
Preface

Radish (*Raphanus sativus* L.) is an important vegetable in East Asia, e.g., Japan, China, and Korea, but not so much in Europe, America, Africa, or Oceania. Therefore, studies on radish are predominantly performed by Asian researchers, and not by Europeans or Americans. In the East Asia, radish roots are thick, long, and mostly white, whereas those are tiny and mostly red in Europe. The East Asian type is called East Asian big long radish, white radish, or daikon (in Japanese), and the European radish type is called European small radish or European garden radish. In this e-book, we use terms “Asian big radish” and “European small radish” for them. In Asian big radish, there is a great variation in root size and shape, especially in Japanese radish. In Southeast Asia, pods are consumed as a vegetable, and seeds are used as oil seeds. On the other hand, *Raphanus raphanistrum*, a species in the same genus as radish, is a serious weed in America and Australia, but not so much in Asia. The recent globalization will change the food culture, and Asian big radish may become an important vegetable in the western countries.

Radish is closely related to the genus *Brassica*, which contains many important crops such as rapeseed, cabbage, broccoli, Chinese cabbage, turnip, and mustard. Genetic and genomic studies of *Brassica* have been intensively carried out, but these studies of radish have been left behind those of *Brassica*. Phylogenetic relationship of radish with *Brassica* species is not established. Although radish is crossable with *R. raphanistrum* and hybrids between radish and *R. raphanistrum* are fully fertile, they have different species names. Asian wild radish growing at seashores is *R. sativus* var. *raphanistroides*. Relationships between the wild radish and cultivated radish are controversial. Besides the importance of radish as a crop itself, radish and wild radish are important genetic resources for breeding of *Brassica* crops.

Development of the next-generation sequencers accelerated whole-genome sequencing of many crop species. Two groups in Japan and one Korean group carried out the whole-genome sequencing of radish independently. Although the group of Tohoku University and Kazusa DNA Research Institute, where high-density linkage maps of DNA markers were constructed to form a standard linkage map, published a draft genome sequence of radish first, the other Japanese group and the Korean group published radish genome sequences with more data soon after that. These genome sequence data will contribute to identification of genes important for breeding of radish and

Brassica crops. Since these three groups joined in publishing this e-book, we hope this cooperative book publication accelerates collaboration of them for integration of three radish genome sequences to make a standard reference genome sequence of radish.

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The Radish Genome

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