



Advances in Molecular Breeding of Vegetable Crops

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Abstract: Molecular vegetable breeding has been progressed intensively in recent years. Huge advances have been made in germplasm evaluation, gene isolation, plant transformation, gene editing and molecular-marker-assisted breeding. The goal of this Special Issue is to highlight, through selected works, frontier research from basic to applied molecular vegetable breeding. The selected papers published in Special Issue of *Horticulturae* exhibit a diversity in molecular vegetable breeding. The papers listed in this editorial are especially noteworthy.

1. Advances in Gene Editing in Context of Vegetable Molecular Breeding

In recent years, it has become certain that genome editing is an efficient and powerful tool for precise genome manipulations in plants. For applications in molecular vegetable breeding, this new technique overcomes the shortcomings of conventional breeding, such as long-term artificial selection and limited genetic germplasm resources [1,2]. Wan et al. reviewed the development and application of CRISPR-Cas9 gene editing in vegetable crops. Currently, this system has been used to improve shelf life, fruit quality and stress resistance in major vegetable crops, such as tomato and cabbage. In the case of broccoli, genome editing has succeeded in limited *B. oleracea* crops [3]. Although the application of genome editing is extensive, how to obtain germplasm resources through gene editing of CREs (Cis-regulatory elements) and create a universal regeneration system for vegetable crops needs to be further studied and improved [1,4].

2. Germplasm Diversity Evaluation for Vegetable Improvement

In the modern breeding process, the evaluation of genetic diversity in agronomic and quality traits is still a fundamental method and approach for germplasm utilization and excavation. Uddin et al. performed phenotypic characterization and genetic diversity evaluation of 130 local eggplant germplasms [5]. Based on an analysis of trait variance, correlation matrix and MGIDI index, numerous traits were evaluated to determine the inherent variation and select applicable parents for eggplant improvement.

Simple sequence repeats (SSRs) are widely used genetic markers for genetic variation research in various crops due to co-dominance traits and high polymorphism. Zhong et al. employed this sequencing technology in *Capsicum frutescens* to provide resources of SSR molecular markers and analysis genetic diversity for pepper breeding [6]. Genome-wide identification of SSR markers revealed that trinucleotides were the dominant repeat motif. A total of 147 collected pepper cultivars were determined, clustered into seven main groups due to genetic diversity and phylogenetic relationships analysis. In *Cucurbita moschata*, 103,056 SSR loci were found by in silico PCR in which di-nucleotide motifs were the most common type [7]. Synteny analysis of cross-species SSR markers indicated that the main syntenic relationships between *Cucurbita* species were highly conserved during evolution.

3. Understanding the Genetic Basis of Biotic Resistance in Vegetable Crops

Fungal diseases remain challenges restricting the sustainable development of vegetable production. Although pesticides can prevent and control fungal diseases, excessive



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use of pesticides has brought great damages to the environment and human beings. Improving disease resistance has become an important breeding objective. The development and establishment of molecular marker technology makes it fast and effective to select germplasm resources directly.

The development of molecular markers associated with resistance to gray mold disease in onion (*Allium cepa* L.) through RAPD-PCR was assessed by Kim et al. [8]. RAPD analysis was performed to identify the genetic relationship between the resistant and susceptible lines and develop the SCAR marker. In addition, RNA-seq of the gray mold-resistant and -susceptible onion lines were analyzed to develop a selectable marker for the resistant line.

Phytophthora blight is a common disease that causes decreased yield and quality in pepper (*Capsicum annuum* L.). Li et al. generated a high-resolution genetic map of pepper associated with resistance to *Phytophthora capsici* by SLAF-seq and QTL analysis [9]. *CQPc5.1* was identified as a major quantitative trait locus (QTL) for the *P. capsici* resistance, including 23 candidate genes located within the interval.

4. Mining Genes Responsible for Abiotic Stresses for Vegetable Improvement

In vegetable crops, abiotic stresses cause serious damages, which limit growth and affect physiological metabolic processes. Therefore, screening genes responsible for abiotic stresses is essential to breeding resistant varieties. Pepper is sensitive to high temperatures, which leads to severe symptoms, such as pollination failure, growth defects and other aspects. Wang et al. identified differential expression genes in pepper leaves through a transcriptomics analysis of heat-tolerant and heat-sensitive varieties [10]. Heat shock (HS) proteins and HS transcription factors were identified as responsive to heat stress or recovery.

A small heat shock protein *CaHSP18.1a* was isolated and characterized from pepper [11]. Liu et al. demonstrated that *CaHSP18.1a* was sensitive to heat stress and showed high expression levels in thermo-tolerant line. The silencing of *CaHSP18.1a* caused elevated MDA contents and decreased resistance to heat, drought, and salt stresses, indicating that *CaHSP18.1a* positively regulates abiotic tolerance.

In eggplant, the genome-wide identification of *Hsf* and *Hsp* genes under heat stress was assessed by Gong et al. [12]. RNA-seq analysis showed that *Hsf* and *Hsp* genes exhibit different expression levels in the thermotolerant line 05-4 and the thermosensitive line 05-1, providing a basis for studying the relationship between thermotolerance and heat-response genes.

Nowadays, the irrational use of nitrogen fertilizer has resulted in undesirable growth and reduced yield in pepper. The molecular basis underlying the genetic variation in N-use efficiency (NUE) remains largely unknown. Based on comparative transcriptome analysis, Wang et al. selected two genotypes with contrasting low-N tolerance to explore the variation in NUE in pepper [13]. Numerous DEGs involved in N metabolism or other physiological processes were identified, providing candidate genes for improving N utilization in pepper.

5. Organic Compounds in Vegetables and Its Interaction with Environment

Flavonoids and volatile organic compounds act as important roles in the growth and developmental processes of vegetable crops, including the attraction of insect pollination, the inhibition of plants diseases and improvement in weed control.

In broccoli, anthocyanins contribute to the purple color and act as health-promoting antioxidants. Liu et al. identified major loci and candidate genes responsible for anthocyanin biosynthesis in broccoli [14]. Two QTLs on chromosomes 7 were identified to be tightly correlated with anthocyanin biosynthesis based on QTL-seq bulk segregant analysis. Further high-resolution mapping identified 14 candidate genes, providing a potential molecular marker into the breeding of novel varieties with abundant anthocyanins.

Volatile organic compounds released from plants are related to the allelopathy phenomenon, a chemical relationship of plant interaction. Xie et al. reviewed the recent advances in the allelopathy of volatile organic compounds (VOCs) of plants [15]. VOCs

had multiple allelopathic effects on plants, such as enzyme activity, dormancy, diseases resistance, ROS scavenging, plant-to-plant communication, and other aspects [15]. The research suggested that the allelopathy of VOCs can be utilized in the development of economical and effective measures for sustainable agriculture [15].

With germplasm evaluation, gene isolation, and marker development, both scientists and breeders are working closely to generate more efficient breeding technology, e.g., gene editing, and to produce more elite cultivars. With emerging substantial genomic data and tools, further collaboration is worthwhile for next-generation breeding technology, e.g., genome-based breeding by design, to generate green, environmentally adaptive vegetable cultivars with high yield and quality.

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