

RESEARCH ARTICLE

Aroma and Agro-morphological Diversity in Traditional Rice (*Oryza sativa*) Germplasm from Eastern India

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Abstract

Traditional aromatic and quality rice (*Oryza sativa* L.) landraces from eastern India harbour valuable grain quality traits, yet their agro-morphological diversity and fragrance genetics remain insufficiently characterized. This study evaluated 183 accessions from the Indian National GeneBank to characterize phenotypic variation and assess allelic diversity at the *BADH2* fragrance locus. Twenty-two agro-morphological traits were recorded, aroma was assessed using the KOH test, and allele-specific PCR was employed to detect the 8-bp functional deletion in exon 7 of *BADH2*. The accessions exhibited wide phenotypic variation, particularly in grain length, grain width, kernel shape, and pigmentation traits. Aroma profiling classified 42% of accessions as strongly aromatic and 36% as moderately aromatic. Multiple-factor analysis and clustering showed weak state-wise structuring, indicating considerable overlap among accessions, likely reflecting historical seed exchange. Genotyping showed that 31% of accessions carried the homozygous aromatic allele; however, a substantial proportion of aromatic accessions lacked the deletion, suggesting that additional genetic factors may contribute to fragrance in this germplasm. These findings highlight the diversity of agro-morphological and aroma-related traits in eastern Indian rice and provide a useful baseline for future genetic studies and quality-oriented breeding programmes, as well as for the conservation and utilization of the aromatic landraces.

Keywords: Aromatic rice, Agro-morphological diversity, *BADH2* gene, Eastern India germplasm, Landraces

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Introduction

Rice is cultivated in more than 117 countries and remains central to global food security, particularly across Asia, Africa, and Latin America. India, a secondary centre of origin for *Oryza sativa*, conserves remarkable genetic variability in both cultivated rice and its wild relatives (Bisne and Sarawgi, 2008; Roy *et al.*, 2020). Among the major varietal groups, aromatic rices occupy a premium niche due to their distinctive fragrance, superior cooking quality, and strong consumer preference. Globally traded types such as Basmati rice from the Indian subcontinent and Jasmine rice from Thailand command high market value, with India exporting over 5.2 million metric tons of Basmati rice valued at USD 5.9 billion in 2024-25 (<https://apeda.gov.in/BasmatiRice>), underscoring the economic importance of fragrant rice.

The key biochemical compound responsible for fragrance, 2-acetyl-1-pyrroline (2-AP), accumulates due to loss-of-function mutations in the *BADH2* gene (Bradbury *et al.*, 2005a). The most widespread allele is the 8-bp deletion in exon 7 (*badh2.1*), originally identified in *Japonica* germplasm and now common across aromatic *Indica* groups (Kovach *et al.*, 2009).

Additional *BADH2* mutations, including G-to-T SNP (single nucleotide polymorphism) in exon 10 (*badh2.7*) and a 1-bp insertion in exon 14 (*badh2.6*), are reported particularly in eastern and north-eastern India (Kovach *et al.*, 2009; Chandanshive *et al.*, 2024). However, *BADH2* variation does not always correlate perfectly with sensory aroma scores, reflecting environmental influences and the possible involvement of other genetic loci (Sakthivel *et al.*, 2009; Prodhan and Qingyao, 2020).

Beyond Basmati, India hosts a wealth of non-Basmati aromatic rice, especially short- and medium-grain landraces cultivated in eastern states such as West Bengal, Bihar, Jharkhand, Odisha, Chhattisgarh, and Assam. Popular examples include 'Gobindabhog', 'Tulaipanji', 'Badshabhog', 'Katarni', 'Sonachur', 'Jeeraphool', and 'Kalajeera'. These landraces are deeply embedded in local food traditions and valued for grain appearance, aroma, and cooking quality. Despite their cultural and economic relevance, they have received limited attention in systematic breeding and characterization efforts. Only a few traditional aromatic varieties, such as 'Gobindabhog', 'Tulaipanji', 'Marcha Dhan', 'Jeeraphool', 'Nagri Dubraj', and 'Koraput Kalajeera', have attained Geographical Indication (GI) status, and none from Jharkhand have yet been recognized. However, many non-basmati landraces have been reported from Jharkhand, including 'Prasad bhog', 'Nanhia', 'Tulshimanjar', 'Baans Phul' and 'Shyam jeera' (Sinha *et al.*, 2016). Lack of formal morphological and genetic characterization constrains their documentation, legal protection, and utilization in quality-oriented breeding.

Aromatic landraces from eastern India exhibit wide morphological diversity, shaped by farmer-driven selection across heterogeneous landscapes. Significant variability has been reported for grain size and shape, awning, pigmentation, plant stature, and flowering behaviour (Ray *et al.*, 2013; Roy *et al.*, 2015; Roy *et al.*, 2016; Behera and Panda, 2023). However, this variation is often poorly structured geographically due to frequent seed exchange and inconsistent naming conventions. Landraces with identical names may be genetically unrelated, whereas distinct names may refer to closely related types. As a result, phenotypic identity and distinctiveness remain unclear, underscoring the need for integrated morphological and molecular approaches.

Despite long-standing interest, comprehensive studies that combine multi-trait agro-morphological evaluation with functional genotyping of the *BADH2* fragrance allele remain scarce in this region. Moreover,

emerging evidence suggests that a substantial proportion of mildly or strongly aromatic eastern Indian cultivars lack the common 8-bp deletion allele (Prodhan and Qingyao, 2020; Chandanshive *et al.*, 2024), indicating the possible presence of additional *BADH2* haplotypes or alternative fragrance mechanisms that remain unexplored.

To address these gaps, the present study evaluates 183 traditional rice accessions from the Indian National GeneBank, predominantly short-grain aromatic and quality landraces originating from Jharkhand, West Bengal, Bihar, Odisha, Chhattisgarh, and Assam. Using 22 agro-morphological descriptors, sensory aroma assessment, and allele-specific PCR targeting the 8-bp deletion in *BADH2*, this study aims to: (i) document the extent and pattern of agro-morphological diversity, (ii) determine the prevalence of the 8-bp FNP in *BADH2* and its association with phenotypic aroma, and (iii) identify unique or distinct landraces with potential for registration, conservation, and quality-breeding programmes. By integrating morphological and molecular evidence, this work provides a clearer understanding of the diversity, fragrance genetics, and distinctiveness of eastern Indian aromatic rice, offering a foundation for GI protection, conservation strategies, and future genomic investigation of fragrance-related loci.

Materials and Methods

Plant material

A total of 219 traditional rice accessions originating from eastern Indian states and Assam were procured from the Indian National GeneBank, ICAR-National Bureau of Plant Genetic Resources (NBPGR), New Delhi. Passport information and collection site coordinates were retrieved from the NBPGR PGR Portal. Initial accession selection was based on vernacular names reported in literatures to represent aromatic or high-quality short-grain landraces. Because accessions with the same vernacular name may differ across collection sites, multiple entries of some landrace names were intentionally included. Before detailed characterization, all 219 accessions were subjected to a preliminary germination test and seed lot examination. Of these, 183 accessions were retained for analysis based on two criteria: (i) satisfactory germination, and (ii) minimal visible seed mixture within the accession (Supplementary Table 1). Accessions showing very low (<5%) germination and/or obvious within-accession seed heterogeneity were excluded. The final set represented collections from Jharkhand, West Bengal,

Bihar, Odisha, Chhattisgarh, and Assam (Fig. 1).



Fig. 1: Collection sites of rice accessions in eastern India, with the inset depicting the count per state.

The map was generated from site coordinates obtained from ICAR-NBPGR and visualized in Google Earth.

Experimental site and growth conditions

The agro-morphological evaluation was conducted during the summer season (February–June 2025) at the phenotyping facility (net-house) of the Central Rainfed Upland Rice Research Station (CRURRS), ICAR–Central Rice Research Institute (CRRI), Hazaribag, Jharkhand. The experiment was laid out in a completely randomized design (CRD). For each accession, three healthy seedlings were transplanted individually into separate 10-kg soil-filled pots and maintained as three biological replicates. Seedlings were first raised in nursery trays and 21-day-old uniform seedlings were transplanted into pots. Pots were randomly arranged within the phenotyping facility (under natural conditions) and periodically repositioned during crop growth to minimize positional or micro-environmental bias. Standard agronomic management was followed, including fertilizer applications of 60:40:40 kg N:P₂O₅:K₂O/ha, irrigation and need-based plant protection measures.

Agro-morphological characterization

A total of 22 phenotypic traits were recorded following the Standard Evaluation System (SES) for Rice (IRRI, 2013), comprising 18 qualitative descriptors and four quantitative grain traits. The qualitative traits included leaf blade pubescence, leaf blade colour, basal leaf sheath colour, leaf angle, pigmentation traits (ligule, collar, and auricle colour), apiculus colour, lemma–palea colour, sterile lemma colour, awn presence and pigmentation, pericarp colour, kernel shape and aroma intensity. The grain traits included

grain length, grain width, kernel length, and 100-grain weight. Quantitative grain traits were measured across the three biological replicates, using 10 grains or kernels per accession per replicate. The 100-grain weight was recorded using well-filled dried grains with an approximate moisture content of 14%.

Aroma was assessed using the 1.7% KOH sensory test following Nagaraju *et al.*, (1991) and IRRI SES guidelines. In short, 2 g of dehusked grains were treated with 10 mL of 1.7% KOH and aroma was scored after 10 min relative to the aromatic check 'Pusa Basmati 1'. Aroma intensity was classified into three categories: 1, absent or very weak; 2, weak; and 3: strong. For accessions that did not flower, aroma was assessed from leaf tissue using the same KOH-based procedure. To minimize scorer bias and olfactory fatigue, samples were evaluated in small batches by three independent evaluators, and the scores were cross-checked before final classification.

Genotyping for BADH2 exon 7, 8-bp deletion

The aroma-linked 8-bp deletion in exon 7 of the *BADH2* gene was detected using the allele-specific amplification (ASA) PCR assay developed by Bradbury *et al.*, (2005b). Genomic DNA was extracted from 21-day-old seedlings using the DNeasy Plant Mini Kit (Qiagen, India). DNA concentration and quality were assessed using a NanoDrop spectrophotometer, and samples were diluted to a working concentration of 50 ng/μl. PCR amplification was performed using four primers: external sense primer (ESP), external antisense primer (EAP), internal fragrant antisense primer (IFAP), and internal non-fragrant sense primer (INSP), following the thermal cycling conditions described by Bradbury *et al.*, (2005b). This primer combinations enable allele-specific amplification of the *BADH2* exon 7 region, producing three diagnostic fragments: a 257 bp fragment corresponding to the aromatic allele (ESP + IFAP), a 355 bp fragment corresponding to the non-aromatic allele (EAP + INSP), and a 580 bp fragment serving as a positive control (ESP + EAP). PCR products were separated on 2% agarose gels stained with DNA-Safedye (SRL, India) and visualized using a Bio-Rad gel documentation system. Based on the observed banding patterns, genotypes were classified as: (i) homozygous non-aromatic (580+355 bp), (ii) heterozygous aromatic/non-aromatic (580+355+257 bp), or (iii) homozygous aromatic (580+257 bp).

Statistical analyses

Descriptive statistics for quantitative traits, including mean, range, standard deviation, coefficient of

variation, and skewness, were computed in R v4.4.3. Differences among accessions for quantitative traits were tested using one-way analysis of variance under the model: $Y_{ijk} = \mu + G_i + R_j + E_{ijk}$ where, Y_{ijk} is trait value, μ is overall mean, G_i is effect of the i^{th} genotype, R_j is the effect of replication, and E_{ijk} is the residual error. Multiple Factor Analysis (MFA) was performed using the FactoMineR package, treating quantitative variables as scaled continuous traits and qualitative variables as categorical traits. Phenotypic dissimilarity among accessions was estimated using Gower's distance, followed by hierarchical clustering with average linkage (UPGMA). The optimal number of clusters was identified using the goodness-of-split criterion implemented in the maptree package. To evaluate genotype–phenotype association between aroma class and *BADH2* genotypic category, a chi-square test of independence was performed using the contingency table of aroma score classes and marker genotypes.

Results and Discussion

Agro-morphological variation among accessions

The 183 traditional rice accessions exhibited substantial phenotypic diversity across the 22 agro-morphological traits evaluated. Qualitative traits showed wide variability, reflecting the heterogeneous evolutionary and cultural histories of these landraces. Traits such as leaf blade pubescence, leaf blade colour, and basal sheath colour demonstrated multiple expression states. Leaf blade colour was predominantly green (71%)

followed by dark green (23%), whereas basal leaf sheath colour ranged from green (85%) to purple-tinged phenotypes, suggesting underlying variation in anthocyanin pigmentation pathways. Leaf angle (LA) also showed even distribution, including erect, horizontal, and droopy forms, suggesting variation in plant architecture possibly linked to environmental adaptation. Other pigmentation traits, such as ligule colour (LC), collar colour (CC), and auricle colour (AC), showed limited variation, with most accessions being light green.

Furthermore, seed coat colour (SCC) and aroma are key grain quality parameters with both consumer and breeding relevance (Zhou *et al.*, 2020). While white pericarp was predominant (70%), the presence of red, brown, and light brown pericarps in a significant proportion of accessions indicates nutritional and phytonutrient diversity, which could be leveraged for biofortification efforts (Rathna Priya *et al.*, 2019). Aroma assessment using the KOH method revealed that, among the 183 accessions, 42% were strongly aromatic, 36% were mildly aromatic, and 23% were non-aromatic. Strongly aromatic landraces included several well-known traditional cultivars such as 'Gobindabhog', 'Katarni', 'Sonachur', 'Samjeera', 'Kalajeera', 'Kalanamak', and 'Tulaipanji'. Notably, many lesser-known cultivars, including 'Nanhia', 'Kusumphul', 'Prasad Bhog', 'Tushi Manjar', and 'Jeeraphul', also exhibited strong aroma. This highlights the underexplored aromatic potential within eastern Indian rice germplasm, particularly from Jharkhand (Table 1).

Table 1: List of highly aromatic landraces from the state of Jharkhand

Sl.No.	Landrace	Origin	BADH2 exon 7, 8-bp polymorphisms	Kernel shape
1	Gopalbhog (IC0385940)	Jharkhand	(580 bp & 257 bp)	1-Slender
2	Sonachur (IC0282478)	Jharkhand	(580 bp & 257 bp)	3-Medium
3	Kusum phool (IC0282466)	Jharkhand	(580 bp & 257 bp)	5-Bold
4	Dhania phool (IC0282519)	Jharkhand	(580 bp & 257 bp)	3-Medium
5	Sonachur (IC0282476)	Jharkhand	(580 bp & 257 bp)	1-Slender
6	Tulsi Manjar (IC0342874)	Jharkhand	(580 bp & 257 bp)	3-Medium
7	Kalajeera (IC0203154)	Bihar	(580 bp & 257 bp)	1-Slender
8	Jeeraphul (IC0267977)	Chattisgarh	(580 bp & 257 bp)	3-Medium
9	Badsha bhog (IC0299955)	Chattisgarh	(580 bp & 257 bp)	1-Slender
10	Katarni (IC0385729)	Bihar	(580 bp & 257 bp)	1-Slender
11	Badshabhog (IC0470970)	West Bengal	(580 bp & 257 bp)	3-Medium
12	Adamchini (IC0553800)	Uttar Pradesh	(580 bp & 257 bp)	3-Medium
13	Shyam Jeera (IC0553879)	Uttar Pradesh	(580 bp & 257 bp)	1-Slender
14	Badsha Pasand (IC0554635)	Uttar Pradesh	(580 bp & 257 bp)	1-Slender
15	Kasturi (IC0574880)	Bihar	(580 bp & 257 bp)	3-Medium
16	Sonachur (IC0574927)	Bihar	(580 bp & 257 bp)	1-Slender

17	Sitabhog (IC0594012)	West Bengal	(580 bp & 257 bp)	3-Medium
18	Sabour Surbhit (IC0595579)	Bihar	(580 bp & 257 bp)	3-Medium
19	Katari bhog (IC0618972)	West Bengal	(580 bp & 257 bp)	3-Medium
20	Radhuni pagol (IC0619255)	West Bengal	(580 bp & 257 bp)	1-Slender
21	Kala jeera (IC0619256)	West Bengal	(580 bp & 257 bp)	3-Medium
22	Kola joha (IC0619302)	Assam	(580 bp & 257 bp)	3-Medium
23	Mohan mala (IC0099217)	Jharkhand	(580 bp & 355 bp)	1-Slender
24	Kohraphool (IC0276799)	Jharkhand	(580 bp & 355 bp)	1-Slender
25	Prasad bhog (IC0282462)	Jharkhand	(580 bp & 355 bp)	1-Slender
26	Nanhia dhan (IC0342866)	Jharkhand	(580 bp & 355 bp)	1-Slender
27	Basmati (IC0282465)	Jharkhand	(580 bp & 355 bp)	3-Medium
28	Prasad bhog (IC0282406)	Jharkhand	(580 bp & 355 bp)	3-Medium
29	Bansbuda (IC0621734)	Jharkhand	(580 bp & 355 bp)	3-Medium
30	Prasad bhog (IC0621769)	Jharkhand	(580 bp & 355 bp)	1-Slender
31	Kamod (IC0396060)	Chattisgarh	(580 bp & 355 bp)	3-Medium
32	Samjeera (IC0332049)	Jharkhand	Heterozygous	1-Slender
33	Tulsi Manjar Dhan (IC0417979)	Jharkhand	Heterozygous	3-Medium
34	Lalmati (IC0640882)	Jharkhand	Heterozygous	3-Medium
35	Sakkar chini (IC0554637)	Uttar Pradesh	Heterozygous	3-Medium
36	Chini Karpoor (IC0554650)	Uttar Pradesh	Heterozygous	3-Medium

Grain-related qualitative traits were considerably diverse (Fig. 2). The apiculus colour was mostly straw (76%) but included brown and black variants, while lemma–palea colour exhibited a wide spectrum from gold and straw to rare reddish or purple forms. Such pigmentation variability aligns with findings in other aromatic landraces, highlighting the polygenic basis of grain colour traits (Ray *et al.*, 2013; Behera and Panda, 2023). Most accessions lacked awns (84%), although several carried long coloured awns, indicating selective retention of primitive traits in certain regional landraces. Pericarp colour was predominantly white (70%), with remaining accessions showing red or brown pericarps, traits associated with nutritional and antioxidant value (Rathna Priya *et al.*, 2019). This diversity is consistent with reports from Bangladesh and eastern India (Islam *et al.*, 2018).



Fig. 2: Grain morphological variation in representative rice accessions.

Quantitative grain traits also displayed considerable variation. Grain length ranged from 5.4–11.0 mm (CV = 16%), with the longest grains recorded in 'Kendu Manja' (IC0438534), 'Kasturi' (IC0438655), 'Kadam Phul' (IC0086591) and 'Vishun bhog' (IC0300024). Grain width showed moderate variation (CV = 15%), while kernel length ranged from 3.9–8.6 mm (CV = 17%). Kernel shape was dominated by medium types (50%), followed by slender (44%) and bold (5%). The widest variation was observed for 100-seed weight (CV = 33%), which ranged from 0.7 g ('Tulsi Manjar' IC0342874) to 3.2 g ('Kala bhuri' IC0421349), reflecting broad differences in endosperm development. These ranges corroborate earlier studies in Indo-Gangetic aromatic rice (Bairwa *et al.*, 2024).

Multivariate analysis revealed weak geographical structuring

To examine the overall pattern of phenotypic variation, Multiple Factor Analysis (MFA) integrating qualitative and quantitative traits was performed. The first five dimensions explained 26% of the total phenotypic

variation. Although this proportion appears modest, it is typical for mixed-data analyses involving a large number of categorical descriptors, where variance is distributed across multiple dimensions rather than concentrated in the leading axes. In the present study, qualitative traits contributed strongly to Dimensions 1–4, while quantitative grain traits such as grain length, grain weight, and kernel length were major contributors to Dimensions 1 and 2, indicating that grain morphology is a primary driver of phenotypic differentiation (Fig. 3A), consistent with earlier studies in aromatic rice landraces (Ray *et al.*, 2013; Roy *et al.*, 2016; Chandraker *et al.*, 2024).

Scatterplots of Dimensions 1 vs. 2 and 3 vs. 4 revealed weak clustering by state, with substantial overlap among accessions (Fig. 3B). This diffuse structure suggests that phenotypic variation is not geographically partitioned, likely reflecting historical seed exchange, cultural diffusion, and farmer-mediated selection across regions. However, future studies involving molecular markers will clarify these aspects. Similar patterns of weak geographic structuring have

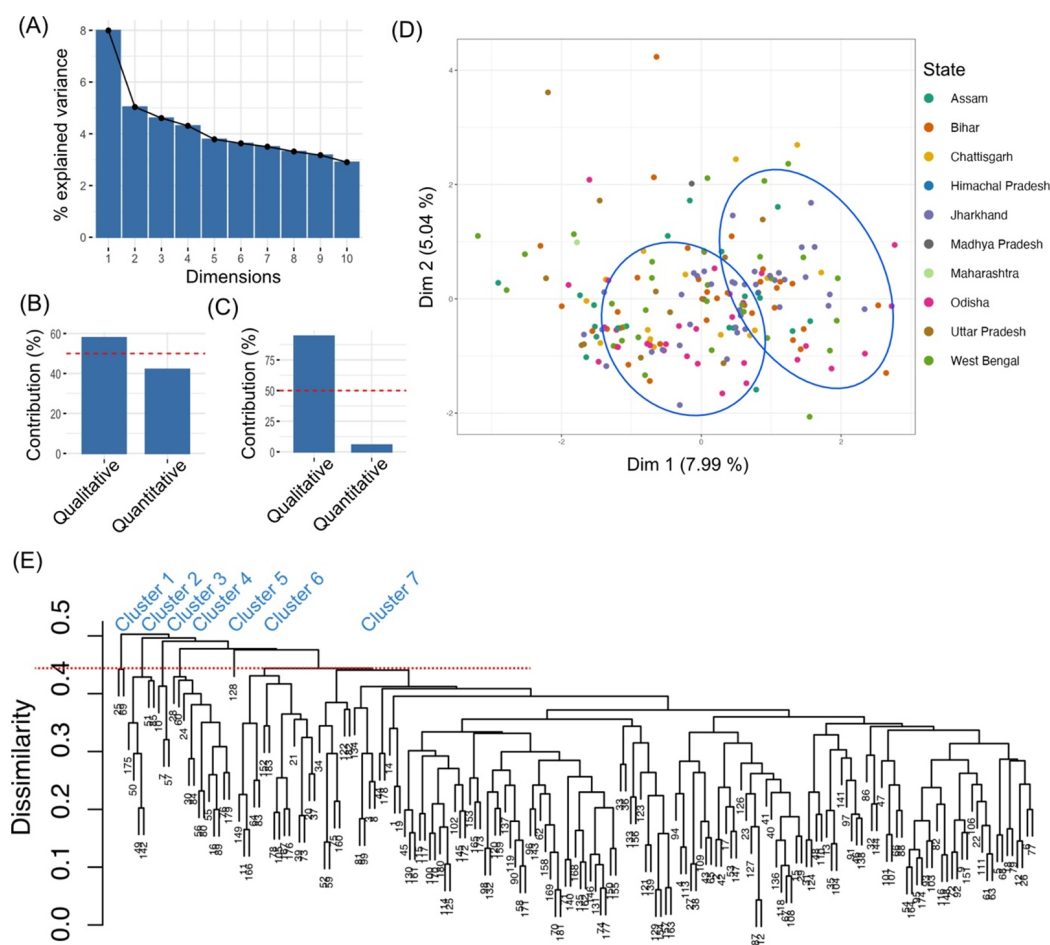


Fig. 3: Multivariate analysis of 183 rice accessions.

(A) Percent contributions of qualitative and quantitative traits in MFA (B) Scatterplot depicting the spatial distribution of the accessions (C) Dendrogram showing grouping of rice accessions in seven clusters.

been reported in aromatic rice germplasm from eastern India and neighbouring regions (Prasad *et al.*, 2020).

Hierarchical clustering based on Gower's distance revealed pairwise dissimilarities ranging from 0.04 to 0.76. The Mantel correlation between the dissimilarity matrix and the dendrogram was significant ($r = 0.62$; $P = 0.001$), indicating a good representation of the underlying phenotypic relationships. Based on the goodness-of-split criterion, seven clusters were identified (Fig. 3C). However, the clustering pattern was highly uneven, with Cluster 3 comprising the majority of accessions ($n = 143$), while the remaining clusters contained relatively few genotypes. This pattern indicates that most accessions share a common morphological core defined by similar combinations of grain and vegetative traits, whereas a smaller subset represents phenotypic extremes or unique trait combinations. Clusters 1, 5, and 6 captured such outlier groups characterized by distinct grain shapes or pigmentation traits. Notably, Cluster 5 contained a single accession ('Tulsi Bhog'), highlighting its exceptional phenotypic distinctiveness within the panel. Clusters 2 and 4 exhibited higher values for grain length and brown rice length, whereas Cluster 6 showed the lowest values. Clusters 3 and 4 had comparatively lower median grain width and grain

weight. Previously, six clusters within aromatic rice accessions from West Bengal have been reported based on agro-morphology (Mondal *et al.*, 2024).

From a breeding perspective, the minor clusters (Clusters 1, 5, and 6) represent valuable sources of unique phenotypic variation, while the large Cluster 3 reflects a broadly adapted and morphologically conserved group. The absence of clear state-wise aggregation further indicates that local nomenclature does not reliably correspond to phenotypic distinctiveness, emphasizing the need for systematic characterization in germplasm management and utilization. However, a comprehensive molecular analysis will be required to fully resolve the underlying population structure and genetic relationships among these accessions.

Allelic variation at the *BADH2* exon 7 polymorphism and its association with aroma

Genotyping of the 8-bp deletion in exon 7 of the *BADH2* gene revealed three genotype classes among the 183 accessions: homozygous non-aromatic allele (580 + 355 bp; 101 accessions, 55%), homozygous aromatic allele (580 + 257 bp; 57 accessions, 31%), and heterozygous (580 + 355 + 257 bp; 25 accessions, 14%) (Fig. 4A). Integration of genotypic data with sensory aroma

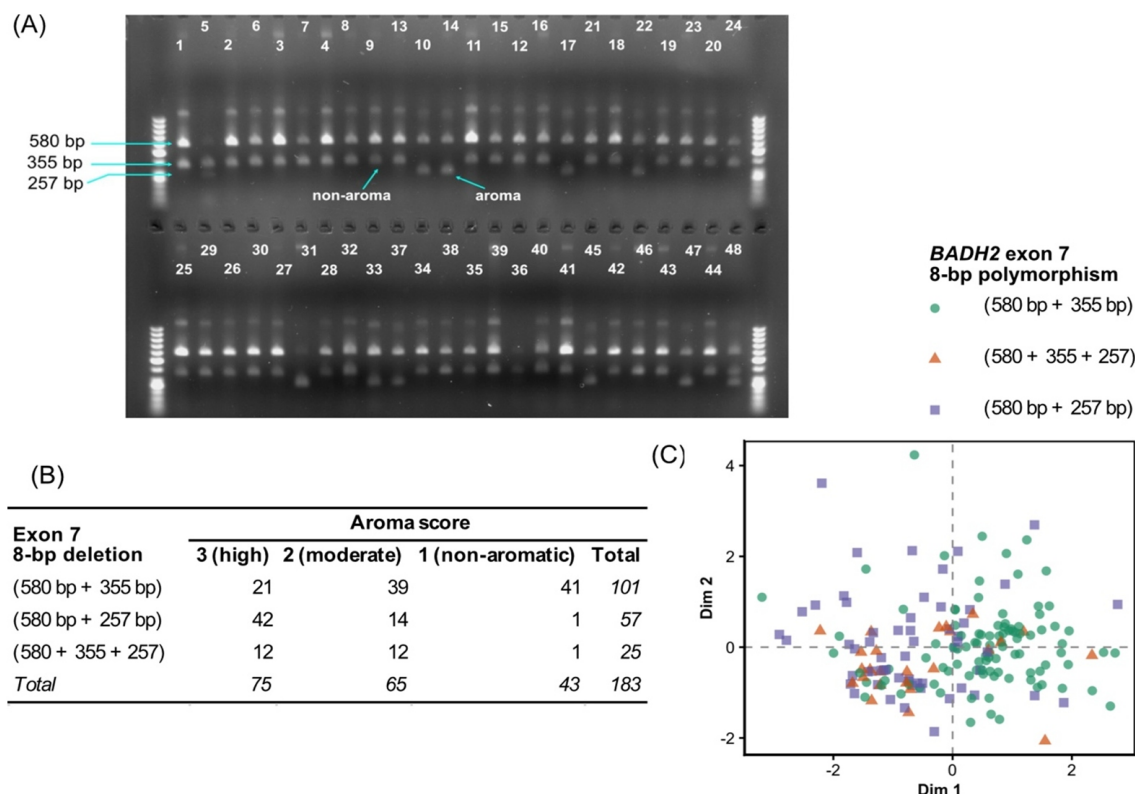


Fig. 4: Genotyping for aroma-associated 8bp-deletion in exon 7 of *BADH2* gene.

(A) Representative gel photograph showing the allelic variations, (B) Polymorphisms detected in 183 accessions, (C) Scatter plot depicting distribution of rice accessions based on variation in 22 phenotypic traits.

classification demonstrated a strong but incomplete association between the *BADH2* exon 7 deletion and aroma phenotype (Fig. 4B). A chi-square test of independence confirmed a highly significant association between genotype and aroma class ($\chi^2 = 56.77$, $df = 4$, $P < 0.001$), indicating that variation at this locus is a major determinant of fragrance expression in the studied germplasm. Accessions carrying the homozygous aromatic allele were predominantly strongly aromatic, whereas those with the homozygous non-aromatic allele were largely non-aromatic or weakly aromatic. Heterozygous accessions exhibited intermediate distributions across aroma classes.

Despite this strong association, notable discordance between genotype and phenotype was observed. Among strongly aromatic accessions, only 56% carried the homozygous aromatic allele, while approximately 43% of strongly or mildly aromatic accessions lacked the exon 7 deletion. This discrepancy may partly reflect environmental influences on aroma expression, as 2-acetyl-1-pyrroline (2-AP) accumulation is affected by temperature, moisture, and nutrient status during crop growth (Guo *et al.*, 2026). As the study was conducted under a single environment, genotype $\times$ environment interactions could not be assessed. Conversely, a small proportion of accessions carrying the aromatic allele exhibited weak or no aroma. Together, these findings indicate that the 8-bp deletion alone does not fully explain aroma variation in this germplasm, consistent with earlier reports (Fitzgerald *et al.*, 2008; Shi *et al.*, 2014).

Previous studies have reported multiple non-functional *BADH2* alleles associated with fragrance, including mutations in exon 10 (*badh2.7*) and exon 14 (*badh2.6*), particularly in *indica* rice from South and Southeast Asia (Kovach *et al.*, 2009; Chandanshive *et al.*, 2024). In the present study, genotyping was done for the exon 7 8-bp deletion (*badh2.1*), as it represents the most widely reported and diagnostically robust allele associated with fragrance across diverse rice germplasm (Bradbury *et al.*, 2005b; Kovach *et al.*, 2009). The allele-specific PCR assay for *BADH2* exon 7 8-bp deletion is simple, easy to score reliably and suitable for screening large germplasm sets. However, this approach does not capture other known functional variants such as *badh2.6* and *badh2.7*. Therefore, the presence of additional fragrance-associated alleles in accessions lacking the exon 7 deletion could not be resolved in this study and warrants further investigation through targeted sequencing or haplotype-based analyses.

Mapping *BADH2* genotypes onto MFA plots

(Fig. 4C) revealed moderate alignment between aromatic allele carriers and specific phenotypic clusters, suggesting that the exon 7 deletion contributes to phenotypic differentiation but does not fully define overall morphological structure. This partial correspondence reinforces the view that aroma, although influenced by *BADH2*, is only one component of the broader phenotypic diversity observed among traditional aromatic rice landraces.

Overall, this study revealed substantial agromorphological and fragrance-related diversity among 183 traditional rice cultivars from eastern India, with 42% classified as highly aromatic, 36% as moderately aromatic, and 23% as non-aromatic based on the KOH test. Key grain traits, particularly grain length, brown rice length, and grain width, were major contributors to phenotypic differentiation across the panel. Genotyping indicated that accessions carrying the *BADH2* exon 7, 8-bp deletion were generally associated with stronger aroma expression; however, a considerable proportion of aromatic accessions lacked this allele, suggesting that additional genetic factors may contribute to fragrance in these landraces. These findings highlight the complexity of the genetic basis of aroma in eastern Indian rice germplasm and underscore the importance of integrating phenotypic and molecular approaches for its characterization. The results provide a useful baseline for future research aimed at elucidating the genetic basis of aroma, as well as for the conservation and protection of unique aromatic landraces in the region.

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