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GENOME SEQUENCING

The Complete Genome Sequences of 12 Species of Plants from the Yucatan Peninsula, Mexico

Yuri J. Peña-Ramírez[1], Natalia Y. Labrín-Sotomayor[1], Patricia A. Becerra-Lucio[1], Hugo Ruiz-González[1], Norka M. Fortuny-Fernández[1], Fulgencio Alatorre-Cobos[2], Stacy Pirro[3]

[1] Department of Sustainability Sciences, El Colegio de la Frontera Sur, Campeche, Mexico , [2] Integrative Biology Unit, CONAHCYT - Centro de Investigación Científica de Yucatán. Yucatán, Mexico, [3] Biodiversity, Iridian Genomes

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Biodiversity Genomes

We present the complete genome sequences of 12 species of plants from Campeche, Mexico and the greater Yucatan Peninsula: *Agave americana*, *Agave angustifolia*, *Agave fourcroydes*, *Agave karwinskii*, *Agave potatorum*, *Agave tequiliana*, *Annona squamosa*, *Cedrela odorata*, *Pouteria campechiana, Pouteria glomerata*, *Trichilia hirta* and *Trichilia minutiflora.*

Methods

Single wild-collected individuals were used for this study. DNA extraction was performed using the Qiagen DNAeasy genomic extraction kit using the standard protocol. A paired-end sequencing library was constructed for each specimen using the Illumina TruSeq kit according to the manufacturer's instructions. The libraries were sequenced on an Illumina Hi-Seq platform in paired-end, 2 × 150 bp format. The resulting fastq files were trimmed of adapter/primer sequence and low-quality regions with Trimmomatic v0.33 (Bolger, Lohse, and Usadel 2014). The trimmed sequence was assembled by SPAdes v2.5 (Bankevich et al. 2012) followed by a finishing step using Zanfona (Kieras, O'Neill, and Pirro 2021).

Results and Data Availability

All data is available via Genbank:

Agave americana	JAVRMC000000000
Agave angustifolia	JAXCLS000000000
Agave fourcroydes	JAVLRU000000000
Agave karwinskii	JAXCLU000000000
Agave potatorum	JAVKLE000000000
Agave tequiliana	JAVJIF000000000
Annona squamosa	JAXCLR000000000
Cedrela odorata	JAXCLQ000000000
Pouteria campechiana	JAYJMB000000000
Pouteria glomerata	JAVXUM000000000
Trichilia hirta	JAWDEX000000000
Trichilia minutiflora	JAVXUL000000000

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REFERENCES

Bankevich, Anton, Sergey Nurk, Dmitry Antipov, Alexey A. Gurevich, Mikhail Dvorkin, Alexander S. Kulikov, Valery M. Lesin, et al. 2012. "SPAdes: A New Genome Assembly Algorithm and Its Applications to Single-Cell Sequencing." *Journal of Computational Biology* 19 (5): 455–77. https://doi.org/10.1089/cmb.2012.0021.

Bolger, Anthony M., Marc Lohse, and Bjoern Usadel. 2014. "Trimmomatic: A Flexible Trimmer for Illumina Sequence Data." *Bioinformatics* 30 (15): 2114–20. https://doi.org/10.1093/bioinformatics/btu170.

Kieras, M., K. O'Neill, and S. Pirro. 2021. *Zanfona, a genome assembly finishing tool for paired-end Illumina reads*. https://github.com/zanfona734/zanfona.