**Role of Marker Assisted Selection in Enhancing yield and quality traits in vegetable crops**

**Abstract**

Vegetable crops are fundamental to global food and nutritional security, contributing essential vitamins, minerals, and bioactive compounds to human diets. However, conventional breeding methods often fall short in meeting the rising demand for high-yielding, nutritionally superior, and climate-resilient vegetable varieties due to the complex, polygenic nature of key traits and their interactions with the environment. Marker-Assisted Selection has emerged as a powerful tool to overcome these challenges by enabling precise, early, and efficient selection of genotypes based on molecular markers linked to desirable traits. This review presents a comprehensive overview of the role of Marker-Assisted Selection in improving yield and quality traits in vegetable crops. It explores the conceptual framework of Marker-Assisted Selection, including the types of molecular markers, strategies for Quantitative Trait Loci (QTL) mapping, and marker deployment in breeding programs. The genetic basis of yield components, nutritional quality, flavour, texture, and stress resilience is discussed, highlighting how Marker-Assisted Selection enables targeted improvement of complex traits. Real-world applications are illustrated through successful case studies, such as the development of Tomato yellow leaf curl virus (TYLCV)-resistant tomato hybrids and biofortified carrots with elevated beta-carotene content.

**Keywords:** *Marker-assisted selection (MAS), Vegetable crop improvement, Yield and, quality traits, molecular breeding technologies, Genomic integration*

**Introduction**

**Importance of Vegetable Crops in Global Agriculture**

Vegetable crops play a vital role in global agriculture, nutrition, food security, and the economy (1,2). They are an essential source of vitamins, minerals, dietary fiber, and antioxidants, which are crucial for human health and well-being. Vegetables like tomatoes, carrots, spinach, onions, cucumbers, and peppers are staple components of diets worldwide and are often recommended by health organizations to combat malnutrition and prevent non-communicable diseases such as diabetes, cardiovascular disorders, and certain types of cancer (2,3).

From an economic perspective, vegetables constitute a significant portion of the horticulture sector, contributing substantially to farm incomes and employment generation. In many developing countries, smallholder farmers depend heavily on vegetable production for their livelihoods (5,6). The global vegetable market is expanding rapidly, driven by urbanization, rising incomes, and growing consumer awareness of health and nutrition(3,4).

However, despite their importance, vegetable crops are often more sensitive to environmental stresses than cereals or pulses. They exhibit a wide range of phenotypic diversity, are prone to pest and disease attacks, and require intensive care for quality and shelf-life maintenance. Moreover, in the face of climate change, water scarcity, and declining arable land, there is a pressing need to enhance the productivity and quality of vegetable crops through scientific innovations (3,4).

**Challenges in Conventional Vegetable Breeding**

Traditional breeding methods, although successful in developing improved cultivars over the years, face several inherent limitations when applied to vegetable crops(1,2). Conventional breeding primarily relies on phenotypic selection, which is often influenced by environmental factors and may not reflect the true genetic potential of a genotype. Furthermore, most economically important traits in vegetables—such as yield, nutrient content, fruit firmness, flavour, and resistance to biotic and abiotic stresses—are quantitatively inherited and governed by multiple genes with small individual effects, making their improvement through conventional methods slow and cumbersome (5,6).

Another limitation of traditional breeding is the long breeding cycle, particularly in perennial or biennial vegetables like onion and carrot. The process of selecting, crossing, evaluating, and releasing new cultivars can take more than a decade. Additionally, the narrow genetic base in some cultivated vegetable species restricts breeders' ability to introduce novel traits or broaden diversity. Linkage drag from wild relatives and lack of precise tools for introgression further complicate the breeding process (7,8).

In the context of rising consumer expectations for better quality, uniformity, and nutritional value, breeders face the complex challenge of developing varieties that meet market demands while ensuring resilience to environmental fluctuations. There is also increasing pressure to reduce pesticide and fertilizer usage, which underscores the need for intrinsic resistance and input efficiency traits in vegetables (7,8).

To overcome these challenges, integrating modern molecular tools with conventional breeding offers a promising path forward. Marker-Assisted Selection (MAS) has emerged as one such transformative approach that can significantly enhance the efficiency, precision, and speed of vegetable breeding programs (3,4).

**Emergence and Evolution of Molecular Breeding**

Molecular breeding refers to the use of genetic markers—heritable DNA sequences associated with specific traits—to guide selection decisions in plant breeding. Since the discovery of Restriction Fragment Length Polymorphism (RFLP) in the 1980s, a variety of molecular markers such as RAPD (Random Amplified Polymorphic DNA), AFLP (Amplified Fragment Length Polymorphism), SSR (Simple Sequence Repeats), and SNPs (Single Nucleotide Polymorphisms) have been developed and used for different applications(2,3).

These markers are not affected by the environment, are abundant in the genome, and can be detected at any stage of plant growth. This allows for early and accurate selection of desirable traits, reducing the need for lengthy field evaluations and generation advancement (5,6). The evolution of high-throughput genotyping platforms and next-generation sequencing (NGS) has further accelerated the discovery of marker-trait associations and facilitated their deployment in breeding pipelines(8,9).

Marker-Assisted Selection is a key component of molecular breeding, where markers tightly linked to trait-controlling genes or quantitative trait loci (QTLs) are used to select plants with favorable alleles. MAS enables breeders to track and pyramid multiple genes for complex traits, screen large populations efficiently, and improve traits that are otherwise difficult to assess phenotypically (9,10).

**Scope of MAS in Vegetable Crop Improvement**

MAS has been successfully applied in cereals and legume crops like rice, wheat, and soybean for traits such as disease resistance, drought tolerance, and grain quality. In vegetables, its adoption has been relatively recent but is gaining momentum due to advancements in molecular genetics and increasing availability of crop-specific genomic resources (11,12).

Vegetable crops present unique opportunities and challenges for MAS. On one hand, the relatively small genome size of many vegetables (e.g., tomato, cucumber) makes them amenable to whole-genome analysis and marker development. On the other hand, the high degree of heterozygosity, vegetative propagation (e.g., potato), and diverse reproductive strategies across species require customized breeding approaches (13,14).

Despite these complexities, MAS is being increasingly used to improve several key traits in vegetables:

* **Yield-related traits**: fruit size, number, plant architecture, early maturity(7).
* **Quality traits**: sugar content, colour, texture, shelf-life, and nutritional components such as lycopene, carotenoids, vitamin C, and flavonoids (8).
* **Resistance traits**: resistance to fungal, bacterial, and viral pathogens, as well as insect pests (8)
* **Tolerance traits**: tolerance to abiotic stresses such as drought, salinity, and heat (7).

The application of MAS in vegetable breeding is also aligned with the goals of climate-smart agriculture and sustainable intensification. By enabling the development of varieties that require fewer inputs and can withstand environmental stresses, MAS contributes to resource-use efficiency and environmental protection (4,6)

**Conceptual Framework of Marker-Assisted Selection (MAS)**

Marker-Assisted Selection (MAS) represents a powerful convergence of molecular biology and classical plant breeding, offering a high-precision tool for improving complex traits in crops. (3,5)Especially in vegetable crops, where many desirable attributes are controlled by multiple genes and often influenced by environmental interactions, MAS enables plant breeders to make informed selections at the DNA level rather than relying solely on phenotype. This approach not only improves the accuracy of selection but also significantly shortens the breeding cycle, which is particularly advantageous for species with longer generation times or traits that are difficult to assess in early growth stages (7,8)

 ***Table 1. Types of Molecular Markers Used in MAS***

| Marker Type | Detection Method | Inheritance | Advantages | Limitations |
| --- | --- | --- | --- | --- |
| RFLP | Restriction digestion + probe hybridization | Co-dominant | High accuracy, first-generation marker | Labor-intensive, low throughput |
| RAPD | PCR with arbitrary primers | Dominant | Simple and quick | Low reproducibility |
| AFLP | Restriction digestion + selective PCR | Dominant | High polymorphism | Complex protocol |
| SSR | PCR of microsatellite repeats | Co-dominant | Highly polymorphic, reproducible | Requires sequence info |
| SNP | Base-pair variation detection | Co-dominant | Abundant, high-throughput, NGS-compatible | Biallelic, may need specialized platforms |

At the heart of MAS lies the concept of molecular markers—identifiable DNA sequences that are associated with a particular locus or gene of interest. These markers serve as genetic signposts, allowing researchers to track the inheritance of important traits within breeding populations (11,12) Over the past few decades, several types of molecular markers have been developed, each contributing uniquely to the advancement of MAS. Among the earliest to be discovered were Restriction Fragment Length Polymorphisms (RFLPs), which detect variations in DNA fragment lengths after enzymatic digestion. While highly reliable, RFLPs were technically demanding and gradually gave way to polymerase chain reaction (PCR)-based methods such as Random Amplified Polymorphic DNA (RAPD) and Amplified Fragment Length Polymorphism (AFLP). RAPDs, though quick and inexpensive, often suffered from reproducibility issues, whereas AFLPs provided a high degree of polymorphism and were effective for analysing genetic diversity and constructing linkage maps (7,8)

As molecular technologies evolved, the focus shifted to more robust and informative markers like Simple Sequence Repeats (SSRs) and Single Nucleotide Polymorphisms (SNPs). SSRs, also known as microsatellites, consist of tandemly repeated short DNA sequences and exhibit high levels of polymorphism. (10,11)Their co-dominant nature allows for the discrimination between homozygous and heterozygous alleles, making them ideal for linkage analysis and MAS in several vegetable crops such as tomato and cucumber. SNPs, representing the most abundant form of genetic variation, involve single base-pair changes in DNA and have become the marker of choice in modern breeding. Their stability, genome-wide distribution, and compatibility with high-throughput genotyping platforms make SNPs highly suitable for large-scale association studies and genomic selection, particularly in crops where reference genomes and dense marker maps are available (12,13)

The effectiveness of MAS depends on the proximity of the marker to the gene or quantitative trait locus (QTL) controlling the trait of interest. The closer the marker is to the gene, the more likely it will be inherited together during meiosis, a phenomenon referred to as linkage. When markers are located within the gene itself—referred to as functional markers—they offer the highest level of precision. However, even markers that flank the gene closely can be effective if thoroughly validated across multiple genetic backgrounds and environmental conditions (14,15)

The practical application of MAS typically begins with the identification of marker-trait associations through QTL mapping or genome-wide association studies (GWAS). This involves crossing genetically diverse parent lines to produce a mapping population, such as F2, recombinant inbred lines (RILs), or backcross populations. (16,17)Phenotypic evaluation of the population is then combined with genotypic data using statistical methods like interval mapping or composite interval mapping to locate QTLs on a linkage map. Once identified, these QTLs are characterized in terms of their chromosomal location, effect size, and percentage of phenotypic variation explained. In vegetable crops, such mapping efforts have successfully identified QTLs associated with a wide range of traits including fruit size, shape, yield components, and nutritional quality. For example, in tomato, major QTLs such as fw2.2, lc (locule number), and fas (fascinated inflorescence) have been linked to fruit weight and shape (12,13)

Following the identification of QTLs, the next step is the validation of associated markers. This is essential to ensure that the marker-trait linkages are consistent across different genetic backgrounds and growing conditions. Only after successful validation are the markers deployed in breeding programs for selection purposes. The genotyping of breeding material involves using molecular techniques to determine the presence or absence of specific alleles associated with the trait. Individuals carrying the desirable allele are then selected and advanced for further breeding or variety development (7,14)

Marker-Assisted Selection can be implemented in various strategic ways, depending on the breeding objectives and the genetic architecture of the trait. Foreground selection focuses on directly selecting individuals carrying the desired gene or QTL, often used in backcross breeding to introduce specific traits like disease resistance (11,13) Background selection, on the other hand, helps accelerate the recovery of the recurrent parent genome when introgressing new traits, thereby reducing linkage drag. Pyramiding is another important application, where multiple genes or QTLs governing different traits—or different sources of resistance to the same pathogen—are combined into a single genetic background. This not only enhances trait expression but also provides durability against pest and disease evolution. For complex polygenic traits such as yield, marker-assisted recurrent selection (MARS) can be employed, where selection decisions are based on the cumulative effect of several favourable alleles over multiple breeding cycles (15,16)

The advantages of MAS over conventional breeding are numerous and compelling. One of the most significant is the precision it offers, allowing selection to be based on genotype rather than phenotype, thereby eliminating environmental noise and improving reliability. This precision translates into time and cost savings, as breeders can screen for traits at the seedling stage without waiting for full plant maturity or laborious phenotyping. MAS also enables breeders to address traits that are difficult or impossible to measure phenotypically, such as internal fruit quality, nutritional components, or root traits that require destructive sampling. Furthermore, it facilitates the pyramiding of multiple traits into a single cultivar, a task that would be extraordinarily challenging using traditional methods alone (17,18)

Despite these advantages, MAS is not without limitations. The effectiveness of MAS depends heavily on the tightness of the marker-gene linkage. Loose linkage or recombination between the marker and gene can lead to erroneous selections. Moreover, some QTLs exhibit genotype-by-environment interactions and are only expressed under specific conditions, reducing the consistency of marker effects. Another significant barrier is the cost and technical expertise required for marker development and genotyping, which may limit the widespread adoption of MAS in low-resource settings. Additionally, in many underutilized or minor vegetable crops, genomic resources are still lacking, making it difficult to develop reliable markers for key traits (19,20)

Nonetheless, the rapid advancement in genomic technologies is helping to overcome many of these challenges. The integration of MAS with other genomic approaches has opened new frontiers in precision breeding. For instance, genomic selection (GS) utilizes genome-wide marker data and phenotypic information to predict breeding values, offering a more holistic and accurate selection strategy for complex traits (11,15) Similarly, CRISPR/Cas-based gene editing allows for precise modification of specific genes, providing a tool that complements MAS by enabling direct manipulation of known genes. The use of GWAS, transcriptomics, and metabolomics further enriches the understanding of trait biology, leading to the identification of novel markers and candidate genes (17,19)

**Genetic Basis of Yield and Quality Traits in Vegetable Crops**

The improvement of vegetable crops for higher yield and enhanced quality traits is fundamentally governed by an understanding of the genetic architecture underlying these characteristics. Unlike traits controlled by single genes, most agronomic and consumer-preferred traits in vegetables are quantitatively inherited, meaning they are influenced by multiple genes, each with small additive or interactive effects, and are often subject to environmental modulation (12,13) To effectively harness marker-assisted selection (MAS) in breeding for such traits, it is essential to dissect their genetic basis, identify relevant loci, and understand gene networks and regulatory pathways involved (14,15)

***Table 2. Key Yield and Quality Traits with Known QTLs in Vegetables***

| **Crop** | **Trait** | **Major Gene/QTL Identified** | **Marker Type Used** | **References** |
| --- | --- | --- | --- | --- |
| Tomato | Fruit weight | *fw2.2*, *lc*, *fas* | SSR, SNP | Frary et al., 2000 |
| Carrot | Beta-carotene content | *Y*, *Y2*, *Or* | SNP | Arango et al., 2010 |
| Cucumber | Flowering earliness | *Ef1.1*, *F* | SSR | Li et al., 2011 |
| Pepper | Fruit pungency | *Pun1*, *pAMT* | SCAR | Stewart et al., 2005 |
| Onion | Bulb colour | *MYB1*, *ACO* | SNP | Martin et al., 2009 |

Yield in vegetable crops is a multifaceted trait that encompasses several components, including total biomass, fruit or tuber number, individual fruit weight, plant architecture, flowering behavior, and the efficiency of resource partitioning. These components can differ drastically among vegetable types—for instance, fruit yield in tomato, leafy biomass in spinach, root mass in carrot, and pod productivity in bean—yet they are all crucial endpoints of yield selection. The genetic control of yield traits is largely polygenic and often involves epistatic interactions, pleiotropic effects, and genotype-by-environment (G × E) interactions, which collectively influence phenotypic expression. Numerous QTLs have been mapped in major vegetable crops for yield-related traits. For example, in tomato, the *fw2.2* QTL has been linked to fruit weight and represents one of the earliest and most significant yield QTLs identified. Similarly, QTLs associated with plant height, fruit set, and harvest index have been mapped in pepper, eggplant, and cucumber (11,16)

The role of flowering and maturity genes in yield determination is also pivotal. Genes regulating photoperiod sensitivity, floral meristem development, and hormonal balance (particularly gibberellins and cytokinins) indirectly control yield potential by influencing the length of vegetative and reproductive phases. MAS has enabled breeders to select for early flowering and determinate growth habits in crops like tomato and cowpea, facilitating synchronized fruit set and mechanical harvest (17,18)

Quality traits in vegetables are equally complex, encompassing a broad spectrum of attributes such as flavour, colour, texture, nutritional composition, shelf life, and processing suitability. These traits are directly linked to consumer preference and marketability. From a breeding standpoint, many quality traits are notoriously difficult to select for phenotypically, as they are often measurable only at maturity or post-harvest and may require sophisticated biochemical assays. Molecular breeding thus offers a viable strategy to select for these traits early and non-destructively (11,12)

Colour and visual appeal are major quality parameters, especially in fruiting vegetables like tomato, pepper, and brinjal. These traits are commonly associated with the accumulation of pigments such as lycopene, beta-carotene, anthocyanins, and chlorophylls. Genetic studies have identified key regulatory genes and QTLs controlling carotenoid biosynthesis pathways. In tomato, for instance, the *Beta* gene controls beta-carotene content, while *old-gold* (og) and *hp* (high pigment) loci influence overall pigment accumulation and intensity. Marker-assisted selection has been utilized to improve fruit colour intensity and nutritional value through targeted introgression of such loci (16,18)

Flavour and taste are dictated by a combination of sugars, acids, volatile compounds, and amino acid profiles. In many vegetable crops, especially tomato and melon, flavour QTLs have been dissected through both traditional mapping and metabolomics-integrated approaches. The *LIN5* gene in tomato, which encodes a cell wall invertase, has been associated with sugar accumulation, influencing sweetness and soluble solids content. Such genes and their linked markers serve as prime candidates for quality improvement via MAS (11,18)

Texture and firmness are vital for post-harvest shelf life and processing quality. These traits are particularly important in crops like tomato and cucumber, where firmness influences transportability and shelf life. Genes related to cell wall degradation (e.g., polygalacturonase, expansin, and pectin methylesterase) are targets of MAS to retain firmness and delay softening. In tomato, for example, the *rin* (ripening inhibitor) and *nor* (non-ripening) genes have been utilized to modify ripening behavior and improve shelf stability (19,20)

Nutritional quality traits, especially those related to vitamin and mineral content, are gaining increasing importance under the global mandate for nutrient-dense diets (7,9) Vegetables are primary sources of micronutrients such as vitamin A (beta-carotene), vitamin C, folate, iron, and zinc. Genetic variability for these traits exists within crop gene pools and can be captured and enhanced through MAS. For instance, orange-fleshed carrot varieties rich in beta-carotene have been developed through QTL mapping of the *Y*, *Y2*, and *Or* genes, which regulate carotenoid accumulation in root tissues. In broccoli and leafy vegetables, QTLs associated with glucosinolate and flavonoid content have been identified and targeted in breeding efforts aimed at developing health-promoting cultivars (20,21)

Shelf life and storability are critical traits from the supply chain and consumer standpoint. These attributes are particularly sensitive to genetic and environmental factors. Ethylene biosynthesis and signalling genes play central roles in ripening and senescence. Markers linked to *ACO* (1-aminocyclopropane-1-carboxylate oxidase) and *ACS* (ACC synthase) genes in tomato and pepper are being used to modulate ethylene response and delay ripening for extended shelf life. Additionally, transcription factors such as *EIN* (ethylene insensitive) and *EIL* (EIN-like) are also being investigated for their utility in regulating post-harvest physiology (22,23)

An additional layer of complexity in the genetic control of both yield and quality traits is introduced by epigenetic regulation and gene-by-environment interactions. Epigenetic mechanisms such as DNA methylation and histone modifications can influence gene expression without altering DNA sequences, thereby affecting trait manifestation. For instance, expression variation in fruit firmness and sugar metabolism genes can be attributed to promoter methylation. While the field of epigenetics in vegetable breeding is still emerging, it holds potential for the development of stable traits that can be fixed through MAS if linked epigenetic markers are identified (21,22)

Moreover, the use of multi-parent advanced generation intercross (MAGIC) populations and nested association mapping (NAM) populations in vegetables is providing new insights into the polygenic control of complex traits. These populations, with their increased recombination and genetic diversity, offer enhanced power for detecting minor-effect QTLs and for constructing high-resolution genetic maps. Such approaches are especially beneficial for unraveling the genetic networks underlying traits like yield stability, flavour complexity, and micronutrient density (23,24)

In the context of breeding for broad adaptability, it is also crucial to understand the genetic basis of phenotypic plasticity—how a genotype performs across varying environments. Recent studies using genotype-by-environment interaction models and stability indices have led to the identification of QTLs associated with yield stability in tomato and other crops. Incorporating these loci through MAS can help in developing cultivars that are not only high yielding under optimal conditions but also resilient under suboptimal or stress-prone environments (27,28)

To effectively exploit the genetic potential of yield and quality traits in vegetables, there is a need for integrated approaches that combine MAS with physiological, biochemical, and omics-based tools. Functional genomics, transcriptomics, proteomics, and metabolomics are being used to complement QTL studies and to validate candidate genes at the expression and metabolic levels. These systems biology approaches offer a holistic understanding of trait development and can guide the prioritization of key markers for MAS programs(23,24)

 **Applications of Marker-Assisted Selection in Vegetable Crops**

The practical deployment of Marker-Assisted Selection (MAS) has significantly transformed breeding strategies in vegetable crops, offering an efficient means to select for complex traits with high precision and speed. (11,17)As the demand for higher productivity, improved nutritional quality, and resilience to environmental and biotic stresses continues to grow, MAS provides a scientific and scalable approach to meet these multidimensional challenges. In vegetables, MAS has been successfully utilized to enhance both yield traits and quality parameters, with growing evidence of its utility in pyramiding multiple genes, reducing breeding cycles, and developing varieties tailored for specific markets and production systems (18,20)

**Enhancing Yield Traits through MAS**

Yield improvement has traditionally been a central objective in vegetable breeding programs. Unlike staple cereals, yield in vegetables is defined not only by total biomass or harvestable unit count but also by size, uniformity, harvest index, and maturity synchronization. MAS has facilitated the introgression and stacking of QTLs linked to these components in several vegetable species (18,20)

In tomato, which serves as a model crop for molecular breeding, several major QTLs have been identified and utilized in yield enhancement programs. The *fw2.2* QTL, for example, regulates cell division and has been strongly associated with increased fruit weight. Other loci such as *lc* (locule number) and *fas* (fascinated inflorescence) contribute to fruit size and morphology. These QTLs, when used in MAS-based selection, have enabled breeders to achieve a balance between yield, shape, and firmness—traits often in trade-off with each other. The use of tightly linked markers has allowed for effective introgression of these QTLs into elite backgrounds without the need for extensive field-based evaluation (27,28)

In brinjal (eggplant), MAS has been employed to select for higher fruit set, improved branching, and flower retention, all of which contribute to increased yield potential. The identification of candidate markers associated with shoot architecture and plant vigor has accelerated hybrid development with better biomass partitioning. Similarly, in cucumber, yield-related traits such as fruit length, girth, and number per plant are being enhanced through QTL mapping of associated markers. Efforts are ongoing to introgress early flowering and monoecious traits to support yield uniformity and increase harvest frequency (19,20)

Cucurbit crops like melon and bitter gourd have also benefited from MAS strategies targeting traits like internode length, node number to first female flower, and earliness. MAS is especially helpful in hybrid breeding programs, where early generation selection for these traits reduces the breeding cycle and enhances genetic gains (17,18)

The use of MAS to develop parthenocarpic varieties—those capable of setting fruit without pollination—has been explored in crops such as cucumber and tomato, with clear implications for improving yield under pollination-constrained environments like greenhouses or during adverse weather conditions (21,22)

 **Quality Trait Improvement Using MAS**

Quality traits in vegetables, which include sensory, nutritional, and post-harvest attributes, directly influence market value, consumer acceptance, and health benefits. These traits are often complex and challenging to measure accurately through phenotypic screening, making them ideal candidates for MAS (12,16)

In tomato, the enhancement of nutritional quality has been a major focus of MAS. Genes such as *Beta*, *old-gold (og)*, and *high pigment (hp)* have been linked to elevated carotenoid content, particularly lycopene and beta-carotene, which contribute to both fruit colour and antioxidant properties (5) Markers associated with these genes have been used to breed tomatoes with deeper red or orange pigmentation, indicating higher phytonutrient content. Additionally, loci associated with sugar accumulation, such as *LIN5*, and acid balance have been deployed to fine-tune the flavour profile and enhance taste appeal (24,26)

Carrot breeding programs have similarly leveraged MAS to improve carotenoid concentration. QTLs linked to the *Or* gene have been associated with the accumulation of alpha- and beta-carotene in the root cortex. Marker-assisted selection using these loci has resulted in the development of carrot lines with intensified orange coloration and enhanced provitamin A content—traits that are crucial in biofortification and public health nutrition contexts (18,19)

In pepper (Capsicum spp.), MAS has been applied to improve capsaicin content and colour attributes. Genes controlling capsaicinoid biosynthesis and carotenoid accumulation, such as *Pun1* and *Ccs*, have been mapped and used to distinguish between pungent and sweet types as well as to manipulate fruit colour for aesthetic and processing purposes (21,22)

Texture and post-harvest quality are also significant targets. In cucumber and zucchini, traits such as fruit firmness and colour retention are being improved using markers linked to cell wall-related enzymes and pigment biosynthetic genes. These traits determine market shelf life, transportability, and overall consumer preference (23,24)

For leafy vegetables such as spinach and lettuce, quality breeding efforts have centered around shelf life, leaf colour, and nutrient density. MAS is being utilized to incorporate slow-bolting traits and resistance to oxidation-induced leaf degradation, which affects shelf stability and fresh-cut quality (27,28)

 **Disease Resistance and Stress Tolerance as Yield & Quality Enhancers**

Though not always classified under yield or quality traits directly, resistance to biotic and abiotic stresses significantly contributes to both by minimizing losses and ensuring consistent performance. MAS has proven especially effective for incorporating disease resistance genes into high-performing vegetable backgrounds (20,21)

In tomato, genes conferring resistance to Tomato yellow leaf curl virus (TYLCV), Fusarium wilt, and bacterial wilt have been identified and used in MAS pipelines. The *Ty* series (Ty-1 to Ty-5) of genes are particularly well-known for their effectiveness against TYLCV and have been pyramided into elite cultivars using linked SSR and SNP markers. The pyramiding strategy ensures durable resistance and minimizes the likelihood of pathogen breakdown (27,28)

In cucumber, MAS has facilitated the introgression of powdery mildew resistance through markers linked to *pm* genes. Similar approaches have been adopted in capsicum, okra, and bottle gourd, where viral and fungal resistances have been enhanced using tightly linked markers. By ensuring crop health and reducing pesticide dependence, MAS indirectly but significantly boosts both yield and quality (24,25)

Abiotic stress tolerance, though more complex due to its polygenic nature, has also seen some progress. In tomato, tolerance to salinity and drought has been linked to QTLs that modulate traits like osmotic balance, root depth, and stomatal behavior. Selection for such traits using MAS, although still in early stages, holds promise for the development of climate-resilient cultivars (27,28)

**MAS in Hybrid Breeding and Seed Purity Maintenance**

MAS has also been applied in hybrid breeding programs, where early identification of parental lines with complementary traits is crucial. In vegetable crops where hybrid vigor (heterosis) is exploited—such as tomato, pepper, and cabbage—markers are used to confirm the presence of restorer or male sterility alleles, identify heterotic groups, and maintain seed purity. In onion, where cytoplasmic male sterility is widely used, MAS has simplified the identification and validation of sterile and fertile lines through mitochondrial and nuclear markers (26,27)

 **Impact and Future Applications**

The success stories of MAS in vegetable crops are expanding, with numerous cultivars developed and released carrying marker-selected traits. Programs supported by international collaborations and public-private partnerships have accelerated MAS adoption in both developed and developing countries (29,30) With the continuous development of high-throughput genotyping platforms, decreasing costs of sequencing, and availability of comprehensive reference genomes, the application scope of MAS is poised to broaden (30,31)

**Case Study: Marker-Assisted Breeding for TYLCV Resistance in Tomato**

**Background**

Tomato Yellow Leaf Curl Virus (TYLCV) is a serious viral disease affecting tomato (Solanum lycopersicum) production across tropical, subtropical, and Mediterranean regions. Transmitted by the whitefly (*Bemisia tabaci*), TYLCV causes stunted growth, leaf curling, flower drop, and substantial yield losses, often up to 90% in severe infestations. Managing TYLCV through vector control alone is ineffective and unsustainable, particularly in low-input farming systems. Thus, developing host-plant resistance has emerged as the most effective and environmentally sound approach to combat this disease 32)

**Discovery of Resistance Genes and Markers**

The earliest sources of TYLCV resistance were identified in wild tomato relatives such as *Solanum chilense* and *Solanum peruvianum*. Through interspecific hybridization and backcrossing, resistance loci were transferred into cultivated tomato backgrounds (32,33) Five major resistance genes—Ty-1, Ty-2, Ty-3, Ty-4, and Ty-5—have been characterized to date:

* Ty-1 and Ty-3 are allelic and encode RNA-dependent RNA polymerase (RDR), contributing to transcriptional gene silencing against TYLCV (32,33).
* Ty-2 originates from *S. habrochaites* and provides monogenic resistance (32,33).
* Ty-5 encodes a mutated version of the *pelota* gene involved in translation, providing recessive resistance (Lapidot et al., 2015) (32,33).

Flanking markers were developed for these genes to facilitate their introgression into commercial lines using marker-assisted backcrossing (MABC). For example, the SCAR marker *P6-25* is tightly linked to the Ty-2 locus on chromosome 11 (Hanson et al., 2000), while *SlNAC1* is used for tracking Ty-1/Ty-3 (34).

**Breeding Strategy and Deployment**

The breeding process typically involves the use of foreground selection to ensure the presence of the resistance gene, background selection to recover the recurrent parent genome, and phenotypic selection for horticultural performance. In India, the Indian Institute of Horticultural Research (IIHR) developed the hybrid Arka Rakshak by pyramiding Ty-2 and Ty-3 using tightly linked markers, ensuring broad-spectrum and durable resistance.

In the Philippines, the East-West Seed Company released the hybrid ‘Diamante Max’, developed by introgressing Ty-2 through marker-assisted backcrossing into an elite recurrent parent. The breeding program used marker-assisted selection in early segregating generations, significantly reducing the breeding cycle while maintaining desirable fruit traits (34,35)

**Impact and Benefits**

The integration of MAS into TYLCV-resistance breeding has had considerable economic and agronomic impact. Resistant hybrids like 'Arka Rakshak' and 'Diamante Max' are widely cultivated in South and Southeast Asia, where TYLCV pressure is high. These hybrids not only reduce the need for chemical sprays (thereby lowering input costs and environmental impact) but also provide stable yields under endemic conditions (35).

Lapidot and Friedmann (2002) demonstrated that plants carrying Ty-1 or Ty-2 showed significantly lower viral titers and symptom expression compared to susceptible lines. Similarly, Vidavski et al. (2008) confirmed that Ty-3 confers tolerance under field conditions even when whitefly populations are high. The use of MAS accelerated the deployment of these genes into adapted germplasm without relying on artificial inoculation or symptom screening, which can be unreliable in field settings (34,35).

 **Integration with Other Genomic Tools**

Marker-Assisted Selection (MAS) has revolutionized plant breeding by enabling precise and early-stage selection of traits based on linked molecular markers. However, the complexity of many agronomic and quality traits—especially those that are polygenic and influenced by environmental interactions—necessitates integration with other genomic tools for enhanced predictive accuracy and genetic gains(2,36).The synergy between MAS and broader genomic technologies such as Genomic Selection (GS), Genome-Wide Association Studies (GWAS), gene editing platforms like CRISPR/Cas, and omics-based approaches (transcriptomics, metabolomics, and phenomics) is shaping a new era of precision breeding in vegetable crops (36,37).

Genomic Selection (GS) represents a paradigm shift from MAS by enabling selection based not just on a few known markers but on genome-wide marker information. While MAS is effective for traits governed by major genes or large-effect QTLs, GS is more suited for complex traits influenced by many small-effect loci, such as yield stability, nutritional content, or abiotic stress tolerance (37,38). In GS, a training population is both genotyped and phenotyped to develop a statistical model that predicts genomic estimated breeding values (GEBVs). These predictions can then be used to select individuals in a testing population solely based on genotypic data, thus accelerating the breeding cycle. In vegetable crops like tomato and pepper, GS models have been developed for traits such as fruit size, shape, and disease resistance. Studies have shown that incorporating both additive and non-additive effects improves prediction accuracy, especially in hybrid breeding programs (39,40).

Genome-Wide Association Studies (GWAS) complement MAS by enabling the identification of novel QTLs and trait-linked markers across diverse germplasm collections. Unlike biparental mapping populations used in traditional QTL analysis, GWAS uses natural populations to uncover marker-trait associations with higher resolution due to historical recombination events. In crops like cucumber, melon, and carrot, GWAS has uncovered markers associated with fruit firmness, sugar content, carotenoid levels, and flowering time (41,42). These markers can then be validated and applied in MAS pipelines. The use of GWAS panels, such as nested association mapping (NAM) and multi-parent advanced generation intercross (MAGIC) populations, has further enhanced the power to detect rare alleles and interactions, expanding the marker repertoire for breeding applications (43,44).

Gene editing technologies, particularly CRISPR/Cas9, are emerging as precise tools for functional validation of candidate genes and for creating novel alleles with improved traits. Unlike MAS, which relies on existing variation, gene editing allows breeders to introduce or knock out specific genes to achieve desired outcomes(43,44). In tomato, CRISPR has been successfully used to create mutations in the *SlCLV3* gene to alter fruit size and locule number, and in *SlAGAMOUS-LIKE6* to delay ripening and improve shelf life. These edited lines, when combined with MAS-selected backgrounds, offer a dual advantage: precision introgression of major traits and rapid tailoring of specific functions. As regulatory landscapes around gene editing become clearer, especially for cisgenic and targeted mutagenesis approaches, CRISPR is likely to be routinely integrated with MAS for trait stacking and accelerated variety development (45,46).

Transcriptomics and proteomics provide valuable insights into gene expression and regulatory networks underlying trait development. For example, RNA-seq analyses in tomato and pepper under drought stress have identified upregulated transcription factors and signaling pathways associated with tolerance mechanisms. Similarly, expression profiling of fruit ripening stages has revealed dynamic gene networks that control firmness and flavour. By overlaying such expression data on QTL maps, breeders can prioritize candidate genes within QTL regions and select markers that represent functionally relevant genetic variation. This integration enhances the biological relevance of MAS and reduces the risk of selecting non-causal markers(47,48).

Metabolomics, the study of the complete set of metabolites in a biological sample, adds another layer of depth by linking genotype to phenotype through biochemical intermediates. In vegetable crops where flavour, nutrition, and pigment content are critical, metabolite profiling can pinpoint key biochemical pathways that differ between genotypes (49,50). For instance, high-performance liquid chromatography (HPLC)-based metabolomics in carrot has been used to quantify beta-carotene and anthocyanin levels, which are then correlated with genetic markers for use in MAS. Similarly, volatile compounds that contribute to flavour in tomato have been associated with specific loci using combined metabolomic and genomic approaches. Such metabolite-assisted breeding, when aligned with MAS, facilitates the improvement of sensory and nutritional traits that are otherwise difficult to select phenotypically(51,52).

Phenomics, the high-throughput measurement of plant traits using imaging, spectroscopy, and remote sensing, addresses one of the key bottlenecks in breeding: precise and large-scale phenotyping. While MAS and genomic tools provide detailed genotypic data, breeding progress is often limited by the capacity to phenotype traits accurately and efficiently. In crops like lettuce, cucumber, and eggplant, phenomics platforms are now used to assess growth rate, leaf area, colour intensity, and stress responses, which are then linked to genetic markers. This enables more accurate QTL mapping and improves the predictive power of MAS models, especially for traits affected by the environment (41,43).

Another promising area of integration is machine learning and artificial intelligence (AI), which are increasingly used to analyze large-scale genomic, phenotypic, and environmental data. Machine learning models can predict genotype performance across multiple environments, identify epistatic interactions, and assist in marker selection for MAS pipelines. In practical breeding programs, decision-support tools powered by AI can guide parental selection, crossing designs, and trait prioritization, making MAS not only more efficient but also more strategic (44).

The convergence of these tools with MAS is leading to the emergence of integrated breeding platforms, where genotyping, phenotyping, and data analytics are harmonized to support real-time breeding decisions. Open-source databases like the Sol Genomics Network (SGN) and G2P-SOL provide access to genomic, phenotypic, and functional data for Solanaceous crops, supporting community-wide efforts in marker development and validation. Similarly, initiatives like the Breeding Insight project aim to deliver scalable digital infrastructure for integrating MAS and genomics in public breeding programs (52,53).

 **Challenges and Limitations**

Despite its promise, Marker-Assisted Selection (MAS) faces several challenges that limit its widespread and effective application in vegetable crop breeding. A key technical limitation lies in the incomplete linkage between markers and target genes. Recombination events can break the association between marker and trait, leading to inaccurate selection, especially in polygenic traits influenced by genotype-by-environment (G×E) interactions (19,31).

Another major constraint is the lack of validated markers and genomic resources in minor or underutilized vegetables, which restricts the application of MAS beyond well-studied crops like tomato and pepper. This challenge is compounded by high genotyping costs and the lack of infrastructure and technical expertise, particularly in public-sector and low-income breeding programs (3,7).

Integration of MAS into breeding pipelines is often hampered by operational disconnects between lab-based genotyping and field-based phenotyping, resulting in underutilization of molecular data. Additionally, intellectual property restrictions on some proprietary markers or technologies can limit accessibility (10.12).

Biologically, traits such as flavour, aroma, and shelf life are complex, with unclear genetic bases, making it difficult to identify reliable markers. Furthermore, over-reliance on a narrow set of resistance genes may lead to genetic vulnerability and rapid breakdown of resistance under field conditions (44).

 **Future Prospects and Strategic Directions**

The continued evolution of molecular breeding technologies is positioning Marker-Assisted Selection (MAS) as a central tool in next-generation vegetable crop improvement. While MAS has already demonstrated its value in enhancing yield, quality, and stress resilience, the future of MAS lies not just in refining current methods but in strategically integrating them with cutting-edge technologies, participatory approaches, and sustainable agricultural systems (47,48).

One of the most promising future directions for MAS is its integration with genomic selection (GS) and artificial intelligence (AI). While MAS typically targets major genes or QTLs, GS captures genome-wide variation and is particularly effective for traits with complex inheritance, such as yield stability or nutritional quality. By combining MAS for known loci with GS models that predict performance based on genome-wide markers, breeders can achieve both trait precision and holistic improvement. AI-driven decision-support systems are also emerging to assist in predicting marker effects, optimizing crosses, and managing large datasets, thereby increasing breeding speed and reducing costs (42,47).

Another critical area for future expansion is the democratization of MAS in underutilized and minor vegetables, many of which are nutritionally dense and locally important but currently lack genomic resources. Investing in reference genomes, diversity panels, and marker libraries for these crops will broaden the impact of MAS and contribute to agrobiodiversity and dietary diversity. Global initiatives like the African Orphan Crops Consortium (AOCC) and G2P-SOL are already working toward this goal, but more coordinated efforts are needed to mainstream MAS across a wider crop base (43,48).

The development of speed breeding protocols, particularly for vegetables with long generation times, presents another opportunity. By combining MAS with controlled-environment breeding cycles, generation time can be significantly reduced, allowing for faster varietal turnover. When supported by high-throughput genotyping platforms and rapid phenotyping technologies, this approach can cut breeding timelines from years to a matter of months (58,59).

The application of multi-omics integration—combining genomics with transcriptomics, proteomics, and metabolomics—is expected to refine MAS further. This systems-level understanding of trait expression will enable breeders to develop more biologically meaningful markers and select for traits that are better aligned with physiological performance. For example, metabolomics-informed MAS could help in developing vegetable varieties with enhanced flavour, post-harvest quality, and functional health compounds, which are increasingly in demand among health-conscious consumers (60,61).

Participatory breeding and product profile-based variety development are also emerging as strategic directions that can complement MAS. Instead of relying solely on trait targets defined in research labs, breeders are now incorporating end-user preferences—farmers, consumers, processors—into variety design. MAS can be aligned with these product profiles to ensure that the improved lines meet both technical standards and market needs. This approach is especially important in smallholder-dominated farming systems, where local acceptability determines varietal success (62,63).

Furthermore, climate change adaptation is a pressing future focus. MAS can be harnessed to stack genes for tolerance to heat, salinity, drought, and emerging pests and diseases, enabling vegetables to perform reliably under stress-prone conditions. Breeding for resilience, rather than just high yield, will become a key mandate. Developing multi-stress tolerant cultivars using MAS-supported pyramiding strategies will be vital for food security under future climate scenarios (47,48).

On the policy and institutional side, building long-term capacity in molecular breeding is essential. This includes establishing regional genotyping hubs, training molecular breeders, and embedding MAS into national agricultural research systems. Public-private partnerships will continue to play a crucial role in scaling MAS tools, sharing markers, and ensuring equitable access to technology. International donor programs and CGIAR centers are well-positioned to support such integrated platforms (54,55).

**Conclusion**

Marker-Assisted Selection (MAS) has emerged as a transformative approach in modern vegetable crop breeding, bridging the gap between molecular genetics and practical cultivar development. By allowing precise and early-stage selection of genotypes based on DNA markers linked to desirable traits, MAS has significantly enhanced the efficiency, speed, and accuracy of breeding programs. Its contributions are evident across a range of vegetable crops—from tomato and pepper to carrot and cucumber—where it has enabled the development of high-yielding, disease-resistant, and nutritionally superior varieties.

The review has demonstrated how MAS has been successfully applied to improve complex traits such as fruit yield, flavour, carotenoid content, shelf life, and resistance to both biotic and abiotic stresses. Furthermore, it has highlighted the value of MAS in hybrid breeding systems, seed purity maintenance, and germplasm enhancement. Through detailed case studies, such as the breeding of TYLCV-resistant tomatoes, the practical utility and socio-economic impact of MAS are clearly evident.

Yet, MAS is not without limitations. Challenges such as incomplete marker-trait linkage, high genotyping costs, lack of infrastructure, and limited resources for minor crops continue to constrain its full potential. Moreover, the integration of MAS into traditional breeding systems requires organizational adaptation, continuous capacity-building, and alignment with farmer and market needs.

Looking ahead, the future of MAS lies in its strategic integration with complementary genomic tools such as genomic selection, GWAS, CRISPR/Cas gene editing, and multi-omics technologies. Speed breeding, AI-assisted prediction tools, and open-access data platforms will further empower breeders to make informed, rapid, and market-driven decisions. Crucially, embedding MAS into participatory breeding models and focusing on climate-resilient and nutritionally enriched cultivars will ensure its relevance in addressing both global food security and local adaptation needs.

**Disclaimer (Artificial intelligence)**

Author(s) hereby declares that NO generative AI technologies such as Large Language Models (ChatGPT, COPILOT, etc.) and text-to-image generators have been used during the writing or editing of this manuscript.

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