non-bioinformaticians a supplemental website which offers a BLAST interface would certainly be welcome. Line 128 - 129: the N50 by itself is not a direct measure for the quality of the assembly. Avoid over-interpretation. Various typos and grammatical mistakes Line 54 and abstract: (DVP01, 4,166) -> the number of genes for the date palm genome is incorrect. In table 2 the authors report 41,660 ! Line 60: facilitating future: missing space Line 78-79: for high tolerant to high salt density: revise grammar Line 80: ...present Hainan Tall... -> ...present the Hainan Tall... Line 82: ...about genome... : revise grammar Line 88 (and other places) : ...pair-end... -> ...paired-end... Line 96: ... removed by using ... -> ... removed using ... Line 116: ...SOAPdenovo2 map ... -> ...SOAPdenovo2 maps ... Line 132: ... reported in previous Fan's research ... : incorrect grammar, should be revised (as previously reported by Fan et al. ..) Line 181: Previous Fan's study : revise grammar Line 192: ... a diagrammatic pipeline is shown ...: revise grammar Line 199: ... completely ... -> complete Line 203 - 204: In sequence similarity step: revise Line 232-233: Font is suddenly somewhat bigger

### Level of Interest

Please indicate how interesting you found the manuscript: An article whose findings are important to those with closely related research interests

### **Quality of Written English**

Please indicate the quality of language in the manuscript: Needs some language corrections before being published

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