

Reviewer Report

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

Version: Original Submission **Date:** 4/12/2017

Reviewer name: Carsten Kulheim

Reviewer Comments to Author:

The manuscript titled 'The genome draft of the Coconut (*Cocos nucifera*)' describes the sequencing, assembly and annotation of the coconut genome. While there are several indicators that the work presented here is well done, the quality of the written work is so poor that it is made difficult to read and assess. The manuscript is full of typographical errors, the formatting is poor and it appears that many small mistakes are present throughout the manuscript that could have been avoided by a careful final evaluation. That said, I believe that the work can be made publishable with some editing and care. Since the authors mention adaptation to salinity, a few results regarding GO or KEGG annotations to this topic would make the study more exciting. Some examples are shown below: line 40: in 93 countries -> the introduction (line 70) says 89 countries line 41: 11 million ha -> the introduction (line 72) says 12 million ha line 44: hinders progress in genetic breeding. Do you mean 'marker assisted breeding' or 'genomic assisted breeding'? line 45: genetic improvement is slow. Do you mean trait improvement with marker or genetic assisted breeding? line 48: The coverage does not add up. 714.67 Gb on a 2.42 Gb genome is 295 x coverage. In any case, only the coverage of the cleaned reads should be shown (177 x) line 54: Do you mean 41,166 genes? line 60: space missing between facilitating and future line 61: should be 'molecular assisted breeding' line 78: '... wide range to environment...' -> unclear, should be explained. Also 'environments' line 78: '... especially for high tolerant to high salt density.' please clarify line 80: '... making it possible to understand its adaptation to to high salinity.' You do not investigate this, you should change the statement to something milder such as: 'This study forms the basis for future research investigating the coconuts tolerance to salt stress.' line 82: provide references. The way this sentence reads at the moment, makes it seem like you are also reporting those genome sequences. line 92: space between 'Illumina', 'HiSeq2000' and 'sequencer' line 129: The data shows that you have higher coverage and a longer N50, it does not show that the assembly is of better quality. line 131: 'tissues', not 'issues' line 134: tables 4 and 5 are mixed up line 165: BLAST not BLSAT line 175 (and others): keep a space between numbers and units, consistently. line 195: Change start of sentence (e.g. 'After the above described steps...') line 196: should read: 'than the predicted gene numbers...' line 203: space between 'by' and 'sequence' line 211: after ref 38, just one dot line 219: remove space between 'mapping' and 'References: need a lot of editing to uniform. Tables: Headers are unclear and many abbreviations within tables are not explained. What is the difference between Tables 4 and 7? Both show BUSCO assessments of palm species. Clarify both in tables and in the text! Figure legend: Figure 1 does not contain any morphological characteristics, they are photographs of coconut plants.

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: Not suitable for publication unless extensively edited

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