

Molecular Markers in Vegetable Crop Improvement

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Markers are essential for identifying specific traits in organisms as they consist of specific DNA sequences or genes with a known location on a chromosome. Markers serve as flag posts or landmarks, directly or indirectly linked to the trait gene of interest, and are typically co-inherited with the trait. Researchers utilize these markers to identify and study particular genetic regions associated with those traits (Nair et al., 2024). Markers are classified into morphological, biochemical, cytological, and molecular markers (Sharma et al., 2021).

Morphological markers

Morphological markers refer to visually characterized phenotypic traits. These traits include plant height, disease response, flower shape or color, fruit characteristics, seed appearance, surface features of plant parts, growth habits, and pigmentation. The gene loci associated with these traits directly influence the morphology of plants. These markers play a crucial role in assessing and evaluating genetic variability within a population. By observing single phenotypic differences, researchers can gain insights into the diversity present among individuals. The main limitations of Morphological markers include their limited number, susceptibility to environmental influences, and dependent on the developmental stage of the plant or its specific organ or tissue. Morphological markers that do not cover the entire genome, cannot be effectively utilized for genotyping or establishing genetic distances. Nevertheless, despite these constraints, morphological markers remain crucial scientific tools in genetic and breeding practices. Many of these markers are genetically linked to economically significant and agronomic traits, enabling cost-effective and simplified production of new varieties essential for advancements in genetics and breeding (Nadeem et al., 2017).

Biochemical markers

Biochemical markers, also known as protein polymorphisms or isozymes with varying molecular weights and electrophoretic mobility perform the same catalytic function. Isozymes reflect the products of different alleles rather than different genes because

the difference in electrophoretic mobility is caused by a point mutation that causes amino acid substitutions in the enzyme structure. These variations in electrophoretic mobility allow isozymes to be used as genetic markers for mapping other genes. In the context of plant breeding, isozymes can be genetically mapped onto chromosomes. Isozymes serve as markers to locate genes on specific chromosomes. They are used to verify the purity of seed lots, ensuring that the desired cultivar is maintained. However, their use in plant breeding is limited due to the small number of isozymes in most crop species, with some only identifiable with specific strains (Dheer et al., 2020).

Cytological markers

Cytological markers refer to variations in the banding patterns of chromosomes used for chromosome characterization, mutation detection, and taxonomical studies. These variations are primarily due to the distribution of euchromatin and heterochromatin, which influences the color, width, order, and position of bands upon chromosome staining. Different banding techniques, such as Q-banding, G-banding, R-banding, C-banding, NOR-banding, and T-banding, have been developed based on specific stains utilized. Additionally, fluorescent in situ hybridization (FISH) has emerged as a modern technique for detecting and pinpointing specific DNA sequences on chromosomes by using fluorescence-labelled DNA or RNA probes. Additionally, fluorescent in situ hybridization (FISH) has emerged as a modern technique for detecting and pinpointing specific DNA sequences on chromosomes by using fluorescence-labelled DNA or RNA probes. Cytological markers have found extensive applications in physical mapping and the identification of linkage groups. They play a crucial role in understanding chromosomal organization and genetic variation (Bharadwaj et al., 2019).

Molecular markers

Molecular markers, also known as genetic markers or DNA markers, are nucleotide sequences with varying levels of polymorphism observed among the nucleotide sequences of different individuals.

These variations can result from mutations such as insertions, deletions, substitutions, or replication errors in tandemly repeated DNA sequences. Since 1980, several DNA marker technologies have been developed, each differing in polymorphism and detection methodology. Molecular markers can be categorized as dominant or codominant markers, based on their ability to differentiate between heterozygous and homozygous individuals. Dominant markers are typically bi-allelic and multi-locus, while codominant markers can be either bi-allelic or multi-allelic and are specific to particular loci (Shende et al., 2023).

Applications of molecular markers in vegetable crop improvement

Genetic diversity assessment

The effectiveness of a breeding program in vegetables primarily depends on the availability of

polymorphism within the crop, and the success of breeding efforts also hinges on genetic diversity. However, genetic diversity has recently encountered challenges such as genetic losses due to the widespread cultivation of high-yielding uniform cultivars and the elimination of natural habitats for flora and fauna due to urbanization and industrial development. Consequently, the conservation and effective use of genetic resources are fundamental to crop improvement programs. Molecular markers play a crucial role in accelerating breeding processes. The application of molecular or genetic markers relies on naturally occurring DNA polymorphisms (Sinha et al., 2023, Bunjkar et al., 2024). Table 2 presents the advancements made in the genetic diversity assessments of vegetables using molecular approaches.

Table 1: Advancements made in the genetic diversity assessments of vegetables using molecular markers			
Vegetable Crop	Markers type	Identification	Reference
Bittergourd	RAPD, ISSR	Genetic diversity	Adarsh et al., 2023
Asparagus	SSR	Genetic diversity	Ahmad et al., 2023
Garlic	RAPD	Genetic diversity	Majeed et al., 2023
Chilli	RAPD	Genetic diversity	Gor et al., 2023
Common Bean	RAPD, SCoT	Genetic diversity	Hromadová et al., 2023
Tomato	ISSR	Genetic diversity	Al-Khayri et al., 2023
Cassava	SSR	Genetic diversity	Sivan et al., 2023
Garlic	SSR, ISSR	Genetic diversity	Papaioannou et al., 2023
Cucumber	SSR	Genetic diversity	Kaur et al., 2023
Potato	SNP	Genetic diversity	Xiao et al., 2023
Potato	SSR	Genetic diversity	Dalamu et al., 2023

Importance of DNA fingerprinting for varietal and hybrid Identification

In the post-Convention on Biological Diversity (CBD) landscape, determining the identity of crop varieties has become increasingly vital for safeguarding the rights of plant breeders and farmers, particularly in developing countries. DNA fingerprinting plays a significant role in differentiating between hybrids and maternal seedlings. One of the earliest techniques utilized for DNA profiling was Restriction Fragment Length Polymorphism (RFLP). However, with modern advancements in molecular biology, a diverse array of molecular markers has been developed for the DNA fingerprinting of cultivars, hybrids, and breeding lines

across various vegetable crops viz tomato (Ahmad et al., 2023, Shahzad et al., 2024), eggplant (Samaha et al., 2023), chilli (Channabasava et al., 2023), melon (Zhang et al., 2023), potato (Rahman et al., 2022, Tiwari et al., 2022). Molecular markers, particularly co-dominant markers such as SSR, and dominant markers like RAPD and ISSR, are widely used for testing hybridity. Besides, DNA fingerprinting helps with genetic diversity assessment, tagging economically useful traits, assessing genetic purity, and parental selection of different vegetable crops (Santhy et al., 2023). Table 3 presents development of markers for major QTLs associated with specific traits in vegetable crops.

Table 3 Molecular markers developed for various traits in vegetable crop

Crop	QTL/gene	Characters	Ch. No.	Marker	Reference
Tomato	<i>Sw-5</i>	Resistance to Tomato spotted wilt virus (TSWV)	9	SCAR/CAPC	Zhang et al., 2021
Eggplant	<i>PI</i>	Lack of prickles	6	Primer pair amplifying I/D	Miyatake et al., 2020
Pepper	<i>up</i>	Fruit orientation	12	CAPS/HRM/AFLP	Solomon et al., 2021
Cucumber	<i>dm4.1.3</i>	Resistance to Downy mildew	4	Retrotransposon insertion	Berg et al., 2021
Spinach	<i>X/Y</i>	Sex determining locus	4	-	She et al., 2021

References

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