

Reviewer Report

Title: Genome sequence and genetic diversity analysis of an under-domesticated orphan crop, white fonio (*Digitaria exilis*)

Version: Original Submission **Date: 9/13/2020**

Reviewer name: Gincy P. Thottathil

Reviewer Comments to Author:

The manuscript entitled "Genome sequence and genetic diversity analysis of an under-domesticated orphan crop, white fonio (*Digitaria exilis*)" is an excellent report on the exemplary research done by the authors. Considering the nutritional importance and the lack of adequate genetic information, fonio needs more research attention. Appreciate the initiative taken by the authors which would definitely be helpful in future breeding programs. But, a more complete assembly of *Digitaria exilis* genome has already been published a few days back.

Abrouk, M., Ahmed, H. I., Cubry, P., Å imonÅ-kovÅj, D., Cauet, S., Pailles, Y., ... & Zekraoui, L. (2020). Fonio millet genome unlocks African orphan crop diversity for agriculture in a changing climate. *Nature Communications*, 11(1), 1-13.

However, considering the additional analysis and information provided in this manuscript, I strongly recommend the publication of this manuscript.

1. Two sequencing platforms were used in the study; PacBio and Illumina. Even though the assembly almost covers the estimated genome size, it is presented as 3333 contigs. What is the difficulty faced by the authors to construct it into chromosome level? Small genome size as well as the availability of long reads could make it more feasible to construct the chromosomes. Also, only 88% of the RNAseq reads could be aligned to genome, which shows the incompleteness of the assembly. How do the authors justify this?

2. Line no. 83

"is some transcript sequence data [13] at NCBI."

Line No. 164

"Illumina RNA sequencing data (paired-end 100 bp) of *Digitaria exilis* [13] were downloaded".

Here the reference cited is wrong.

3. 67855 protein coding genes were identified from the assembly. This is quite a large number compared to other related plants. However, it is expected due to the allotetraploid nature of the plant and 4.3% single nucleotide variation was observed in between the sub-genomes. All analyzed domestication genes are duplicated in fonio compared to other related plants. Apart from the expected doubling, is there an expansion in any particular gene family?

4. Is there any gene unique to either of the sub-genomes?

5. Please provide legends for Fig. S1- A and B.

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