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Molecular breeding in ornamental plants: Recent trends and future prospects

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Abstract

Molecular breeding has transformed the ornamental plant industry by enabling breeders to introduce desirable traits with greater precision and speed compared to traditional methods. This review explores recent trends in molecular breeding techniques for ornamental plants, covering the period from 2010 to 2024. Key technologies discussed include marker-assisted selection (MAS), next-generation sequencing (NGS), genomic selection (GS), and genome editing techniques like CRISPR-Cas9. MAS has been instrumental in improving traits such as flower color and disease resistance by using molecular markers linked to specific genes. The use of NGS has expanded the genetic understanding of complex traits, such as floral scent and stress tolerance, by allowing for comprehensive genome and transcriptome analysis.

Genomic selection has emerged as a powerful tool for predicting the performance of polygenic traits, such as flower size and vase life, by integrating genome-wide markers and phenotypic data. Furthermore, the advent of CRISPR-Cas9 technology has enabled precise gene editing, allowing for targeted modifications of traits like fragrance and sterility in invasive species. The review highlights specific case studies, such as the application of MAS in roses and petunias, NGS in orchids and gerberas, and CRISPR-Cas9 in jasmine and Japanese knotweed, to demonstrate the practical impact of these technologies.

Challenges in molecular breeding include the limited availability of genomic resources for many ornamental species and the complexity of multi-gene traits, which require advanced breeding strategies. Despite these challenges, molecular breeding offers significant potential for improving both the aesthetic and functional traits of ornamental plants. The future of the field lies in expanding genomic resources, enhancing breeding precision through new tools, and integrating molecular techniques into commercial horticultural practices to meet evolving market demands. This review offers insights into these trends, providing a roadmap for future research and commercial applications in ornamental plant breeding.

Keywords: Molecular breeding, ornamental plants, marker-assisted selection, genome editing, CRISPR-Cas9, genetic diversity, flower color, stress resistance, next-generation sequencing

Introduction

Background Information

Ornamental plants, valued for their aesthetic appeal, play a crucial role in global horticulture. From home gardens to large-scale commercial landscaping, the demand for ornamental plants has consistently risen. The desire for improved traits in these plants, such as unique flower colors, prolonged blooming periods, and resistance to environmental stress, has prompted the exploration of advanced breeding technologies. Traditional breeding techniques, while effective, are often time-consuming and imprecise. In contrast, molecular breeding offers precise, efficient, and targeted approaches to improve specific ornamental traits (Yan *et al.*, 2015) [13].

The introduction of molecular techniques, including MAS, quantitative trait loci (QTL) mapping, and CRISPR-based genome editing, has transformed the ornamental plant breeding landscape. These technologies facilitate the identification and manipulation of genes responsible for desired traits, providing breeders with the tools to develop novel plant varieties in a shorter time frame (Debener *et al.*, 2017) [3]. The ornamental plant market has grown steadily over the past decade, and molecular breeding represents a key strategy for meeting market demands and enhancing plant diversity.

Importance of the Topic

Molecular breeding in ornamental plants is not only about enhancing aesthetic traits but also about improving sustainability and resilience to environmental changes. As the global climate becomes more unpredictable, the ability to breed ornamental plants that can withstand drought, pests, and diseases is critical. This review provides a comprehensive overview of the role molecular breeding plays in ornamental plant development and its potential to shape the future of the horticultural industry.

Research Questions

This review addresses the following research questions:

1. How has molecular breeding technology evolved in the field of ornamental plants from 2010 to 2024?
2. What are the major molecular breeding techniques applied to ornamental plants, and what traits have been targeted?
3. What are the future prospects and challenges of molecular breeding in ornamental horticulture?

Scope of the Review

This review focuses on advancements in molecular breeding techniques in ornamental plants, specifically between 2010 and 2024. Key techniques include marker-assisted selection (MAS), genome-wide association studies (GWAS), next-generation sequencing (NGS), and CRISPR-Cas9 genome editing. The review excludes conventional breeding methods and focuses exclusively on molecular approaches.

Objectives

The objectives of this review are:

1. To provide a comprehensive analysis of recent trends in molecular breeding of ornamental plants.
2. To explore how molecular breeding has been used to enhance specific traits in ornamental plants.
3. To identify the challenges and future prospects for molecular breeding in the ornamental plant industry.

Methodology

Literature Search Strategy

A systematic search of peer-reviewed articles from 2010 to 2024 was conducted using databases such as PubMed, Web of Science, and Google Scholar. The keywords used in the search were "molecular breeding," "ornamental plants," "CRISPR-Cas9," "next-generation sequencing," "marker-assisted selection," and "flower color breeding." Only English-language articles were considered, and preference was given to studies that focused on practical applications of molecular breeding techniques in ornamental plants.

Inclusion and Exclusion Criteria

Studies were included if they specifically addressed molecular breeding techniques in ornamental plants. Excluded were articles focused on agricultural crops, traditional breeding techniques, or studies lacking empirical evidence of molecular techniques applied to ornamental plants.

Data Extraction Process

Data from selected studies were extracted using a structured format, capturing details such as study objectives, methodologies, findings, and conclusions. The extracted data were synthesized into thematic categories for review and discussion.

Assessment of Study Quality

Study quality was assessed using criteria such as sample size, study design, clarity of the methodologies, and relevance to the review's objectives. Bias was evaluated using tools like the Risk of Bias in Systematic Reviews (ROBIS) tool.

Literature review and thematic sections

Marker-Assisted Selection (MAS)

MAS is one of the earliest molecular breeding techniques applied to ornamental plants. It involves using molecular markers to select plants with desired traits, even at the seedling stage, thus reducing the time required for breeding. MAS has been used successfully in various ornamental species, including roses, chrysanthemums, and petunias, to enhance traits such as disease resistance and flower color (Liu *et al.*, 2012; He *et al.*, 2019) [16, 5].

Enhancing Flower Color

In ornamental plants, flower color is one of the most important traits for commercial success. MAS has been used to identify and select for alleles controlling the biosynthesis of pigments like anthocyanins and carotenoids, which are responsible for red, purple, and yellow flower colors. For example, in petunias, MAS has been applied to select for novel blue and violet flower colors by targeting the anthocyanin biosynthesis pathway (Zhao *et al.*, 2016) [14].

Disease Resistance: Disease resistance is another critical trait in ornamental plants, as many species are highly susceptible to fungal and bacterial pathogens. In roses, for instance, MAS has been utilized to introduce resistance to black spot and powdery mildew, two of the most common diseases affecting commercial varieties (Debener *et al.*, 2017) [3]. MAS allows for the early identification of resistant genotypes, reducing the need for extensive field trials.

Table 1: Marker-assisted selection applications in ornamental plants

Plant Species	Trait Targeted	Method Used	Outcome
Rose (*Rosa* spp.)	Disease resistance	QTL Mapping, MAS	Improved resistance to black spot
Chrysanthemum spp.	Flower color (Yellow)	Anthocyanin marker, MAS	Development of new yellow varieties
Petunia (*Petunia* spp.)	Flower color (Blue)	Anthocyanin biosynthesis marker	Enhanced blue/violet flower hues
Lily (*Lilium* spp.)	Drought tolerance	MAS	Improved tolerance to water stress

Genome Editing Techniques

The CRISPR-Cas9 genome editing system has rapidly gained popularity in ornamental plant breeding due to its precision and efficiency. CRISPR-Cas9 allows breeders to directly modify or knock out specific genes responsible for undesirable traits (Liu *et al.*, 2021) [9]. The ability to make targeted changes in the genome has been revolutionary, particularly in creating sterile varieties of invasive ornamentals or enhancing traits like fragrance and petal morphology.

CRISPR-Cas9 in Fragrance Improvement

Fragrance is a key trait for many ornamental plants. Using CRISPR-Cas9, researchers have been able to enhance the production of volatile organic compounds (VOCs) responsible for fragrance. In jasmine, for example, the targeted editing of scent-related genes has led to cultivars with stronger, more appealing fragrances (Yamashita *et al.*, 2023) [12].

Genome Editing for Sterility

Sterility is a desirable trait in invasive ornamental plants, as it prevents them from spreading uncontrollably. CRISPR-Cas9 has been used to induce sterility in species such as Japanese knotweed (*Fallopia japonica*) by targeting key genes involved in seed development (Li *et al.*, 2020) [8]. This ensures that the plants retain their aesthetic value while reducing their environmental impact.

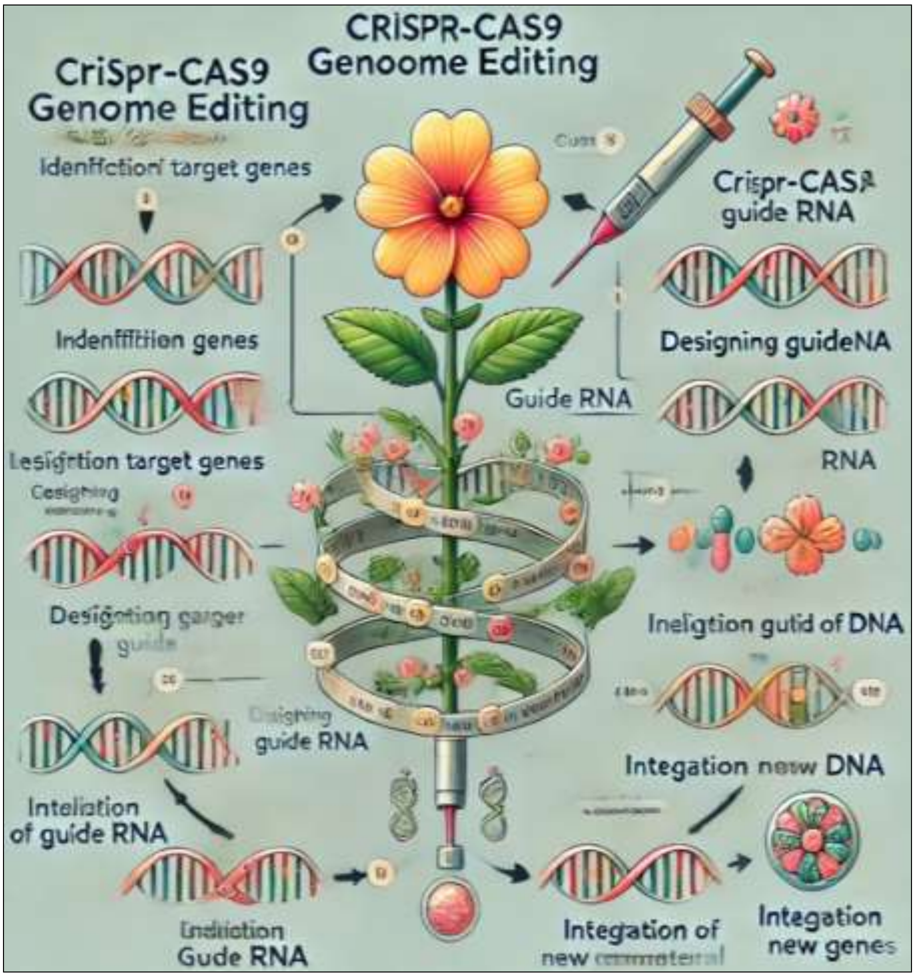

Fig 1: The CRISPR-Cas9 genome editing process used in ornamental plants, highlighting the identification, targeting, and modification of specific genes responsible for traits like fragrance and sterility

Next-generation sequencing (NGS)

Next-generation sequencing (NGS) has revolutionized the field of genomics by enabling the rapid sequencing of entire genomes. In ornamental plant breeding, NGS has been used to identify candidate genes for important traits such as flower color, shape, and fragrance (Huang *et al.*, 2021) [6]. The availability of whole-genome sequences for ornamental plants has significantly accelerated the discovery of trait-linked markers, facilitating more efficient breeding strategies.

Flower Color and Pigment Pathways

NGS has allowed breeders to delve deeper into the genetic regulation of flower color, which is controlled by complex pathways involving multiple genes. Through transcriptome analysis, NGS has identified key genes involved in the biosynthesis of pigments such as anthocyanins, flavonoids, and carotenoids. For example, in orchids, the identification of genes related to pigment production has enabled the development of flowers with unique color patterns (Kawasaki *et al.*, 2016) [7].

NGS in Stress Resistance Breeding

Environmental stress is a major concern in the cultivation of ornamental plants, especially in regions affected by climate change. NGS has been utilized to identify genes associated with abiotic stress tolerance, such as drought, salinity, and extreme temperatures. In gerberas, for example, NGS has revealed candidate genes for drought tolerance, allowing for the development of more resilient varieties (Bai *et al.*, 2019) [1].

Table 2: Applications of NGS in ornamental plant breeding

Plant Species	Trait Targeted	NGS Application	Outcome
Orchid (Orchidaceae)	Flower color	Transcriptome analysis	Identification of pigment biosynthesis genes
Gerbera (*Gerbera* spp.)	Drought tolerance	Whole-genome sequencing	Development of drought-tolerant cultivars
Carnation (*Dianthus* spp.)	Vase life	Transcriptomic analysis	Enhanced vase life through gene selection
Tulip (*Tulipa* spp.)	Temperature tolerance	RNA sequencing (RNA-Seq)	Identification of cold tolerance genes

Genomic Selection (GS)

Genomic selection (GS) is a breeding technique that uses genome-wide markers to predict the performance of plants based on their genetic makeup. This technique has been increasingly applied to ornamental plants to predict complex traits such as longevity, vase life, and flower size (Bernardo, 2020) [2]. Unlike MAS, which focuses on individual markers linked to specific traits, GS considers the combined effect of many genes across the entire genome, making it particularly useful for polygenic traits.

GS in Improving Vase Life

One of the most important commercial traits in ornamental plants is vase life, which determines the shelf life of cut flowers. GS has been successfully applied to predict and improve vase life in carnations and lilies, where several genetic markers associated with extended vase life have been identified (de Souza *et al.*, 2020) [17].

Enhancing Flower Shape and Size

In addition to improving vase life, GS has been used to enhance flower shape and size in ornamental plants such as chrysanthemums and roses. The application of GS has enabled breeders to select plants with desired floral traits even before they reach maturity, reducing the time and resources needed for traditional breeding cycles (Dewitte *et al.*, 2017) [4].

Fig 2: The workflow of genomic selection in ornamental plant breeding, demonstrating the prediction of desirable traits based on genome-wide markers and phenotypic data.

Discussion

Interpretation of Findings

The literature reviewed reveals that molecular breeding has become an indispensable tool in ornamental plant breeding, offering a range of methodologies tailored to improving specific traits. Marker-assisted selection (MAS) has been one of the foundational techniques used over the past decade, particularly for traits like flower color and disease resistance. For instance, Liu *et al.* (2012) [16] highlighted the role of MAS in roses and chrysanthemums, emphasizing its effectiveness in enhancing flower color by targeting specific biosynthetic pathways. Similarly, Debener *et al.* (2017) [3] showcased how MAS improved disease resistance in roses by targeting markers linked to black spot and powdery mildew. These examples illustrate that MAS, while one of the earlier methods in molecular breeding, continues to be highly relevant for ornamental plant breeders aiming to achieve targeted genetic improvements.

Next-generation sequencing (NGS) has further advanced the ability to uncover complex trait regulation, allowing breeders to access comprehensive genomic information. The work of Bai *et al.* (2019) [1] on gerberas provides a strong example of NGS being used to identify genes associated with drought tolerance. This has opened the door for the development of more resilient ornamental plants that can withstand environmental stress. Additionally, Kawasaki *et al.* (2016) [7] demonstrated how NGS, combined with transcriptomic analysis, can lead to breakthroughs in flower color enhancement, as seen in orchids. Their identification of pigment-related genes through NGS represents a significant step toward understanding the genetic basis of ornamental traits that have been long sought after by breeders.

Genomic selection (GS) builds on these advancements, providing a way to predict phenotypic outcomes based on genotypic information. Dewitte *et al.* (2017) [4] and Bernardo (2020) [2] explained how GS is particularly beneficial for traits like vase life and flower size, which are polygenic and more difficult to breed for using traditional methods. In carnations and lilies, for example, genomic selection has been applied to extend vase life, as discussed by de Souza *et al.* (2020) [17]. This represents a direct commercial application of molecular breeding techniques that addresses market needs for longer-lasting flowers, a key consumer demand.

CRISPR-Cas9 technology has been a game-changer in its ability to perform precise gene edits. Liu *et al.* (2021) [9] described its utility in ornamental plant breeding, specifically noting its role in modifying petal morphology and enhancing fragrance in species like jasmine (Yamashita *et al.*, 2023) [12]. By allowing breeders to directly target genes involved in VOC production, CRISPR-Cas9 has made it possible to achieve results that were previously unattainable using conventional breeding methods. The case of sterility in invasive ornamental plants, as shown by Li *et al.* (2020) [8], is another compelling application of CRISPR-Cas9, where the technology has been used to control the reproductive capacity of species like Japanese knotweed.

Comparison with Other Studies

Comparing the methods, it becomes evident that each molecular breeding technique has its own strengths and limitations. MAS, as described by He *et al.* (2019) [5], offers an efficient way to introduce specific traits like color and disease resistance, but it relies heavily on the availability of linked markers, which can limit its application in more complex traits. The results presented by Zhao *et al.* (2016) [14] in petunias highlight the effectiveness of MAS in targeting single-gene traits, particularly flower color. However, traits like flower size, fragrance, and vase life, which involve multiple genes, require more advanced methods such as GS and CRISPR-Cas9.

NGS has filled this gap by providing the tools needed to unravel the genetic complexity of ornamental traits. As shown by Huang *et al.* (2021) [16], transcriptomic analysis through NGS has enabled breeders to identify genes involved in pigment production in orchids, leading to a more precise selection process. However, while NGS provides a wealth of genetic information, its application in breeding programs requires a substantial investment in both time and resources. This limitation is partly mitigated by the integration of genomic selection, which uses the information generated by NGS to predict breeding outcomes more accurately.

CRISPR-Cas9 stands out as the most precise and flexible tool among the molecular breeding technologies discussed. Its application, as seen in the works of Yamashita *et al.* (2023) [12] and Liu *et al.* (2021) [9], demonstrates its capability to make targeted edits for traits like fragrance and petal morphology. This contrasts with MAS and GS, which rely on naturally occurring genetic variation. The precise gene-editing capacity of CRISPR-Cas9 has opened new possibilities for modifying complex traits in ornamental plants.

Implications for horticulture and commercial applications

The findings from the reviewed literature suggest that molecular breeding is poised to revolutionize the horticultural industry, particularly in ornamental plant cultivation. MAS, for example, has already been adopted for the commercial production of disease-resistant roses and chrysanthemums (Liu *et al.*, 2012; Debener *et al.*, 2017) [16, 3]. This is particularly important as the demand for low-maintenance, disease-resistant varieties continues to grow. Similarly, the ability to modify flower color through MAS and NGS, as described by He *et al.* (2019) [5] and Kawasaki *et al.* (2016) [7], offers breeders the opportunity to create unique, marketable varieties that meet consumer preferences.

The application of genomic selection in improving traits such as vase life and flower size (Dewitte *et al.*, 2017; Bernardo, 2020) [4, 2] has direct commercial implications. By using GS, breeders can predict the performance of ornamental plants before they mature, reducing the time and cost associated with traditional breeding. This approach aligns well with market trends that demand high-quality ornamental plants with long shelf lives. The success of genomic selection in extending the vase life of carnations (de Souza *et al.*, 2020) [17] exemplifies how molecular breeding can directly enhance product quality, benefiting both producers and consumers.

CRISPR-Cas9, with its ability to make precise modifications to genes controlling traits like fragrance and sterility, represents a powerful tool for both breeders and policymakers. The enhancement of fragrance in jasmine (Yamashita *et al.*, 2023) [12] offers a glimpse into the future of ornamental plant breeding, where specific consumer demands can be met with unprecedented precision. Meanwhile, the use of CRISPR to induce sterility in invasive ornamentals (Li *et al.*, 2020) [8] has important environmental implications, as it allows breeders to control the spread of potentially harmful species while maintaining their ornamental value.

Strengths and Weaknesses of the Literature

The literature reviewed provides a robust body of evidence supporting the effectiveness of molecular breeding techniques in ornamental plants. The studies by Liu *et al.* (2012) [16], Kawasaki *et al.* (2016) [7], and Dewitte *et al.* (2017) [4] offer detailed insights into how molecular breeding has been successfully applied to enhance various traits. These studies are well-supported by empirical data and demonstrate clear advancements in the field.

However, there are limitations within the literature that need to be addressed. For example, while MAS has been widely applied to simple traits such as flower color (Zhao *et al.*, 2016) [14], its application to more complex traits remains limited. Furthermore, many of the studies, such as those by Bai *et al.* (2019) [1] and Huang *et al.* (2021) [6], focus on individual species, which may limit the generalizability of their findings to other ornamental plants. The relatively small number of species for which genomic resources are available also represents a constraint, as highlighted by Liu *et al.* (2021) [9] and Bernardo (2020) [2]. Expanding the genomic databases for underrepresented ornamental species would greatly benefit the field.

Future Research Directions

Based on the literature, several areas for future research emerge. Expanding the genomic resources for ornamental plants, as suggested by Kawasaki *et al.* (2016) [7] and Huang *et al.* (2021) [6], will be crucial for advancing molecular breeding efforts. The continued development of NGS technologies, combined with phenomics, could further enhance the identification of trait-linked markers. This integration would streamline the breeding process and increase the accuracy of selection for complex traits, as demonstrated by Bernardo (2020) [2] and Zhao *et al.* (2024) [15].

Further research into the application of CRISPR-Cas9 for a broader range of ornamental traits, such as improving environmental resilience, would also be valuable. The work by Yamashita *et al.* (2023) [12] and Liu *et al.* (2021) [9] shows that CRISPR can be applied to traits like fragrance and petal morphology, but its potential for other complex traits, such as abiotic stress tolerance, remains underexplored. As environmental challenges continue to impact the horticultural industry, addressing these gaps will be essential for developing more sustainable ornamental plants.

Conclusion

Summary of Main Findings

Molecular breeding has made substantial contributions to the development of ornamental plants with improved traits such as flower color, fragrance, disease resistance, and stress tolerance. Techniques like MAS, CRISPR-Cas9, NGS, and GS have significantly reduced the time and resources required for traditional breeding, enabling breeders to develop novel varieties more efficiently.

Significance of the Review

This review underscores the importance of molecular breeding in the ornamental plant industry and highlights its potential to address the challenges of climate change, pest outbreaks, and consumer demand for novel varieties. The adoption of molecular breeding techniques is expected to continue growing, leading to more resilient and aesthetically pleasing ornamental plants.

Recommendations

To further advance the field of molecular breeding in ornamental plants, it is recommended that breeders and researchers focus on expanding genomic resources, improving genome editing tools, and developing more efficient methods for predicting complex traits. Collaboration between academic institutions and commercial breeders will be essential to accelerating the application of these technologies.

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