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Identification of SSR Molecular Markers Associated with the Creeping Trait in Crape Myrtle

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Introduction

Crape myrtle (*Lagerstroemia indica*) is a versatile and widely cultivated ornamental plant appreciated for its colourful flowers, attractive bark and ability to thrive in various climates. Among its diverse phenotypic traits, the creeping habit stands out for its aesthetic appeal and practical landscaping uses, such as ground cover and erosion control. Understanding the genetic basis of the creeping trait in crape myrtle is crucial for advancing breeding efforts aimed at developing new cultivars with enhanced ornamental value and environmental adaptability. Traditional breeding methods for crape myrtle have relied on phenotypic evaluations and crosses between selected individuals to improve desirable traits. However, these approaches are time-consuming and often limited by the complexity of trait inheritance [1]. Molecular markers, particularly Simple Sequence Repeats (SSRs) or microsatellites, offer a promising alternative by providing insights into the genetic architecture underlying complex traits like the creeping habit. SSR markers are highly polymorphic, abundant throughout the genome and amenable to high-throughput genotyping, making them invaluable tools for Marker-Assisted Selection (MAS) in breeding programs. The identification of SSR molecular markers associated with the creeping trait involves a multidisciplinary approach integrating genomics, bioinformatics and molecular genetics. This comprehensive strategy aims to uncover specific genomic regions and alleles linked to the expression of the creeping phenotype, facilitating targeted breeding for improved crape myrtle varieties [2].

Description

The quest to identify SSR molecular markers associated with the creeping trait in crape myrtle begins with the selection and characterization of diverse germplasm collections encompassing a range of growth habits, including both creeping and non-creeping forms. These collections serve as the foundation for genetic studies aimed at elucidating the genetic basis of the creeping phenotype. Genomic DNA extraction from crape myrtle samples is followed by Next-Generation Sequencing (NGS) technologies to generate large-scale sequence data. Bioinformatics tools are employed to analyse these data, identifying SSR loci distributed across the genome [3]. SSRs consist of short, tandemly repeated DNA motifs, typically 1-6 base pairs in length and are characterized by high levels of polymorphism due to variation in the number of repeat units among individuals. Once SSR loci associated with the creeping trait are identified computationally, primer pairs flanking these regions are designed for PCR-based marker development. The primers are validated for their ability to amplify target SSR loci consistently across a diverse panel of crape myrtle genotypes, ensuring robustness and reproducibility of the markers. The next phase involves genotyping the crape myrtle populations using the developed SSR markers to assess allelic variation associated with the creeping phenotype [4]. Statistical analyses, such as association mapping and linkage disequilibrium studies, are employed to establish correlations between specific SSR marker alleles and the expression of the creeping trait. These analyses provide insights into the genetic architecture and inheritance patterns underlying the trait, shedding light on the molecular mechanisms regulating growth habit in crape myrtle. The integration of SSR markers into crape myrtle breeding programs enhances breeding efficiency by enabling targeted selection of genotypes carrying desired traits. MAS allow breeders to identify and propagate individuals with superior creeping characteristics without relying solely on subjective phenotypic evaluations. This approach accelerates the development of new crape myrtle cultivars with enhanced ornamental features, adaptability to diverse environmental conditions and resilience to pests and diseases [5].

Conclusion

In conclusion, the identification of SSR molecular markers associated with the creeping trait in crape myrtle represents a significant advancement in ornamental plant breeding and genetics. By leveraging genomic technologies and bioinformatics tools, researchers have made strides in unravelling the genetic basis of complex traits like growth habit. The availability of SSR markers provides breeders with precise tools to accelerate the development of new cultivars with improved creeping characteristics, meeting consumer demand for aesthetically pleasing and resilient landscape plants. The application of SSR markers in crape myrtle breeding not only enhances breeding efficiency but also contributes to the conservation and utilization of genetic diversity within cultivated populations. Continued research efforts could expand upon identified SSR markers or explore additional genomic regions influencing the creeping phenotype, further refining breeding strategies and broadening our understanding of genetic mechanisms in ornamental plants. Future directions may involve integrating genomic data with phenotypic data from field trials and environmental studies to enhance predictive breeding models and improve cultivar performance under varying climatic conditions. Advances in genome editing technologies, such as CRISPR-Cas9, also hold promise for manipulating specific genomic regions associated with desired traits, including creeping habit, thereby accelerating the pace of cultivar development and innovation in crape myrtle breeding. Overall, the identification and application of SSR molecular markers associated with the creeping trait in crape myrtle exemplify the transformative potential of molecular genetics in modern plant breeding. By harnessing the power of genomics and molecular biology, breeders can cultivate new varieties that not only enhance urban landscapes but also contribute to sustainable horticulture practices and environmental stewardship in the face of global challenges such as climate change and urbanization.

Acknowledgement

None.

Conflict of Interest

None.

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