

Series on
Genetics, Genomics and Breeding of Crop Plants

Series Editor
Chittaranjan Kole, Clemson University, Clemson, SC, USA

Genetics, Genomics and Breeding of Stone Fruits

Editors
Chittaranjan Kole • Albert G. Abbott



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ABOUT THE SERIES

Basic and advanced concepts, strategies, tools and achievements of genetics, genomics and breeding of crops have been comprehensively deliberated in 30 volumes each dedicated to an individual crop or crop group.

The series editor and one of the editors of this volume, Prof. Chittaranjan Koie, is globally renowned for his pioneering contributions in teaching and research for nearly three decades on plant genetics, genomics, breeding and biotechnology. His works and edited books have been appreciated by several internationally reputed scientists including six Nobel Laureates for the impact of his publications on science and society.

ABOUT THE VOLUME

The stone fruits, including peaches, apricots, almonds, plums and cherries, have been bred and grown for thousands of years and today are significant agricultural crops in many local economies worldwide providing important components to healthy diets. This volume, comprising 14 chapters authored by 37 scientists from 7 countries, presents a comprehensive commentary on classical genetics and breeding; molecular mapping and breeding of agronomic traits; cloning of genes of interest; recent advances on 'omics' sciences including structural and functional genomics, proteomics and metabolomics with an enumeration on the whole genome sequencing of the model fruit plant peach; and application of bioinformatic strategies and tools for stone fruit research.

ABOUT THE EDITOR

Albert Abbott is a world renowned plant molecular geneticist working primarily on fruit and forest tree genetics and genomics. He has been a leader in efforts to promote research devoted to understanding the underlying genetic foundations of both basic tree biology and traits that are critical to sustaining and improving our tree resources. His own research efforts have centered on developing the peach [*Prunus persica* (L.) Batsch] as a model tree genome species focusing on development of genomic and genetic resources for the species, as well as investigating genetic networks involved in phenological as well as agriculturally important traits. Presently, he is working to translate genomic information in peach to other fruit and forest tree species through cooperative research investigations with the Rosaceae research community and the international forest tree research communities. He holds the Coker Endowed Research Chair in Plant Molecular Genetics at Clemson University and currently is also an ANR Chaire d'Excellence at the INRA-Bordeaux, France.

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6000 Broken Sound Parkway, NW
Suite 300, Boca Raton, FL 33487
711 Third Avenue
New York, NY 10017
2 Park Square, Milton Park
Abingdon, Oxon OX14 4RN, UK

Functional Genomics: Transcriptomics

Livio Trainotti,^{1,*} Stefano Cagnin,^{1,2} Claudio Forcato,²
Claudio Bonghi,³ Amit Dhingra,⁴ Tyson Koepke,⁴ Loreto Prat,⁵
Jonathan Maldonado⁵ and Herman Silva^{5,*}

ABSTRACT

Transcriptomics approaches in the *Prunus* genus started to be developed since the beginning of the new century. In few years, a set of tools have been developed and used, mainly in peach, apricot and almond. Transcriptomics tools have been primarily used to investigate fruit ripening and post-harvest physiology, but also disease resistance and flower transition. At the beginning of the second decade of the century, more than 100,000 ESTs are available in public databases, the majority of which were obtained from peach fruit. This repertoire has been used for digital expression analyses of transcriptome changes associated with fruit ripening and the appearance of chilling-induced post-harvest fruit disorders. The microarrays developed on peach ESTs have been extensively used mainly to investigate fruit biology but are soon going to be replaced by genome-wide platforms based on the recently released peach genome sequence. Transcriptome profiling based on second generation DNA sequencing (SGS) technologies are also expected

¹Department of Biology, University of Padova, Via U. Bassi 58/B, 35121 Padova, Italy.

²CRIBI Biotechnology Centre, University of Padova, Via U. Bassi 58/B, 35121 Padova, Italy.

³Department of Environmental Agronomy and Crop Science, University of Padova, Agripolis, Legnaro (PD) 35020, Italy.

⁴Department of Horticulture and Landscape Architecture and Molecular Plant Sciences Graduate Program, Washington State University, PO BOX 646414, Pullman, WA 99164, USA.

⁵Millennium Nucleus in Plant Cell Biotechnology and Functional Genomics & Bioinformatic Lab, Departamento de Producción Agrícola, Facultad de Ciencias Agronómicas, Universidad de Chile, Av. Santa Rosa 11315, 8820808 La Pintana, Casilla 1004, Santiago, Chile.

*Corresponding authors: livio.trainotti@unipd.it; hesilva@uchile.cl