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Marker-assisted selection in ornamental plant breeding

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Abstract

Ornamental plants play a vital role in the global horticulture industry due to their aesthetic, economic, and cultural importance. Breeding of ornamental crops focuses on traits such as flower colour, shape, fragrance, vase life, flowering time, and resistance to biotic and abiotic stresses. Conventional breeding methods in ornamentals are often limited by long breeding cycles, high heterozygosity, polyploidy, and strong environmental influence on phenotypic expression. Marker-assisted selection (MAS) has emerged as a powerful molecular breeding tool that enhances selection efficiency by utilizing DNA markers linked to desirable genes or quantitative trait loci (QTLs). This review paper discusses the principles of MAS, types of molecular markers, applications in ornamental crop improvement, advantages, limitations, and future prospects of MAS in floriculture breeding.

Keywords: Marker-assisted selection, ornamental plants, molecular markers, floriculture, plant breeding.

Introduction

Floriculture is a rapidly expanding sector of horticulture, contributing significantly to the global agricultural economy. Ornamental crops such as rose, chrysanthemum, carnation, gladiolus, gerbera, orchid, and marigold are cultivated for cut flowers, loose flowers, potted plants, and landscaping purposes. Breeding programs in ornamental crops aim to improve aesthetic traits, adaptability, yield, and resistance to diseases and environmental stresses.

Traditional breeding methods rely mainly on phenotypic selection, which is time-consuming and often inefficient due to environmental effects on trait expression. Moreover, ornamental crops exhibit complex genetic features such as polyploidy, vegetative propagation, self-incompatibility, and high heterozygosity. These challenges limit the progress of conventional breeding. Marker-assisted selection integrates molecular genetics with classical breeding, allowing

precise and early selection of superior genotypes and accelerating the development of improved ornamental varieties.

Concept and Principles of Marker-Assisted Selection

Marker-assisted selection is a breeding technique in which selection is based on molecular markers tightly linked to genes or QTLs governing traits of interest. Molecular markers serve as genetic landmarks, enabling indirect selection of target traits without waiting for phenotypic expression.

The basic principles of MAS include:

- Identification of polymorphic DNA markers
- Establishment of linkage between markers and target traits
- Validation of markers across populations
- Application of markers for selection in breeding programs

MAS is particularly useful for traits that are:

- Difficult to measure phenotypically
- Expressed late in the plant's life cycle
- Controlled by multiple genes
- Influenced strongly by environmental factors

Workflow of Marker-Assisted Selection in Ornamental Breeding

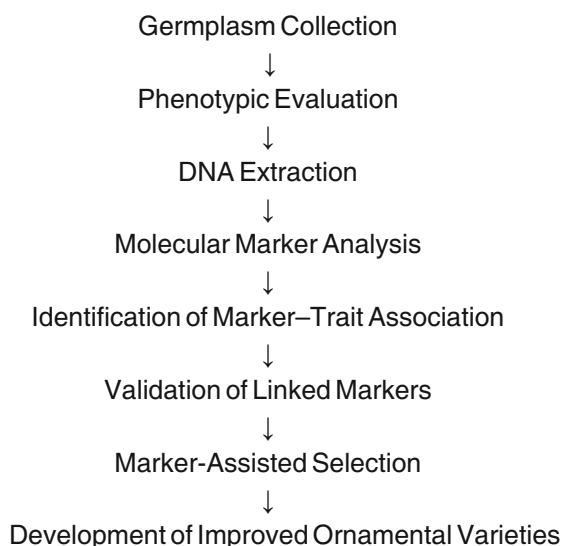


Fig. 1: General workflow of marker-assisted selection in ornamental plant breeding

Types of Molecular Markers Used in MAS

Several molecular markers have been employed in ornamental plant breeding:

Restriction Fragment Length Polymorphism (RFLP)

RFLP markers were among the first DNA-based markers used in plant breeding. Restriction Fragment Length Polymorphism (RFLP) detects genetic variation by identifying differences in DNA fragment lengths generated after digestion with restriction enzymes. Although highly reliable, the technique is labour-intensive and requires large amounts of high-quality DNA.

Restriction Fragment Length Polymorphism (RFLP) is a DNA-based molecular marker technique used to identify genetic variation among individuals by detecting differences in the length of DNA fragments produced after digestion with specific restriction enzymes. These variations arise due to mutations such as insertions, deletions, or single base changes that create or eliminate restriction enzyme recognition sites within the genome. As a result, individuals show distinct fragment patterns, which can be used to compare genetic makeup, assess diversity, and study inheritance in plant breeding and genetics.

Advantages of RFLP:

Co-dominant nature: Allows clear differentiation between homozygous and heterozygous genotypes, making it useful for inheritance and segregation studies.

High reproducibility: Results are consistent across laboratories since RFLP is not PCR-dependent.

High reliability and accuracy: Detects true DNA sequence variations with low error rates.

Locus-specific markers: Probes hybridize to specific genomic regions, enabling precise genetic analysis.

Neutral markers: Generally unaffected by environmental conditions or developmental stages.

Limitations of RFLP:

Large DNA requirement: Needs a high quantity of intact, high-quality genomic DNA, which is difficult to obtain from some plant tissues.

Labor-intensive and time-consuming: Involves multiple steps such as restriction digestion, gel

electrophoresis, and Southern blotting, making it slow.

Low throughput: Not suitable for analysing a large number of samples simultaneously.

Use of labelled probes: Often requires radioactive or chemically labelled probes, raising safety and disposal concerns.

High cost: Expenses related to enzymes, probes, membranes, and labour make it less economical.

Limited automation: Difficult to automate compared to PCR-based marker techniques.

Random Amplified Polymorphic DNA (RAPD)

RAPD markers are simple and cost-effective but show poor reproducibility, limiting their widespread use in MAS.

Random Amplified Polymorphic DNA (RAPD) is a PCR-based molecular marker technique used to detect genetic variation among organisms by amplifying random segments of genomic DNA using short, arbitrary primers. Random Amplified Polymorphic DNA (RAPD) is a PCR-based molecular marker technique used to detect DNA polymorphism among individuals by amplifying random segments of genomic DNA using short, single primers of arbitrary nucleotide sequence. RAPD does not require prior knowledge of the DNA sequence, making it a simple and rapid method for genetic analysis.

Advantages:

- Simple, rapid, and cost-effective
- No prior sequence information required
- Requires small quantity of DNA
- Simple, rapid, and cost-effective technique
- Does not require prior DNA sequence information
- Requires only a small quantity of DNA
- Useful for screening a large number of samples
- Suitable for laboratories with limited resources

Limitations:

- Dominant marker (cannot distinguish heterozygotes)
- Low reproducibility due to sensitivity to PCR conditions
- Less reliable for detailed genetic analysis
- Poor reproducibility due to sensitivity to PCR conditions
- Dominant markers; cannot distinguish between homozygous and heterozygous genotypes

Results can vary between laboratories

Limited reliability for precise genetic mapping

Not suitable for detailed or high-resolution genetic analysis

Amplified Fragment Length Polymorphism (AFLP)

AFLP markers provide high polymorphism and genome coverage, making them useful in genetic diversity and linkage studies in ornamentals.

Amplified Fragment Length Polymorphism (AFLP) is a highly sensitive DNA fingerprinting technique that combines the principles of restriction digestion and PCR amplification to detect genetic variation across the genome. Amplified Fragment Length Polymorphism (AFLP) is a highly sensitive and reliable DNA-based molecular marker technique that combines the principles of restriction digestion and polymerase chain reaction (PCR) to detect genetic polymorphism across the entire genome. AFLP does not require prior sequence information and is widely used for genetic diversity analysis, linkage mapping, and population genetics studies.

Advantages:

- High reproducibility and reliability
- Detects large numbers of polymorphic loci
- No prior sequence information required
- High reproducibility and reliability
- Detects large numbers of polymorphic loci
- No prior sequence information required
- Wide genome coverage
- High sensitivity
- Applicable to many species
- Useful for genetic diversity and mapping studies

Limitations:

- Dominant marker (limited detection of heterozygosity)
- Technically demanding and relatively expensive
- High cost
- Requires high-quality DNA
- Time-consuming
- Difficult band scoring
- Limited transferability of markers

Simple Sequence Repeats (SSR)

SSR markers are co-dominant, highly polymorphic, and reproducible. They are widely used in MAS for ornamental crops like rose and chrysanthemum.

Simple Sequence Repeats (SSR), also known as

microsatellites, are **PCR-based molecular markers** consisting of short tandemly repeated DNA sequences (1–6 base pairs) such as $(CA)_n$, $(AT)_n$, $(GATA)_n$ distributed throughout the genome. Simple Sequence Repeats (SSRs), also known as microsatellites, are short tandemly repeated DNA sequences consisting of 1–6 base pair motifs (e.g., A, AT, GA, CAG) that are widely distributed throughout the genome. The number of repeat units at a given SSR locus varies among individuals, resulting in length polymorphism that can be detected using PCR.

Advantages:

- Co-dominant marker (detects heterozygotes)
- Highly polymorphic and reproducible
- Requires small amount of DNA
- Locus-specific markers
- Excellent reproducibility
- Wide genome distribution
- Requires small amount of DNA
- Amenable to automation
- Data easily comparable
- Useful for long-term studies

Limitations:

- Development of SSR primers is time-consuming and costly
- Requires prior sequence information

Single Nucleotide Polymorphism (SNP)

SNP markers are abundant throughout the genome and are increasingly used due to advances in next-generation sequencing technologies.

Single Nucleotide Polymorphism (SNP) is a DNA-based molecular marker representing a variation at a single nucleotide (A, T, C, or G) position in the genome among individuals of a species. Single Nucleotide Polymorphisms (SNPs) are the most basic form of DNA variation, involving a change of a single nucleotide (A, T, C, or G) at a specific position in the genome among individuals of a species. SNPs are abundant, stable, and widely distributed across coding and non-coding regions of the genome.

Advantages:

- Abundant and evenly distributed across the genome
- Highly stable and reproducible
- Suitable for high-throughput and automated analysis

Highly abundant and stable throughout the genome
Co-dominant markers, allowing detection of heterozygotes

Amenable to high-throughput automated analysis

Useful for fine-scale genetic mapping and trait association studies

Limitations:

Mostly bi-allelic, providing lower polymorphism per locus

Requires advanced equipment and bioinformatics support

Typically, bi-allelic, providing less information per locus than SSRs

High initial cost for SNP discovery and genotyping platforms

Requires advanced equipment and bioinformatics support

May require high-quality DNA for reliable detection

Applications of MAS in Ornamental Plant Breeding

Marker-assisted selection has been applied to improve several important traits in ornamental crops.

Improvement of Flower Colour and Pigmentation

Flower colour is a key aesthetic trait controlled by pigment biosynthesis pathways such as anthocyanins and carotenoids. Molecular markers linked to colour genes enable early selection of desired flower colours in crops like rose, petunia, and chrysanthemum.

Breeding for Disease Resistance

Ornamental crops are susceptible to fungal, bacterial, and viral diseases. MAS facilitates selection for resistance genes against diseases such as powdery mildew, rust, and wilt, reducing reliance on chemical control.

Enhancement of Vase Life and Post-Harvest Quality

Vase life is an economically important trait in cut flowers. MAS allows indirect selection for delayed senescence, ethylene insensitivity, and improved post-harvest performance.

Flowering Time and Floral Traits

Markers linked to genes controlling flowering time, inflorescence architecture, and flower size are used to develop varieties with synchronized flowering and improved market value.

Stress Tolerance

Abiotic stresses such as heat, drought, and salinity

affect ornamental crop production. MAS helps in identifying QTLs associated with stress tolerance, enabling the development of resilient ornamental varieties.

Advantages of Marker-Assisted Selection

MAS offers several advantages over conventional breeding:

- Reduces breeding cycle duration
- Enables early selection at seedling stage
- Increases accuracy and efficiency of selection
- Minimizes environmental influence on selection
- Facilitates pyramiding of multiple genes
- Particularly useful for complex and low-heritability traits

Limitations and Challenges of MAS in Ornamentals

Despite its potential, MAS faces several challenges in ornamental breeding:

- Limited genomic resources for many ornamental crops
- High cost of molecular infrastructure and expertise
- Complex genome structures and polyploidy
- Poor marker-trait association due to genetic background effects
- Limited availability of validated markers.

Integration of MAS with Advanced Breeding Technologies

Recent advancements in genomics and biotechnology have enhanced the effectiveness of MAS. Integration with:

- Genomic selection (GS)
- High-throughput phenotyping
- Next-generation sequencing (NGS)
- Gene editing tools such as CRISPR-Cas9

is expected to revolutionize ornamental plant breeding and enable precise genetic improvement.

Future Prospects

The future of MAS in ornamental crops is promising due to declining costs of sequencing and increased availability of genomic data. Development of crop-specific molecular markers, improved bioinformatics tools, and international collaboration will further strengthen MAS-based breeding programs. MAS will play a crucial role in developing climate-resilient, high-quality ornamental varieties to meet global market demands.

The future of Marker-Assisted Selection (MAS) in ornamental crop improvement is highly promising due to rapid advancements in molecular biology and genomics. The declining cost of DNA sequencing and the increased availability of genomic and transcriptomic data have made MAS more accessible and efficient for ornamental breeding programs.

The development of crop-specific and trait-linked molecular markers will enhance the precision and reliability of selection for important ornamental traits such as flower color, fragrance, vase life, disease resistance, and stress tolerance. Improved bioinformatics tools and databases will further support the identification, validation, and utilization of markers in complex ornamental genomes.

International collaboration among research institutions and breeding companies will accelerate the exchange of genomic resources and breeding technologies. MAS is expected to play a key role in developing climate-resilient ornamental varieties capable of withstanding biotic and abiotic stresses. Overall, MAS will significantly contribute to the production of high-quality, uniform, and market-oriented ornamental crops, meeting the growing global demand of the floriculture industry.

Conclusion

Marker-assisted selection has emerged as an efficient and reliable approach for ornamental plant breeding. By overcoming the limitations of conventional breeding, MAS enables rapid and precise selection of desirable traits. Although challenges remain, continued advancements in molecular genetics and genomics will ensure the wider adoption of MAS, contributing significantly to sustainable floriculture development.

Marker-Assisted Selection (MAS) has emerged as a powerful and efficient tool in ornamental plant breeding, enabling precise and rapid improvement of economically important traits. By combining molecular markers with conventional breeding methods, MAS reduces breeding time, enhances selection accuracy, and overcomes limitations associated with complex traits and long breeding cycles in ornamental crops. The integration of MAS with advanced genomic technologies will further strengthen breeding programs, leading to the development of high-quality,

Table 1: Types of Molecular Markers Used in MAS

Molecular Marker	Nature	Advantages	Limitations
RFLP	Co-dominant	High reliability	Labor -intensive
RAPD	Dominant	Simple, low cost	Poor reproducibility
AFLP	Dominant	High polymorphism	Complex procedure
SSR	Co-dominant	Highly polymorphic, reproducible	Development cost
SNP	Co-dominant	Abundant, high throughput	Requires advanced tools

Table 2: Advantages of MAS in Ornamental Plant Breeding

Aspect	Benefit
Selection stage	Early seedling selection
Accuracy	High precision
Breeding cycle	Reduced time
Environment effect	Minimal
Gene pyramiding	Possible

Table 3: Limitations of MAS in Ornamentals

Constraint	Description
Genomic complexity	Polyploidy and heterozygosity
Marker availability	Limited in some crops
Cost	High initial investment
Technical skill	Requires trained personnel

disease-resistant, and climate-resilient ornamental varieties. Overall, MAS holds great potential for sustaining innovation and competitiveness in the global floriculture industry.

Conflict of Interest

The authors declare that there is no conflict of interest associated with this publication.

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