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Screening for aroma in rice genotypes with African and Asian backgrounds

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Abstract

Aromatic rice is highly preferred by consumers and has an important market worldwide. The demand for aromatic rice is high in East African countries, mainly in urban areas. Among the rice varieties that are grown in Burundi, few of them have a slight aroma which is not enough to satisfy the consumers' demand and preference. There is no published report on the status of aroma in locally grown varieties and breeding lines in Burundi yet. This study aimed to identify aromatic genotypes that can be used in the breeding program to meet preferences of consumers. Two hundred fifteen genotypes were subjected to kompetitive allele-specific PCR genotyping and sensory evaluation methods. Fifty-three genotypes had the betaine aldehyde dehydrogenase ($BADH_2$) gene for fragrance and displayed different levels of aroma expression. The sensory evaluation revealed two strongly aromatic genotypes, 43 moderately aromatic genotypes, 131 slightly aromatic genotypes, and 32 nonaromatic genotypes.The results of this study showed that $BADH_2$ gene is significantly associated with rice aroma in accordance with previous reports. Furthermore, aroma and taste were positively and significantly correlated. Strongly aromatic genotypes (SUPA KATRIN and SUPA DE NYANZA –LAC) having the $BADH_2$ gene for fragrance are of great interest for use in the breeding program to improve rice varieties to meet consumers' preferences in Burundi.

1 | INTRODUCTION

Rice is the principal food grain consumed in the world (Rezvi et al., 2022). Rice is an important source of calories and proteins such as albumin, globulins, prolamins, and glutelin (Webster, 2019). Rice provides energy and other essential nutrients including vitamin E, zinc, and iron (Rezvi et al., 2022). Rice grain quality such as milling, storage, cooking, eating, and nutrition value are the main parameters that determine the extent of acceptance of rice by consumers (Sultana et al., 2022). Consumers' preferences for rice grain quality vary worldwide (Kaewmungkun et al., 2022; Ndikuryayo et al., 2022; Sultana et al., 2022). Among the grain quality traits, aroma is the key characteristic that influences the rice price in both national and international markets (Hui et al., 2022). In the countries of East African Community, urban consumers prefer aromatic rice (Kilimo Trust, 2018). Aroma and taste are the main components of the flavor defined as the impression perceived through the chemical senses (Champagne, 2008).

Flavor is genetically controlled and influenced by many factors including preharvest and postharvest factors (Champagne, 2008; Ndikuryayo et al., 2022). Sucrose, glucose, fructose, umami amino acids, sweet amino acids, and bitter amino acids were reported to be the main chemical components of rice taste (Zhao et al., 2020). Gustative perceptions such as salty, sweet, sour, bitter, and umami are induced by these chemical substances when they are dissolved in the mouth (Champagne, 2008).

Seven aroma-active compounds were detected in Jasmine rice. These compounds include hexanal, octanal, nonanal, (E)-2-octenal, decanal, 1-heptanol, and 1-octanol (Zhao et al., 2020). However, aroma is mainly induced by high concentration of 2-acetyl-1-pyrroline (2AP), an N-heterocycle compound that is produced by a mutation in the betaine aldehyde dehydrogenase ($BADH_2$) gene (Akwero et al., 2020; Ocan et al., 2019; Wang et al., 2016; Withana et al., 2020). That mutation is responsible for accumulation of 4-aminobutanal, its acetylation, and cyclization (Daygon et al., 2017).

This implies that rice aroma is mainly controlled by a nonfunctional allele of $BADH_2$ gene coding for the enzyme betaine aldehyde dehydrogenase (Hui et al., 2022; Pachauri et al., 2010). If there is no mutation, functional $BADH_2$ leads to the production of gamma-aminobutyric acid (GABA) responsible for a phenotype without aroma (Luo et al., 2022; Withana et al., 2020) as shown in Figure 1.

The most significant quantitative trait loci (QTLs) for rice aroma, qaro8.1, was mapped on chromosome 8 (Pachauri et al., 2010). The QTL qaro3-1 located on chromosome 3 was also reported to be significant for aroma (Singh et al., 2007). Moreover, the QTL qaro4.1 mapped on chromosome 4 had specific alleles of the $BADH_1$ gene that exhibited an association with rice aroma (Pachauri et al., 2010).

A single recessive gene was reported to control aroma in rice varieties. However, some researchers reported dominant gene (s) (Pachauri et al., 2010) and multiple factors/polygenes responsible for rice aroma (Singh et al., 2007). Some genetic studies revealed 19 alleles of the $BADH_2$ gene having an association with aroma (Akwero et al., 2020; Withana et al., 2020).

Generally, it is difficult to directly select for a quantitively inherited trait. The partial success of the traditional breeding approaches that prioritize phenotypic selection can be explained by the genotype by environment interactions, genetic interactions including epistasis, and the related low heritability (Sahebi et al., 2018). The use of the results from genotyping is the most effective method to predict the performance of a genotype and accurately select the individuals with gene(s) of interest (Swamy et al., 2017).

Several methods have been implemented for aroma assessment in rice leaves or grains. Some researchers analyzed aroma strength using a gas chromatography method by determining the amount of 2AP content in rice (Daygon et al., 2017; Ocan et al., 2019). Kaewmungkun et al. (2022) selected aromatic lines based on the presence of $BADH_2$ gene and the 2AP content. The findings of a study conducted by Ocan et al. (2019) suggested the use of quantitative information about 2AP and sensory evaluation while improving aroma trait in rice varieties. Akwero et al. (2020) suggested the combination of molecular and sensory evaluation for selecting the most aromatic lines for use in breeding program to meet consumers' preferences. Aroma status in rice can be assessed by smelling rice grains that are soaked in KOH solution (Akwero et al., 2020; Kibria et al., 2008; Ocan et al., 2019). However, nasal passages can be damaged while evaluating many rice samples using KOH solution. This may have a negative impact on the data collected from evaluated genotypes (Akwero et al., 2020). Therefore, if the quantity of rice grains is not a limiting factor, the assessment of aroma and other flavor attributes such as taste can be done at once by cooking the milled rice in a rice cooker (Kim, 2020).

According to Kilimo Trust (2018), 71% of imported rice to Burundi was from Tanzania in 2016. Rice from Tanzania is preferred due to its large grains with good taste and aroma (Gahiro, 2011; Ndikuryayo et al., 2022). In Bujumbura and some centers of provinces, the demand for high-quality aromatic rice is high (Ministère de l'Agriculture et de l'Elevage [MINAGRIE], 2014). Previous studies emphasized on improving Supa rice lines for disease resistance including blast (Kanyange et al., 2019).

However, there is no information related to the formal identification of aromatic rice varieties or lines in Burundi. Very little is known on the status of aroma in the grown rice varieties and in the lines used by the breeding program (Kanyange et al., 2019; Ndikuryayo et al., 2022). This study aimed to identify aromatic genotypes that can be used in the breeding program to meet preferences of consumers, especially in Burundi.

Core Ideas

- Genotyping revealed 53 rice genotypes with the betaine aldehyde dehydrogenase gene for fragrance.
- Sensory evaluation revealed strongly aromatic, moderately aromatic, slightly aromatic, and nonaromatic genotypes.
- Identified aromatic genotypes with the gene for fragrance are of great interest for the breeding program.

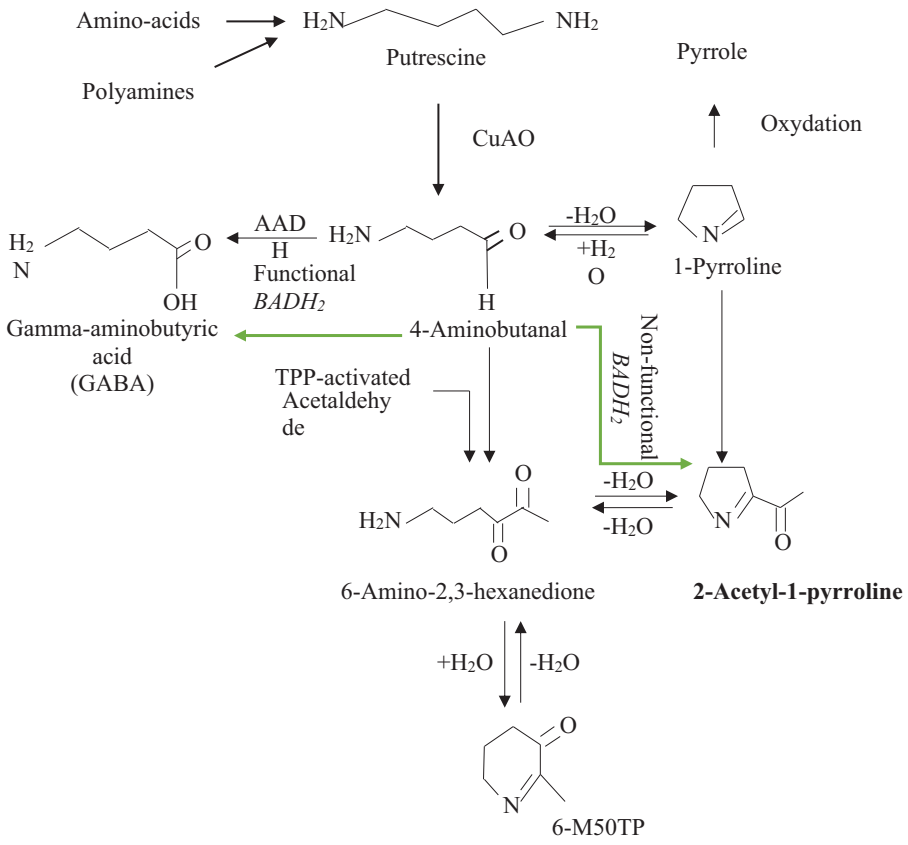

FIGURE 1 *BADH*$_2$ dependent pathways of 2AP biosynthesis in rice.

2 | MATERIALS AND METHODS

2.1 | Plant materials and environmental conditions in the area of the study

Two hundred fifteen rice genotypes with diverse origins (Africa and Asia) were collected through the research institutions in accordance with the national and international regulations of plant materials exchange. More details on the evaluated genotypes are provided in the Supporting Information. These genotypes were grown under irrigated conditions in the field at Gihanga, a lowland area in Burundi. Soil samples were taken from the field to the laboratory for analysis. The results showed that the soil type varied from loamy sand to sandy loam in the plots where the experiment was set. Other soil characteristics such as the hydrogen potential (pH), the content in organic matter (C), the exchangeable sodium (Na), the exchangeable zinc (Zn), and the exchangeable iron (Fe) accounted for 5.5, 0.65%, 0.14 meq/100 g, 0.37 mg/kg, and 443 mg/kg, respectively.

The rice genotypes underwent the standard agricultural practices as recommended by the Ministry of Environment, Agriculture and Livestock (Ministère de l'Environnement, de l'Agriculture et de l'Elevage [MINEAGRIE], 2019). Among these cultural practices, fertilizers were applied at a rate of 65 kg of diammonium phosphate, 29 kg of urea, and 50 kg of K_2O in accordance with the formula NPK 75-30-30. The weather conditions were recorded during the field experiment where the mean temperature was 23.4˚C during the maturity period. The rice grains were harvested from each genotype when plants had completely matured. The rice grains were then dried to get a moisture content of approximately 13% and stored for 1 month at the room temperature.

2.2 | Sensory evaluation of aroma and taste in the evaluated rice genotypes

The rice samples were husked and milled in the same conditions. From each genotype, 750 g of milled rice was cooked in a rice cooker as described by the manufacturer (Kim, 2020). Aroma expression was assessed by smelling the odor once the rice cooker had automatically stopped cooking. The rice cookers were well washed and then labeled before cooking each genotype. The rice samples were cooked from five rooms. The windows and the doors were opened for 15 min before cooking each genotype and then closed while cooking until finishing the activity of smelling.

TABLE 1 Sensory attributes, definitions, and orientations.

Attribute	Definition	Orientation
Aroma		
Popcorn	Aromatics reminiscent of popcorn	2-Acetyl-1-pyrroline
Floral	Fragrant aromatics associated with flowers	Jasmine tea
Dairy	Aromatics associated with milk, especially the skin of cooked milk	UHT Devondale milk
Hay/sour	Aromatics associated with hay, not decaying vegetation	Hay
Earthy	Aromatics associated with soil, dirt, raw mushrooms, and decomposed wood	Sliced mushrooms and soil
Grain	Aromatics associated with grains, for example, barley, cooked porridge, raw oats, and fiber	Cooked barley
Nutty	Aromatics associated with mixed nuts	Peanut butter
Green	Aromatics associated with green, grassy	*cis*-3-Hexanol
Sulfur	Aromatics associated with boiled eggs	Hardboiled egg
Taste		
Sweet	Basic sweet taste associated with sugar	Sucrose
Bitter	Basic bitter taste	Caffeine
Metallic	Flavor and mouthfeel of minerals and metals, such as a metal spoon and iron	Various rice types spiked with liquid ferrous sulfate
Nutty	Flavors associated with mixed nuts	Various rice types with peanut butter

Source: Maleki et al. (2020), Champagne (2008), Zhao et al. (2020).

The score for each rice sample was recorded by eight evaluators, including five women and three men, chosen among the technicians working on rice, the rice millers, and traders. Each evaluator tasted 30 genotypes per day. These evaluators were the same throughout the process of sensory evaluation and during the whole period of that activity. The evaluators were first trained by the researchers of the International Rice Research Institute (IRRI) in Burundi. These researchers are experienced in rice sensory evaluation, and they trained the panel based on the definitions of aroma and taste that are provided in Table 1.

Each of the eight evaluators smelled and scored all the 215 genotypes. The samples were scored on 1–4 scale with 1, 2, 3, and 4 corresponding to absence of aroma, slight aroma, moderate aroma, and strong aroma, respectively (Kibria et al., 2008). SUPA rice from Tanzania with strong aroma and IR 64 nonaromatic rice were used as control. After the activity of smelling, rice was shifted from the room where it was cooked and smelt to the conference room where tasting was performed after 15 min. Using disposable cups and spoons, the evaluators stated above assessed the taste of the cooked rice. Each evaluator tasted and scored all the 215 genotypes. The sensory evaluation took 8 days. After tasting each genotype, the evaluators used to refresh their mouth/tongues using water.

A hedonic scaling method (Minh et al., 2023) was used, with 1, 2, 3, 4, 5, 6, 7, 8, and 9 corresponding to dislike extremely, dislike very much, dislike moderately, dislike slightly, neither like nor dislike, like slightly, like moderately, like very much, and like extremely, respectively.

2.3 | Genotyping procedure

To check the presence or the absence of $BADH_2$ gene in the evaluated rice, two leaf samples were taken from each genotype in the field at 6 weeks after transplanting, before booting. Gloves were put on the hands and then sterilized together with scissors before cutting each leaf. Each leaf was directly put in one labeled envelop inside the ice container. These samples were taken to the laboratory where they were punched and kept in wells of plates at −80°C (Akwero et al., 2020) for 14 h. Each plate was also labeled. Samples were later transferred to a lyophilizer for 48 h for drying (Kanyange et al., 2019).

Genomic deoxyribonucleic acid (DNA) was extracted using a modified cetyl trimethylammonium bromide)–based method (Aboul-Maaty et al., 2019; Kanyange et al., 2019). Extracted genomic DNA was subjected to the kompetitive allele-specific PCR method (Kanyange et al., 2019). The single nucleotide polymorphism (SNP) marker (snpOS0022) targeting the $BADH_2$ gene for aromatic fragrance was used with TATA as favorable allele and AAAAGATTATGGC as unfavorable allele. Note that 5′CTGGTAAAAAGATTATGGCTTCA3′ and

TABLE 2 Groups of genotypes according to their level of aroma expression.

Number of genotypes	Aroma median value	Group of aroma
2	3.5–4	Strongly aromatic
43	2.5–3	Moderately aromatic
138	1.5–2	Slightly aromatic
32	1	Nonaromatic

5′ACATAGTGACTGGATTAGGTTCTG3′ were used as forward primers, and 5′CATCAACATCATCAAACACCACT3′ was used as reverse primer.

2.4 | Data analysis

The scores for aroma and taste were subjected to Friedman sum rank test (Niedoba et al., 2023) using R statistical software (R Core Team, 2020) to determine differences among tested genotypes. The Friedman sum rank test was performed using scores from the eight evaluators. The genotypic data underwent a numerical scoring method by assigning one to a positive allele and zero to a negative allele.

Chi-square test of independence was done to test the association between aroma and $BADH_2$ gene, using the Statistical Tool for Agricultural Research (STAR) software. The median values were used to perform Pearson's correlation analysis in order to check the relationship between aroma and taste using R statistical software.

3 | RESULTS

3.1 | Outputs for sensory evaluation of aroma and taste

Significant (Friedman chi-squared = 302.88, $df = 214$, $p < 0.001$) differences in aroma scores were detected among the tested genotypes by Friedman sum rank test. The sensory evaluation revealed two strongly aromatic genotypes, 43 moderately aromatic genotypes, 138 slightly aromatic genotypes, and 32 nonaromatic genotypes (Table 2 and Table A1).

Differences in taste scores among the evaluated genotypes were significant (Friedman chi-squared = 268.08, $df = 214$, $p < 0.01$). The outputs of taste assessment showed that four genotypes were much liked, 35 were moderately liked, 82 were slightly liked, 57 were neither liked nor disliked, 31 were slightly disliked, and 6 were moderately disliked by the evaluators (Table 3 and Table S1). The correlation between aroma and taste was positive and significant (correlation coefficient = 0.40, $p < 0.001$).

3.2 | Status of $BADH_2$ gene for fragrance in the evaluated genotypes

Out of the 215 genotypes subjected to genotyping, 52 genotypes were homozygous while 1 genotype was heterozygous at the locus of $BADH_2$ gene for fragrance. The genotypes having the gene for fragrance are presented in Table 4. Chi-square test of independence showed that aroma scores and $BADH_2$ were significantly associated ($\chi^2 = 24.01$, $p < 0.001$).

4 | DISCUSSION

The level of aroma expression perceived by the evaluators varied among the tested genotypes. The current results agree with other recent studies that found differences in the strength of aroma among rice genotypes (Akwero et al., 2020; Ocan et al., 2019). As the evaluated genotypes were grown in the same field and handled in the same way after harvesting, these differences in level of aroma expression can mostly be explained by the genetic background of each genotype (Ndikuryayo et al., 2022; Ocan et al., 2019). Genetic factor has been reported to be the main basis of aroma in rice even if the same rice variety might result in different aroma expression because of different planting, processing, and storage conditions (Hu et al., 2020).

The genotypic screening revealed 53 genotypes to be aromatic having $BADH_2$ gene for fragrance. However, the sensory evaluation suggested 183 genotypes to be aromatic with different levels of aroma expression. This can be explained by the fact that aroma is a quantitative trait controlled by more than one gene (Singh et al., 2007). According to Pachauri et al. (2010), there are many chemical compounds in varying proportions that are responsible for significant variation in the intensity of aroma.

Chi-square test of independence showed that aroma and $BADH_2$ were significantly associated. Although aroma is controlled by many genes in rice, the most important is fgr/*badh2*/Os2AP homologous to betaine aldehyde dehydrogenase (*BADH*) on chromosome 8 (Hashemi et al., 2013). It has been reported that aroma is mainly induced by high concentration of 2AP, an N-heterocycle compound

TABLE 3 Groups of genotypes according to their taste intensity.

Number of genotypes	Taste median value	Group of taste
4	7.5	Much liked
35	6.5–7	Moderately liked
82	5.5–6	Slightly liked
57	4.5–5	Neither liked nor disliked
31	3.5–4	Slightly disliked
6	2.5–3	Moderately disliked

that is produced by a mutation in the $BADH_2$ gene. The mutation induces the accumulation of 4-aminobutanal, its acetylation, and cyclization (Daygon et al., 2017; Luo et al., 2022).

Seven genotypes that had $BADH_2$ gene for fragrance were scored nonaromatic by most of evaluators. This can be explained by low concentration of 2AP. A similar finding was recorded by Mathure et al. (2014) while analyzing the concentration of 2-AP in rice samples. They realized that 2-AP volatile compound was also present in some nonfragrance varieties for which the average concentration was about 10 times less in the nonfragrant compared to fragrant rice varieties. During our experiment, any potential mistake in scores was controlled by evaluating few genotypes per day and making sure that none of the evaluators had the flu. Indeed, successive analysis reduces the ability to differentiate aromatic and nonaromatic genotypes because the senses may become saturated (Akwero et al., 2020). Therefore, these results can also be explained by the occurrence of known or unknown mutations in a different part of the $BADH_2$ gene or in the promoter region (Bindusree et al., 2017). In few cases, the mutations can occur in the noncoding regions (Wang et al., 2016). These mutations consist of insertions, deletions, and SNPs (Bindusree et al., 2017). It has been concluded that rice aroma has a highly complex nature (Hu et al., 2020; Ocan et al., 2019).

The scores for taste were significantly different among the tested genotypes. This result agrees with other research findings that revealed significant differences in sensory scores among the evaluated rice genotypes (Akwero et al., 2020; Kwak et al., 2015; Ocan et al., 2019). In a study conducted by Kwak et al. (2015), significant differences in the sensory profiles and consumer acceptability were detected among frozen-cooked rice samples. It has been reported that flavor intensity depends on genetic factors, oxidation products, preharvest (environment and cultural methods), and postharvest (drying, milling, storage, and cooking method) factors (Champagne, 2008). In this study, these differences in sensory scores can mostly be attributed to the genetic factors because the evaluated genotypes were grown and handled in the same conditions.

Significant and positive correlation between the scores of aroma and taste was noticed for the genotypes subjected to sensory evaluation in this study. This suggests that most of aromatic genotypes are likely to be much liked by consumers. Similar results were obtained and reported by Daygon et al. (2017) who discovered positive correlation between flavor attributes. The lipid oxidation products and 2-AP concentration have been reported as main compounds that contribute to the attributes of flavor and aroma in rice (Champagne, 2008; Kaewmungkun et al., 2022).

Among the genotypes that had the $BADH_2$ gene for fragrance, SUPA KATRIN and SUPA DE NYANZA –LAC had the highest aroma median values. This suggests the high level of 2AP content in these genotypes as $BADH_2$ gene expression is mainly controlled by high concentration of 2AP (Kaewmungkun et al., 2022 Ocan et al., 2019; Withana et al., 2020). These genotypes are potential parents that can be suggested for aroma improvement of the genotypes having other preferred traits. Indeed, it was reported that any parent is expected to have elite traits for use in the breeding program (Kaewmungkun et al., 2022; Singh et al., 2022).

5 | CONCLUSION

Considerable variations in taste and aroma expression detected among the evaluated genotypes imply the genetic diversity in these genotypes and the possibility for selection. The findings of this study proved that selecting aroma may favor selection of good taste. The current study has revealed two strongly aromatic (SUPA KATRIN and SUPA DE NYANZA–LAC) genotypes that are more interesting for aroma improvement of elite varieties in Burundi. Among the moderately aromatic genotypes, IR 106172:496-2006-12-21-2, BASMATI 370, BR11 sub 1 (IR85260-148), IR 97013-19-1-3-1-B, IR 97013-19-1-4-1-B, IR 97013-19-1-1-1-B, and SUKARI are of great interest for the breeding program as they carry the $BADH_2$ gene for fragrance and have a good taste. The choice of parents to use in the breeding program can be made among these genotypes after checking their general and specific combining ability but also their perfor-

TABLE 4 Genotypes with *BADH*$_2$ gene and the summary of their sensory evaluation.

Entry No.	Designation	AM	*BADH*$_2$	TM	Origin
1	SUPA KATRIN	4	+:+	5	Tanzania
2	SUPA DE NYANZA –LAC	3.5	+:+	4.5	Burundi
3	BASMATI 370	3	+:+	7	Kenya
4	BR11 sub 1(IR85260-148)	3	+:+	7	–
5	IR 97013-19-1-4-1-B	3	+:+	7	IRRI
6	IR 106172:496-2006-12-21-2	3	+:+	6.5	IRRI
7	IR 97013-19-1-3-1-B	3	+:+	6.5	IRRI
8	FRX 92-14	3	+:+	6	Malawi
9	IR 97012-27-3-1-1-B	3	+:+	3.5*	IRRI
10	SUKARI	2.5	+:+	6.5	Tanzania
11	IR 97013-19-1-1-1-B	2.5	+:+	6.5	IRRI
12	IR 74371-46-1-1	2.5	+:+	6	IRRI
13	IR 97011-1-1-2-3-B	2.5	+:+	6	IRRI
14	SHINGO YA MWALI	2.5	+:+	6	Tanzania
15	IR 106172:502-2029-21-20-2	2.5	+:+	5	IRRI
16	RANGI MBILI	2.5	+:+	5	Tanzania
17	IR 106172:496-2007-23-3-6	2.5	+:+	4.5	IRRI
18	IR 106172:496-2006-12-21-1	2	+:+	7	IRRI
19	IR 97011-1-1-2-1-B	2	+:+	7	IRRI
20	IR 106172:490-2017-4-1-1	2	+:+	6.5	IRRI
21	BASMATI 217	2	+:+	6	Kenya
22	FAYA DUME 5	2	+:+	6	Tanzania
23	FRX 472	2	+:+	6	Malawi
24	GSR IR1-1-Y4-Y1	2	+:+	6	–
25	IR 106172:496-2021-11-5-1	2	+:+	6	IRRI
26	IR 106172:496-2007-20-11-3	2	+:+	5.5	IRRI
27	BARAMATA	2	+:+	5	Zanzibar
28	IR 102858:68-4-2032-16-14-1	2	+:+	4.5	IRRI
29	SIFARA	2	+:+	7	Tanzania
30	IR 97013-8-1-3-2-B	2	+:+	6.5	IRRI
31	MBAWAMBILI KYELA	2	+:+	6	Burundi
32	IR 97012-5-4-3-2-B	2	+:+	6	IRRI
33	MBAWAMBILI	2	+:+	5.5	Tanzania
34	MUGWIZA	2	+:+	5.5	–
35	TXD 307	2	+:+	5.5	Tanzania
36	IR 97011-7-4-1-2-B	2	+:-	5	IRRI
37	IR15L1222	2	+:+	5	IRRI
38	IR 106172:496-2007-19-8-3	2	+:+	4*	IRRI
39	KOMBOKA	2	+:+	4*	Tanzania
40	SUPA SURUNGAI	2	+:+	4*	Tanzania
41	Rumonge	2	+:+	2.5*	Burundi
42	LINE-8A-2	1.5	+:+	6	Kenya
43	KIVULI	1.5	+:+	4.5	Tanzania
44	NERICA 1	1.5	+:+	4.5	Kenya
45	IR 106172:496-2007-19-8-2	1.5	+:+	4*	IRRI
46	IR 12A 164	1.5	+:+	4*	IRRI

(Continues)

TABLE 4 (Continued)

Entry No.	Designation	AM	*BADH*$_2$	TM	Origin
47	IR97012-4-TZA-1-2-1-1	1	+:+	7	IRRI
48	IR 101840-1-1-11-2-1	1	+:+	6	IRRI
49	IR 117796-10-1-1-1	1	+:-	5	IRRI
50	YASIMIN AROMATIC	1	+:+	5	Egypt
51	HUA 565	1	+:+	4*	Mozambique
52	IR 107015-6-5-3-1	1	+:+	4*	IRRI
53	SUPA 1052	1	+:+	4*	IRRI

Note: +:+ = Homozygote for *BADH*$_2$ gene, 4 and 3.5 = strongly aromatic, 3 and 2.5 = moderately aromatic, 2 and 1.5 = slightly aromatic, 1 = nonaromatic, 7.5–7 = moderately liked, 5.5–6 = slightly liked, 4.5–5 = neither liked nor disliked, 4* = slightly disliked, 3.5* = slightly disliked, 2.5* = moderately disliked.
Abbreviations: AM, aroma median value; IRRI, International Rice Research Institute; TM, taste median value.

mance in other important traits including yield depending on the targeted environment.

As aroma is a complex trait, further study to assess the level of aroma expression in rice genotypes may use a combination of multiple methods including sensory evaluation, genotyping, and gas chromatography. Furthermore, genotypes with different backgrounds including segregating populations can be used to generate phenotypic data from Burundi to detect the QTLs controlling aroma in rice and determine the gene(s) within these QTLs.

AUTHOR CONTRIBUTIONS

Cyprien Ndikuryayo: Conceptualization; data curation; formal analysis; investigation; methodology; resources; software; visualization; writing—original draft; writing—review and editing. **Alexis Ndayiragije**: Conceptualization; funding acquisition; methodology; project administration; resources; supervision; validation; writing—review and editing. **Newton Kilasi**: Conceptualization; funding acquisition; methodology; resources; supervision; validation; writing—review and editing. **Paul Kusolwa**: Conceptualization; methodology; resources; supervision; validation; writing—review and editing.

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CONFLICT OF INTEREST STATEMENT

The authors declare no conflicts of interest.

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SUPPORTING INFORMATION

Additional supporting information can be found online in the Supporting Information section at the end of this article.

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APPENDIX

TABLE A1 Level of aroma expression in the evaluated genotypes.

Group of aroma	Genotypes
Strongly aromatic	SUPA KATRIN, SUPA DE NYANZA–LAC
Moderately aromatic	IR 97011-7-4-1-3-B, IR16F1172, IR 106172:496-2006-12-21-2, IR05N221, FRX 92-14, IR 97012-B-2-1-3-B, IR 108267-28-1:4-B RGA-B RGA-1, IR 97013-19-1-3-1-B, IR 117794-32-1-2-2, IR13A515, BASMATI 370, GAMTI, IR 102858:68-4-2032-16-14-2, GIZA 178, IR 97012-27-3-1-1-B, BR11 sub 1(IR85260-148), IR 97013-19-1-4-1-B, WITA 9, IR 107015-18-3-1-B, IR 108031-B-B-B-2-B-B, BASMATI, IR 127156-2-27, IR 97011-1-1-2-3-B, IR 82077-B-B-71-1, IR 100692-AJY 5-1-AJY 1, RANGI MBILI, IR 108043-B-B-B-6-B-B, TXD 306 IMPROVED, GWIZUMWIMBU, IR 13N 154, IR 106172:502-2029-21-20-2, IR 04A115, SHINGO YA MWALI, IR 97011-7-7-3-1-B, IR 103404-B-B-1-3, IR 74371-46-1-1, IR 86385-84-1-1-B, SUKARI, IR 97013-19-1-3-2-B, IR 97013-19-1-1-1-B, IR 106172:496-2007-23-3-6, MKIA WA NYUMBU, IR 103803-B-B-2-1
Slightly aromatic	IR 106172:496-2006-12-21-1, IR 97011-1-1-2-1-B, SIFARA, IR 106172:490-2017-4-1-1, IR 97013-8-1-3-2-B, BASMATI 217, FAYA DUME 5, FRX 472, GSR IR1-1-Y4-Y1, IR 106172:496-2021-11-5-1, IR 97012-5-4-3-2-B, MBAWAMBILI KYELA, IR 106172:496-2007-20-11-3, MBAWAMBILI, MUGWIZA, TXD 307, BARAMATA, IR 97011-7-4-1-2-B, IR15L1222, IR 102858:68-4-2032-16-14-1, IR 106172:496-2007-19-8-3, KOMBOKA, SUPA SURUNGAI, Rumonge, NZAHARA, IR 101793-1-1-1-3-5-4, IR 112661-150-1:1-B RGA-B RGA-1, IR 117795-10-1-2-1, IR 2793-80-1, IR 92522-45-3-1-4, IR14L345, KAZOSI, IR 97012-4-1-2-3-B, IR 97012-4-3-1-1-B, IR09A228, IR16L1499, MET108, FACAGRO 906, IR 103421-B-B-5-3, IR 106172:502-2029-21-20-1, IR 108044-B-B-B-3-B-B, IR 108135-B-1-AJY 1-B-1, IR 108175-B-22-AJY 3-B-1, IR 118170-B-18-1-1-3, IR 127167-2-99, IR 13240-108-2-2-3, IR 55423-01, IR 79913-B-176-B-4, IR 83388-B-B-108-3, IR 97011-6-1-2-1-B, IR 97011-7-2-1-2-B, IR 97012-B-2-1-1-B, IR08A176, IR11A306, IR14F713, IR14L545, IR15T1133, IR15T1330, IR16L1478, RF101, BRRI DHAN 55, EDIGET (WAB189-B-B-B-HB), FACAGRO 904-4, INTSINZI, IR 09N516, IR 103414-B-B-6-1, IR 107015-80-2-B-1, IR 112655-9-1:2-B RGA-B RGA-1, IR 112671-126-1:4-B RGA-B RGA-1, IR 81412-B-B-82-1, IR 97011-7-7-2-1-B, IR 97012-4-1-1-1-B, IR06N188, IR13N134, NAWA TULE NA BWANA, PIR-26>C0-2071-1-4-2-1, TXD 85 IMPROVED, TXD 88 IMPROVED, CYICARO, IR 100842-B-B RGA-B RGA-B RGA-9, IR 103406-B-B-3-2, IR 103419-B-B-1-3, IR 64-SUB1, IR 74371-70-1-1, IR 86384-55-2-1-B, IR 86781-3-3-1-1, IR 95781-15-1-1-4, IR 97013-21-5-B-B-B, IR 99054-B-B-1, IR05N359, IR09L226, IR12A173, IR15L1564, NERICA 10, Ciherang-Sub1, IR 108289-B-AJY 1-2-B-1, IR 99047-B-B-B-B-47, IR14L362, IR16L1421, IRON, LINE 11 WARDA, NERICA 4, PR44420-36-4-3, RUMBUKA 179, SALT TOL SIN THWE LATT, VUNINZARA, CIHERANG, IR 117795-41-3-1-2, IR 117824-B-50-1-2-5, IR 74371-54-1-1, IR 97011-7-7-2-2-B, IR16F1079, LUNYUKI, IR 100638-12-AJY 3-CMU 2, IR13N131, IRGEO, LINE-8A-2, KIVULI, NERICA 1, IR 106172:496-2007-19-8-2, IR 12A 164, IR11N202, IR15L1008, IR 117795-49-3-3-1, IR15D1058, IR 97011-7-4-3-2-B, IR15L1419, PR42071-14-2-2-2, IR 103802-B-B-2-3, IR15A1410, IR 103782-B-B-1-1, IR 106172:496-2007-23-3-5, IR 117787-5-1-2-1, IR16F1045, WAHIWAHI, IR 103387-B-B-3-3, IR06A150, IR13N143, A69-1, AFAA MWANZA1/159, HUA 565
Nonaromatic	IR 101840-1-1-11-2-1IR 107015-15-9-B-1, IR 107015-6-5-3-1, IR 108028-B-B-B-1-B-B, IR 108028-B-B-B-4-B-B, IR 112675-28-2:1-B RGA-B RGA-1, IR 117795-10-1-3-1, IR 117796-10-1-1-1, IR 127136-11-40, IR 64, IR 82589-B-B-84-3, IR05N341, IR10N237, IR11A293, IR11N121, IR12A282, IR13A107, IR13A153, IR14L156, IR14L440, IR16F1014, IR97012-4-TZA-1-2-1-1, JAMBO TWENDE, KDML, MUSESEKARA, YASIMIN AROMATIC, NEMEYUBUTAKA, SUPA 1052, MPEMBUKE