
Preface

The kiwifruit (*Actinidia chinensis* var. *chinensis*/*A. chinensis* var. *deliciosa* complex, with diploid, tetraploid and hexaploid races) is one of the most recently domesticated fruit crops. Native to China, like most taxa of the genus *Actinidia*, the kiwifruit was introduced to New Zealand as seed in 1904. By the 1930s small orchards were established and in the 1960s its fruit became known to western consumers. Growers of the world's temperate regions introduced its cultivation to their own countries leading to a rapid expansion of this crop that currently accounts for ca. 200,000 hectares with nearly 3 million tons of fruits produced annually. Kiwifruit is now cultivated also in its homeland, China: indeed, China produces more kiwifruits than any other country.

The genome of a *A. chinensis* var. *chinensis* genotype was sequenced in 2013 by a Chinese team (Huang et al. Nature Communications 4:2640), following the classical procedures that brought analogous achievements in other crops: development of markers and genetic maps, large EST collections, and finally whole-genome sequencing based on Next Generation Sequencing platforms.

The draft sequence has a total length of 616.1 MB and contains 39,040 annotated genes, an unusually high number that indicates repeated polyploidization of this species. Analysis of the genome structure has indeed revealed ancient polyploidization events shared by core eudicots and two more recent whole-genome duplications, which occurred after the divergence of kiwifruit from tomato and potato. The assembly of the diploid ($x = 29$) kiwifruit genome was challenging not only because of the multiple chromosomal copies but also because of the dioecy of the species that implies high genome heterozygosity. In the absence of haploids, seemingly never described in this species, the production of well-saturated genetic maps based on genotype-by-sequencing protocols together with resequencing of a number of genotypes are improving the genome assembly.

This book starts with a description of the basic botanical features of kiwifruit and its wild relatives, then reports on the steps that led to the genome sequencing and discusses the results obtained with the assembly and annotation. The book has been planned and is intended as a tool for taxonomists, biologists, horticulturists, geneticists, and especially for breeders. For this reason, the core chapters are dedicated to a description of the main gene families that characterize this species as a crop, including genes

controlling sugar and starch metabolism, pigment biosynthesis and degradation, the ascorbic acid pathway, fruit softening and postharvest metabolism, and allergens.

Being a book specially intended as a guide for kiwifruit breeders, the last chapters are dedicated to gene introgression from wild relatives and genome-based breeding, in the belief that information from the genome sequence may be an extraordinarily useful tool for the evaluation of the breeding value of individuals based on whole-genome scans.

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The Kiwifruit Genome

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2016, XV, 269 p. 55 illus., 38 illus. in color., Hardcover

ISBN: 978-3-319-32272-8