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MOLECULAR MARKERS IN IMPROVING QUALITY TRAITS OF VEGETABLE CROPS: A REVIEW

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ABSTRACT

Global food and nutritional security is greatly enhanced by vegetable crops, which are essential to human nourishment. They are abundant in vital vitamins, minerals, dietary fiber, and bioactive substances that promote general health. The importance of enhancing quality characteristics in vegetable crops, such as flavor, texture, color, nutritional composition, and shelf life, has been highlighted in recent years by rising consumer awareness and market demand. However, because of their complicated inheritance patterns and significant environmental effect, improving these qualities through traditional breeding techniques is still difficult. One effective way to get around these restrictions is through the use of molecular marker technology in plant breeding. Molecular markers are DNA-based instruments that make it easier to identify genes linked to desired characteristics and detect genetic variation. Vegetable crop development initiatives have made extensive use of methods including restriction fragment length polymorphism, random amplified polymorphic DNA, simple sequence repeats, and single nucleotide polymorphisms. These markers facilitate accurate selection using marker-assisted selection and effective mapping of quantitative trait loci. Furthermore, the effectiveness and precision of molecular breeding have been improved by recent developments in genomic technology, including as next-generation sequencing and genome-wide association studies. These methods facilitate the development of superior vegetable varieties with enhanced quality features and make it possible to identify complex trait-associated genes. Molecular markers are still essential to contemporary breeding techniques, despite certain drawbacks including expense and technical demands. In addition to discussing their applications and future prospects in vegetable crop improvement, this review emphasizes their importance in enhancing quality features.

***Key words*: Molecular markers; Vegetable crops; Quality traits; MAS; QTL; NGS; GWAS; CRISPR.

Introduction

In addition to being a vital part of human meals, vegetable crops are vital to the world's food and nutritional security. They are abundant in vitamins, minerals, dietary fiber, and antioxidants all of which are critical for preserving human health and averting chronic illnesses (Dias, 2012). The demand for vegetables with superior quality characteristics, such as improved flavor, texture, color, and increased nutritional content, has increased dramatically in recent years due to growing awareness of healthy lifestyles (Klee & Tieman, 2018). Vegetable crops can have a variety of qualities, including nutritional components (vitamins and minerals), biochemical features (sugars, acids, and secondary metabolites), and morphological aspects (size, shape, and color) (Beckles, 2012). These characteristics are frequently complicated and quantitatively inherited, which means that they are modified by environmental circumstances and regulated by several genes. Because of their complexity, improving them using traditional breeding methods is challenging and time-consuming (Giovannucci, 1999). Phenotypic selection, which selects plants based on visible traits, is the primary strategy used in traditional plant breeding. Despite their success in improving crops, these techniques are frequently constrained by environmental variability and need several generations to get consistent outcomes (Collard & Mackill, 2008). Additionally, because it is challenging to pinpoint the individual genes causing desired qualities, the enhancement of complex features is less accurate (Moose & Mumm, 2008). Plant breeding is now much more accurate and efficient thanks to the development of molecular marker technology. Molecular markers are dependable for genetic analysis since they are DNA-based instruments that identify genetic variation and are unaffected by environmental factors (Gupta *et al.*, 2001). These markers provide precise selection in breeding programs and make it possible to identify genetic areas linked to significant features. Marker-assisted selection (MAS), which enables indirect selection of desired features based on linked DNA markers, is one of the main uses of molecular markers. Early plant screening made possible by MAS shortens breeding times and increases selection precision (Ribaut & Hoisington, 1998). This strategy is especially helpful for enhancing complicated features that are challenging to evaluate using phenotypic techniques. The field of molecular breeding has been further enlarged by recent developments in genomic technology, like as next-generation sequencing. The production of better vegetable varieties can be accelerated by using these technologies to identify genes and quantitative trait loci linked to significant quality attributes (Varshney *et al.*, 2009).

Types and Principles Molecular Markers

DNA-based instruments called molecular markers are frequently employed to identify genetic variation at the genomic level. Because these markers are stable between generations and unaffected by environmental factors, they offer a dependable and effective way to differentiate between genotypes (Semagn, 2006). The discovery of polymorphisms in DNA sequences is the basis of the basic idea behind molecular markers. These polymorphisms result from changes that can be identified using a variety of molecular approaches, such as insertions, deletions, or nucleotide substitutions. Molecular markers are crucial tools in agricultural improvement projects, genetic mapping, and plant breeding because of their capacity to identify such differences (Gupta, 2001).

Types of Molecular Markers

Restriction Fragment Length Polymorphism (RFLP):

Variations in DNA fragment lengths produced by restriction enzyme digestion serve as the basis for RFLP markers. Heterozygous and homozygous individuals can be identified using these co-dominant, very reliable indicators for genetic study (Tanksley, 1989).

Random Amplified Polymorphic DNA (RAPD):

Using short primers in polymerase chain reactions, random DNA fragments are amplified to create RAPD identifiers. This method is helpful for first genetic research because it is straightforward and doesn't require previous sequencing information (Welsh, 1990).

Simple Sequence Repeats (SSR):

Short tandem repeats of DNA sequences make up SSR markers, which are highly polymorphic because of differences in repeat counts. For genetic mapping and diversification research, these co-dominant markers are frequently employed (Powell, 1995).

Single Nucleotide Polymorphisms (SNP):

SNP markers show differences at a single genetic nucleotide location. They are perfect for contemporary breeding programs due to their high abundance and suitability for high-throughput genotyping (Vignal, 2002).

Amplified Fragment Length Polymorphism (AFLP):

AFLP markers provide many polymorphic markers by combining selective PCR amplification with restriction digestion. These markers yield high-resolution genetic information and are very repeatable (Mueller, 1999).

Inter Simple Sequence Repeats (ISSR):

ISSR markers do not require prior sequence information; instead, they amplify areas between microsatellites. These markers are frequently employed for characterizing germplasm and analyzing genetic diversity (Reddy, 2002).

Principles of Molecular Marker Application

The use of molecular markers is predicated on their association with genes governing significant characteristics. In breeding programs, a marker that is closely associated with a gene can be used to select for that gene indirectly. This linkage-based selection lessens

Table 1: Comparison of Molecular Markers.

Marker Type	Principle	Advantages	Limitations
RFLP	Restriction digestion	Reliable, co-dominant	Labor-intensive
RAPD	Random PCR amplification	Simple, low cost	Low reproducibility
SSR	Tandem repeats	Highly polymorphic	Expensive
SNP	Single base variation	High-throughput	Requires advanced tools
AFLP	Restriction + PCR	High resolution	Technically complex
ISSR	Between SSR regions	No prior sequence needed	Dominant marker

Source: Botstein *et al*., (1980); Williams *et al*., (1990); Tautz (1989); Rafalski (2002); Vos *et al*., (1995); Zietkiewicz *et al*., (1994); Agarwal *et al*., (2008)

reliance on phenotypic evaluation and increases accuracy (Young, 1999). The creation of genetic linkage maps, which aid in finding genes on chromosomes, heavily relies on molecular markers. These maps are crucial for locating quantitative trait loci linked to complex variables like vegetable crop quality attributes (Paterson, 1991).

Marker-Assisted Selection (MAS):

Molecular markers are used in marker-assisted selection, a contemporary breeding technique, to identify plants with desired characteristics. This method greatly shortens the time needed for breeding operations and allows for early genotype screening (Melchinger, 1990). MAS is especially helpful for enhancing complex characteristics that are hard to assess phenotypically, such flavor and nutritional content. Additionally, it permits the pyramiding of several genes, which results in the creation of improved crop types (Bernardo, 2008).

Importance in Vegetable Crop Improvement:

In order to increase the effectiveness and accuracy of vegetable breeding programs, molecular markers are essential. They make it possible to identify the genes linked to significant quality attributes including color, flavor, and nutrient content. Molecular markers greatly boost crop development efforts by promoting early selection and shortening breeding cycles (Xu, 2010). Furthermore, genetic diversity studies and germplasm conservation make extensive use of molecular markers. These uses are crucial for preserving genetic resources and creating better vegetable cultivars with higher-quality characteristics (Varshney, 2005).

Quality Traits in Vegetable Crops

Vegetable crops' nutritional worth, marketability, and customer acceptability are all determined by their quality attributes. These characteristics, which affect overall quality, include dietary, physical, biochemical, and genetic elements (Shewfelt, 1999).

Nutritional Quality Traits

Since vegetable crops are the main source of vital vitamins, minerals, and bioactive chemicals needed for human health, their nutritional content is one of its most significant characteristics. Micronutrients found in vegetables, such as vitamin C, carotenoids, folates, and antioxidants, are essential for supporting physiological processes and preventing illness (Davey *et al*., 2000). Improving these nutrients through breeding initiatives has emerged as a major goal, especially in malnutrition-affected areas. Vegetable nutrient accumulation is influenced by both environmental and genetic factors. For instance, both genotype and growth conditions affect the amount of carotenoid in tomatoes and carrots. A thorough understanding of metabolic pathways and gene regulation is necessary for improving nutritional characteristics. The identification of genes involved in nutrient production has been made possible by developments in molecular biology, allowing for the targeted enhancement of nutritional quality (Fraser & Bramley, 2004).

Physical and Visual Quality Traits

Vegetable crops' commercial worth and consumer attractiveness are largely determined by their physical and visual characteristics, such as size, shape, color, and hardness. These qualities are crucial for business success since they are frequently the first things taken into account when making purchases (Kader, 2008). For example, veggies like tomatoes, capsicums, and carrots should have consistent size and vibrant coloring. Both genetic and environmental factors, such as temperature, light, and soil conditions, have an impact on these characteristics. Pigments like anthocyanins, carotenoids, and chlorophyll are frequently linked to the genetic regulation of color. While preserving other crucial attributes like yield and nutritional value, breeding efforts seek to enhance these qualities to satisfy market demands (Lancaster *et al*., 1997).

Biochemical and Sensory Quality Traits

Vegetable flavor, fragrance, and general sensory experience are all influenced by biochemical characteristics. chemicals including sugars, organic acids, amino acids, and volatile chemicals determine these

Table 2: Applications of Molecular Markers in Vegetable Crops.

Crop	Trait Improved	Marker Type	Outcome
Tomato	Lycopene content	SSR/SNP	Improved color & nutrition
Carrot	Beta-carotene	QTL/SSR	Enhanced vitamin A
Potato	Starch quality	AFLP/SNP	Better processing quality
Onion	Flavor compounds	SSR	Improved taste
Capsicum	Fruit color	SNP	Enhanced visual appeal
Source: (Foolad, 2007); (Simon, 2000); (Gebhardt *et al.*, 2004); (Kumar *et al.*, 2011); (Collard & Mackill, 2008); (Xu & Crouch, 2008); (Tanksley, 1993)			

characteristics (Baldwin *et al.*, 2000). Taste is largely determined by the ratio of sugars to acids, notably in crops like tomatoes and onions. Flavor is a multifaceted characteristic that is impacted by several biochemical processes and environmental factors. The polygenic character of flavor and the difficulties of assessing sensory traits make it difficult to increase flavor through conventional breeding. However, the identification of genes involved in flavor production has been made possible by breakthroughs in molecular techniques, opening up new possibilities for improving sensory quality (Tieman *et al.*, 2017).

Genetic and Environmental Influences on Quality Traits

Vegetable crops typically have quantitative quality attributes that are regulated by several genes, which are known as quantitative trait loci (QTLs). These characteristics show constant fluctuation and are impacted by both environmental and genetic factors (Falconer & Mackay, 1996). Precise improvement by conventional breeding techniques is challenging due to the intricacy of genetic regulation. Furthermore, the expression of quality features is greatly influenced by interactions between genetics and environment. The buildup of nutrients and other quality-related chemicals can be influenced by environmental factors as temperature, light intensity, and agricultural techniques (Dumas *et al.*, 2003). Therefore, to guarantee stability and consistency in quality attributes, it is crucial to assess genotypes under various environmental situations. Because molecular markers make it possible to identify QTLs and genes linked to quality, they have been crucial in helping us understand the genetic basis of these attributes. This has made it easier to use more accurate breeding techniques to enhance complex traits in vegetable crops (Grandillo *et al.*, 1999).

Application of Molecular Markers in Quality Improvement

In developing the possible to precisely identify, map, and select genes linked to significant quality features, molecular markers have completely transformed the improvement of vegetable crops. Molecular marker-based techniques enable breeders to directly target particular genetic areas controlling desired qualities, in contrast to conventional breeding, which depends on phenotypic selection. This has greatly increased breeding programs' accuracy and efficiency, especially for complex qualities like flavor, nutritional quality, and shelf life (Collard & Mackill, 2008). The quick production of superior vegetable varieties with improved qualitative attributes and improved environmental tolerance has been made possible by the incorporation of molecular markers into breeding procedures.

Marker-Assisted Selection (MAS) in Quality Improvement

One of the most popular uses of molecular markers in plant breeding is marker-assisted selection (MAS). Instead of depending only on phenotypic assessment, it entails choosing plants based on DNA markers that are strongly associated with desired characteristics. This method reduces the time and resources needed for breeding programs by enabling early genotype screening (Xu & Crouch, 2008). MAS has been effectively used to enhance a number of vegetable crop quality attributes. For example, markers connected with sugar content have contributed to increased flavor, while markers associated with carotenoid concentration have been utilized to improve the nutritional quality of tomatoes and carrots. Furthermore, MAS has been applied to enhance characteristics that are crucial for post-harvest quality, like firmness and shelf life (Foolad, 2007).

Quantitative Trait Loci (QTL) Mapping

One effective method for locating genomic areas linked to complex phenotypes is quantitative trait loci (QTL) mapping. QTL mapping is essential to comprehending the genetic basis of vegetable quality attributes because the majority of these qualities are quantitatively inherited (Paterson *et al.*, 1988). Researchers have found loci linked to significant characteristics like fruit size, color, and nutrient content through QTL mapping. Breeding programs can employ these QTLs to more precisely improve particular features.

Table 3: Modern Molecular Breeding Technologies.

Technology	Key Feature	Application	Outcome
NGS	High-throughput sequencing	Gene discovery	Faster breeding
GWAS	Association mapping	Trait identification	High precision
GS	Genome-wide prediction	Selection	Reduced breeding time
CRISPR	Gene editing	Trait modification	Targeted improvement
Source: (Metzker, 2010); (Yu *et al.*, 2006); (Meuwissen *et al.*, 2001); (Jinek *et al.*, 2012)			

Developing cultivars with consistent quality performance requires the identification of stable QTLs in various conditions (Tanksley, 1993).

Gene Tagging and Mapping

Finding molecular markers that are strongly associated with genes governing significant features is known as “gene tagging.” This approach allows breeders to track the inheritance of specific genes and incorporate them into new varieties more efficiently (Young, 1996). Gene tagging has been used to identify genes linked to characteristics including ripening processes, taste compounds, and pigment synthesis in vegetable crops. When combined with molecular markers, gene tagging improves breeding precision and makes it easier to create superior varieties with desired quality traits (Saliba-Colombani *et al.*, 2001).

Case Studies in Vegetable Crops

Most vegetable crops have shown notable increases in quality features as a result of the use of molecular markers. Markers associated with lycopene content have been applied to tomatoes to improve fruit color and nutritional value. Molecular indicators linked to beta-carotene content have been used to raise provitamin A levels in carrots. Similarly, increased processing quality in potatoes has been attributed to indicators associated with starch content (Gebhardt *et al.*, 2004). These illustrations demonstrate how molecular markers can enhance both commercial and nutritional quality attributes. The effective application of these methods shows that they have the ability to overcome the drawbacks of traditional breeding and satisfy the growing demand for premium vegetables (Blanca *et al.*, 2012).

Advances in Molecular Breeding Techniques for Quality Improvement

The accuracy, effectiveness, and speed of enhancing quality attributes in vegetable crops have been greatly increased by recent developments in molecular breeding. A better understanding of the genetic basis of complex traits has been made possible by the merging of genomics, high-throughput sequencing, and sophisticated computational methods. These contemporary methods enable breeders to more precisely discover, choose, and modify genes linked to crucial quality characteristics including flavor, nutritional value, and shelf life (Varshney *et al.*, 2014).

Next-Generation Sequencing (NGS)

Plant genomics has undergone a revolution thanks to next-generation sequencing (NGS) technologies, which make it possible to quickly and affordably sequence whole genomes. Large-scale genomic data produced by these technologies can be utilized to find genetic variants such insertions and deletions and single nucleotide polymorphisms (Metzker, 2010). NGS has made it easier to identify genes linked to significant quality attributes in vegetable crops and has helped create high-density genetic maps. These maps aid in locating the genetic areas governing important features and are crucial for accurate breeding. Breeding operations have accelerated due to the availability of genome sequences for crops like potatoes and tomatoes (Shendure & Ji, 2008).

Genome-Wide Association Studies (GWAS)

In examining natural variation in a variety of populations, genome-wide association studies (GWAS) have become effective instruments for locating genetic loci linked to complex traits. This method allows for the simultaneous identification of several loci and offers a greater resolution than conventional QTL mapping (Yu *et al.*, 2006). Vegetable crops have made extensive use of GWAS to find genes linked to quality attributes like fruit composition, color, and nutritional value. By facilitating accurate marker-assisted selection, the data produced by GWAS aids in the creation of better varieties (Zhu *et al.*, 2008).

Genomic Selection (GS)

Genomic selection (GS) is a sophisticated breeding technique that predicts an individual’s genetic potential using genome-wide markers. Without waiting for phenotypic evaluation, this technique enables breeders to choose superior genotypes based on genetic data (Meuwissen *et al.*, 2001). GS is very successful at enhancing complicated traits like qualitative qualities since it greatly shortens the breeding cycle and improves selection accuracy. The effectiveness of creating superior vegetable varieties has increased after GS was incorporated into breeding programs (Heffner *et al.*, 2009).

Gene Editing and CRISPR Technology

CRISPR/Cas9 and other gene-editing technologies have become effective tools for precisely modifying genes linked to desirable traits. Through targeted genome modifications made possible by this technique, particular features can be improved without the introduction of foreign DNA (Jinek *et al.*, 2012). CRISPR has been applied to vegetable crops to improve characteristics like shelf life, resilience to biotic and abiotic stressors, and nutritional quality. A very effective method for creating better crop varieties is to combine gene editing with molecular markers (Bortesi & Fischer, 2015).

Challenges and Future Prospects

The efficiency and precision of breeding have been greatly improved by the use of molecular markers in vegetable crop development. However, a number of biological, technological, and financial obstacles continue to prevent their widespread use. Rapid developments in biotechnology and genomics are also creating new avenues for overcoming these constraints and enhancing the efficacy of molecular breeding techniques (Varshney *et al.*, 2005).

Challenges in the Use of Molecular Markers

High Cost and Technical Requirements:

The high expense of sophisticated genomic tools like next-generation sequencing and high-throughput genotyping platforms is one of the main issues with molecular marker technology. According to (Edwards and Batley, 2010), underdeveloped nations might not have access to the sophisticated infrastructure and trained workers needed for these technologies. This restricts their availability and practical application in numerous breeding initiatives.

Complexity of Quality Traits:

Vegetable crop quality traits are frequently quantitatively inherited and regulated by several genes. Finding trustworthy markers that are consistently linked to desired attributes across many genetic backgrounds is challenging due to this complexity (Xu & Crouch, 2008). Because of this, marker-assisted selection might not always yield reliable results.

Genotype × Environment Interaction:

Environmental elements including temperature, light, and soil conditions have a big impact on how quality qualities manifest. Finding permanent markers is made more difficult by this genotype × environment interaction since differing environmental variables might affect how effective a marker is (Collard & Mackill, 2008). It is difficult to create widely adaptable types because of this variability.

Limited Genetic Resources:

Effective molecular breeding requires the availability of well-characterized germplasm. However, the identification of novel alleles linked to quality attributes is limited due to low genetic diversity and inadequate genetic resource characterisation (Tanksley & McCouch, 1997). This restricts the possibility of genetic advancement.

Integration with Conventional Breeding:

Integrating molecular marker technology with conventional breeding techniques is another significant difficulty. Incorporating genetic techniques necessitates adjustments to breeding strategies and staff training, as many breeding programs still mainly rely on phenotypic selection (Bernardo, 2008). This shift may take a long time and require a lot of resources.

Future Prospects of Molecular Breeding

Reduction in Cost of Genomic Technologies:

Researchers and breeders can now more easily access molecular breeding thanks to ongoing advancements in sequencing technology that lower the cost of genetic analysis (Mardis, 2008). This is anticipated to boost the use of molecular techniques in improving vegetable crops.

Integration of Advanced Genomic Tools:

It is anticipated that the incorporation of technologies like genomic selection, genome-wide association studies, and next-generation sequencing would improve the accuracy of breeding programs. These methods facilitate effective selection and offer comprehensive insights into the genetic foundation of complex traits (Varshney *et al.*, 2014).

Utilizing Gene Editing Technologies:

CRISPR/Cas systems and other gene-editing techniques provide new opportunities for precise manipulation of genes linked to desirable traits. Without adding foreign DNA, these technologies provide focused enhancements in flavor, nutritional value, and shelf life (Chen *et al.*, 2019). This is a significant development in crop improvement.

Utilizing Big Data and Bioinformatics:

Advanced bioinformatics tools for data processing and interpretation have been developed as a result of the growing availability of genomic data. These tools facilitate the effective management of huge datasets and aid in breeding program decision-making (Batley & Edwards, 2009). It is anticipated that the application of big data analytics will improve breeding efficiency even more.

Creation of Varieties Resistant to Climate 1Change:

Future breeding initiatives will concentrate on creating vegetable types that are both high-quality and climate-resistant. The identification of genes linked to stress tolerance and adaptability will be greatly aided by molecular markers (Tester & Langridge, 2010).

Conclusion

In contemporary plant breeding, molecular markers have become potent instruments that provide notable benefits over traditional techniques for enhancing quality attributes in vegetable crops. Their capacity to identify genetic diversity at the DNA level makes it possible to precisely identify and choose desired features, improving breeding programs' accuracy and efficiency. The production of vegetable varieties with enhanced nutritional value, flavor, appearance, and shelf life has been significantly hastened by the application of methods including gene tagging, QTL mapping, and marker-assisted selection. The scope of molecular breeding has been further extended by the use of cutting-edge genomic technology, such as next-generation sequencing, genome-wide association studies, genomic selection, and gene-editing tools. These methods have permitted targeted improvement at a previously unheard-of level of accuracy and have given deeper insights into the genetic architecture of complex quality attributes. Because of this, breeders are now more capable of handling the difficulties involved in improving quantitatively inherited features. Despite these developments, the broad use of molecular marker technologies is still constrained by a number of issues, including high costs, technical limitations, and the complexity of trait inheritance. However, it is anticipated that in the near future, ongoing advancements in biotechnology and genetics will get over these restrictions and make these technologies more useful and accessible. In conclusion, molecular markers have enormous potential for the future of sustainable agriculture and are essential for enhancing quality attributes in vegetable crops. The development of superior vegetable varieties that satisfy changing consumer preferences and support global food and nutritional security will depend on their continuing integration with cutting-edge technologies.

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