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REVIEW ARTICLE

The journey of aromatic rice: genetic diversity, global trade, and prospects for improvement: a review

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ABSTRACT

Aromatic rice, a globally esteemed crop, holds significant cultural and economic value due to its unique fragrance and delicate flavor. Originating in the Indian subcontinent around 400 BC, now grown in over 30 countries. Its evolution is hypothesized to have resulted from hybridization between newly introduced japonica rice, carrying the *betaine aldehyde dehydrogenase 2* (*BADH2*) aroma mutation, and local Aus varieties. This market, dominated by Basmati and Jasmine types, constitutes 15-18% of the global rice trade and commands a significantly higher market value than non-aromatic rice. The distinctive aroma is primarily attributed to 2-acetyl-1-pyrroline (2-AP) alongside over 300-500 other volatile compounds, whose synthesis is regulated by *BADH2*, a recessive gene on chromosome 8. While *BADH2* is a key driver, minor quantitative trait loci (QTLs) and other genes contribute to aroma complexity, revealing its polygenicity. Conventional breeding has developed prominent cultivars like Pusa Basmati-1of India and KDML105 of Thailand. Recently, Marker-aided selection (MAS) has facilitated the precise introgression of aroma genes into high-yielding, non-aromatic backgrounds, evading the limitations of traditional phenotyping. The expanding global market for aromatic rice, driven by consumer preference for premium quality and rising demand, necessitates continued improvement. Recent innovations in genomics and genome editing technologies will offer unprecedented precision for genetic alterations of aroma. This review highlights the evolutionary history, genetic basis, global market dynamics, and breeding advancements in aromatic rice, emphasizing the need for continued exploration of its rich genetic diversity to ensure sustainable production and enduring international appeal.

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Introduction

A particular kind of rice called aromatic rice is distinguished by its unique flavor, which is sometimes characterized as floral or nutty. The aromatic rice genotypes are thought to have evolved in the Indian subcontinent approximately 2400–4000 years ago. According to Siddiq *et al.* (2012), the first recorded reference to fragrant rice was made by the renowned Indian surgeon and physician Susrutha (400 BC). The evolution of aromatic rice is assumed to be a result of an admixture between newly introduced *japonica* rice, which carried the *BADH2* mutation responsible for aroma, and the local Aus rice varieties (Lu, 2023; Singh *et al.,* 2000). Aromatic rice varieties, prized for their distinct fragrance and delicate flavor, represent a significant and cherished category within the global rice market. Nowadays, these varieties are cultivated across diverse regions. There is scientific evidence of aromatic rice cultivation in over 38 countries worldwide, including countries from all continents (Singh *et al*., 2000; Verma *et al*., 2018). The primary categories of scented rice genotypes include jasmine, basmati, and other aromatic rice varieties.

Basmati rice cultivars are of Indian and Pakistani origin, known for their delicate aroma and extra-long elongation after cooking (Siddiq *et al*., 2012). Originating in Thailand, jasmine-type rice boasts a kernel that is relatively longer than basmati. Both of these main aromatic groups are complemented by a plethora of minor aromatic groups found in various parts of the world. The strong aroma of rice is associated with more than 500 volatile compounds, among which 2-AP is the principal component (Behera and Panda, 2023). Beyond 2-AP, rice aroma results from a complex mixture of plentiful volatile compounds (Hu *et al*., 2020; Verma and Srivastav, 2018). Quantitative analyses show that fragrant rice varieties typically contain 0.04-0.09 ppm of 2-AP, a level significantly higher than the 0.006-0.008 ppm found in non-fragrant varieties (Varatharajan et al., 2022). 2-AP is also found in some other foods, like popcorn, green tea, and bread, and can be produced by certain microbes. This unique character helped aromatic rice be promoted as an essential group with the highest quality rice and attracted a higher selling price than non-aromatic rice (Hien *et al*., 2007). However, significant differences in the aroma intensity, grain character, and elements among aromatic rice varieties suggest that various chemical groups play a role in varying amounts.

Extensive research has been done to elucidate the genetic basis of rice aroma and to map genes or QTLs responsible for aroma expression (Behera and Panda, 2023; Chen *et al*., 2008). The genetic control of 2-AP synthesis and rice aroma expression is primarily understood to be governed by a recessive gene on the long arm of chromosome 8 between the SSR markers RM223 and RM515 (2.34 cM), known as *BADH2* (Hui et al., 2022). Various other fragrance genes have also been found in the rice genome. Three major QTLs related to rice aroma on chromosomes 3, 4, and 8 were mapped (Chen *et al.*, 2008; Choudhury *et al.*, 2024). Fine mapping of the qaro3-1, qaro4-1, and other QTLs for rice aroma was carried out to confirm their role in aroma production of rice (Pachauri *et al.*, 2010). These diverse genes/QTLs provide opportunities for breeders to design and develop new aromatic rice cultivars. There is evidence of successful introgression of aroma genes in a high-yielding rice background to create new aromatic rice cultivars. For Instance, semi-dwarf Basmati 370 in India, Shenyou R3 in Japan, and MR84, MR219 in Malaysia (Cheng *et al.*, 2017; Zhang *et al.*, 2025). Scientists have fruitfully edited the concerned gene, resulting to the down-regulated expression of *OsBADH2*, and amplified 2-AP content and fragrance (Hui *et al.*, 2022).

The global market for aromatic rice is a significant part of the broader rice industry, with the market size reaching USD 309.8 billion in 2024 (IMARC Group, 2025). The global aromatic rice market is substantial, with fragrant rice accounting for 15-18% of the global rice trade (Hashim *et al.*, 2021). It has a higher market price of more than USD 1050 per ton, whereas the non-aromatic rice is selling at USD 440--580 per metric ton (Hashim *et al.*, 2021). Only a handful of well-known aromatic rice varieties are available in the world market, where Basmati and Jasmine are at the top of the list. India is one of the leading players in aromatic rice segment and Basmati rice dominates the other varieties. The top position goes to India, where nearly 70% of the world's Basmati is grown. Apart from India, Basmati rice has been producing in Pakistan and Kenya. While India is a leading exporter of aromatic rice, it is vital to recall that other countries are also contributing significantly to the global aromatic rice market. Jasmine-type rice is mostly from Southeast Asia, with Thailand, Vietnam, and Cambodia being main producers and exporters. Although Basmati and Jasmine grasp the largest market share, several other aromatic varieties are grown and consumed globally, often playing a magnificent role in the regional economy. Kalijira, Kataribhog, Chinigura, and Tulshimala are popular aromatic rice cultivars in Bangladesh. Other privileged aromatic rice from different countries includes Sadri from Iran, the Afghani Bahar, Della, Texmati, and Kasmati from the USA, Paw San Hmwe of Myanmar (Hien *et al.*, 2006; Verma *et al.*, 2018). These rice varieties have a specific, potent charm that brands them popular in the area. Climatic and edaphic conditions are ecological components that affect the fragrance of rice.

Aromatic rice is naturally biofortified with Fe, Zn, and other nutrients (Islam *et al.*, 2020). To avert micronutrient shortages in kids and senior citizens, scented rice is now in high demand. Using traditional breeding techniques, the Fe and Zn-rich, high-yielding, fragrant rice varieties were produced and cultivating. However, there are challenges to the steady improvement of aromatic rice. For instance, intricate genetic backgrounds, complex phenotyping, insufficient understanding of molecular markers, as well as genotype-environment interactions (Zhang *et al*., 2014). This review research was conducted to summarize information on aromatic rice, focusing on its evolutionary history, the connection between rice availability and genetic diversity of aromatic rice, global consumption, and the present market scenario. The additional objective is to explore the opportunities for further qualitative and quantitative improvement of aromatic rice through utilizing advanced breeding tools.

Materials and Methods

We searched for scientific papers and reliable sources on the evolutionary history, genetic diversity, type of rice aroma, utilization pattern, global trade, genetic resources, and breeding methods of aromatic rice. The electronic databases, such as Web of Science, Scopus, PubMed, and Google Scholar, were searched systematically using keywords or their combinations such as "aromatic rice", "evolutionary history of rice", "world consumption and trade of rice", "aroma biosynthesis mechanism in rice, and "genetic improvement for aromatic rice". The search was restricted to peer-reviewed papers, books, university websites, and influential reports written in English from 1950 up to 2025 provided a wide-ranging perspectives and current summaries.

Types of rice aroma and aromatic rice across the world

Around the world, there are numerous varieties of fragrant rice, each tailored to a particular area and distinguished by its distinct aroma, grain quality, and culinary potential. In general, they differ in terms of size, elongation ratio, texture, cooking methods, and sensory appeal. After cooking, some become soft and sticky, while others stay solid and distinct. Aromatic cultivars have various aroma types due to their diversity in volatile compounds. Among these, 2-AP is the most important; other compounds that have been demonstrated to increase consumer acceptability include 2-acetyl-pyrrole, α-pyrrolidone, and pyridine, among others. However, some volatile compounds like hexanal, acetic acid, and pentanoic acid could be detrimental to flavor (Bryant and McClung, 2011). When it comes to rice scents, these substances fall into some sensory categories. Researchers have reported several types of aroma in rice, including Sweet, Green, Popcorn, Nutty, Floral, and Fruity (Table 1). The vast diversity of genetic resources of aromatic rice needs to be conserved for further development of this crop.

Aromatic rice is esteemed globally for its unusual aroma, superior grain quality, and exceptional palatability. Different countries have their famous aromatic varieties. For instance, irrigated fields provide the famously long grains, strong aroma, and prolonged cooking time of Basmati rice from Pakistan

Table 1. A list of popular aromatic rice cultivars with their grain quality and aroma types cultivated across the world

Country	Growing Season	Cultivars	Grain quality	Aroma type	References
Bangladesh	Wet season	Kataktara, Chinigura, Kalijira, BRRI dhan34, BRRI dhan80, Kataribhog, Dadkhani, BRAC dhan2,	Fine, slender grain with a strong aroma	Sweet	Kader et al., 2020
	Dry season	BRRI dhan50, BRRI Dhan104, GAU dhan3, Binadhan-7, Binadhan-9	Fine, slender grain with a strong aroma	Sweet	Kader et al., 2023
India	Wet season	Basmati-370, Basmati-386, Dehradun, Haryana Basmati-1,	Fine, slender grain with a strong aroma	Green	Singh et al., 2018
	Dry season	Pusa-33, Sabarmati, Mahi Sugandha, etc.	Medium slender with mild aroma	Nutty	Verma et al., 2018
Pakistan	Wet season	Basmati-385, Basmati-185, Basmati-370, Super Basmati, Basmati Pak	Long, slender, with a moderate aroma	Green	Kishor et al., 2020
	Dry season	PK 4048-3, Basmati 50021-1, PK 50005-3,	Long-slender with moderate aroma	Green	Verma et al., 2018; Akhtar et al., 2018
Vietnam	Wet season	Di Huong, Jasmine 85, Lua Tam, Tam Xoan, Nang Thom Cho Dao	Long-slender, with a strong aroma	Floral	Pachauri et al., 2010
	Dry season	Tam Canh, Tam On, VD20,	Long-slender, with a strong aroma	Floral	Verma et al., 2018
China	Wet season	Congjiangxixiangmi, Huanglongxiangmi, De Chang Xiang Mi, Gan wan-xian 22	Medium-slender with strong aroma	Nutty aroma	Verma et al., 2018
	Dry season	Shuang-Zhu-Zhan, SR 5041, Xiang Keng 3	Moderate aroma	Nutty aroma	Potcho et al., 2021
Thailand	Wet season	KDML5, Hom Mali 105	Long-slender with strong aroma	Fruity	Vanavichit et al., 2018;
	Dry season	RD15, Hom Pathum	Long, slender, mild aroma	Fruity	Vinavichit et al., 2018
Iran	Wet season	Domsiah, Tarom Hashemi, Binam	Long-slender with strong aroma	popcorn-like	Kiani et al., 2012
	Dry season	Kadus, Fajr	Long, slender, with a mild aroma	popcorn	Xie et al., 2024
Myanmar	Wet season	Paw San Hmwe	Medium bold with powerful aroma	slightly sweet.	Oo et al., 2015
USA	Wet season	Texas Jasmine, California Basmati	Extra-long with moderate aroma	slightly sweet	Mohan et al., 2013;
	Dry season	Frontier Rice, Textmati	Long grain with strong aroma	nutty, popcorn	Verma et al., 2018
Japan	Dry season	Milky Queen	Short grain with sweet aroma	Sweet	Yamamoto et al., 2014
	Wet season	Hitomebore, Koshihikari	Short grain with mild aroma	slightly sweet	Nishikawa et al., 2015
Cambodia	Wet season	Phka Rumdeng	Medium grain, mild aroma	jasmine-like aroma	Thong et al., 2020
	Dry season	Sen Pidao,	Medium grain, mild aroma	Tantalizing aroma	FAO,2017
Malaysia	Wet season	MR219	Long slender grain with strong aroma	floral	Chen et al., 2017
Indonesia	Wet season	Rojolele	Medium to long grain with aroma	Nut-like aroma	Dwiningsih and Alkahtani, 2022

and India. In the United States, Texmati is an aromatic rice variety with medium-long grains and moderate aroma, while in Iran, Hashemi rice is a traditional variety with fine grains and a mild fragrance. Aromatic rice type is determined by ecotype, grain size and shape, intensity of scent, and cooking quality. These features depend on both rice genotype and the environment in which it is grown. The combination of these factors determines the visual appeal, flavor, and overall satisfaction of rice across regions and cultures. A country-wise list of popular aromatic rice is presented in Table 2.

Biosynthesis of rice aroma: Aroma is an innate trait. The volatile aromatic compounds are synthesized in the aerial parts of rice seedlings in the early vegetative stage, and final accumulation takes place in the seeds (Fayaz *et al*., 2024). Since rice aroma is an important trait, the synthesis of 2-AP has been rigorously studied utilizing biochemical and molecular techniques. The primary mechanism for aroma development is the inactivation of the *BADH2* enzyme and the synthesis of 2-AP (Bradbury *et al*., 2008; Chen *et al*., 2008). The biosynthesis of 2-AP is a multifaceted process that mainly depends on specific amino acids as starting

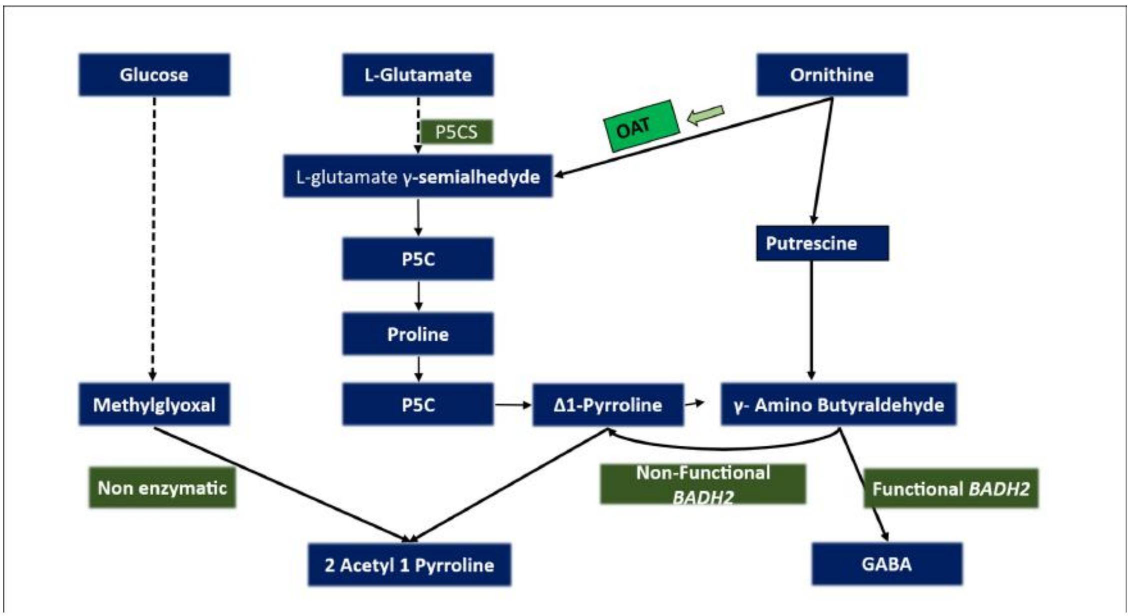

Figure 1. A schematic diagram of the *BADH2*-dependent and independent pathways of aroma biosynthesis in rice plants. P5CS-Pyrollin 5-carboxylic acid synthetase, OAT- ornithine aminotransferase, P5C-1-pyrroline-5-carboxylic acid. BADH2-Betain aldehyde dehydrogenase, GABA-γ Amino Butyraldehyde. This figure was created by putting together the results of two studies: Renuka et al. (2022) and Prodhan and Qingyao (2020), which investigated the aroma production of rice.

materials. The primary vital precursor molecules in this apparatus are glucose, ornithine, and glutamate. These precursors are digested toward a common intermediate, 1-pyrroline-5-carboxylic acid (P5C). P5C is then metabolized into 1-pyrroline, a compound recognized as a decisive factor for 2-AP production in rice. Finally, the reaction of 1-pyrroline with methylglyoxal produced 2-AP. In addition to glucose, sodium acetate, and sodium octanoate are proposed as possible sources of the acetyl group incorporated into 2-AP. Sodium acetate and sodium octanoate have been suggested as potential donors for the acetyl group incorporated into 2-AP (Poonlaphdecha *et al.*, 2016). There are two pathways that have been identified for the synthesis of 2-AP: the BADH2-dependent pathway and the BADH2-independent mechanism (Vanavichit et al., 2018). In the case of the *BADH2*-dependent pathway, precursor molecules like L-proline, γ-aminobutyric acid (GABA), and ornithine are linked to the production of 2-AP. When the *BADH2*-dependent conversion of γ-amino butyraldehyde (GAB-ald) to γ-aminobutyric acid (GABA) is functional, the accumulation of 1-pyroline, the precursor molecule of 2-AP, will be inhibited. While in the *BADH2*-independent pathway, accumulation of GAB-ald and 1-pyrroline occurs, and these compounds react with acetyl groups to produce 2-AP (Fitzgerald, 2010; Kovach *et al.*, 2010).

Genetic resources of aromatic rice

The Aromatic rice has enjoyed great demand for more than 45 years with its pleasing aroma and other qualities of grains (Verma and Srivastav, 2018). Varieties like Basmati, Jasmine, Texmati, and indigenous landraces are appreciated because of their distinct scent and other nutrients (Ashokkumar *et al.*, 2020). The expanding global demand points to the necessity to preserve the genetic resources of aromatic rice because it will boost production, counter climate change, and prevent genetic erosion (Sharma *et al.*, 2021). Moreover, many nations have been conducting research on aromatic rice to develop new aromatic rice genotypes to adapt to their environment due to their consumer preferences. The genetic resources would be one of the determinants of the successful breeding of aromatic rice. Landraces, primitive cultivars, modern cultivars, mutants, and wild progenitors with the preferred characteristics are examples of these resources. Fortunately, in most of the cases, there is an established network and collaboration system for germplasm exchange among the concerned countries or organizations for aromatic rice. These exchanges of germplasm are critical for breeding and development of aromatic rice. Advances in genomics and metabolomics have improved the understanding of aroma biosynthesis, aiding breeding efforts to develop improved aromatic genotypes (Zhang *et al.*, 2023). However, elite genotypes raise concerns about stress vulnerability, adaptability, and stable productivity due

Table 2. Country-wise representation of aromatic rice germplasm with their released varieties until 2024

Country	Aromatic accession	Released varieties	Major Aromatic genotypes	References
Afghanistan	More than 40 genotypes	13	Bahra, Lawangi, Sela Takhar, Bala, Lawangin, Pashadi, Germa Bala, Sarda Bala, Luke Qasan, Torishi, Sela Doshi, Surkha-Bala, Pashadi Konar	Singh, 2000; Itani, 2002
Bangladesh	Over 113	14	Kataribhog, Bau-pagal, Badshabhog, Dadkhani, Kalazira, Banshful, Chinigura, BRRI dhan 70, Binadhan 13, BRRI dhan 38, BRRI dhan37, BRRI dhan38, BRRI dhan50, BRRI dhan70, BRRI dhan80, BRRI dhan 104, BR5, BRRI dhan34, Binadhan-13, BRAC dhan 2.	Anik and Talukder, 2002; Vemireddy et al., 2021; Islam et al., 2018
Benin	Over 35 accession	12	Bagou 19, Bagou 22, Tchaka 34, Foun 15, Tchaka 41, Nana 32, Kan 61, Kung 69, Kung 67, Bagou 20, Agbab 101, Koum 55	Nanoukon et al., 2024
Combodia	About 20	4	Somali, Phka Rumduol, Phka Rumdeng, Phka Roment, CSP70	Pachauri et al, 2010; Roy et al, 2020
China	Over 50 accessions	19	Xianggeng 3, Xiangyou 63, Zhe 9248, Ganwanxian 22, SR5041, Dechangxiangmi, Beijingkoutou, Shuangzhuzhan, Xiangnuo 4, Tainung Sen 20, Yongshunxingdao, Qingbuxiangjingmi, Congjiangxixiangmi,	Yang et al, 2012; Verma et al, 2019
France	30 accessions	3	Ajchad, Fidji, and Red Camargue rice	Maraval et al,. 2008
India	Over 500 accessions	20	Basmati 370, Joha rice, Haryana Basmati 1, Kalanamak, Ranbir Basmati, Taraori Basmati, Basmati 386, Type 3, Pusa Basmati 1, Pusa Basmati 1121, Mullan Kazhama, Seeraga Samba, Punjab Basmati 1, CSR30, Pusa 33,	Nagaraju et al, 2002; Kiani et al, 2012; Singh et al, 2018;Verma et al, 2019
Indonesia	More than 40 landraces	10	Rojo Lele, Bengwan Solo, Pare Kembang, Batang Gadis, Mentik Wangi, Sukanandi, Sinyanur, Pulu Mandoti, Pandanawangi, Gunung Perak	Kamath et al, 2008; Pachauri et al, 2010; Verma et al, 2019
Italy	Not recognized	03	Apollo, Ermes, and Venere	Griglione et al., 2015
Iran	Over 60 local fragrant cultivars	15	Tarom Mahalli, Anbar-boo, Mirza, Fajr, Champa, Mir tarom, Hassani, Shiroudi,Nemat,Mehr, Mosa Tarom, Poya, Domsiah, Hasan, Sadri, Hashemi	Kiani et al., 012; Vemireddy et al, 2021
Japan	20 aromatic genotype	8	Miyakaori, Iwaga, Sari Queen, Kouikuka 37, Hieri, Jakou, Kabashiko, Oitakoutou	Hien et al, 2007; Ootsuka et al, 2014
Myanmar	Around 50 accessions	6	Nama the Lay, Taungpyan Hmwe, Balugyun, Boke Hmwe, Ngakywe, Pawsan Hmwe	Singh, et al., 2000
Nepal	Approx. 15 developed types	22	Masino, Bayarni, Biramphool, Gauria, Gurdi kalo, Gurdi seto, Khalte kholo, Mansara, Masino, Sisuwa panheli, Jethobudho, Panhele, Anpjhutte, Rato	Rayamajhi, et al. 2023; Thakuri et al. 2023; Pachauri et al., 2010
Pakistan	Over 100 accessions	8	Basmati Pak, Basmati 385, Super Basmati, PK50005-3, Basmati 185, Basmati 50021-1, Basmati 377, Sathi Basmati	Khush, 2000; Kishor et al, 2020
Philippines	10 indigenous	3	Azucena, Milagrosa, Milfore	Pachauri et al., 2010
South Korea	33	0	Daebunhyangdo2, Hyangmi2ho	Kim et al., 2008
Thailand	Over 70 accessions	18	Buer Neo Moo, Hawm Klong Luang, Buer Ner Moo Pho Phi, Hawn Mali, RD15, Baow Hawm 62, Buer Ner Moo Phardo, Jao Mali, KDML105, Siamati, Hawm, Som Hung, Hawm Baow, RD6, Hawm Supanburi, Pla Sew.	Itani et al, 2004; Pachauri et al, 2010; Verma et al, 2019; Roy et al, 2020
USA	10 genotypes	6	A-201, Della, Dellamont, Jasmine-85, Kasmati, Texamati	Kush et al., 2000
Vietnam	50 indigenous genotypes	17	Di Huang, Tam Xuan Hai Hau, VD 20, Nang Thom, Nep Hoa Vang, Tam On, Nang Huong Ran, Nang Thom Muong, Tam Canh, Lam Thao	Hien et al, 2007; Pachauri et al, 2010; Verma et al, 2019

Table 3. The key *BADH2* alleles, their molecular characteristics, and effects on aroma expression in rice

Allele Name	Mutation Type(s)	Location(s)	Effect on *BADH2* Protein	Associated Varieties/Regions
badh2-E2	7-bp deletion	Exon 2	Truncated (82 residues), non-functional	General fragrant rice
badh2-E7	8-bp deletion + 3-bp SNP	Exon 7	Truncated (lacks 252 C-terminal residues), non-functional, premature stop codon.	Basmati, Jasmine, Daohuaxiang, RD6, KDML105, in most aromatic rice
badh2-E4/5	806-bp deletion	Between Exons 4 and 5	Leads to non-functional *BADH2*	General fragrant rice
badh2.7	G insertion	Exon 14	frameshift mutation, non-functional	India, Bangladesh, Pakistan, Sri Lanka
badh2-p	250-bp deletion	Promoter region	Leads to non-functional *BADH2*	Indica and japonica rice, frequency is more than *badh2-E7* in some aromatic varieties
badh2-E12	3-bp deletion	Exon 12	*BADH2* activity is reduced, not fully lost	Chinese rice accession A30, A29, and A28
Novel Exon 7	1 SNP (A/T) + 2 INDELs (5bp, 3bp)	Exon 7	premature stop codon, truncated BADH2 protein.	76 accessions from the 3K rice genome project
Other INDELs/ SNPs	Various INDELs and SNPs	Introns, other exons, 5'-UTR	Lead to non-functional *BADH2* (e.g., premature stop codons)	Diverse aromatic rice accessions

to limited genetic diversity. A broader genetic diversity is essential for sustainable aromatic rice improvement (Biswas *et al.*, 2021). Genetic resources empower breeders to effectively observe and characterize germplasm, to predict genetic potential, and identify novel genes and traits crucial for crop improvement. While understanding available resources of aromatic rice and easy exchange can enhance breeding efforts, summarizing global aromatic rice germplasm remains challenging. Many samples have not been tested for aroma, new genotypes are emerging, and duplicates exist, with variation in names for the same genotype across regions. We are presenting a list of country-wise documented available aromatic rice resources in Table 2.

Genetics of rice aroma

Rice fragrance has been the subject of extensive genetic analysis, which has shown a complex interplay between genes, metabolic pathways, and environment. Knowledge about these genetic mechanisms is important in breeding programs to enhance aromatic rice but retain the desirable properties of the rice. The aroma of rice is predominantly regulated by the *BADH2* gene on the 8^{th} chromosome. The *BADH2* gene of *Oryza sativa* has 15 exons and 14 introns that encodes a protein consisting of 503 amino acids. At least 19 different alleles of *BADH2* have been described so far; they include a combination of insertions, deletions, and single-nucleotide polymorphisms that are located at different introns, promoter regions, and the 5' UTR (Kovach *et al.*, 2009). As *BADH2* is considered the key genetic switch of rice aroma, there is an urgent need to explore and target *BADH2* mutants to fine-tune the aromatic characteristics of rice. The reality of multiple types of mutations strongly suggests a pattern of convergent evolution. This extensive genetic base is a valuable resource for breeders to improve fragrance in rice. The accurate transfer of the aroma genes into high-yielding but non-aromatic rice varieties has been made possible by this crucial breakthrough in marker-assisted breeding. While a predominant *BADH2* allele (*badh2.1*) originating from Japonica rice and introgressed into Indica varieties accounts for much of the global aromatic rice, significant allelic diversity exists, suggesting multiple independent origins of the trait.

In addition to *BADH2*, minor QTLs on chromosomes 3 (qaro3-1) and 4 (qaro4-1) contribute to the variation in aroma intensity in aromatic rice groups (Pachauri *et al.*, 2010). These QTLs highlight the polygenic nature of rice fragrance and the influence of genetic background on aroma expression. Nonetheless, the phenotypic expression of aroma can be modulated due to epistatic effects of genes**.** Certain reports show that there is a particular genetic background that can facilitate or inhibit the 2-AP production even with *BADH2* mutation (Sakthivel et al., 2009). The complexity of this fact highlights the need for a detailed genetic study during breeding aromatic rice, since the presence of the *BADH2* mutant gene does not ensure the desirable aroma profile.

Table 4. A list of significant QTLs associated with rice aroma that mapped across several chromosomes

Candidate gene	Chrom. number	Tissue specificity	Protein interaction	Subcellular localization	Mutation type	Key function	Reference
OsBadh2 (fgr)	8	Flower buds, flowers	Glutamate synthase	Chloroplast, cytoplasm, nucleus	8-bp deletion + 3 SNPs in exon 7	Primary gene for fragrance; elevate 2-AP	Bradbury et al., 2005; Chen et al., 2008
OsBadh1	4	Flowers, roots before flowering	Glutamate synthase	Peroxisome, cytoplasm, nucleus	Rare SNPs/ promoter mutations	Secondary contributor; enhances aroma under stress	Amarawathi et al., 2008; Pachauri et al., 2014
OsP5CS1, and OsP5CS2	5	Milk grains, flower buds, flowers	Ferredoxin-dependent glutamate synthase	Cytoplasm, nucleus, and Cell membrane	Upregulation under stress (e.g., drought)	Stress-inducible; links nitrogen metabolism to 2-AP synthesis.	Kaikavoosi et al., 2015
OsGlyI	5	Flower buds, leaves before flowering	Glyoxalase	Chloroplast, cytoplasm	Knockdown	Links glycolysis to aroma; promotes 2-AP formation.	Talukdar et al., 2017
OsGlyII	3	Flowers, flower buds	Glyoxalase	Cytoplasm, chloroplast, nucleus	Overexpression	Antagonistic role; reduces aroma under high MG detoxification.	Pachauri et al., 2014
OsGlyIII	3	Leaves and roots before flowering	Ferredoxin-nitrite reductase	Chloroplast, peroxisome, cytoplasm, Golgi body	Regulatory SNPs	Potential regulatory link between nitrogen and aroma	Pachauri et al., 2014

A more comprehensive understanding and manipulation of these minor QTLs is required for fine-tuning aroma profiles during breeding superior aromatic rice.

Global scenario of the aromatic rice market

The world market of aromatic rice is experiencing a continuous growth, which is due to shifting of consumers preferences. According to the IMARC Group (2025) statistics, the aromatic rice market, in the context of the broader rice industry, has a valuation of around USD 309.8 billion in 2024, which proves the significance of the rice entire industry. In addition, according to the projections by the IMARC Group (2025), the value of the aromatic varieties will reach about USD 380.4 billion by 2033. The importance of aromatic rice in international trade is also explained by the fact that it comprises 15-18% of the total volume of rice trade in the world (Hashim *et al*., 2021). A market price of aromatic rice is approximately USD 1,050 per metric ton, equated to non-aromatic rice at USD 440-580 per metric ton (Hashim et al, 2021). The world aromatic rice market is controlled by a small set of outstanding cultivars, with Basmati and Jasmine rice taking the top section of the pyramid. Most of the global Basmati is produced in Indian subcontinent, especially in Pakistan and India. India has strategically located itself in the aromatic rice industry largely owing to its mass production of the Basmati-type scented grains. India supplies about 70 percent of the world Basmati, thus creating a web of its dominance. Besides India, Pakistan and Kenya are also suppliers of Basmati. As of 2024, the Basmati rice alone was estimated at approximately USD 5 billion and is expected to continue an upward trend to USD 7.5 billion by 2033, with a robust CAGR of 4.6%. While India is a leading exporter of aromatic rice, it's important to note that other countries like Thailand, Vietnam, Pakistan, and the United States also contribute significantly to the global aromatic rice market. Jasmine rice is predominantly from Southeast Asia, with Thailand, Vietnam, and Cambodia being major producers and exporters. The Jasmine type fragrant rice market demonstrates an even more rapid expansion, estimated at US$35.25 billion in 2024 and forecast to reach US$57.73 billion by 2031, with an impressive CAGR of 7.3%. While Basmati and Jasmine rice hold the largest market share, numerous other aromatic varieties are cultivated and consumed globally, often playing significant regional or local economic roles. Paw San Hmwe, an aromatic rice from Myanmar, was honored as the world's best rice in a conference of rice traders in 2011 (Myint and San, 2020). North American and European countries are importing Basmati rice from India. Bangladesh produces varieties of aromatic rice, including Kalijira, Kataribhog, Chinigura, and Tulsimala. Other popular aromatic rice from different countries includes Sadri of Iran, Bahra of Afghanistan, Della, Texamati, and Kasmati of the USA, Paw San Hmwe of Myanmar (Hashim et al, 2021; Win et al., 2024). These aromatic rice varieties are regionally popular due to their scent, which gives them a uniquely strong allure. The agro-climatic parameters, including appropriate soil, precipitation, and temperature, are very favorable for fragrant rice.

Breeding methods used to develop aromatic rice

Researchers worldwide have been endeavoring to cultivate aromatic rice from many perspectives. From prehistoric selection to contemporary genome editing, and from traditional breeding to genetic engineering, rice has consistently been a focal crop. While the anticipated result is consistently a superior fragrant rice genotype, the associated efforts and costs fluctuated significantly. The successful outcomes are analyzed here according to methodology.

Conventional breeding

Improving aromatic rice through conventional breeding is challenging due to the influence of the environment, the low heritability of the trait, and polygenic control. Many traditional and widely recognized aromatic cultivars were developed through conventional breeding, such as KDML105 and its mutants, RD6 and RD15. These rice varieties now cover over 70% of Thailand's rice area due to stress tolerance (Vanavichit *et al.*, 2018). The advent of Pusa Basmati-1 (PB-1) in 1989 was a significant advancement, as it is a high-yielding, semidwarf, photoperiod-insensitive basmati variety that dominated exports from 1995 to 2007. Varieties like Pusa Basmati-1, BRRI dhan50 (Bangladesh), Texmati (USA), and Paw Sam Hwme (Myanmar) have been developed using conventional methods, with some dominating exports and covering large areas due to their yield and quality.

Molecular breeding

Marker-assisted selection (MAS) is an effective method for developing aromatic rice varieties by introgression aroma genes into elite non-aromatic lines. Since high-quality, fine-scale rice genome sequences are now available, several genetic loci have been found and used in marker-assisted backcross breeding to overcome the challenge of traditional phenotyping of aroma. Molecular markers are easier and more reliable (Kottearachchi *et al.*, 2010) as they can be linked to particular genes. A key advantage of MAS is its ability to facilitate the pyramiding of aroma genes with other crucial agronomic traits, such as resistance to diseases. For instance, the new hybrid japonica rice "Shenyou R3" and indica variety "Yishenxiangsimiao" was developed by incorporating *fgr* alleles (for aroma) alongside resistance genes (*Lgc-1, Pi-2, Xa23*) into a single genetic background (Bergman *et al.*, 2000). Additionally, stress-resistant basmati and jasmine rice varieties like Pusa1460, Pusa1121, and PB1718 were developed through MAS (Akter *et al.*, 2018). Precision gene editing tools like CRISPR/Cas9 and TALEN have revolutionized plant breeding by enabling highly targeted and efficient modifications at specific genomic loci, particularly the *BADH2* gene, to enhance aroma profiles in rice (Desigan *et al.*, 2024). CRISPR/Cas9 has been successfully used to create novel *BADH2* alleles in non-fragrant japonica and indica varieties, effectively improving aroma (Liao *et al*., 2024). Furthermore, aromatic thermosensitive genic male sterile (TGMS) lines, such as Huahang 48s, have been accomplished by using CRISPR/Cas9 to enhance aroma and male sterility simultaneously (Chen *et al*., 2025).

Mutation breeding

Mutation breeding has been a valuable tool for developing improved fragrant rice species. With 861 recognized mutant varieties worldwide, 37% and 29% of which are from China and Japan, respectively. Mutation breeding has so far been a significant factor in improving rice (IAEA Mutant Database). 25 of the 861 varieties were of aromatic rice, while the remaining genotypes were created for characteristics including drought tolerance (20), dwarfism (156), and disease resistance (271) (IAEA Mutant Database). Mutation breeding has successfully addressed some of the common drawbacks of traditional aromatic rice landraces, resulting in improved genotypes. For instance, TCDM-1, a highly scented, dwarf, high-yielding, non-lodging variety developed from the aromatic rice 'Dubraj' in India (Kumar *et al*., 2021). Similarly, Roshan is a new mutant aromatic rice derived from the Nemat variety, exhibiting high yield (8.23 ton/ha) and early maturity, while retaining fragrance (Arefrad *et al*., 2021). In Pakistan, Khushboo-95, developed from Jajai-77, is a short-statured, highly productive aromatic rice (Bughio *et al*., 2007). Mutation breeding will be dignified for even greater impact in the future improvement of aromatic rice.

Genetic improvement of aromatic rice

Historically, aromatic rice cultivars are characterized by low grain production, tall stature, and low stress tolerance compared to modern high-yield varieties. Therefore, breeding programs focused on incorporating aromaticity with high yield potential, resistance to diseases, and adaptation to environmental stresses. The traditional breeding methods such as selection, pedigree breeding, and backcrossing, have generated significant developments in the last few decades together with the current use of modern molecule methods. High-yielding, semi-dwarf Basmati varieties in India and Pakistan retained their long-aromatic characteristics and, nonetheless, yielded better and had shorter maturity times; the emergence of Pusa Basmati 1121 later changed the dynamics of the Basmati market worldwide (Singh *et al.* 2018). Aromatic varieties like Hom Mali 105-Sub1 have gained submergence tolerance in Thailand, and Meixiangzhan 2 have gained fragrance and blast resistance properties in China via marker-assisted selection (Deng *et al*., 2012). Bangladesh has introduced a number of superior aromatic varieties that can be used in both wet and dry seasons, and the United States has come up with jasmine-type varieties that are characterized by better yield and grain quality (Kader *et al.*, 2020; Sha *et al*., 2011).

One of these developments was the discovery of BADH2 as the key aromatic gene, thus making it easier to use to select fragrance by marker-assisted selection (MAS) (Bradbury *et al*., 2005). Therefore, breeders have come to practice the combination of BADH2 with genes that provide resistance against the blast, bacterial blight, and flood tolerance (Ndikuryayo *et al*., 2022). In India, *Xa21, Xa13, Xa5*, and *BADH2* alleles were combined through marker-assisted backcrossing (MABC) to create Pusa Basmati 1728 (blast resistance) and Pusa Basmati 1885 (bacterial blight resistance). CRISPR/Cas9 gene editing has been used more recently to improve the aroma content of hybrid and colored rice, as well as to produce fragrant versions of high-yielding cultivars without compromising other agronomic traits (Zhang *et al*., 2023). Researchers generated aroma in a three-line hybrid rice restorer line (SH313) by knocking out BADH2, leading to significantly increased 2AP in grains (Liao *et al*., 2024). Genome-wide studies continue to discover additional genes and alleles influencing aroma and grain quality, providing new opportunities to broaden the genetic base and further enhance aromatic rice in the future.

Challenges of aromatic rice production

Significant advancements in aromatic rice have been achieved due to high demand and ongoing research efforts. However, obstacles remain that must be addressed to produce excellent aromatic rice. These include genotype-environment interactions, environmental factors that alter volatile chemical molecules, and the complex polygenic nature. Climatic conditions significantly influence both the yield and quality of aromatic rice. Temperature and humidity are two environmental elements that might affect the aroma of rice in addition to the cultivation practices, post-harvest handling, and storage. High temperature during the grain filling stage can enhance the aroma production (Zhao *et al*., 2025). Aromatic inundation can surely be reduced by delayed harvesting due to increased amylose and protein (Marzempi *et al*., 1990). The genetic resources of aromatic rice are disappearing due to a combination of factors, primarily driven by human activities and the pursuit of higher yields in conventional rice varieties. Low productivity and susceptibility to pests, as well as poor availability of quality seed, are constraints holding back farmers from cultivating traditional aromatic rice. In the last two decades, high-yielding rice monoculture has led to the extinction or threat to other valuable aromatic rice varieties (Biswas *et al*., 2021). A lack of empirical understanding and official recognition contributes to their disregard and eventual vanishing. Multiple breeding objectives, lack of quality measurement methodologies, and complex selection criteria are the key challenges.

Future prospects of global aromatic rice

The global aromatic rice production is expected to experience significant growth due to a combination of technological advancement, deliberate breeding initiatives, and expanding growing areas. Although facing challenges from biotic and abiotic stresses threatening production and quality, auspicious scenarios exist for enhancing resistance and increasing the spread of aromatic rice. A comprehensive knowledge of the genetic basis of stress tolerance is crucial in the further quest to discover and characterize genes that will provide resistance. The ultimate goal is to introgress these resistance mechanisms while keeping the unique quality traits. Combining multiple resistance and aroma genes could be a key strategy for developing sustainable and wide-spectrum resistance (Wang *et al*., 2023). Molecular breeding has already demonstrated its effectiveness in transferring and combining genes that provide resistance to commercially successful aromatic varieties (Chen *et al*., 2025; Chukwu *et al*., 2020). The development of the MH725 line in China that combined blast and bacterial blight resistance with submergence tolerance and aroma (Luo *et al*., 2016), and the water-saving and drought-resistant 'Huhan 1516 (Xie et al., 2024) are evidence of successful application of MAS for the improvement of aromatic rice. Aroma is complex, involving over 380 compounds, but breeders currently rely on only the *fgr*1 marker for 2-AP. The solution requires a disciplined MABC strategy combining foreground and phenotypic selection, plus gene discovery for other aroma loci. New genome-editing technologies like TALE nuclease, zinc-finger nuclease, and CRISPR-Cas9 provide unparalleled specificity to customize the rice genome to not only improve agronomic outcomes and sensory traits without the incorporation of foreign DNA (Usman et al., 2020) but also to improve blast resistance (Wang *et al.*, 2016).

A recent important opportunity for expanding the aromatic rice is extending its production to harsh climatic conditions and non-conventional growing areas. For example, the introduction of CSR 36, an aromatic in Kenya, which is a salinity-tolerant and high-yielding variety, shows that there is a chance to produce rice in places that were considered to be unsuitable because of salinity (Sackey *et al.*, 2025). Beyond this, aromatic rice cultivation in the USA, the development of ORYLUX varieties by AfricaRice for Sub-Saharan Africa (Zozo *et al.*, 2021), and temperate Basmati for high-altitude regions, Uganda's NARORICE-1 (Alibu *et al.*, 2022), and Indonesia's local Basmati variants (Susmita and Nugraha, 2020) further underscore the successful adoption of aromatic rice in diverse settings. Lastly, biofortification is a valid solution that can be used to enhance nutritional security by increasing the levels of micronutrients without compromising the desirable sensory properties, thereby enabling a greater acceptance by consumers. Such combined policies are set to support the international aromatic rice industry, which guarantees a more robust, delicious future of the rice production for the next generation. Finally, breeders must be supported with functional molecular markers and bioinformatics tools. Ultimately, collaboration between universities and research institutions is crucial to applying basic science to practical breeding.

Conclusion

Aromatic rice, a crop of global reputation of economic and cultural, has evolved through a long journey from Asia to all continents with a vast genetic diversity, shaped by both natural and human selection for its unique properties. However, its sustainability is currently threatened in some places due to genetic erosion, low yields, and various environmental pressures. Although there are limitations, ongoing breeding efforts, recent advancements in technologies like molecular breeding and genome editing offer promising avenues for enhancing the genetic background of aromatic rice without compromising its quality. The next generation breeding should focus on the development of aromatic rice genotypes resistant to biotic and abiotic stresses, with a wide range of environmental adaptation, and nutritionally biofortification. Collective research and breeding efforts are vital to conserve the total diversity of this valuable and distinct agrarian resource for the steady supply of aromatic rice to meet escalating consumer demand. Such coordinated endeavors will support the sustainable production of aromatic rice, ensuring its viability for future generations.

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Conflict of Interest

The authors affirm that no financial or commercial relationships that might be construed as a potential conflict of interest existed during the course of the research.

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Conceptualization, Mohaimin Islam and Liakat Ali; methodology, Mohaimin Islam, Azmia Patwary, and Liakat Ali; resources, Liakat Ali and Nasrin Akter Ivy; data curation, Nur Islam, Azmia Patwary, Sumaiya Khatun, and Nahid Hasan; writing-preparation of the initial draft, Mohaimin Islam, Sumaiya Khatun, and Nur Islam; writing, review, and editing, Sheikh Maniruzzaman, Nasrin Akter Ivy, and Liakat Ali; visualization, Mohaimin Islam, Nahid Hasan; supervision, Liakat Ali, Nasrin Akter Ivy; project administration, Liakat Ali. All authors have reviewed the manuscript in its current form and given their approval.

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