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NOT ONLY TRANSPOSONS: THE PECULIAR EVOLUTION OF OLIVE GENOME STRUCTURE

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The current view of plant genome evolution proposes that genome size is determined by processes such as polyploidization and amplification and/or loss of transposable elements. Other types of repeated sequences, including tandem repeats, usually have a minor role in shaping plant genome structure and size, accounting for a small portion of the genomes sequenced so far.

In the cultivated olive (*Olea europaea* L. subsp. *europaea* var. *europaea*), available data suggest the occurrence of a singular model of genome evolution, in which polyploidization and amplification/loss of transposons were accompanied by a massive expansion of the tandem repeated fraction. This fraction is composed by six major families of satellites, that make almost one third of the genome. This peculiarity highlights the necessity of further studies about the evolution of the *Olea* genus, to shed light on mechanisms of genome expansion and the possible function of the different types of repeated sequences.

Massively parallel sequencing technologies, advanced bioinformatic analyses and in situ hybridization, were applied to study in detail the genome structure of cultivated olive and other 4 related species or subspecies (*O. europaea* subsp. *cuspidata*, *O. europaea* subsp. *guanchica*, *O. exasperata*, and *O. paniculata*). They originated at different times from the common ancestor from which the cultivated form derived.

Our analysis led to a complete characterization of the repeated fraction of the genomes of the selected *Olea* species, with emphasis on the tandem repeats. On average, repetitive DNA in *Olea* species ranges from 42% in *O. paniculata* to 66% in *O. europaea* subsp. *cuspidata*, showing remarkable differences in terms of composition. In fact, the 11 major families of tandem repeats identified across the analyzed species presented different redundancy levels. Thus, some families were barely represented in one species and highly redundant in another. A large number of long-terminal-repeat (LTR) retrotransposons (of different lineages) were also found in every *Olea* species. Interestingly, overall tandem repeat redundancy was inversely correlated to that of retrotransposons. This trend might implicate a competition in the proliferation of these two classes of repeats. As a matter of fact, *O. paniculata*, the closer species to the *Olea* common ancestor, presents very few tandemly-repeated sequences (as most plant species) while it is rich in LTR-retrotransposons, suggesting that the amplification of tandem repeats occurred after its speciation from the common ancestor of the other four species (which include the cultivated olive tree).

In conclusion, our research identified the temporal dynamics shaping the genome structure during the evolution of the genus *Olea*. This genus represents a very peculiar model of genome evolution in higher plants. Studies are in progress to estimate the intraspecifc variation of the repeat component, in order to decipher the possible role that tandem repeats played during the evolution of the olive genome.