
Preface

Olive (*Olea europaea* L., subsp. *europaea*, var. *europaea*), a multifunctional long-living tree crop, is relevant not only for table olive and oil production, but also for shaping and protecting the landscape and for its impact on human nutrition and rural lifestyle.

It is usually accepted that olive has been primarily domesticated in the Levant. Then, three main clusters of the var. *europaea* inside the primary gene pools have been identified for the cultivated olive in Eastern, Central, and Western Mediterranean. These centers of diversity likely reflect crop diversification from East to West, but could also result from independent domestications.

Gene exchanges between wild (*Olea europaea* L., subsp. *europaea*, var. *sylvestris*, named as oleaster) and cultivated olive have played a major role in the diversification of the crop. In the Mediterranean area, where minimum winter temperatures do not usually fall below -7°C , olive cultivation occupies 12 million hectares, representing about 95 % of total world olive cultivated area. Recently, its cultivation has spread to non-traditionally olive-growing countries, i.e., USA, Argentina, Chile, South Africa, and Australia, with intensive and super high-density systems, for which high productive, high oil producing, and low vigor varieties are required.

The *Olea* species belongs to the Oleaceae family that comprises nearly 25 genera and 600 species distributed in the temperate and tropical regions. In this family, plants are mostly evergreen trees, bushes, and vines, many of them producing essential oils in their flowers and fruits. The olive has a medium-sized genome (about 1.4 Gb), but the high number of chromosomes ($n = 23$), the large amount of the repetitive component ($>70\%$, made up by 30 % of tandem repeat sequences and 40 % of transposable elements), and the high level of heterozygosity have made very difficult the sequencing tasks and only a first draft of the olive genome sequence has recently been released.

The molecular bases underlying the phenotypic differences among cultivars still remain poorly understood. Nowadays, the acknowledged beneficial health properties of the extra-virgin olive oil and the ability of the species to produce under harsh conditions (e.g., drought stress) have provided new impulses for introducing innovation through olive genomics and breeding, leading to a deeper understanding of the biological processes underlying oil accumulation, polyphenol synthesis, adaptation to environmental constraints,

and response to threatening epidemics by biological agents. The ‘omics’ studies have particularly been useful to unravel the intricacy of main biochemical pathways and to characterize genes involved in the expression of complex traits.

Information about olive phylogeny, domestication, and relationships with related wild forms represents a fundamental prerequisite for the genetic improvement of the species, allowing for the introgression of important alleles from oleaster or from other *O. europaea* subspecies. The intercompatibility between cultivated olive and related forms has been analyzed for numerous subspecies, resulting compatible with the subsp. *cuspidata*, *laperrinei* and tetraploid *cerasiformis*, while a pre- or post-zygotic incompatibility has been observed in other cases (e.g., *ferruginea* and *Olea capensis*, respectively). The in vitro techniques now available may overcome these intercross limitations, opening the road toward new hybridization approaches.

Although the poor knowledge available on the genetic basis of the main olive characters, the lack of sound QTL markers, the limited experience on gene-transfer technologies, and the long generation interval, significant programs of genetic improvement may be undertaken profiting of the new information rising from biotechnology and genomics research. Harnessing innovations in these two research fields will help the development of fast-track breeding procedures, to improve important economical and agro-nomical traits, shorten the prefruiting period, and increase the selection efficiency of the designed new olive varieties through the cloning and genotyping of in vitro germinated embryos or developed seedlings.

Topics of this book cover the description of olive genetic resources, the classical and modern breeding methods for releasing new cultivars, the genotype/environment interactions determining the response to biotic and abiotic stresses, the fruit metabolism related to oil production and synthesis of health beneficial molecules, the mapping of genes and QTLs, the genome sequencing, and the transcriptomic and proteomic strategies pertinent to the development of molecular platforms and templates amenable to the precise and rapid genetic modifications using the recently developed genome-editing tools.

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