



Editorial

Harvesting Knowledge: Illuminating Advances in *Brassica* Crops Genomics and Breeding

Xu Cai , Jian Wu * and Xiaowu Wang *

Institute of Vegetables and Flowers, Chinese Academy of Agricultural Sciences, No. 12, Haidian District, Beijing 100081, China; caixu@caas.cn

* Correspondence: wujian@caas.cn (J.W.); wangxiaowu@caas.cn (X.W.)

Brassica crops encompass a diverse array, including vegetables, oil crops, ornamentals, and condiments. In particular, some *Brassica* crops such as turnip, Chinese cabbage, cabbage, and rapeseed have solidified their status as global agricultural cash crops. Beyond their economic significance, *Brassica* species stand out due to the domestication of extreme morphological types, offering a distinctive spectrum of leafy heading, root/stem enlarging, and florescence heading. Moreover, the occurrence of polyploidization events within *Brassica* species positions them as ideal models for investigating the complexities of polyploidization. With these distinctive features, research on *Brassica* crops has remained a hot research area. In the ever-evolving landscape of agricultural research, the Special Issue (SI) on “Advances in *Brassica* Crops Genomics and Breeding” emerges as a crucial guide for understanding the key research trends in the genomics and breeding of *Brassica* crops.

Genomic Exploration: The rapid progress in sequencing technologies has propelled *Brassica* crops into the genomic spotlight. Numerous genomes of *Brassica* crop species have been meticulously sequenced, yielding high-quality chromosome-scale assemblies. This groundbreaking achievement has been complemented by the availability of large-scale resequencing data of germplasm resources in *B. rapa*, *B. oleracea*, *B. juncea*, and *B. napus*. This wealth of data empowers researchers with the tools necessary for genome-wide association studies (GWAS) and domestication analyses, unlocking the genetic mechanisms embedded for the agricultural traits of these vital crops. One feature paper [1] conducted a reanalysis of previously published resequencing data encompassing various *B. rapa* morphotypes. It revealed a significant biased distribution of haplotypes for variations on *BrFLC1* across diverse population accessions, including turnip, Chinese cabbage, Pak choi, Caixin, Wutacai, and Taicai. This observation implies a close association between the evolutionary patterns of *BrFLC1* haplotypes and the dissemination of different *B. rapa* morphotypes, highlighting the vital role of natural variation in the diversification of *Brassica* crops.

Functional Genomics: One of the primary objectives of the *Brassica* community is to showcase the functional aspects of important genes within *Brassica* crops. The investigation into complex *Brassica* genomes extends beyond mere sequencing, seeking to reveal the functions of key genes that contribute to the adaptability and unique characteristics of these crops. The intersection of genomics and functionality provides a holistic understanding that is pivotal for informed breeding strategies. Nine research papers, exploring various aspects of *Brassica* crops, contribute valuable insights into their genetic regulation, stress responses, and biochemical composition of *Brassica* crops. The featured analyses cover a diverse range of topics, including exploring the regulatory role of miR398a and its target gene *BraCSD1-1* in Chinese cabbage’s response to heat stress [2], uncovering the significance of *BnA.JAZ5* in *B. napus* and highlighting its key role as a genetic regulator in drought stress [3], and investigating the involvement of *PARP1* in *B. rapa*’s response to drought stress, with a specific emphasis on its impact on root growth and stress-related gene expression [4]. Additionally, the issue delves into the effects of TuMV on *B. rapa*, conducting detailed analyses of the volatile metabolome and transcriptome in resistant and



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susceptible lines [5]. The physiological and biochemical responses in *B. juncea* cultivars under drought stress influenced by brassinolide are explored as well [6]. Furthermore, there is an analysis of the poorly understood group of enzymes, *BrPAPs*, in *B. rapa*, with a focus on their roles and potential implications [7]. Other studies identify a key mutation (Pe1 + 58) in the *BrFLC1* gene that impacts flowering time variation in *B. rapa* [1], explore the glucosinolate (GSL) profile of *B. nigra*, and emphasize the identification of sinigrin as the predominant GSL [8]. Lastly, the issue investigates pollen abortion and abnormal development in Chinese cabbage under Ogura CMS, providing comprehensive insights [9]. Collectively, these studies contribute to advancing our understanding of *Brassica* crops, encompassing genetic mechanisms, stress responses, and biochemical characteristics.

Molecular Marker-Assisted Breeding: Advancements in genomics are not confined to the laboratory; they have a tangible impact on the field through molecular marker-assisted breeding. It is very important to explore how the fusion of genomics and breeding is accelerating the development of *Brassica* cultivars with enhanced traits. This marks a transformative era in agriculture, where precision breeding aligns with the specific needs of farmers and global food security. The SI features three papers, each focusing on essential aspects of genetic mapping and improvement in *B. rapa*. The first paper places a primary emphasis on constructing a comprehensive genetic map with 105 intragenic SSR markers distributed across 10 linkage groups [10]. This map serves as a valuable resource, providing insights into the intricate genetic architecture governing essential agronomic traits in Chinese cabbage. The research identified 48 QTLs associated with various traits, offering significant contributions to molecular breeding and marker-assisted genetic enhancement initiatives for Chinese cabbage accessions. The second paper highlights the successful application of molecular marker-assisted gene pyramiding and backcrossing techniques to improve Chinese cabbage accessions. This study stands out for its focus on integrating self-compatibility, multilocular ovaries, and resistance to clubroot through precise molecular marker identification [11]. Together, these papers contribute to advancing genetic knowledge and practical applications for the genetic improvement of Chinese cabbage. The third paper maps 102 QTLs associated with biochemical traits, primarily located on the fifth, sixth, seventh, and ninth linkage groups [12]. These findings offer insights for genetic and breeding work, aiding in the development of genotypes with desirable biochemical compositions adapted to specific photoperiodic conditions through marker-assisted selection in *B. rapa*.

Additionally, a review is focused on discussing the emerging use of rapeseed (*B. napus*) as an ornamental crop, particularly in China where tourism centered around fields of blooming yellow flowers has become an economic opportunity [13]. Additionally, there is a paper that addresses the crucial issue of seed quality in vegetable production. Employing instrumental automated methods, the study specifically focuses on the digital X-ray analysis of seeds from *B. oleracea*, *Raphanus sativus*, and *Lepidium sativum* [14]. These works are of particular interest to breeders of *Brassica* crops.

Conclusion: “Advances in *Brassica* Crops Genomics and Breeding” shows the collective efforts of researchers unraveling the genetic intricacies of *Brassica* crops. From the economic significance of these diverse crops to the exploration of their complex genomes, these research findings will contribute to advancements in breeding research on *Brassica* crops. As we glean insights from the latest breakthroughs in genomics and breeding, the future of *Brassica* crops appears brighter, promising enhanced productivity, adaptability, and nutritional value.

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