

GENOMIC DYNAMICS OF OLIVE TREES IN THE MEDITERRANEAN BASIN: INSIGHTS FROM THE REPETITIVE COMPONENT EVOLUTION

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Understanding the processes of plant genome evolution is crucial for unravelling the complexities of species domestication, not only to provide insights into how organisms had adapted to human influence but also to anticipate how crops will respond to future global changes, enabling us to improve breeding programs.

One of the most iconic fruit trees in the Mediterranean basin is the olive tree. The cultivated olive (*Olea europaea* L. subsp. *europaea* var. *europaea*), besides being an economic pillar and cornerstone of Mediterranean agriculture, presents a fascinating case study in genome evolution. In fact, while it is generally accepted that polyploidization and amplification/loss of transposable elements are key factors determining genome structure in plants, the olive showcases a distinct pattern. Alongside these processes, there has been a notable expansion of the tandem repeated fraction in its genome, which encompasses several major families of satellites, accounting for nearly one third of the olive genome. This unique characteristic calls for further investigation into the dynamics of olive domestication in order to unravel the mechanisms that led to such genome structure and understand the potential functions of different types of repeated sequences.

Massively parallel sequencing technologies and advanced bioinformatic analyses were applied to 11 cultivars of olive and 11 oleaster from the Mediterranean Basin to study in detail the genomic dynamics that led to the presently cultivated olive genome.

Our analysis led to a fine characterization of the tandem repeat sequences and, in general, of the repeated fraction of the genotypes of olive. On average, repetitive DNA in *Olea europaea* genotypes ranges from 32.50 % to 41.40%, showing a remarkable difference in terms of abundance and composition. A total of 7 major families of tandem repeats was identified across the genotypes analyzed alongside a substantial number of LTR-retrotransposons from different lineages, showing an inverse correlation between the redundancy of tandem repeats and retrotransposons. Notably, this suggests a potential competition in the proliferation of these two repeat classes. Multivariate analysis of tandem and interspersed repeat abundance highlighted a clear separation between cultivars and oleasters, with an effect of the geographical origin on the latter group.

Finally, analyses of ancient DNA greatly enhanced our research to identify the temporal dynamics which shaped the genome structure during the evolution of the genus *Olea*, which represents a remarkable and peculiar model of genome evolution in higher plants.