



Vegetable Crops Improvement by Molecular Approaches

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Abstract

Molecular vegetable breeding is a technique that merges conventional breeding methods with contemporary molecular biology techniques to generate enhanced vegetable cultivars with desirable characteristics such as increased yields, improved nutritional composition, resistance to diseases and pests, tolerance to environmental pressures, and enhanced flavour profiles. Recent advancements in gene editing have transformed genome editing into a very effective method for accurately manipulating the genetic makeup of plants, beyond the limitations of traditional breeding techniques. CRISPR-Cas9 gene editing has been used to enhance the longevity, fruit characteristics, and ability to withstand stress in prominent vegetable crops such as tomato and cabbage. Additional research is required to acquire germplasm resources and develop a universally applicable regeneration method for vegetable crops. Evaluating the variety of germplasm is a crucial approach for using and exploring germplasm. Gaining knowledge about the genetic foundation of biotic resistance in vegetable crops is crucial for the long-term sustainability of vegetable production. The development of molecular marker technology enables direct selection of genetic resources, but additional study is required to enhance disease resistance and optimise crop output. The Special Issue of Horticulture focuses on advancements in molecular vegetable breeding, including a wide range of research that include gene editing and the examination of genetic foundations for both biotic and abiotic stressors. Abiotic stressors have detrimental effects on vegetable crops, impeding development and disrupting physiological metabolic processes. Identifying the genes responsible for abiotic stressors is crucial for developing resistant cultivars via breeding. The finding of Hsf and Hsp genes in eggplant's genome under heat stress serves as a foundation for investigating the connection between thermo tolerance and heat-response genes. The presence of anthocyanin in broccoli is responsible for both its purple colour and its health-promoting antioxidants. The use of volatile organic compounds (VOCs) in allelopathy may contribute to the development of cost-effective and efficient strategies for sustainable agriculture. The cooperation between scientists and breeders is crucial for the development of advanced breeding technology, which aims to produce environmentally resilient vegetable cultivars with high productivity and quality.

Keyword- Molecular vegetable breeding, Molecular Marker, Anthocyanin, CRISPR-Cas9 gene editing

Introduction

Molecular vegetable breeding is an advanced strategy that combines conventional breeding procedures with contemporary molecular biology approaches to improve the effectiveness

and accuracy of creating new vegetable types. This novel strategy utilises our knowledge of plant genetics and genomics to expedite the breeding procedure, resulting in the development of enhanced vegetable varieties with desirable characteristics such as increased productivity, enhanced nutritional value, resistance to diseases and pests, tolerance to environmental pressures, and improved flavour profiles.

Advances in Gene Editing in Context of Vegetable Molecular Breeding

Genome editing has emerged as a reliable and potent technique for accurately manipulating the genetic makeup of plants. This novel strategy addresses the limitations of traditional breeding methods, such as prolonged artificial selection and restricted genetic germplasm supplies, in the context of molecular vegetable breeding applications. Examined the progress and use of CRISPR-Cas9 gene editing in vegetable crops.

Presently, this approach has been used to enhance the longevity of produce, the calibre of fruits, and the ability of main vegetable crops, such as tomato and cabbage, to withstand stress. Genome editing has achieved success in a restricted range of B. oleracea crops, namely in the case of broccoli. While the use of genome editing is widespread, there is a need for more research and improvement in obtaining germplasm resources via gene editing of Cis-regulatory elements (CREs) and developing a universal regeneration system for vegetable crops.

Germplasm Diversity Evaluation for Vegetable Improvement

Genetic diversity assessment is a crucial tool in the contemporary breeding process for utilising and exploring germplasm in agriculture. In this study, we conducted phenotypic characterisation and genetic diversity evaluation of 130 local aubergine germplasms. The inherent variation of various attributes was determined and eligible parents for aubergine enhancement were selected based on an examination of trait variance, correlation matrix, and MGIDI index. Simple sequence repeats (SSRs) are commonly utilised genetic markers in crop research to study genetic variation. These markers are favoured for their co-dominant nature and high level of polymorphism. In this study, we applied sequencing technology to *Capsicum frutescens* to generate a collection of SSR molecular markers. We then used these markers to analyse the genetic diversity of pepper plants for the purpose of breeding. The analysis of the whole genome identified SSR markers, which showed that trinucleotides were the most prevalent repeating pattern. A total of 147 pepper cultivars were identified and classified into seven primary groups based on an investigation of their genetic diversity and phylogenetic linkages. A total of 103,056 SSR loci were identified in *Cucurbita moschata* using in silico PCR, with di-nucleotide motifs being the most prevalent form. An study of cross-species SSR markers revealed that the primary syntenic links across *Cucurbita* species have remained remarkably maintained throughout evolution.

Understanding the Genetic Basis of Biotic Resistance in Vegetable Crops

Fungal infections continue to pose issues that impede the sustainable growth of vegetable production. While pesticides have the ability to prevent and manage fungal illnesses, their overuse has caused significant harm to both the environment and human health. Enhancing disease resistance has emerged as a crucial goal in breeding. The advent and use of molecular marker technology enables the direct and efficient selection of germplasm resources. An evaluation was conducted on the use of RAPD-PCR to create molecular markers linked to graymold disease resistance in onion (*Allium cepa* L.). The genetic link between the resistant and susceptible lines was determined and a SCAR marker was developed using RAPD analysis. Furthermore, an analysis of the RNA-seq data from the onion lines that are resistant and vulnerable to grey mould was conducted in order to create a selectable marker specifically for the resistant line. Phytophthora blight is a prevalent disease that leads to

reduced productivity and quality in pepper plants (*Capsicum annuum* L.) Produced a detailed genetic map of pepper using SLAF-seq and QTL analysis to identify the genes responsible for resistance to *Phytophthora capsici*. CQPc5.1 was discovered as a prominent quantitative trait locus (QTL) responsible for *P. capsici* resistance. This locus encompasses a range where 23 potential genes are situated.

Mining Genes Responsible for Abiotic Stresses for Vegetable Improvement

Abiotic stressors in vegetable crops result in significant damage, leading to growth limitations and disruptions in physiological metabolic systems. Hence, it is essential to conduct gene screening for abiotic challenges in order to develop resilient plant kinds via breeding. Pepper has a heightened sensitivity to high temperatures, resulting in the manifestation of severe symptoms like pollination failure, growth abnormalities, and other related issues. Pepper leaves were analysed using transcriptomics to identify genes that show differential expression between heat-tolerant and heat-sensitive types. Heat shock proteins (HSPs) and heat shock transcription factors (HSFs) were shown to be sensitive to heat stress or recovery. A tiny heat shock protein, CaHSP18.1a, was identified and characterised from pepper. It was shown that CaHSP18.1a is sensitive to heat stress and exhibits high levels of expression in a thermo-tolerant line. When CaHSP18.1a was silenced, it led to an increase in MDA levels and a loss in resistance to heat, drought, and salt stressors. This suggests that CaHSP18.1a has a favourable role in regulating tolerance to abiotic stress.

We conducted a comprehensive analysis to identify the Hsf and Hsp genes in eggplant that are affected by heat stress at the genome-wide level. An initial framework for studying the relationship between thermal tolerance and heat-response genes was established by RNA-seq analysis. This research showed that the Hsf and Hsp genes exhibit different levels of expression in the thermo tolerant line 05-4 and the thermo sensitive line 05-1. The overuse of nitrogen fertiliser in pepper cultivation has resulted in undesirable growth and reduced crop productivity. There is still a significant amount of information that remains unknown about the molecular foundation of the genetic diversity in N-use efficiency (NUE). We conducted a comparative transcriptome study to select two pepper genotypes that exhibit contrasting degrees of low-N tolerance. Our objective was to investigate the variations in nitrogen use efficiency (NUE) between these genotypes. Several differentially expressed genes (DEGs) associated with nitrogen (N) metabolism or other physiological processes were identified to enhance pepper's N utilisation.

Organic Compounds in Vegetables and Its Interaction with Environment

Flavonoids and volatile organic compounds play a crucial role in the development and expansion of vegetable crops. They serve several functions such as attracting pollinators, preventing plant illnesses, and enhancing weed control. The presence of anthocyanins in broccoli gives it its purple colour and antioxidant capabilities. Identify the specific loci and probable genes responsible for the formation of anthocyanin in broccoli. QTL-seq bulk segregant analysis identified two strongly linked quantitative trait loci (QTLs) on chromosome 7 that are responsible for anthocyanin production. Further high-resolution mapping identified fourteen potential genes, providing a potential molecular indicator for the creation of novel cultivars with high levels of anthocyanins. Allelopathy is the process by which plants release volatile organic molecules into the air, creating a chemical connection between them. The coordinated efforts of scientists and breeders involved in germplasm assessment, gene isolation, and marker design have led to the development of advanced breeding methods, such as gene editing, and the production of superior cultivars. To develop vegetable cultivars that are both ecologically friendly and have high yields and quality, superior breeding technique is needed. This technology may be enhanced by using new, extensive genomic data and tools. Genome-based breeding by design is a specific approach

that may be used. Funding sources: This endeavour received money from the National Key Research and Development Plan. The listed projects have been granted funding from multiple sources, including the National Natural Science Foundation of China, the Wuhan Biological Breeding Major Project, the International Cooperation Promotion Plan of Shihezi University (GJHZ202104), the Key Project of Hubei Hong Shan Laboratory (2021hszd007), and the Fundamental Research Funds for the Central Universities.

Conclusion

The Special Issue of Horticulture focuses on the notable advancements in molecular vegetable breeding, presenting a wide range of research that include gene editing and the discovery of genetic foundations for both biotic and abiotic challenges. The abstract highlights the significance of molecular tools in expediting the advancement of high-quality vegetable varieties, with the goal of achieving sustainable agriculture and improved crop output. Furthermore, it is crucial to have cooperation between scientists and breeders, with the backing of diverse funding sources, in order to make progress in the development of advanced breeding methods. This will finally result in the production of vegetable cultivars that are both environmentally adaptable and of superior quality.

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