

Editorial Note on Olive (*Olea europaea* L.) crucial to life on Earth

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Received: March 20, 2021; **Accepted:** April 25, 2021; **Published:** April 30, 2021

Olive (*Olea europaea* L.) is internationally renowned for its high-end product, extra virgin olive oil. An incomplete genome of *O. europaea* was previously obtained using shotgun sequencing in 2016. To further explore the genetic and breeding utilization of olive, an updated draft genome of olive was obtained using Oxford Nanopore third-generation sequencing and Hi-C technology. Seven different assembly strategies were used to assemble the final genome of 1.30 Gb, with contig and scaffold N50 sizes of 4.67 Mb and 42.60 Mb, respectively. This greatly increased the quality of the olive genome. We assembled 1.1 Gb of sequences of the total olive genome to 23 pseudochromosomes by Hi-C, and 53,518 protein-coding genes were predicted in the current assembly. Comparative genomics analyses, including gene family expansion and contraction, whole-genome replication, phylogenetic analysis, and positive selection, were performed. Based on the obtained high-quality olive genome, a total of nine gene families with 202 genes were identified in the oleuropein biosynthesis pathway, which is twice the number of genes

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Citation: Michel (2021) Editorial Note on Olive (*Olea europaea* L.) crucial to life on Earth. Am J Phytomed Clin Ther Vol.9 No.4:14

identified from the previous data. This new accession of the olive genome is of sufficient quality for genome-wide studies on gene function in olive and has provided a foundation for the molecular breeding of olive species.