

Reviewer Report

Title: De novo genome assembly of the red silk cotton tree (*Bombax ceiba*)

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Reviewer Comments to Author:

Thank authors for improving the manuscript and providing a quick response to my comments. Based on the reply I still have some concerns and suggestions. For my previous question 1: the authors pointed out that heterozygosity may affect the estimation of genome size by using Kmers. Do authors believe <1% heterozygosity rate can lead to ~100 Mb assembly differences (the final assembly is 895Mb)? Is that possible 17-mer underestimated the genome size (I understand that in BGI's paper they used 17-mer to estimate giant panda's genome size. Is 17-mer suitable for *B.ceiba*? If authors test different kmers, I suppose you will have different results). For my previous question 2: I appreciate that authors used BLASTN to confirm contaminations. However, shouldn't authors use the non-plant database instead of bacteria? Why did authors randomly select some contigs (how many?) instead of all of them? I understand that using random selection to avoid bias, but since the contamination rate is low (I suppose), you will have less chance to select a contamination contig if you only select a few contigs from the pool. For my previous question 3: I understand that there are some discrepancies between Bionano consensus maps and the NGS reference. I want to know how many Bionano consensus maps can align to the Pacbio assembly or the total size of the aligned PacBio assembly? Since Bionano gives 1.09Gb consensus maps, does that mean the real genome size of *B.ceiba* is around 1.09 Gb? Does that mean the Pacbio assembly is still underestimated? For the 'Ns' added through Bionano scaffolding, it can be easily checked. New questions: 1. why did authors change the final assembled genome size from 869Mb to 895Mb, but didn't change any stats, is anything wrong with the previous calculation? 2. From the density of Bionano label, it seems it is low. Which enzyme did authors use to generate the Bionano data? Is that Nt. BspQI?

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