Reviewer Report

Title: The draft genome sequence of a desert tree Populus pruinosa

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Reviewer name: John Mackay

Reviewer Comments to Author:

The Data note presents the genome assembly of Populus pruinosa - a poplar tree species that is adapted to the deserts of western China and neighbouring regions. It is the third genome of the Populus genus to be sequenced, and others are being developed. Poplars are important forest tree species from ecological and economic standpoints throughout the Northern hemisphere; therefore, the development of genome resources for poplars will have wide ranging impacts. The development of several genome sequences enables comparative and evolutionary studies and, the analysis of a desert-adapted species helps to develop knowledge that is relevant for adaptation to climate change and for combating desertification.This note describes the sequencing, assembly, annotation and evolutionary analysis of the genome. The methods are appropriate and the analyses are extensive. The data metrics indicate that the assembly is of high quality. The evolutionary analyses indicate that this resource is likely to lead to valuable developments in the understanding of adaptation and evolution in plants.The outcomes of several analyses are presented in the supplemental materials but why not include a composite figure presenting the key findings in the main paper? I feel it would be off interest to readers and strengthen the paper.I verified that the data have been deposited at the Short read archive for 7 Illumina libraries. I tried searching the project website (Salinity Tolerant Poplar Database) for information on the assembly. I did find a link but I was unsuccessful at downloading. Unfortunately I attempted this over Wifi which may be the problem. Could the authors give more detail on what is available and in what format? Could the authors also post an update on the website describing the genome assembly and its release?In the section 'Evolutionary analyses', the last sentence of the 1st paragraph states that the functional categories are probably related to the differences in the adaptations... Please explain the basis for the statement / hypothesis.In the next paragraph in the same sectin, the authors wrote that they identified 6,925 genes that are specific to P. pruinosa, which seems like a large number given what is known about gene conservation in plants. The authors should explain on what basis is the number obtained. Is the result relative to other poplars or relative to all plants?In the last sentence of the closing paragraph, the authors wrote that pan-analyses will be necessary in poplar but they do not explain why they believe this to be the case nor what it will achieve. I do not dispute the potential interest of the idea but I do feel it needs at least some explanation.

Level of Interest

Please indicate how interesting you found the manuscript: An article of importance in its field

Quality of Written English

Please indicate the quality of language in the manuscript: Acceptable

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