

1. Record Nr.	UNINA9910156337203321
Titolo	The Olive Tree Genome // edited by Eddo Rugini, Luciana Baldoni, Rosario Muleo, Luca Sebastiani
Pubbl/distr/stampa	Cham : , : Springer International Publishing : , : Imprint : Springer, , 2016
Edizione	[1st ed. 2016.]
Descrizione fisica	1 online resource (XI, 193 p. 42 illus., 35 illus. in color.)
Collana	Compendium of Plant Genomes, , 2199-4781
Disciplina	572.86
Soggetti	Plant breeding Plant genetics Agriculture Plant Breeding/Biotechnology Plant Genetics and Genomics
Lingua di pubblicazione	Inglese
Formato	Materiale a stampa
Livello bibliografico	Monografia
Nota di bibliografia	Includes bibliographical references at the end of each chapters.
Nota di contenuto	Economical/Academic importance Shimon LAVEE -- Biology of the species (botanical description, taxonomy, growth, reproduction, cytology, etc.) -- Genetic resources -- Olive origin and domestication -- Plant-environment interactions - abiotic interactions -- Plant-environment interactions - biotic interactions -- Fruit and oil metabolomics - health compounds.
Sommario/riassunto	This book provides an introduction to the genetics, genomics, and breeding of the olive tree, a multi-functional long-lived crop plant that is relevant not only for culinary olive and oil production, but also for shaping the landscape and history of many rural areas for centuries. Today, the recognized health benefits of extra-virgin olive oil provide new impulses for introducing innovation in olive crop management and olive breeding for a deeper understanding of the biological processes underlying fruit quality, adaptation to crop environment and response to threatening epidemics due to biological agents such as Xylella fastidiosa. The individual chapters discuss genetic resources; classic and modern breeding methods for providing new olive cultivars; the genotype x environment interactions determining the response to

biotic and abiotic stresses; fruit metabolism related to oil production and the synthesis of health beneficial molecules; the mapping of genes and quantitative trait locus; and genomic, transcriptomic and proteomic strategies pertinent to the development of a molecular platform and template amenable to precise and rapid genetic modifications using recently developed genome editing tools.

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