
Preface

Brassica rapa is a crop species of the genus *Brassia*, which belongs to the plant family Brassicaceae (Cruciferae). It has ten chromosomes ($2n = 20$) and is widely cultivated as oil and vegetables crop across the world. It is also one of the basic species of the other two widely cultivated crops *Brassica napus* and *Brassica juncea*. Owing to its close relationship to the model species, *Arabidopsis* and relatively smaller genome size among the *Brassica* species, it was identified as the first *Brassica* species to be sequenced by the BrGSP. The consortium developed a plan based on the experience of *Arabidopsis* genome sequencing by using BAC to BAC strategy and a complete chromosome A03 was assembled by a Korea team using this traditional sequencing technology. However, the project was finally completed by using the second generation sequencing technology, which adopted completely different assembling strategies from that of traditional Sanger sequencing. The reporting of the whole genome sequence of *B. rapa* in 2011 was a milestone in the field of *Brassica* research. It was the first example of a complex genome with recent whole genome duplication (WGT) that was assembled using short sequencing reads generated by second generation sequencing technology. The assembly covered $\sim 98\%$ of the gene region or 60% of the ~ 500 Mb genome of *B. rapa* and the 40% unassembled sequences were mainly due to the highly repetitive nature of this portion of the genome. With this genome assembly, dedicated tools were developed not only to compare—at the whole genome level—with the extensively studied *Arabidopsis* genome, but also to transfer the rich research information from the model plant to a cultivated crop. We thus could investigate the whole genome detail of the WGT event in the *Brassica* genome now. The subgenomes of *B. rapa* are not equally important. One of the three subgenomes generated from WGT has not only more genes, but also a higher gene expression level over the other two. Such a subgenome dominance phenomenon leads to a hypothesis that the WGT event was occurred through a two-step duplication process. Although the genome of *Arabidopsis* was frequently used to compare with the *Brassica* genome, it was inferred from the *B. rapa* genome that the direct diploid ancestor of *Brassica* has a genome structure of the translocation Proto-Calepineae Karyotype (tPCK), which is the same as for the extant species *Schrenkiella parvula*. The WGT created large number of duplicated genes which may evolve interactively and even concertedly through homoeologous recombination. It was detected that 8%

of these duplicated genes were converted by one another after the divergence of *B. rapa* and *Brassica oleracea*. The release of the *B. rapa* genome reference promoted genome evolution research and facilitates gene discovery and functional studies, as well as the breeding of *Brassica* crops. However, the quality of the genome assembly still has room for improvement and the accuracy of the annotation will be increased with the accumulation of more mRNA-Seq data, and more tools and resources need to be established to help the breeders using the genomic data.

Xiaowu Wang

The Brassica rapa Genome

Wang, X.; Kole, C. (Eds.)

2015, VIII, 169 p. 38 illus., 36 illus. in color., Hardcover

ISBN: 978-3-662-47900-1