



The Singular Evolution of *Olea* Genome Structure

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OPEN ACCESS

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Specialty section:

This article was submitted to
Plant Systematics and Evolution,
a section of the journal
Frontiers in Plant Science

Received: 03 February 2022

Accepted: 07 March 2022

Published: 31 March 2022

Citation:

Mascagni F, Barghini E, Ceccarelli M, Baldoni L, Trapero C, Díez CM, Natali L, Cavallini A and Giordani T (2022) The Singular Evolution of *Olea* Genome Structure. *Front. Plant Sci.* 13:869048. doi: 10.3389/fpls.2022.869048

The current view of plant genome evolution proposes that genome size has mainly been determined by polyploidisation and amplification/loss of transposons, with a minor role played by other repeated sequences, such as tandem repeats. In cultivated olive (*Olea europaea* subsp. *europaea* var. *europaea*), available data suggest a singular model of genome evolution, in which a massive expansion of tandem-repeated sequences accompanied changes in nuclear architecture. This peculiar scenario highlights the importance of focusing on *Olea* genus evolution, to shed light on mechanisms that led to its present genomic structure. Next-generation sequencing technologies, bioinformatics and *in situ* hybridisation were applied to study the genomic structure of five related *Olea* taxa, which originated at different times from their last common ancestor. On average, repetitive DNA in the *Olea* taxa ranged from ~59% to ~73% of the total genome, showing remarkable differences in terms of composition. Among repeats, we identified 11 major families of tandem repeats, with different abundances in the analysed taxa, five of which were novel discoveries. Interestingly, overall tandem repeat abundance was inversely correlated to that of retrotransposons. This trend might imply a competition in the proliferation of these repeat classes. Indeed, *O. paniculata*, the species closest to the *Olea* common ancestor, showed very few tandem-repeated sequences, while it was rich in long terminal repeat retrotransposons, suggesting that the amplification of tandem repeats occurred after its divergence from the *Olea* ancestor. Furthermore, some tandem repeats were physically localised in closely related *O. europaea* subspecies (i.e., cultivated olive and *O. europaea* subsp. *cuspidata*), which showed a significant difference in tandem repeats abundance. For 4 tandem repeats families, a similar number of hybridisation signals were observed in both subspecies, apparently indicating that, after their dissemination throughout the olive genome, these tandem repeats families differentially amplified maintaining the same positions in each genome. Overall, our research identified the temporal dynamics shaping genome structure during *Olea* speciation, which represented a singular model of genome evolution in higher plants.

Keywords: *Olea* evolution, tandem repeats, retrotransposons, genome landscape, NGS analyses, genome evolution

