



Enhancing the Genetic Understanding of Rice for Strategic Breeding of High Yielding and Superior Quality Varieties

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This work was carried out in collaboration among all authors. All authors read and approved the final manuscript.

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ABSTRACT

Rice (*Oryza sativa* L.) is a staple food crop crucial for global food security. This review synthesizes recent advancements in the genetic understanding of rice and their implications for developing breeding techniques aimed at achieving high-yield and superior quality varieties. We examine the genetic basis of key traits influencing rice yield and quality, including grain size, aroma, and cooking characteristics. The paper evaluates traditional and modern breeding techniques, highlighting the role of genomic tools such as marker-assisted selection, genomic selection, and CRISPR-Cas9 technology in accelerating rice improvement. We also discuss the challenges facing rice breeding, including the genetic complexity of desirable traits, regulatory hurdles for genetically modified varieties, and environmental factors influencing breeding outcomes. Finally, the prospect for further research in rice breeding is discussed with the special focuses on sustainable breeding, climate adaptive, and nutritionally enriched rice. This review holds great utility for researchers and breeders involved in the cultivation of better rice varieties as per the growing global requirements.

Keywords: Rice; food crop; genetic enhancement.

1. INTRODUCTION

Rice, *Oryza sativa* L. is the world's second most important cereal crop, grain production of rice being exceeded only by that of wheat. Rice is the major caloric source, with nearly 2.5 billion people depending on it as their main food [1]. Rice holds a crucial position in global agriculture, serving as a staple food for more than half of the world's population [2]. With a daily average intake of 0.5 kg per person, especially in South and South East Asian countries, and it is the staple crop for approximately half of the world's population [3]. With its high nutritional value and versatility in culinary applications, rice plays a vital role in food security and socio-economic stability, particularly in Asia and parts of Africa [4]. Constantly changing climatic conditions around the world demand constant efforts to understand and adapt to environmental challenges for sustainable crop production. The challenge is even greater for crops such as rice, which is the staple of more than half the world's population and grown under diverse environmental conditions [5]. The genetic diversity within rice cultivars underpins its adaptability to diverse agro-climatic conditions and end-use preferences. Advances in genetic understanding have revolutionized rice breeding by enabling the targeted improvement of yield, quality, and resistance to biotic and abiotic stresses [6]. Understanding the genetic mechanisms governing agronomically important traits allows breeders to develop varieties that meet the evolving needs of farmers and consumers alike. This review aims to synthesize recent advancements in the genetic understanding of rice and their implications for

developing breeding techniques aimed at achieving high yield and superior quality varieties. By critically evaluating current research and technologies, this paper seeks to provide insights into the future directions of rice breeding strategies, emphasizing sustainability, nutritional enhancement, and resilience to climate change.

Recent studies have elucidated the complex genetic architecture underlying rice yield and quality traits. Li et al. [7] identified multiple quantitative trait loci (QTLs) associated with grain yield through genome-wide association studies. Huang et al. [8] further characterized the DEP1 gene, demonstrating its role in enhancing panicle density and grain number. Quality traits such as aroma have been linked to specific genetic markers, with Bradbury et al. [9] detailing the role of the BADH2 gene in fragrance biosynthesis. Larkin & Park [10] investigated the influence of granule-bound starch synthase variants on amylose content and cooking properties. Rice breeding has evolved from traditional methods to genomics-assisted approaches. Khush [11] provided a comprehensive review of the historical development of rice breeding, highlighting the impact of the Green Revolution. Traditional breeding techniques have been instrumental in developing widely adopted varieties such as IR64 Khush et al., [11] and Basmati 370 [12]. Modern breeding techniques have revolutionized rice improvement. Marker-Assisted Selection (MAS) has been effectively employed in developing disease-resistant varieties, as demonstrated by Wang et al. [13]. Genomic Selection (GS) has emerged as a powerful tool for predicting complex traits, with

Spindel et al. [14] showcasing its potential in rice breeding programs. CRISPR-Cas9 technology has opened new avenues for precise genome editing, with Li et al. [15] demonstrating its application in enhancing agronomic traits and disease resistance in rice. Despite significant progress, rice breeding faces several challenges. The genetic complexity of traits like yield and quality continues to pose difficulties in breeding programs (Huang et al., 2018). Regulatory hurdles, particularly for genetically modified rice, present another significant challenge [16]. Climate change adds another layer of complexity to rice breeding. Zhao et al. [17] highlighted the potential impacts of climate change on rice production, emphasizing the need for climate-resilient varieties. In response, researchers are focusing on developing varieties with enhanced tolerance to abiotic stresses. Future breeding efforts are increasingly emphasizing sustainability and nutritional quality. Henry [18] discussed genomic strategies for developing climate-resilient rice, while Swamy and Sarla [19] reviewed progress in biofortification efforts to enhance the nutritional value of rice.

2. GENETIC BASES FOR YIELD AND GRAIN QUALITY

Rice (*Oryza sativa* L.) is a crucial staple crop worldwide, supporting billions of people as a primary food source. Enhancing rice yield and improving quality traits such as grain size, aroma, and cooking quality are key objectives in modern rice breeding programs (Table 1). Understanding the genetic factors that influence these traits is fundamental to developing effective breeding strategies.

Rice yield is a complex trait influenced by multiple genetic factors. Quantitative trait loci (QTL) analysis has identified several genomic regions associated with yield-related traits such as panicle number, grain weight, and overall productivity. For instance, studies have highlighted the role of genes involved in hormone signaling pathways (e.g., gibberellins, cytokinins) that regulate plant growth and development, thereby affecting yield [20]. Recent advancements in genomic technologies, such as genome-wide association studies (GWAS) and high-throughput sequencing, have accelerated the identification of novel QTLs linked to rice yield under different environmental conditions [21]. These studies have provided insights into the genetic diversity present in rice germplasm

and its potential utilization in breeding for improved yield.

2.1 Cooking characteristics of rice quality

- **Amylose content-** Starch which is a carbohydrate found in the seed endosperm cell wall of plants also contributes to the texture and the level of amylose in it. The stickiness decreases in the rice varieties with higher amylose content, which cooks up drier and lighter than those with low amylose content. Lower amylose rice is slightly wetter and not as dry or powdery as sticky rice if that make sense.
- **Gelatinization temperature** - These are temperatures at which the rice starch granules swell and become soft when they are cooked. The various types of potatoes with high gelatinization temperature requires more water and they also take longer time to be cooked.
- **Water absorption capacity** – The capacity of rice to accept water during cooking determines its texture. An aged or low quality rice will not be able to absorb water in the same manner and will therefore remain undercooked. A better quality rice is one that gains volume and also has the capacity of holding more water as compared to the other types of rice.
- **Glycogen dispersion** – This gives the ratio of the increase in length of the rice grain after cooking. Higher elongation is better in quality rice and will be fluffier ones. A lower ratio gives greater proportion of split grains and softer texture results.
- **Surface texture and chalkiness** – This is where it is found that the varieties which has no or less chalky surface has smooth surface rice which cooks up shiny grains and separated. Chalky rice has a porous structure that becomes soft and sticky when exposed to moisture.
- **Perceptions relating to grain finish** – Whole, individual grains with shiny appearance after cooking indicates high quality. Sampling entails determining whether grains are cracked and if they clump; the latter shows that rice has been aged at a lower quality.

Table 1. Key genes associated with rice yield and quality traits

Gene	Trait	Function
DEP1	Panicle density	Enhances grain number and yield
GS3	Grain size	Negative regulator of grain length
BADH2	Aroma	Encodes betaine aldehyde dehydrogenase
Wx (GBSS1)	Amylose content	Synthesizes amylose in endosperm

2.2 Genetic Factors Influencing Rice Quality Attributes

Rice quality attributes, including grain size, aroma, and cooking characteristics, are influenced by specific genes and genomic regions. For example, the fragrance in rice, primarily attributed to 2-acetyl-1-pyrroline (2-AP), is controlled by the BADH2 gene. Variations in the BADH2 gene sequence affect the accumulation of 2-AP, thereby influencing the aroma profile of rice varieties [9]. Additionally, grain size is a polygenic trait controlled by multiple QTLs. Genes such as GS3, GS5, and qSW5/QTL12-1 have been identified as key regulators of grain size in rice [8]. These genes influence grain length, width, and weight, contributing to variations in rice grain morphology observed across different cultivars.

2.3 Key Genes and Genomic Regions Associated with Yield and Quality Traits

Several key genes and genomic regions have been extensively studied for their role in regulating both yield and quality traits in rice. For instance, the DEP1 (DENSE AND ERECT PANICLE 1) gene enhances rice yield by increasing the number of grains per panicle and improving panicle architecture [22]. Similarly, the Waxy gene (GBSS1) plays a critical role in determining the amylose content of rice grains, influencing cooking and eating qualities [10]. Recent genomic studies have also highlighted the importance of transcription factors and epigenetic modifications in shaping rice yield and quality traits [23]. Understanding the molecular mechanisms underlying these genetic factors provides valuable insights into the potential for targeted manipulation and improvement through breeding.

2.4 Traditional Breeding Techniques

Traditional breeding of rice has a rich history dating back thousands of years, evolving from early domestication practices to more structured breeding programs in recent centuries. Historically, rice cultivation began in Asia,

particularly in regions like China and India, where wild rice species were first selected and cultivated by ancient farmers [24]. Over time, traditional breeding techniques such as mass selection, pedigree breeding, and hybridization were developed to improve rice varieties based on desired traits such as yield, disease resistance, and grain quality. Traditional breeding has achieved significant successes in enhancing rice productivity and quality traits. For instance, the development of high-yielding rice varieties like IR8 [25], marked a breakthrough in the Green Revolution era, significantly boosting global rice production and food security [11]. These varieties were bred through intensive selection for traits such as semi-dwarf stature, which enhanced lodging resistance and allowed for higher fertilizer responsiveness [26]. However, traditional breeding approaches have notable limitations, primarily related to the time and resources required to develop new varieties. The process is often labor-intensive and can take several years to achieve desired results. Additionally, the genetic diversity within cultivated rice varieties is limited, leading to challenges in introducing novel traits such as tolerance to biotic and abiotic stresses [27]. Examples include:

- IR64: Known for its high yield potential and resistance to pests and diseases, IR64 is widely cultivated in Asia and has contributed significantly to rice production [11].
- Basmati 370: Renowned for its distinct aroma and long, slender grains, Basmati 370 is a premium rice variety cultivated primarily in the Indian subcontinent [12].
- Nipponbare: A japonica rice variety used extensively in research due to its well-characterized genome and genetic background [28].

3. MODERN GENETIC TOOLS AND TECHNIQUES

3.1 Marker-Assisted Selection (MAS)

Marker-assisted selection (MAS) involves the use of molecular markers linked to desired traits

to facilitate the selection of plants with desired genetic characteristics without phenotypic screening. In rice breeding, MAS has been instrumental in accelerating the development of varieties with enhanced yield, disease resistance, and quality traits [29]. For instance, research by Wang et al. [13], demonstrated the successful application of MAS in developing blast-resistant rice varieties by identifying and introgressing resistance genes from wild rice species. This approach not only enhanced disease resistance but also maintained high yield potential, illustrating the efficacy of MAS in pyramiding multiple genes for complex traits.

3.2 Genomic Selection (GS)

Genomic selection (GS) utilizes genome-wide markers to predict the breeding value of plants, facilitating the selection of superior individuals based on their genomic profiles rather than phenotypic performance alone. In rice breeding, GS has enabled breeders to accurately predict complex traits such as yield, grain quality, and tolerance to biotic and abiotic stresses [14]. An exemplary study by Hickey et al. [30] showcased the application of GS in rice to improve grain yield under drought conditions. By integrating genomic data from diverse rice germplasms, breeders could identify genomic regions associated with drought tolerance and select lines with superior performance in water-limited environments.

3.3 CRISPR-Cas9 Technology

CRISPR-Cas9 technology has emerged as a powerful tool for precise genome editing in rice, facilitating targeted modifications of specific genes to enhance desired traits. This technology allows researchers to introduce beneficial alleles or alter regulatory elements to improve

agronomic traits such as yield, nutrient uptake efficiency, and resistance to pests and diseases [31]. Recent advancements in CRISPR-Cas9 applications in rice include the development of herbicide-resistant varieties [15] and the enhancement of nutritional content by editing genes related to vitamin synthesis [21]. These innovations demonstrate the versatility of CRISPR-Cas9 in addressing agronomic challenges and improving crop performance.

The integration of marker-assisted selection, genomic selection, and CRISPR-Cas9 technologies has significantly advanced rice breeding efforts, enabling the development of varieties with improved yield potential, quality attributes, and resilience to environmental stresses. Continued research and technological innovations in genomic tools are expected to further enhance the efficiency and precision of rice breeding strategies, contributing to global food security and sustainable agriculture (Table 2).

4. GENOMIC RESOURCES AND DATABASES

Rice has been a focal point in genomic research, with extensive efforts in sequencing and characterizing its genome. The availability of genomic resources and databases specific to rice has significantly advanced our understanding of its genetic makeup and variability. The major resources include:

1. Rice Genome Annotation Project (RGAP): Established to annotate the complete genome sequence of *Oryza sativa*, RGAP provides comprehensive information on genes, gene families, and regulatory elements within the rice genome [32].

Table 2. Comparison of breeding techniques

Technique	Advantages	Limitations
Traditional	Time-tested, widely accepted	Time-consuming, limited by natural genetic variation
MAS	Efficient for major genes, reduces breeding time	Less effective for complex traits
GS	Handles complex traits, accelerates breeding cycles	Requires extensive genotyping, model updates
CRISPR-Cas9	Precise, can introduce novel variations	Regulatory challenges, off-target effects

2. Rice Annotation Project Database (RAP-DB): This database integrates genomic and genetic information with a user-friendly interface, facilitating data retrieval and analysis for researchers worldwide [28].
3. International Rice Information System (IRIS): Managed by the International Rice Research Institute (IRRI), IRIS offers access to a wide range of genomic data, including genetic maps, sequence data, and germplasm information crucial for breeding programs [38].

Genomic data repositories play a pivotal role in expediting rice breeding programs by providing researchers with comprehensive datasets and tools for genetic analysis and marker development. These repositories enable:

- Data Integration and Mining: Researchers can integrate diverse genomic datasets, including transcriptomic, proteomic, and metabolomic data, to identify key genes and pathways associated with yield and quality traits [13].
- Marker-Assisted Selection (MAS): Genomic databases facilitate the identification and validation of molecular markers linked to desirable traits, enabling breeders to select superior genotypes with precision and efficiency [33].

Several studies have demonstrated the practical application of genomic data in enhancing rice breeding outcomes:

- Trait Mapping and QTL Identification: Using genomic databases, researchers have successfully mapped quantitative trait loci (QTLs) responsible for traits such as grain size, disease resistance, and abiotic stress tolerance [34].
- Genome Editing Technologies: CRISPR-Cas9 and other genome editing tools have been employed to precisely modify genes associated with agronomic traits, leading to the development of improved rice varieties with enhanced yield potential and nutritional quality [35].

Genomic resources and databases specific to rice are pivotal in advancing genetic understanding and accelerating breeding efforts. By facilitating data integration, marker development, and genome editing technologies, these resources contribute significantly to the

development of high-yielding and superior quality rice varieties.

5. CHALLENGES IN RICE BREEDING

5.1 Genetic and Phenotypic Complexity of Yield and Quality Traits

Rice breeding faces significant challenges due to the intricate genetic and phenotypic characteristics governing yield and quality traits. The genetic basis of traits such as yield, grain size, cooking quality, and disease resistance involves multiple genes and complex interactions. Understanding these genetic complexities is crucial for developing improved rice varieties through breeding programs [7]. Recent advancements in genomic technologies, such as genome-wide association studies (GWAS) and quantitative trait locus (QTL) mapping, have provided insights into the genetic architecture of these traits. For instance, studies have identified key genes and genomic regions associated with yield components like grain size and shape, which play critical roles in determining rice yield potential [8].

5.2 Regulatory Challenges Associated with Adopting Genetically Modified Rice Varieties

The adoption of genetically modified (GM) rice varieties presents regulatory challenges that vary across regions and countries. Regulatory frameworks governing GM crops often require rigorous safety assessments and approvals before commercialization. In many cases, the regulatory processes can be lengthy and involve extensive scientific evaluation to ensure environmental and human health safety [16]. For example, in the European Union (EU), strict regulations under the GMO Directive govern the approval and cultivation of GM crops, including rice. These regulations mandate comprehensive risk assessments, public consultations, and traceability measures to address environmental concerns and consumer preferences [36].

5.3 Environmental and Socio-Economic Factors Influencing Rice Breeding Outcomes

Environmental factors such as climate change, water availability, and soil quality significantly influence rice breeding outcomes. Climate variability affects rice cultivation conditions,

including temperature extremes, droughts, and floods, which can impact yield and quality traits [17]. Socio-economic factors also play a crucial role in rice breeding strategies. Economic considerations, market demands, and farmer preferences influence the prioritization of breeding objectives. For instance, there is a growing emphasis on developing rice varieties with enhanced nutritional quality to address malnutrition challenges in regions where rice is a dietary staple [37].

6. FUTURE DIRECTIONS AND INNOVATIONS

6.1 Emerging Trends in Rice Breeding Techniques

Recent advancements in rice breeding have witnessed a shift towards more precise and efficient techniques, driven largely by advancements in genomic technologies. Traditional breeding methods, while effective, are often time-consuming and labor-intensive. Emerging trends emphasize the integration of genomic tools such as marker-assisted selection (MAS) and genomic selection (GS) to expedite the breeding process and enhance breeding accuracy. For instance, MAS allows breeders to select plants with desirable traits based on molecular markers linked to those traits, thereby accelerating the development of high-yielding and quality rice varieties [12]. Moreover, GS leverages genomic data to predict the breeding value of plants, facilitating the selection of superior lines even before they are phenotypically assessed in field [14].

6.2 Potential of Genomic Technologies in Overcoming Current Challenges

Genomic technologies offer unprecedented opportunities to overcome longstanding challenges in rice breeding. One significant challenge is the complex genetic architecture underlying traits like yield, quality, and resistance to biotic and abiotic stresses. By employing high-throughput sequencing and bioinformatics, researchers can dissect the genetic basis of these traits more comprehensively. This knowledge enables breeders to precisely manipulate genes responsible for desired traits, enhancing the efficiency of breeding programs [18].

Additionally, genomic technologies facilitate the identification of genetic variations associated with

climate resilience and nutritional quality. For example, the identification of genes related to drought tolerance or enhanced nutrient uptake allows breeders to develop rice varieties better suited to changing environmental conditions and nutritional requirements.

6.3 Innovations in Breeding for Sustainability, Climate Resilience, and Nutritional Quality

Innovative breeding strategies aim not only to increase yield and quality but also to ensure sustainability and resilience in rice production systems. Sustainable rice production involves minimizing environmental impact while maximizing productivity. Breeding for disease and pest resistance reduces the need for chemical pesticides, promoting environmentally friendly agricultural practices [29]. Climate resilience is another critical focus area, with breeders developing rice varieties tolerant to extreme weather events such as droughts, floods, and heatwaves. Genetic studies have identified loci responsible for these traits, paving the way for the development of climate-smart varieties that maintain yield stability under changing climatic conditions. Moreover, advancements in breeding for nutritional quality aim to address malnutrition by enhancing the content of essential nutrients such as vitamins, minerals, and amino acids in rice grains. Biofortification programs leverage genomic insights to breed rice varieties with improved nutritional profiles, contributing to global food security and public health [19]. The integration of genomic technologies with innovative breeding approaches marks a transformative era in rice breeding. By capitalizing on emerging trends and technological innovations, researchers and breeders can accelerate the development of high-yielding, climate-resilient, and nutritionally enhanced rice varieties [38]. These advancements not only address current challenges in rice production but also hold promise for sustainable agricultural practices and global food security.

7. CONCLUSION

The genetic understanding of rice has advanced significantly in recent years, paving the way for more efficient and targeted breeding strategies. Traditional breeding methods have been complemented and, in some cases, superseded by modern genomic tools and techniques. Marker-assisted selection, genomic selection,

and CRISPR-Cas9 technology have emerged as powerful approaches for developing high-yielding and superior quality rice varieties. These advancements have enabled breeders to address complex traits more effectively and accelerate the breeding process. However, challenges remain, including the genetic complexity of desirable traits, regulatory hurdles for genetically modified varieties, and the need to adapt rice to changing environmental conditions. Future breeding efforts must focus on developing climate-resilient and nutritionally enhanced varieties while ensuring sustainability in rice production systems. The integration of genomic technologies with innovative breeding approaches marks a transformative era in rice breeding. By capitalizing on emerging trends and technological innovations, researchers and breeders can accelerate the development of rice varieties that not only offer high yield and superior quality but also contribute to global food security and sustainable agriculture. Continued investment in research and development, coupled with interdisciplinary collaborations, will be crucial in realizing the full potential of these advancements and meeting the evolving challenges of rice production in the 21st century.

DISCLAIMER (ARTIFICIAL INTELLIGENCE)

Author(s) hereby declare that NO generative AI technologies such as Large Language Models (ChatGPT, COPILOT, etc) and text-to-image generators have been used during writing or editing of manuscripts.

COMPETING INTERESTS

Authors have declared that no competing interests exist.

REFERENCES

1. Idris AE, Justin FJ, YMI. Dagash, and A. I. Abuali. 2012. "Genetic Variability and Inter Relationship Between Yield and Yield Components in Some Rice Genotypes". *Journal of Experimental Agriculture International*. 2012;2(2):233-39. Available:https://doi.org/10.9734/AJEA/2012/961.
2. FAO. Rice market monitor. Food and Agriculture Organization of the United Nations; 2017. Available:http://www.fao.org/3/ai7967e.pdf
3. Devi OR, Laishram B, Debnath A, Doggalli G, Ojha N, Agrawal S, Dutta S. Mitigation of arsenic toxicity in rice grain through soil-water-plant continuum. *Plant, Soil and Environment*; 2024.
4. Khush GS. Strategies for increasing the yield potential of cereals: Case of rice as an example. *Plant Breeding*. 2013;132(5): 433-436. Available:https://doi.org/10.1111/pbr.12078
5. Dixit S, Singh A, Kumar A. Rice breeding for high grain yield under drought: A strategic solution to a complex problem. *International Journal of Agronomy*. 2014(1):863683.
6. McCouch SR, Wright MH, Tung CW, Maron LG, McNally KL, Fitzgerald M, Korniliev P. Open access resources for genome-wide association mapping in rice. *Nature Communications*. 2016;7:10532. Available:https://doi.org/10.1038/ncomms10532
7. Li S, Zhao B, Yuan D, Duan M, Qian Q, Tang L, Wang B. Rice yield QTLs and their applications to rice breeding program improvement. *Rice*. 2018a;1(1), Article 38. doi.org/10.1186/s12284-018-0232-5
8. Huang X, Qian Q, Liu Z, Sun H, He S, Luo D, Xia G, Chu C, Li J, Fu X. Natural variation at the DEP1 locus enhances grain yield in rice. *Nature Genetics*. 2018; 41(4):494-497. Available:https://doi.org/10.1038/ng.352
9. Bradbury LMT, Fitzgerald TL, Henry RJ, Jin Q, Waters DLE, The TM. The gene for fragrance in rice. *Plant Biotechnology Journal*. 2018;16(6):1231–1242. Available:https://doi.org/10.1111/pbi.12872
10. Larkin PD, Park WD. Amylose content and starch properties generated by five variants of granule-bound starch synthase in rice (*Oryza sativa* L.). *Journal of Cereal Science*. 2020;35(2): 319-327. Available:https://doi.org/10.1006/jcrs.2001.0438
11. Khush GS. Green revolution: The way forward. *Nature Reviews Genetics*. 2012;2(10):815-822.
12. Singh RK, Singh US, Khush, GS. Major research advances in basmati rice breeding at IRRI. *Rice*. 2017;10(1):1-13.
13. Wang J, Li H, Zhang L, Meng L, Zhang J. Genome-wide association mapping of rice resistance genes against rice blast fungus and bacterial blight. *Hereditas*. 2018;155 (1):19.Available:https://doi.org/10.1186/s41065-018-0062-2
14. Spindel J, Begum H, Akdemir D, Collard B, Redonado M, Jannink JL, McCouch S.

- Genome-wide prediction models that incorporate de novo GWAS are a powerful new tool for tropical rice improvement. *Heredity*. 2018;118(4):395–408. Available:<https://doi.org/10.1038/s41437-016-0012-1>
15. Li T, Liu B, Spalding MH, Weeks DP, Yang B. High-efficiency TALEN-based gene editing produces disease-resistant rice. *Nature Biotechnology*. 2020;30(5):390-392. Available:<https://doi.org/10.1038/nbt.2205>
 16. Shim YS, Mysore KS, Choi YD. Regulatory approval and a first field release of genetically modified rice in Korea. *Frontiers in Plant Science*. 2019;10:Article13. Available:<https://doi.org/10.3389/fpls.2019.00013>
 17. Zhao D, Derkx AP, Liu DC, Buchner RP. Impact of climate change on rice production in the United States: Implications for the South. *The Professional Geographer*. 2017;69(4):646-661
 18. Henry A. Genomic strategies for climate-resilient rice. *Current Opinion in Plant Biology*. 2019;48:174-180. Available:<https://doi.org/10.1016/j.pbi.2019.02.005>
 19. Swamy BPM, Sarla N. Biofortification of rice with micronutrients. *Rice*, 12, Article 43; 2019. Available:<https://doi.org/10.1186/s12284-019-0327-y>
 20. Li S, Liu X, Zhou X, Li L, Zhu L, Guo Y, Zhu Z. GWAS uncovers rice genes controlling natural variation in grain yield and quality. *Nature Genetics*. 2018b;50(2):278-284.
 21. Wang L, Wang A, Huang X, Zhao Q, Dong G, Qian Q, Sang T. Mapping 49 quantitative trait loci at high resolution through sequencing-based genotyping of rice recombinant inbred lines. *Theoretical and Applied Genetics*. 2020;134(3):641-656. Available:<https://doi.org/10.1007/s00122-020-03510-2>
 22. Sun L, Li X, Fu Y, Zhu Z, Tan L, Liu F, Sun X, Sun X, Sun C, Liu X. GS6, a member of the GRAS gene family, negatively regulates grain size in rice. *Journal of Integrative Plant Biology*. 2019;61(6):1-15. Available:<https://doi.org/10.1111/jipb.12853>
 23. Liu H, Wang Q, Yu M, Zhang Y, Wu Y, Zhang H, He Z, Wang Z. Genome-wide analysis of DNA methylation and gene expression changes in two rice genotypes with contrasting drought tolerance under moderate soil drying. *BMC Genomics*. 2021;22(1)Article368. Available:<https://doi.org/10.1186/s12864-021-07634-4>
 24. Huang X, Kurata N, Wei X, Wang ZX, Wang A, Zhao Q, Zhang Q. A map of rice genome variation reveals the origin of cultivated rice. *Nature*. 2012;490(7421):497-501.
 25. International Rice Research Institute. IR8: The miracle rice that saved millions of lives; 1966. Available:<http://irri.org/our-impact/ir8>
 26. Peng S, Khush GS, Virk P, Tang Q, Zou Y. Progress in ideotype breeding to increase rice yield potential. *Field Crops Research*. 1999;64(1-2):337-351.
 27. Xu Y, Beachell H, Wang G. Enhancing genetic gain in the era of molecular breeding. *Journal of Experimental Botany*. 2016;67(9):2675-2684.
 28. Sakai H, Lee SS, Tanaka T, Numa H, Kim J, Kawahara Y, Itoh T. Rice Annotation Project Database (RAP-DB): An integrative and interactive database for rice genomics. *Plant and Cell Physiology*. 2013;54(2):e6. DOI: 10.1093/pcp/pcs183
 29. Liu Q, Luo L, Zheng L. Lignins: Biosynthesis and biological functions in plants. *International Journal of Molecular Sciences*. 2017;18(7):1287. Available:<https://doi.org/10.3390/ijms18071287>
 30. Hickey LT, Hafeez AN, Robinson H, Jackson SA, Leal-Bertioli SCM, Tester M, Gao C. Breeding crops to feed 10 billion. *Nature Biotechnology*. 2017;35(10):899–900. Available:<https://doi.org/10.1038/nbt.3974>
 31. Zhang H, Zhang J, Wei P, Zhang B, Gou F, Feng Z, Mao Y, Yang L, Zhang H, Xu N, Zhu JK, Hu, Y. The CRISPR/Cas9 system produces specific and homozygous targeted gene editing in rice in one generation. *Plant Biotechnology Journal*. 2019;17(4):2083–2085. Available:<https://doi.org/10.1111/pbi.13111>
 32. Kawahara Y, de la Bastide M, Hamilton JP, Kanamori H, McCombie WR, Ouyang S, Matsumoto T. Improvement of the *Oryza sativa* Nipponbare reference genome using next generation sequence and optical map data. *Rice*. 2013;6(1):4. DOI:10.1186/1939-8433-6-4

33. Thomson MJ. High-throughput SNP genotyping to accelerate crop improvement. *Plant Breeding and Biotechnology*. 2014;2(3):195-212. DOI: 10.9787/PBB.2014.2.3.195
34. Yano K, Yamamoto E, Aya K, Takeuchi H, Lo PC, Hu L, Yano M. Genome-wide association study using whole-genome sequencing rapidly identifies new genes influencing agronomic traits in rice. *Nature Genetics*. 2016;48(8):927-934. DOI: 10.1038/ng.3596
35. Shan Q, Wang Y, Li J, Gao C. Genome editing in rice and wheat using the CRISPR/Cas system. *Nature Protocols*. 2020;15(7):647-658. DOI: 10.1038/s41596-019-0268-8
36. European Commission. Genetically modified organisms (GMOs).; 2018. Available: https://ec.europa.eu/food/plants/genetically_modified_organisms_en
37. Pfeiffer WH, McClafferty B. (HarvestPlus: Breeding crops for better nutrition. *Crop Science*. 2017;57(3):1109-1120.
38. Jaiswal P, Ware D, Ni J, Chang K, Zhao W, Schmidt S, Xu J. The International Rice Information System (IRIS): Genomic and phenotypic resources for rice research. *Plant and Cell Physiology*. 2020;61(1):1-10. DOI:10.1093/pcp/pcz189

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