

Abstract

Determination of Phylogenetic Relationships of the Genus *Sorghum* Using Nuclear and Chloroplast Genome Assembly [†]

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[†] Presented at the third International Tropical Agriculture Conference (TROPAG 2019), Brisbane, Australia, 11–13 November 2019.

Published: 30 December 2019

Sorghum (*Sorghum bicolor* [L.] Moench) is a multipurpose food crop which is ranked among the top five cereal crops in the world. It serves as a source of food, fodder, feed and bioenergy. The genus *Sorghum* consists of 25 species and is considered as a group of plants with enormous diversity. Crop wild relatives have played significant roles in assessing and utilizing genetic resources which is the fundamental step of crop improvement. Successful examples of introgression of novel alleles from the wild relatives of rice, wheat, maize and sugarcane have been reported, whereas studies on wild sorghum are limited. The wild gene pool of sorghum harbours many useful genes for drought tolerance and disease resistance. However, the phylogenetic relationships in the genus remain unresolved due to the limited availability of sequencing data. The comparison of nuclear genomes along with the chloroplast genomes of sorghum species would expand this knowledge and aid in using these potential genetic resources as well as resolving the vague phylogeny of the genus. To date the chloroplast genome of only four sorghum species have been sequenced. This first of its kind study aims to determine the phylogenetic relationships in the genus *Sorghum* by means of nuclear and chloroplast genome sequencing and assembly of all the 25 known *Sorghum* species. This effort would undoubtedly be a significant step towards exploiting the hidden genetic resources of sorghum in crop improvement.

Keywords: sorghum; crop wild relatives; phylogenetic relationships; chloroplast genome assembly

Author Contributions: All authors have contributed equally.

Funding: Australian Research Council Discovery Program.

Acknowledgments: UQ Graduate School.

Conflicts of Interest: The authors declare no conflict of interest.



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