

Review and Progress

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Key Bottlenecks and Breakthrough Strategies in Modern Durian Breeding: From Hybridization to Precision Genomic Selection

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Abstract The breeding of durian (*Durio zibethinus* L.) faces many challenges, including limited genetic diversity and sensitivity to environmental changes. This study summarized the key bottlenecks encountered in durian breeding, and discussed the breakthrough strategies to improve the efficiency of durian breeding. In recent years, the development of genome selection, marker-assisted breeding and CRISPR gene editing technology has provided new opportunities to accelerate durian breeding. Agronomic management strategies to optimize durian production, such as soil nutrient regulation, water-saving irrigation techniques and integrated pest control, were also explored. The successful practice of genomic tools in durian breeding was illustrated through case studies in Thailand and Malaysia. In the future, we need to further promote precision breeding technology, improve regulatory policies, strengthen international cooperation, and further promote the sustainable development of the durian industry.

Keywords Durian breeding; Genomic selection; CRISPR gene editing; Marker-assisted breeding; Agronomic management

1 Introduction

Durian (*Durio zibethinus* L.), known as the "king of fruits", occupies an important position in the economy and culture of Southeast Asia. Durian has a special taste and rich nutrition, and is very popular in the international market, especially in China. The growing market demand for durian has prompted researchers to try to improve the yield and quality of durian through various advanced breeding methods (Lin et al., 2022). Durian also has great economic value in international trade, and Thailand and Malaysia are the main exporters of durian. In this situation where consumers' interest in durian is increasing, it has become urgent to improve durian varieties so that their flavor, taste, shelf life and other aspects can meet market requirements.

Lin et al. 's study in 2022 showed that the genetic diversity of durian is not fully understood, which brings certain difficulties to improve and protect durian germplasm resources. Research by Akdemir and Isidro-Sanchez in 2019 shows that traditional breeding methods are time-consuming and laborious, coupled with the durian's long childhood growth period, which makes the whole breeding process complicated, and the relatively high cost of identifying complex traits such as flavor and disease resistance, which also adds difficulty. Peixoto et al. (2023) showed that genome selection and advanced high-throughput phenotypic identification techniques could be applied in durian breeding, but these techniques are still in the early stage of development and need some financial support and technical improvements to make them more effective.

This study will analyze the problems encountered in durian breeding, explore relevant solutions, and explore ways to optimize durian planting management. By analyzing the successful cases of durian breeding in Thailand and Malaysia, this study will evaluate the practical application effect of genomic tools in durian breeding, hoping to provide scientific basis for the development of durian industry.

2 Genetic and Agronomic Challenges in Durian Breeding

2.1 Long juvenile phase and reproductive barriers

Because durian has a relatively long juvenile period, its flowering and fruiting time will be delayed, and the breeding cycle will be extended. The selection and evaluation of target traits is also complicated by the long



juvenile period, especially for breeders, who are faced with a situation where the reproductive success and fruit quality of new hybrids can be assessed over several years. The self-incompatibility of durian and not too high fruit setting rate, these reproductive obstacles also hinder breeding work, so that cross-pollination or cross-breeding attempts face many difficulties, and the success rate is difficult to reach an ideal degree.

2.2 Limited genetic diversity and breeding stocks

According to the study by Lin et al in 2022, so far, the genetic basis of durian populations is limited, and most genotypes in durian populations seem to have similar genetic backgrounds, which will limit the number of new traits that can be introduced, and reduce the resistance of durians to some pests and diseases and climate change. Lin et al. (2022) developed 79,178 simple repeat sequence SSR markers in the research process, which provided help for expanding genetic resources through marker-assisted selection and quantitative trait loci positioning, and was conducive to integrating new genetic materials into the current breeding system.

2.3 Disease susceptibility and climate sensitivity

Durians lack genetic diversity, have a low number of disease resistance genotypes, and are vulnerable to biological or abiotic stresses and climate change. Because of the complex interactions between durian plants and their environment, developing durian varieties that are resistant to disease and weather conditions is not straightforward. According to Lin et al. 's research in 2022, they have identified relevant genetic markers that provide useful information for improving breeding methods and making it easier to screen out durian varieties with good disease resistance and adaptability.

3 Conventional Breeding Methods and Their Limitations

3.1 Open pollination and mass selection

Open pollination is natural selection, and quality selection is the selection of individuals with excellent phenotypic characteristics. Rembe et al. (2018) believe that both open pollination and quality selection have weak control over genetic diversity, leading to inbreeding and genetic drift, while Anand et al. (2023) believe that they take longer to achieve significant genetic improvement.

3.2 Hybridization techniques

A 2023 study by De Vries et al. showed that hybridization is a technique that combines the best characteristics of different breeds or species to produce better offspring. The hybridization technique has remarkable effect in improving crop yield and disease resistance. Hickey et al. (2017) argued that hybridization is challenging to implement due to its complexity and resource requirements, and hybridization also requires multi-generation selection and testing to stably express desired characteristics.

3.3 Grafting and clonal propagation

Grafting and clonal reproduction are techniques to maintain good individual characteristics through asexual reproduction, and have advantages in rapidly propagating good varieties, especially in cases where researchers need to maintain a specific genotype of the crop. Rembe et al. (2018) suggested that grafting and clonal reproduction may reduce genetic diversity, and they are less adaptive to environmental changes.

4 Genomic Advances in Durian Breeding

4.1 Durian genome sequencing and its implications

Complete genome sequences can be used by researchers to identify specific genomic regions, genes, and alleles associated with desirable traits. Key traits such as fruit quality, disease resistance and environmental adaptability were proposed by Xu et al. (2012) and Salgotra and Stewart (2020). This genetic information facilitates the development of molecular markers for use in breeding programs to improve important traits. Durian genome sequencing facilitated the construction of high-density genetic maps, which helped to identify quantitative trait loci associated with key agronomic traits.

4.2 Marker-assisted selection (MAS) for trait improvement

The researchers used marker-assisted selection to select durians with good traits at an early stage. Tiwari et al.



(2022) and Wang and Zhang in 2024 proposed that marker-assisted selection uses DNA markers associated with specific traits to allow breeders to select more efficiently for complex traits. Research by Migicovsky and Myles in 2017 showed that marker-assisted selection is well suited for perennial crops such as durians, which tend to consume a lot of time and money due to their long young growing periods (Figure 1). He et al. (2014) pointed out that the combination of MAS and high-throughput genotyping technology can accelerate the breeding process by economically and efficiently screening good traits in large populations.



Figure 1 Schematic of breeding using marker-assisted selection (MAS) (Adopted from Migicovsky and Myles, 2017)

Image caption: Wild relatives containing a trait of interest are crossed with a cultivated crop. In this example, the wild parent is heterozygous for a dominant Mendelian trait. With a marker associated with this trait, offspring can be screened for the trait and eliminated at the seedling stage. MAS ensures that the trait of interest is present in the progeny through several generations of backcrossing. Not shown here is that, with each generation, there is an increase in the proportion of cultivated ancestry while maintaining the desirable wild trait (Adopted from Migicovsky and Myles, 2017)

4.3 Genome-wide association studies in durian

GWAS scans the durian's entire genome to identify genetic variants associated with specific phenotypic traits. Yue (2013) and Tiwari et al. in 2022 showed that GWAS was applied in durian and revealed the genetic basis of complex traits in other crops to improve breeding efficiency. Researchers used GWAS to identify single nucleotide polymorphism markers associated with target traits and develop new durian varieties with better traits. Meuwissen et al. (2013) suggested that whole-genome marker data could improve the accuracy and speed of breeding by combining GWAS with genomic selection methods to predict individual breeding values.

5 Precision Genomic Selection and CRISPR Applications

5.1 High-throughput genotyping for durian improvement

In their study in 2020, Salgotra and Stewart proposed that high-throughput sequencing technology could rapidly identify functional markers highly correlated with durian phenotypic variation, improve selection efficiency, and



promote the development of excellent varieties. Through the application of high-throughput sequencing technology, breeders can more accurately select genes related to target traits and accelerate the improvement of durians.

5.2 CRISPR/Cas9 genome editing in durian

Studies by Bortesi and Fischer (2015) and Zhang et al. (2017) have shown that CRISPR/Cas9 can be used for gene function research and crop improvement in a variety of crops. Studies by Arora and Narula (2017) and Liu et al. (2021) showed that CRISPR/Cas9 improved durian fruit quality, disease resistance and nutritional composition by improving specific traits through precise gene editing. Zhou et al. (2023) stated that CRISPR/Cas9's high efficiency and specificity make it a promising tool in durian breeding.

5.3 Functional genomics for future durian breeding

Functional genomics provides a new method for durian breeding by studying the function and interaction of genes. Salgotra and Stewart's findings in 2020 suggest that strategies such as transcriptomics, TILLING, homologous recombination, and association mapping can be used to identify functional markers relevant to breeding goals, understand the genetic basis of durian, improve breeding efficiency, and promote the development of new durian varieties (Figure 2).



Figure 2 Different approaches involved in development of functional markers (FMs) (Adopted from Salgotra and Stewart, 2020)

6 Environmental and Agronomic Management for Durian Yield Optimization

6.1 Soil and nutrient management

The yield of durian is affected by the content of nitrogen (N), phosphorus (P) and potassium (K) in soil. The improved RBF neural network algorithm can more accurately predict the soil nutrient content and its relationship with durian yield, help farmers apply fertilizer more effectively according to the predicted results, not only improve the soil nutrient utilization efficiency, but also reduce the negative environmental impact, ensure that durian trees get the right amount of nutrients, maximize the growth potential of durian, and reduce production costs. Increase yield (Tang et al., 2024).

6.2 Water and climate adaptation strategies

Wild species have adaptations to drought and other adverse environmental conditions. The studies of Zhang and Batley (2020) and Renzi et al. (2022) illustrate that researchers can improve the adaptability of crops in marginal environments by utilizing the genetic diversity of crop wild relatives, and can also enhance the stress resistance of modern crops through gene introduction. Richards et al. 's study in 2010 showed that accurate phenotypic analysis and the use of quantitative trait loci markers could help identify and select good traits adapted to arid environments, thereby improving crop yield in arid environments.



6.3 Pest and disease integrated management

Durian and other high economic value crops are facing the harm of pests and diseases in the planting process. The resistance of crops to biotic and abiotic stresses can be enhanced through microbiome selection and co-propagation of symbionts. Co-evolution of plants with their microbial symbiotes provides additional genetic variability to crops that can be used to breed crop varieties resistant to pests and climate change (Gopal and Gupta, 2016). Field phenotyping by drones and high-resolution imaging systems can rapidly assess crop resistance to biological and abiotic stresses and further optimize pest and disease management (Sankaran et al., 2015).

7 Case Study

7.1 Case study 1: successful hybrid durian breeding in Thailand

The researchers resequenced the genomes of three durian species popular in Thailand (Kradumthong (KD), Monthong (MT) and Puangmanee (PM)), enabling cross-breeding of durians and revealing significant genetic variation between the different varieties. Nawae et al. 's 2023 study explored the genetic diversity of durians by analyzing the genomic assembly of these varieties, and in the study compared Thai durian with Malaysian durian variety Musang King (MK) to explore the evolutionary differences between the two types of durian varieties. The findings revealed that Thai durians, especially the Monthong variety, are unique in genomic evolution, with genetic variants related to disease resistance and flowering mechanisms.

7.2 Case study 2: genomic selection for durian cultivar development in Malaysia

Genome selection combined with genome prediction improves the accuracy of selection and reduces the cost of breeding. Breeders have unified breeding methods and accelerated the process of genetic improvement through genome selection. Genomic selection has been proven effective in other plant breeding projects, indicating that it also has certain application potential in durian breeding in Malaysia. Genomic selection is based on genomic data to predict breeding values, optimize the screening process, and promote the breeding of excellent durian varieties (Figure 3) (Gaynor et al., 2017; Hickey et al., 2017).

Population Improvement

Product Development



Figure 3 Overview of the two-part program with PYT genomic selection (2Part) and two-part program with headrow genomic selection (2Part+H) (Adopted from Gaynor et al., 2017)

Image caption: DH, doubled haploid; GS, genomic selection; PYT, preliminary yield trial; AYT, advanced yield trial; EYT, elite yield trial. The number of DH lines per cross (N) differs for each breeding program to maintain equal operating costs (Adopted from Gaynor et al., 2017)



7.3 Key takeaways from case studies

The Thai case study focuses on the analysis of genetic diversity and evolutionary differences of varieties to provide genetic information for crossbreeding; The Malaysian case study focuses on the use of genomic selection techniques to demonstrate an efficient and accurate modern breeding method. Both cases highlight the potential of genomic tools to overcome the difficulties encountered in traditional breeding and achieve rapid development of high-quality durian varieties, providing the scientific basis to meet the growing demand of the durian market and ensure the development of the durian industry in Southeast Asia.

8 Economic and Market Considerations in Durian Breeding

8.1 Consumer preferences and market trends

Breeding goals are more or less influenced by consumer preferences for durian characteristics such as taste, aroma and appearance. Lin et al. 's study in 2022 showed that the implementation of breeding plans requires researchers to make relevant adjustments according to market trends and changes in consumer demand, which can not only ensure that new varieties meet market demand, but also bring economic benefits to people.

8.2 Cost-benefit analysis of advanced breeding programs

Advanced techniques such as genome selection have improved the efficiency and genetic gains of modern durian breeding, but for researchers, the implementation of the technology also needs to take into account the cost. Studies by Grenier et al. (2015), Crossa et al. (2017), and Merrick et al. (2022) respectively indicate that genomic selection can speed up the breeding process and improve the accuracy of researchers' selection, but high initial investment and operating costs can also affect small breeding projects.

8.3 Intellectual property and seedling certification

Intellectual property protection and seedling certification guarantee the legitimate rights and interests of new varieties and market competitiveness. Lin et al. (2022) pointed out that the development and application of molecular marker technology can effectively identify and protect varieties, and De Vries et al. (2023) pointed out that the establishment of seed and seedling certification system will help regulate the market, prevent the circulation of counterfeit and shoddy products, protect the interests of breeders and increase market trust.

9 Conclusion

The application of genome selection technology in durian breeding lies in the development of accurate genome prediction model, which requires a large number of genetic markers and phenotypic traits data. The high cost and operating expenses of genome selection make it economically viable for some users, but it does improve breeding efficiency and optimize trait selection. Successful implementation of genome selection techniques requires the development of cost-effective breeding strategies, increased efficiency of data collection, and enhanced use of genomic tools by researchers.

The use of advanced breeding techniques is subject to legal and ethical restrictions in some countries due to the lack of relevant policies to regulate their use. The recognition and acceptance of breeding technology by the general public and society also determines whether breeding technology can be quickly incorporated into commercial breeding projects. Therefore, countries that have not yet formulated relevant policies need to formulate regulations to ensure the safety and transparency of genome breeding. The international trade of GM durian varieties will be complicated by differences in regulations between countries, which will require policy makers, scientists and industry stakeholders to work together to develop standard laws that balance scientific progress and ethics.

In this study, it is believed that the subsequent breeding of durian should focus on improving drought resistance, insect resistance and climate adaptability, etc. It happens that the application of genome-assisted breeding technology accelerates the development of climate adaptability varieties, improves the selection efficiency, and quickly identifies genetic traits that enhance stress resistance. The optimization of sustainable agricultural practices is important to increase durian yields in the face of environmental changes. The application of genome selection technology in durian breeding faces multiple challenges, but through the efforts of all parties, genome selection technology can certainly promote the subsequent development of durian breeding.



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Conflict of Interest Disclosure

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

References

- Akdemir D., and Isidro-Sánchez J., 2019, Design of training populations for selective phenotyping in genomic prediction, Scientific Reports, 9: 1446. https://doi.org/10.1038/s41598-018-38081-6
- Anand A., Subramanian M., and Kar D., 2023, Breeding techniques to dispense higher genetic gains, Frontiers in Plant Science, 13: 1076094. https://doi.org/10.3389/fpls.2022.1076094
- Arora L., and Narula A., 2017, Gene editing and crop improvement using CRISPR-Cas9 system, Frontiers in Plant Science, 8: 1932. https://doi.org/10.3389/fpls.2017.01932
- Bortesi L., and Fischer R., 2015, The CRISPR/Cas9 system for plant genome editing and beyond, Biotechnology advances, 33(1): 41-52. https://doi.org/10.1016/j.biotechadv.2014.12.006
- Crossa J., Pérez-Rodríguez P., Cuevas J., Montesinos-López O., Jarquín D., De Los Campos G., Burgueño J., González-Camacho J., Pérez-Elizalde S., Beyene Y., Dreisigacker S., Singh R., Zhang X., Gowda M., Roorkiwal M., Rutkoski J., and Varshney R., 2017, Genomic selection in plant breeding: methods, models, and perspectives, Trends in Plant Science, 22(11): 961-975. https://doi.org/10.1016/j.tplants.2017.08.011
- De Vries M., Adams J., Eggers E., Ying S., Stockem J., Kacheyo O., Van Dijk L., Khera P., Bachem C., Lindhout P., and Van Der Vossen E., 2023, Converting hybrid potato breeding science into practice, Plants, 12(2): 230. https://doi.org/10.3390/plants12020230
- Gaynor R., Gorjanc G., Bentley A., Ober E., Howell P., Jackson R., Mackay I., and Hickey J., 2017, A two part strategy for using genomic selection to develop inbred lines, Crop Science, 57: 2372-2386. <u>https://doi.org/10.2135/CROPSCI2016.09.0742</u>
- Gopal M., and Gupta A., 2016, Microbiome selection could spur next-generation plant breeding strategies, Frontiers in Microbiology, 7: 1971. https://doi.org/10.3389/fmicb.2016.01971
- Grenier C., Cao T., Ospina Y., Quintero C., Chatel M., Tohme J., Courtois B., and Ahmadi N., 2015, Accuracy of genomic selection in a rice synthetic population developed for recurrent selection breeding, PLoS One, 10(5): e0154976. <u>https://doi.org/10.1371/journal.pone.0154976</u>
- He J., Zhao X., Laroche A., Lu Z., Liu H., and Li Z., 2014, Genotyping-by-sequencing (GBS), an ultimate marker-assisted selection (MAS) tool to accelerate plant breeding, Frontiers in Plant Science, 5: 484. <u>https://doi.org/10.3389/fpls.2014.00484</u>
- Hickey J., Chiurugwi T., Mackay I., Powell W., Eggen A., Kilian A., Jones C., Canales C., Grattapaglia D., Bassi F., Atlin G., Gorjane G., Dawson I., Rabbi I., Ribaut J., Rutkoski J., Benzie J., Lightner J., Mwacharo J., Parmentier J., Robbins K., Skøt L., Wolfe M., Rouard M., Clark M., Amer P., Gardiner P., Hendre P., Mrode R., Sivasankar S., Rasmussen S., Groh S., Jackson V., Thomas W., and Beyene Y., 2017, Genomic prediction unifies animal and plant breeding programs to form platforms for biological discovery, Nature Genetics, 49: 1297-1303. https://doi.org/10.1038/ng.3920
- Lin X., Liu X., Chen M., Gao H., Zhu Z., Ding Z., and Zhou Z., 2022, Assessment of genetic diversity and discovery of molecular markers in durian (*Durio zibethinus* L.) in China, Diversity, 14(9): 769. https://doi.org/10.3390/d14090769
- Liu Q., Yang F., Zhang J., Liu H., Rahman S., Islam S., Ma W., and She M., 2021, Application of CRISPR/Cas9 in crop quality improvement, International Journal of Molecular Sciences, 22(8): 4206. <u>https://doi.org/10.3390/ijms22084206</u>
- Merrick L., Herr A., Sandhu K., Lozada D., and Carter A., 2022, Optimizing plant breeding programs for genomic selection, Agronomy, 12(3): 714. https://doi.org/10.3390/agronomy12030714
- Meuwissen T., Hayes B., and Goddard M., 2013, Accelerating improvement of livestock with genomic selection, Annual Review of Animal Biosciences, 1: 221-237.

https://doi.org/10.1146/annurev-animal-031412-103705

Migicovsky Z., and Myles S., 2017, Exploiting wild relatives for genomics-assisted breeding of perennial crops, Frontiers in Plant Science, 8: 460. https://doi.org/10.3389/fpls.2017.00460



- Nawae W., Naktang C., Charoensri S., U-Thoomporn S., Narong N., Chusri O., Tangphatsornruang S., and Pootakham W., 2023, Resequencing of durian genomes reveals large genetic variations among different cultivars, Frontiers in Plant Science, 14: 1137077. <u>https://doi.org/10.3389/fpls.2023.1137077</u>
- Peixoto M., Coelho I., Leach K., Bhering L., and Resende M., 2023, Simulation based decision making and implementation of tools in hybrid crop breeding pipelines, Crop Science, 64(1): 110-125.

https://doi.org/10.1002/csc2.21139

Rembe M., Zhao Y., Jiang Y., and Reif J., 2018, Reciprocal recurrent genomic selection: an attractive tool to leverage hybrid wheat breeding, Theoretical and Applied Genetics, 132: 687-698.

https://doi.org/10.1007/s00122-018-3244-x

- Renzi J., Coyne C., Berger J., Von Wettberg E., Nelson M., Ureta S., Hernández F., Smýkal P., and Brus J., 2022, How could the use of crop wild relatives in breeding increase the adaptation of crops to marginal environments, Frontiers in Plant Science, 13: 886162. https://doi.org/10.3389/fpls.2022.886162
- Richards R., Rebetzke G., Watt M., Condon A., Spielmeyer W., and Dolferus R., 2010, Breeding for improved water productivity in temperate cereals: phenotyping, quantitative trait loci, markers and the selection environment, Functional Plant Biology, 37: 85-97. https://doi.org/10.1071/FP09219
- Salgotra R., and Stewart C., 2020, Functional markers for precision plant breeding, International Journal of Molecular Sciences, 21(13): 4792. https://doi.org/10.3390/ijms21134792
- Sankaran S., Khot L., Espinoza C., Jarolmasjed S., Sathuvalli V., Vandemark G., Miklas P., Carter A., Pumphrey M., Knowles N., and Pavek M., 2015, Low-altitude, high-resolution aerial imaging systems for row and field crop phenotyping: a review, European Journal of Agronomy, 70: 112-123.
- Tang R., Wei S., Tang J., Aridas N., and Talip M., 2024, A method for durian precise fertilization based on improved radial basis neural network algorithm, Frontiers in Plant Science, 15: 1387977.

https://doi.org/10.3389/fpls.2024.1387977

- Tiwari J., Yerasu S., Rai N., Singh D., Singh A., Karkute S., Singh P., and Behera T., 2022, Progress in marker-assisted selection to genomics-assisted breeding in tomato, Critical Reviews in Plant Sciences, 41: 321-350.
- Wang Y.F., and Zhang L.M., 2024, Gene-driven future: breakthroughs and applications of marker-assisted selection in tree breeding, Molecular Plant Breeding, 15(3): 132-143.
- Xu Y., Lu Y., Xie C., Gao S., Wan J., and Prasanna B., 2012, Whole-genome strategies for marker-assisted plant breeding, Molecular Breeding, 29: 833-854. Yue G., 2013, Recent advances of genome mapping and marker - assisted selection in aquaculture, Fish and Fisheries, 15: 376-396.
- Zhang F., and Batley J., 2020, Exploring the application of wild species for crop improvement in a changing climate, Current Opinion in Plant Biology, 56: 218-222.

https://doi.org/10.1016/j.pbi.2019.12.013

- Zhang H., Zhang J., Lang Z., Botella J., and Zhu J., 2017, Genome editing-principles and applications for functional genomics research and crop improvement, Critical Reviews in Plant Sciences, 36: 291-309.
- Zhou J., Luan X., Liu Y., Wang L., Wang J., Yang S., Liu S., Zhang J., Liu H., and Yao D., 2023, Strategies and methods for improving the efficiency of CRISPR/Cas9 gene editing in plant molecular breeding, Plants, 12(7): 1478. <u>https://doi.org/10.3390/plants12071478</u>

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