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Meta-analysis **Open Access**

Meta-analysis of Genetic Markers for Yield and Quality Traits in Dragon Fruit

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Abstract This study conducted a meta-analysis of genetic markers associated with yield and quality traits in dragon fruit, revealing significant genetic diversity among different genotypes and their potential applications. Dragon fruit has gained increasing attention in the global market due to its nutritional value and economic benefits; however, breeding efforts still face challenges in balancing yield and quality. By integrating existing genetic data, this study highlights the potential of genetic markers such as simple sequence repeats (SSR) and inter-simple sequence repeats (ISSR) in identifying key loci associated with yield and quality traits. These markers facilitate the dissection of the genetic architecture of complex traits, providing a scientific basis for molecular breeding of dragon fruit. Furthermore, a detailed case study compared the antioxidant capacity and nutritional characteristics of specific genotypes, offering valuable references for cultivar selection.

Keywords Genetic diversity; Marker-assisted selection (MAS); Yield traits; Quality traits; Simple sequence repeat (SSR) markers

1 Introduction

Dragon fruit, belonging to the *Hylocereus* species, has garnered significant attention due to its economic value and nutritional benefits, as well as its remarkable drought tolerance (Tao et al., 2014). This fruit is not only a staple in tropical regions but also a growing favorite in global markets, thanks to its rich content of essential nutrients, antioxidants, and bioactive components (Morillo et al., 2020; Zaman et al., 2023). Despite its popularity, breeding dragon fruit for enhanced yield and quality remains a challenge. The genetic diversity within dragon fruit species is vast, yet underexplored, particularly in regions like Colombia where genetic studies are limited. This diversity presents both an opportunity and a challenge for breeders aiming to improve traits such as yield, fruit quality, and resistance to environmental stresses.

Current breeding efforts face several challenges, including the need to balance yield and quality traits while maintaining genetic diversity. The complexity of these traits, often influenced by multiple genetic and environmental factors, complicates the breeding process. Moreover, the lack of comprehensive genetic studies and the limited understanding of the genetic architecture of these traits hinder the development of effective breeding strategies (Kumar et al., 2022; Zaman et al., 2024). The use of genetic markers, such as Inter-Simple Sequence Repeat (ISSR) markers, has shown promise in characterizing genetic diversity and identifying potential breeding lines (Tao et al., 2014). However, the integration of these markers into breeding programs is still in its nascent stages.

Genetic markers play a crucial role in the improvement of yield and quality traits in dragon fruit. They provide a means to dissect the genetic architecture of complex traits, allowing breeders to identify and select for desirable traits more efficiently. Meta-QTL analysis, for instance, has been successfully used in other crops to identify stable quantitative trait loci (QTLs) that can be targeted in breeding programs (Lin et al., 2024). By leveraging genetic markers, breeders can enhance the precision of selection processes, ultimately leading to the development of superior dragon fruit varieties with improved yield and quality (Maan et al., 2023).

The objective of this meta-analysis is to synthesize existing genetic data to identify key genetic markers associated with yield and quality traits in dragon fruit. By consolidating findings from various studies, this analysis aims to provide a comprehensive understanding of the genetic factors influencing these traits. The scope of this study includes evaluating the effectiveness of different genetic markers and their potential application in breeding programs to enhance dragon fruit production and quality. Through this meta-analysis, we seek to bridge the gap between genetic research and practical breeding applications, paving the way for more efficient and targeted breeding strategies.

2 Overview of Genetic Markers in Dragon Fruit

Genetic markers are essential tools in the study and improvement of dragon fruit, aiding in the identification of genetic variations associated with yield and quality traits. These markers facilitate the understanding of genetic diversity, assist in marker-assisted selection (MAS), and contribute to the development of improved cultivars. The use of genetic markers in dragon fruit research has evolved over time, with various types being employed to address specific breeding and research objectives.

2.1 Types of genetic markers used

Simple sequence repeats (SSRs), also known as microsatellites, are co-dominant markers widely used in horticultural crop improvement due to their high polymorphism and reproducibility. SSRs have been effectively utilized in the characterization of genetic diversity and the identification of quantitative trait loci (QTL) in various fruit crops, including citrus and guava, which share similar breeding challenges with dragon fruit. The development of SSR databases, such as citSATdb for citrus, highlights their utility in germplasm characterization and molecular breeding (Morillo et al., 2022; De Mori and Cipriani, 2023).

Single nucleotide polymorphisms (SNPs) are another class of genetic markers that provide high-resolution insights into genetic variation. Although not explicitly mentioned in the provided data, SNPs are generally favored for their abundance and potential for high-throughput genotyping, making them suitable for detailed genetic mapping and association studies in fruit crops (Cockerton et al., 2021).

Other marker types, such as amplified fragment length polymorphisms (AFLPs) and random amplified polymorphic DNA (RAPDs), have been used in the study of genetic variability and diversity. In the context of guava, sequence specific amplified polymorphism (SSAP) markers have shown higher polymorphism and intraspecific variability compared to AFLPs, indicating their potential utility in dragon fruit research for similar purposes (Maan et al., 2023).

2.2 Marker-trait associations reported

Marker-trait associations are crucial for understanding the genetic basis of important agronomic traits. In guava, SSR markers have been linked to QTLs related to fruit characteristics such as pulp thickness, color, and soluble solids, demonstrating their applicability in early selection and MAS (Chen et al., 2024; Lin et al., 2024). These findings suggest that similar approaches could be applied to dragon fruit to identify markers associated with desirable yield and quality traits.

2.3 Trends in marker application over time

The application of genetic markers in fruit crop research has evolved significantly, with a shift towards more informative and high-throughput markers like SSRs and SNPs. The development of comprehensive marker databases and the integration of advanced genotyping techniques have enhanced the precision and efficiency of breeding programs. This trend is expected to continue, with ongoing advancements in molecular technologies further facilitating the genetic improvement of dragon fruit and other horticultural crops (Rifat et al., 2019).

3 Yield Traits in Dragon Fruit

3.1 Genetic basis of yield-related traits

The genetic basis of fruit weight and size in dragon fruit is influenced by a variety of genetic markers that contribute to the phenotypic diversity observed in different genotypes. Studies utilizing Inter-Simple Sequence Repeat (ISSR) markers have revealed significant genetic diversity among dragon fruit accessions, which is crucial for breeding programs aimed at improving yield traits such as fruit weight and size. For instance, research conducted on *Hylocereus* spp. in China demonstrated high polymorphism in genetic markers, indicating a broad genetic base that can be exploited to select for larger and heavier fruits (Cockerton et al., 2023). This genetic variability is essential for developing new cultivars with enhanced fruit size and weight, which are key determinants of market value and consumer preference.

Flowering time and pollination success are critical components of yield in dragon fruit, as they directly affect fruit set and overall productivity. Genetic studies have shown that these traits are influenced by both genetic and environmental factors. The genetic diversity observed in dragon fruit populations, as indicated by high heterozygosity and polymorphic loci, suggests that there is potential for selecting genotypes with optimal flowering times and improved pollination success (Maan et al., 2023). This diversity allows for the identification of genetic markers associated with these traits, facilitating the development of varieties that can thrive in different environmental conditions and have higher yield potential.

3.2 Significant markers associated with yield

Significant genetic markers associated with yield traits in dragon fruit have been identified through the use of ISSR markers, which have proven effective in distinguishing between high-yielding and low-yielding genotypes. In particular, studies have highlighted the utility of specific ISSR primers, such as UBC824, UBC891, and UBC900, in fingerprinting genotypes with desirable yield characteristics (Lopez-Nieves et al., 2018; Forcada et al., 2019). These markers provide a valuable tool for breeders to select and propagate dragon fruit varieties with superior yield traits, thereby enhancing productivity and meeting market demands. The identification of these markers is a crucial step in the development of targeted breeding strategies aimed at improving yield and quality traits in dragon fruit.

4 Quality Traits in Dragon Fruit

4.1 Genetic basis of quality-related traits

The sugar content and acidity in dragon fruit are critical quality traits that significantly influence consumer preference and market value. These traits are largely determined by the genetic makeup of the fruit, which varies widely among different genotypes. Studies have shown that the genetic diversity within dragon fruit species, such as *Selenicereus megalanthus*, is substantial, with a high level of heterozygosity and polymorphic loci, indicating a broad genetic base that can be exploited for breeding programs aimed at enhancing these quality traits (Morillo et al., 2022). The genetic parameters, such as expected average heterozygosity and genetic distances, provide insights into the potential for selecting genotypes with optimal sugar content and acidity levels (Kenis et al., 2008; Khan et al., 2024).

Pigmentation and antioxidant properties are other essential quality traits in dragon fruit, contributing to its nutritional value and appeal. The pigmentation, primarily due to betalains, and the antioxidant capacity are influenced by the genetic diversity present in the fruit. Research utilizing ISSR markers has revealed significant genetic variation among dragon fruit accessions, which correlates with differences in pigmentation and antioxidant levels (Figure 1) (Forcada et al., 2019; Chen et al., 2021; Zheng et al., 2021). This genetic diversity is crucial for breeding programs focused on enhancing these traits, as it allows for the selection of genotypes with superior pigmentation and antioxidant properties, thereby improving the fruit's health benefits and marketability (Fernández-López et al., 2020; Lin et al., 2024).

4.2 Significant markers associated with quality

Significant genetic markers associated with quality traits in dragon fruit have been identified through various molecular techniques, such as ISSR markers. These markers are instrumental in distinguishing between different genotypes and understanding the genetic basis of quality traits. For instance, the use of ISSR markers has enabled the identification of polymorphic bands that are associated with specific quality traits, such as sugar content, acidity, pigmentation, and antioxidant properties (Capel et al., 2015; Zhao et al., 2024). The high percentage of polymorphic bands and the polymorphism information content (PIC) values indicate a rich genetic diversity that can be harnessed to improve quality traits through targeted breeding strategies (Forcada et al., 2019; Tel-Zur et al., 2022). This genetic information is vital for developing dragon fruit varieties with enhanced quality traits, meeting consumer demands, and increasing the fruit's economic value.

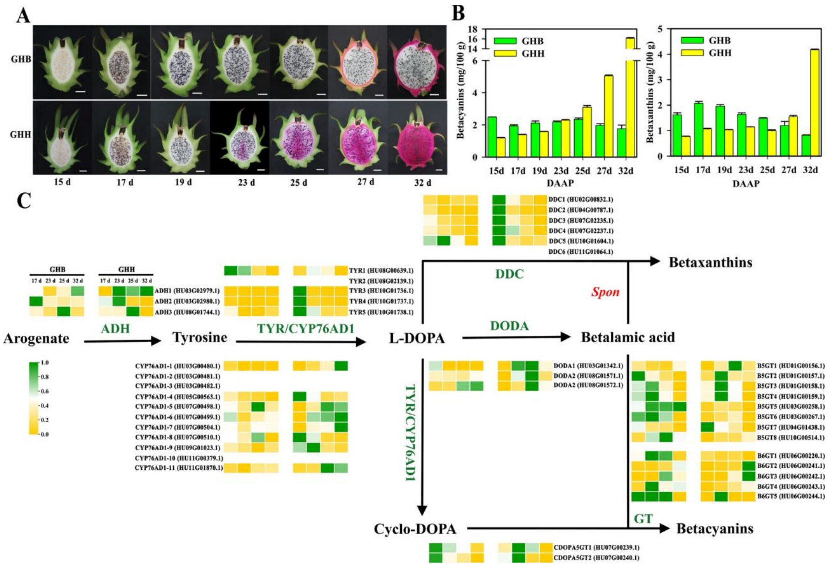

Figure 1 Genes involved in the betalain biosynthesis cascade (Adopted from Chen et al., 2021)

Image caption: A The development of ‘Guanhuabai’ (GHB) and ‘Guanhuahong’ (GHH) pitaya pulp. B The betacyanin and betaxanthin contents of ‘GHB’ and ‘GHH’ pitaya pulp. C The expression profiles of genes related to betalain biosynthesis according to the RNA-Seq datasets of ‘GHB’ and ‘GHH’ pitaya pulp. The gene IDs are in brackets. Spon, spontaneous. Bar =2 cm (Adopted from Chen et al., 2021)

5 Case Study: Biochemical Characterization of Four Genotypes from Three Species of Pitaya (*Hylocereus* spp.)

5.1 Selection criteria for the case study

A case study was selected to analyze the biochemical characteristics of four genotypes of pitaya, it was observed that DGF4 demonstrated significant advantages in total phenol, flavonoid, and β-carotene content, with notably high antioxidant activity in the peel. DGF2 exhibited outstanding performance in antioxidant activity and xanthophyll content, while DGF3 led in carotenoid and xanthophyll accumulation. These results provide a scientific basis for evaluating the nutritional value and functional properties of different dragon fruit genotypes, offering valuable references for breeding and cultivar selection, particularly for enhancing fruit antioxidant capacity and nutritional composition.

5.2 Biochemical characteristics and antioxidant capacity of different dragon fruit genotypes

This study systematically compared the biochemical characteristics of four different genotypes (DGF1, DGF2, DGF3, and DGF4) of three *Hylocereus* spp. species, focusing on total phenol content (TPC), total flavonoid content (TFC), total carotenoid content (TCC), β-carotene, xanthophyll, and color parameters (L, a, b, hue, and chroma). In terms of total phenol content, the DGF4 genotype showed significant advantages, with phenolic content in the peel and pulp reaching 161.3 mg GAE 100 g^{-1} and 130.0 mg GAE 100 g^{-1}, respectively, far exceeding the other genotypes. This was followed by DGF3, while DGF1 and DGF2 exhibited relatively lower phenolic content, indicating that DGF4 might possess stronger antioxidant potential (Abirami et al., 2021).

For total flavonoid content, DGF4 demonstrated the highest flavonoid content in the peel, reaching 508.2 mg RE 100 g^{-1}, while its pulp flavonoid content also surpassed other genotypes at 258.2 mg RE 100 g^{-1}. In contrast, DGF2 had the lowest flavonoid content. Flavonoids, as natural antioxidants, contribute significant nutritional value, and the high levels observed in DGF4 further enhance its functional importance. Additionally, carotenoid content analysis revealed that DGF3 had the highest total carotenoid content in the pulp (33.8 μg 100 g^{-1}), while DGF2 exhibited the highest value in the peel (24.3 μg 100 g^{-1}). For β-carotene, both DGF4 and DGF2 displayed high accumulation, particularly in the pulp, with values of 55.9 μg 100 g^{-1} and 53.2 μg 100 g^{-1}, respectively. These results highlight the nutritional superiority of these two genotypes as excellent sources of vitamin A precursors (Abirami et al., 2021).

The differences in xanthophyll content were also notable, with DGF3 recording the highest xanthophyll content in the pulp (32.7 μg/g), while DGF2 showed the highest value in the peel (24.1 μg/g), demonstrating favorable nutritional accumulation. Antioxidant capacity was evaluated using the DPPH and ABTS methods. The results revealed that DGF2 had the highest antioxidant activity in the pulp, reaching 75.3% with the DPPH method and 87.9% with the ABTS method. In contrast, DGF4 exhibited the highest antioxidant activity in the peel, with DPPH and ABTS values of 81.2% and 89.8%, respectively (Abirami et al., 2021). These findings indicate that DGF2 and DGF4 genotypes exhibit exceptional antioxidant capacity, which contributes to their ability to scavenge free radicals and delay aging.

Color parameter analysis further revealed variations in pigment composition between the peel and pulp of the four genotypes. The L value (brightness), a value (red-green), and b value (yellow-blue) ranged from 11.7-51.0, -0.6 to 21.4, and -2.5 to 2.5, respectively, for the pulp, and 13.6-40.8, 3.8 to 24.0, and 4.4 to 19.0, respectively, for the peel. The hue and chroma values for the pulp ranged from -76.0 to 77.5 and 2.1 to 21.5, respectively, while for the peel, they varied from 16.3 to 78.5 and 12.0 to 26.0. These color variations reflect differences in pigment accumulation and fruit appearance among the genotypes, which are likely associated with phenolic and carotenoid content (Figure 2) (Abirami et al., 2021).

Figure 2 An illustration of important traits of three different *Hylocereus* species of dragon fruit (Adopted from Abirami et al., 2021)
Image caption: Cladode characters: (A) length of segments (cm), (B) number of spines and (C) margin ribs of cladode; Flower characters: (D) flower bud shape and (E) shape of apex; fruit characters: (F) fruit length (cm) and (G) position towards the peel (Adopted from Abirami et al., 2021)

5.3 Lessons learned and future applications

The case studies highlight the importance of genetic diversity in breeding programs, DGF4 exhibited significant advantages in total phenolic, flavonoid, and β-carotene content, with particularly high antioxidant activity in the peel. DGF2 excelled in antioxidant capacity and xanthophyll content, while DGF3 stood out for its high accumulation of carotenoids and xanthophyll. These findings provide a scientific basis for evaluating the nutritional value and functional properties of dragon fruit genotypes, offering insights into varietal selection and breeding strategies to meet market demands for highly nutritious and antioxidant-rich fruits.

6 Discussion

6.1 Key findings from the meta-analysis

The meta-analysis of genetic markers for yield and quality traits in dragon fruit has revealed significant genetic diversity among different genotypes. Studies utilizing Inter-Simple Sequence Repeat (ISSR) markers have demonstrated high polymorphism, with polymorphic bands ranging from 25% to 100% and an average polymorphism information content (PIC) of 0.85, indicating substantial genetic variation (Saini et al., 2021). This diversity is crucial for breeding programs aimed at improving yield and quality traits. The genetic differentiation coefficient (Fst) of 0.26 further supports the presence of considerable genetic diversity within dragon fruit populations, which is essential for developing genotypes with superior traits (Salazar et al., 2020).

6.2 Challenges in applying genetic markers to breeding

Despite the promising findings, several challenges exist in applying genetic markers to dragon fruit breeding. One major challenge is the discrepancy observed between morphological traits and ISSR loci, which complicates the accurate assessment of genetic relatedness (Lin et al., 2024). Additionally, the limited number of genetic studies in certain regions, such as Colombia, highlights the need for more comprehensive research to fully understand the genetic architecture of dragon fruit (Morillo et al., 2022). The integration of genetic markers into breeding programs also requires significant resources and expertise, which may not be readily available in all breeding contexts.

6.3 Comparison with other crops

When compared to other crops, such as Indian mustard, the genetic analysis of dragon fruit is still in its nascent stages. In Indian mustard, meta-QTL analysis has identified robust and stable meta-QTLs for yield and quality traits, with significantly reduced confidence intervals, facilitating more precise breeding strategies (Saini et al., 2021). In contrast, dragon fruit research is primarily focused on genetic diversity and structure, with less emphasis on identifying specific QTLs for targeted breeding. This highlights the potential for dragon fruit breeding programs to benefit from methodologies applied in more extensively studied crops.

6.4 Future prospects for marker-assisted breeding

The future of marker-assisted breeding in dragon fruit looks promising, with the potential to significantly enhance yield and quality traits. The high genetic diversity observed provides a rich resource for selecting desirable traits (García-Gómez et al., 2019). Future research should focus on identifying specific QTLs associated with key traits, similar to the approaches used in Indian mustard, to enable more targeted breeding efforts (Salazar et al., 2020). Additionally, advancements in genetic engineering and genome editing technologies could further accelerate the development of improved dragon fruit varieties, offering resistance to biotic and abiotic stresses and meeting market demands for high-quality produce.

7 Conclusion

The meta-analysis of genetic markers for yield and quality traits in dragon fruit has provided significant insights into the genetic diversity and potential for breeding improvements in this economically valuable fruit. The study synthesized data from various genetic analyses, highlighting the substantial genetic variability present in dragon fruit populations, as evidenced by the high percentage of polymorphic loci and genetic diversity indices observed in studies from different regions. This genetic diversity is crucial for breeding programs aimed at enhancing yield and quality traits, as it provides a broad genetic base from which to select superior genotypes.

For researchers and breeders, the findings underscore the importance of utilizing genetic markers such as ISSR to assess and exploit the genetic diversity within dragon fruit populations. The identification of specific genetic clusters and the correlation between morphological and genetic data can guide the selection of parent plants for breeding programs, aiming to develop new varieties with improved traits such as higher yield, better quality, and increased resistance to environmental stresses. Additionally, the study suggests that integrating molecular markers with traditional breeding methods could accelerate the development of superior dragon fruit cultivars.

This meta-analysis highlights the potential of genetic markers in advancing dragon fruit breeding efforts. By leveraging the genetic diversity and understanding the genetic architecture of yield and quality traits, breeders can make informed decisions to enhance the productivity and quality of dragon fruit. The study's findings provide a foundation for future research and breeding strategies, emphasizing the need for continued exploration of genetic resources to meet the growing demand for this nutritious and economically important fruit.

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Conflict of Interest Disclosure

The authors affirm that this research was conducted without any commercial or financial relationships that could be construed as a potential conflict of interest.

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