
Compendium of Plant Genomes

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Eddo Rugini · Luciana Baldoni
Rosario Muleo · Luca Sebastiani
Editors

The Olive Tree Genome

 Springer

Editors

Eddo Rugini
DAFNE
University of Tuscia
Viterbo
Italy

Rosario Muleo
DAFNE
University of Tuscia
Viterbo
Italy

Luciana Baldoni
Institute of Biosciences and Bioresources
National Research Council
Perugia
Italy

Luca Sebastiani
Scuola Superiore Sant'Anna
Pisa
Italy

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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 agronomical 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.

Viterbo, Italy
Perugia, Italy
Viterbo, Italy
Pisa, Italy

Eddo Rugini
Luciana Baldoni
Rosario Muleo
Luca Sebastiani

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Abbreviations

ABA	Abscisic acid
AChE	Acetylcholinesterase
ADH	Alcohol dehydrogenase
AFLP	Amplified fragment length polymorphism
ArMV	Arabidopsis mosaic virus
ATT	Alcohol acetyl transferases
BCA	Biological control agent
BSseq	Bisulfite sequencing
CAP	Common Agrarian Policy
CDD	Cumulated degree day
cDNA	Complementary DNA
ChIPseq	Chromatin immunoprecipitation sequencing
CLRV	Cherry leaf roll virus
cM	centiMorgan
CMV	Cucumber mosaic virus
CoDiRO	Complesso del disseccamento rapido dell'Olivo
cpDNA	Chloroplast DNA
DAF	Days after flowering
DArT	Diversity arrays technology
dsRNAs	Double-stranded RNA
Ece	Saturated paste extract
Eco-TILLING	Targeting-induced local lesions in genomes
EFSA	Commission of the European Food Safety Authority
ELISA	Enzyme-linked immunosorbent assay
EST	Expressed sequence tag
EU	European Union
EVOO	Extra-virgin olive oil
FAD	Fatty acid desaturase
FAO	Food and Agriculture Organization
FsRIDL	Female-specific release of insects carrying a 'Dominant Lethal'
GBS	Genotyping by sequencing
GP	Gene pool
GSI	Gametophytic self-incompatibility
GWAS	Genome-wide association study
HD	High density
IAA	Indole-3-acetic acid
IBA	Indole-3-butyric acid

IOGC	International olive genome consortium
IOC	International olive council
ISSR	Inter-simple sequence repeat
JERF	Jasmonate and ethylene response factor
LAI	Leaf area index
LA	Linoleic acid
LDR-UA	Ligation detection reaction-universal array
LG	Linkage group
LnA	Linolenic acid
LN	Liquid nitrogen
LOX	Lipoxygenase
MAS	Marker-assisted selection
MFO	Mixed function oxidase
MS	Murashige and Skoog (medium)
NAA	Naphthalene acetic acid
NaCl	Sodium chloride
NGS	Next-generation sequencing
nsSNPs	Non-synonymous single nucleotide polymorphisms
OCWE	Olive crop wild relatives
OLF	Olive fly
OLRV	Olive latent ring spot virus
OLS	Olive leaf spot
OLV-3	Olive latent virus
OLYaV	Olive leaf yellowing-associated virus
OM	Olive medium-Rugini olive medium
OMMV	Olive mild mosaic virus
Ops	Organophosphates
OQDS	Olive quick decline virus
OSLV	Olive semi-latent virus
OWGB	Olive World Germplasm Bank
OYMDaV	Olive yellow mottle and decline-associated virus
PCD	Programmed cell death
PCR	Polymerase chain reaction
PDO	Protected designation of origin
PEG	Polyethylene glycol
PGIP	Polygalacturonase-inhibiting protein
PGI	Protected geographic identification
PPM	Plant preservative mixture
PR	Pathogen-related protein
PrsS	Pistil S determinant
PSII	Photosystem II
PVS1	Plant vitrification solution 1
PVS2	Plant vitrification solution 2
QTL	Quantitative trait loci
RAPD	Random amplified polymorphic DNA
RFLP	Restriction fragment length polymorphism
RIDL	Release of insects carrying a 'Dominant Lethal'
RNAseq	RNA sequencing
ROS	Reactive oxygen species

RWC	Relative water content
SA	Salicylic acid
SCAR	Sequence characterized amplified region
SCR	S-locus cysteine rich protein
SHD	Super high density
SIT	Sterile insect technique
SLG	S-locus glycoprotein
SLRSV	Strawberry latent ring spot virus
SNP	Single nucleotide polymorphism
SRK	S-locus receptor kinase
SSH	Suppression subtractive hybridization
SSR	Simple sequence repeat
TDZ	Thidiazuron
TF	Transcription factor
TG	Taxon group
TNA	Total nucleic acid
TNV-D	Tobacco necrosis virus D
UNESCO	United Nations Educational, Scientific and Cultural Organization
VOCs	Volatile organic compounds
VOO	Virgin olive oil
VWO	Verticillium wilt of olive
Wt	Wild type
WUE	Water use efficiency
Xf	<i>Xylella fastidiosa</i>