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RESEARCH ARTICLE

Unravelling genetic variability and character association study for cooking quality attributing traits for the selection of promising genotypes in rice

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Abstract

Rice (*Oryza sativa* L.) is a major cereal crop in the world, particularly in Asia, where it is a staple food for 90 % of the population. The current research was aimed at determining the better genotypes for cooking quality characteristics by utilizing forty-three genotypes of rice along with two checks, *viz*: Pooja and RNR 15048. The experiment was carried out during the summer season of 2024 at Post Graduate Research Farm, M.S. Swaminathan School of Agriculture, Centurion University of Technology and Management, Paralakhemundi, India. The design of experiment was Randomized Block Design (RBD) with three replications. Study revealed significant difference among all the studied parameters through analysis of variance which extend scope of further study. Genetic parameters revealed that phenotypic coefficient variation is higher than genotypic coefficient of variation indicates along with genotypic environment also played key role to influence the studied characters. High heritability coupled with high to moderate genetic advance as percent of mean noted for all the studied characters signify the predominance of additive gene action henceforth, direct selection would be rewarding. Character association and partial regression study revealed significant association among the studied variables. The significant character such as seed protein content highest exhibited by POO7SD (8 %), amylose content exhibited highest in Durgasal (24 %), on contrary lowest was revealed by Mugi (10 %). Genotypes RNR 15048, Pusa Basmati and POO7SD were found to be superior for biochemical and cooking quality traits and hold promise for future programs of improvement. Which clearly signify future potential to unravel qualitative breeding by seeing India's opportunities in global market through Basmati rice. Therefore, further exploration of aforementioned genotypes will ultimately help to strengthen India's qualitative rice market in domestic and international pace.

Keywords: amylose; cooking quality parameters; correlation; path coefficient; rice

Introduction

Rice (*Oryza sativa* L.) is one of the world's most significant cereal crops and a nutritional mainstay of over half of the world's population. Rice has inestimable agricultural, economic and cultural importance in India which plays a significant contribution to food security and rural livelihoods (1). As the population has been growing and consumer preferences have been shifting, the requirement for rice varieties not only with enhanced yield but also it has observed that in 2024-25 Indian domestic market is moving towards packaged rice and a rise in demand for health-conscious options like low-Glycaemic Index, organic and unpolished rice. Rice grain quality is a multifaceted trait controlled by various physical and biochemical properties. Amongst the physical parameters characters such as; kernel length and kernel breadth, before and after cooking act as an important predictor of grain appearance which eventually decides cooking quality and consumer acceptability (2). These traits have direct implications on market price and are frequently employed to discriminate premium quality rice varieties, like India's and overseas-preferred long-grain Basmati types. Grain elongation following cooking is particularly appreciated, as it makes cooked rice more visually appealing and better textured.

Besides, of physical attributes, biochemical properties like protein content, amylose content and gelatinization temperature play as critical determinants of rice nutritional and cooking quality (3). Protein content is a very important nutritional factor, as rice is one of the primary sources of dietary protein for hundreds of millions, particularly for low-income groups Malnutrition due to lack of sufficient protein energy is one of most serious concern causing bottleneck issue in social and economic front. Amylose content has a great influence on the texture of cooked rice, with high amylose types having a dry, fluffy texture and low amylose types having a soft, sticky texture Moreover, character like low glycaemic index highly associated with amylose content in the concerned genotypes. Gelatinization temperature, a term describing the temperature at which starch granules swell and take in water when cooking, has implications for cooking time and texture (4). India, being richly endowed with genetic variation in rice, offers a great chance to study variation in these characters. These studies are helpful in the identification of genotypes with combinations of desirable traits, which can be successfully utilized in selection and hybridization schemes. High eating quality Indica rice varieties have diverse texture properties when cooked. Selection of texture properties of cooked rice should focus on grain amylose content rather than grain protein content for high eating quality Indica rice (5). While global trends in rice consumption increasingly favour long-grain, aromatic and high to moderate amylose varieties with soft texture, regional preferences remain diverse. In Odisha, consumers traditionally prefer parboiled bold grain types of rice which continues to influence varietal adoption and breeding targets in the region.

Rice grain quality is a multifaceted trait influenced by various characteristics, including kernel size, protein content and amylose content (6). While previous studies have examined genetic variation for these traits, unexplored genetic diversity in landraces holds promise for identifying valuable parents to enhance heterosis and quality in rice breeding programs.

The purpose of this study is to explore the genetic variation in many rice genotypes about kernel length and breadth (uncooked and cooked), together with biochemical traits like seed protein content, amylose content and gelatinization temperature. The discovery will be beneficial information for breeders and scientists in the development of rice varieties that retain high nutritional quality along with better grain and cooking quality, ensuring sustainable rice production and addressing the changing needs of Indian and global markets.

Materials and Methods

Experimental site

The present investigation was conducted at Post Graduate Research farm of M.S. Swaminathan School of Agriculture, Centurion University of Technology and Management, Gajapati, Northeastern Ghats zone of India, during the summer season of 2024. The site's geographical coordinates are 84.14195°E longitude, 18.80027°N latitude, with an altitude of 91 meters above mean sea level.

Experimental materials

The study utilized 43 rice genotypes obtained from across the different states of India and even beyond as mentioned in Table 1 and evaluated as per standard agronomical package and practices. The type of soil was sandy loam with good drainage and a pH of 6.3.

Experimental layout

The experiment utilized a Randomized Complete Block Design (RCBD) with three replications to evaluate 43 rice genotypes for biochemical and cooking quality characteristics. Plot size was 2mx1.5 m and 15 cm spacing between plants and 20 cm between rows where, each genotype were having three rows. Fertilizers used were 80:40:40 kg hectare^{-1} N:P_2O_5:K_2O as basal P_2O_5, K_2O and half N at land preparation followed by standard agronomic practices were adopted.

Observation recorded

To reduce the border impact, plants from the border were not included as samples. Five plants were randomly tagged prior to flowering in order to record the data. Kernel length, kernel breadth, kernel length after cooking, kernel breadth after cooking, kernel linear elongation ratio (KLER), gelatinization temperature, amylose content estimated followed by previous studies where, 100 mg of rice grain flour dissolved into 1 mL of 95 % of ethanol solution followed by adding 9 mL of 1 N NaOH and mixed gently (7). Afterwards the solution was heated in hot water bath for nearly 10 min to dissolved the starch afterwards cooled in room temperature and transferred it into 100 mL of flask and volume makeup with distilled water. 5mL of starch solution pipette out into a new test tube and added 1 mL of 1 N acetic acid later added 2 mL of iodine reagent and diluted it with 10 mL of distilled water until the colour develop for nearly 20 min at room temperature (25 °C) and observation were recorded with spectrophotometric method at 660 nm against a blank (Model UV-1900I Shimadzu, Japan). Seed protein content measured after (8) where, 0.2 g of the sample was weighed and ground with 4mL of sodium phosphate buffer in a mortar pestle. It was then centrifuged at 10000 rpm for 20 min and the supernatant was used for protein estimation. 0.1 mL of the sample extract was pipetted out into a test tube. The volume was made up to 1mL with distilled water. 5 mL of solution C was added and with the help of shaker mixed well and incubated at room temperature for 10 min. Afterwards 0.5 mL of FCR was added in the test tube

Table 1. List of rice genotypes

Sl no.	Genotype	Origin	Sl no.	Genotype	Origin	Sl no.	Genotype	Origin
1	Kamalabhog	West Bengal	16	Binni	Bangladesh	31	BIB3	Unknown
2	Durgasal	Unknown	17	Bidhansuruchi	West Bengal	32	Dhanurban	bidha
3	Bhutmuri	West Bengal	18	Gobindobhog	West Bengal	33	Ananya	Maharashtra
4	Ratansal	Tamil Nadu	19	Babui	West Bengal	34	Kanakchur	West Bengal
5	Sitasal	West Bengal	20	TN1	Taiwan	35	Swarna	Andhra Pradesh
6	Kataribhog	West Bengal	21	Kalma	Uttar Pradesh	36	POO7SD	Unknown
7	Malati	Uttar Pradesh	22	Hathi pajar	Unknown	37	Shatabdi	Odisha
8	Badshahbhog	West Bengal	23	Pokshali	Kerala	38	Santoshi	Odisha
9	Tulai Panji	West Bengal	24	Sonalu	Andhra Pradesh	39	Kabirajsal	West Bengal
10	Abita	United States of America	25	IR36	Philippines	40	IR64	Philippines
11	MTU1075	Andhra Pradesh	26	Pratiksha	Odisha	41	MTU1010	Andhra Pradesh
12	PRS101		27	Dudheshwar	West Bengal	42	Pooja	Odisha
13	MTU1153	Andhra Pradesh	28	Indrabam	Odisha	43	RNR15048	Andhra Pradesh
14	Sukumar	West Bengal	29	Pusa Basmati	New Delhi			
15	Barsha	Andhra Pradesh	30	Mugi	Unknown			

and mixed well with the help of shaker and incubated at room temperature in dark for 30 min. The intensity of the blue colour was measured calorimetrically at 660 nm against the blank in a spectrophotometer (Model UV-1900I Shimadzu, Japan). The amount of protein present in the seed sample was calculated with the help of standard graph prepared using different concentration of bovine serum albumin and the result was expressed as gm100g-1 of sample. Using an ALPA Megaline AA029 model digital slide caliper, the length and breadth of ten randomly chosen kernels (after de-husking) was measured and the mean value was calculated. KLER was measured by dividing the length of cooked rice by the length of original (uncooked) kernel (9). The alkali spreading value, was measured which is related to the amylose concentration of the starch, which is a measurement of the gelatinization temperature of whole kernel milled rice in contact with diluted alkali where, 1.7 % of potassium hydroxide dissolve 8.5 g KOH pellets in 500 mL of recently boiled and cooled distilled water. Stored at 24 hrs before use and data were observed between low to high gelatinization temperature. The cooking temperature at which water is absorbed and the starch granules irreversibly enlarge while simultaneously losing their crystalline structure is known as the endosperm starch's gelatinization temperature. Given that amylose content is a key factor in determining the fluff or stickiness of rice, which is directly related to consumer behavior and end-use suitability, it is important to take it into account in this experiment (10). On the other hand, qualities like gel consistency indicate how firm the cooked rice is and lowering the gelatinization temperature uses less energy and takes less time to cook, which is advantageous for both domestic household and industry (11).

Statistical analysis

A RBD was employed to analyse data from three replications, allowing for the identification of significant variation. Analysis was done using 'R' software version 4.3.3. The statistical method for figuring out whether there is a substantial difference present between treatments is the analysis of variance. Followed by character association and partial regression study among cooking quality and biochemical traits to determine traits association at both 1 % and 5 % level of significance as mentioned (12). Test of significance for every character was carried out against the corresponding error degrees of freedom using standard 'F' table values (13). The research entails moderate material and energy inputs throughout field trials, post-harvest processing and laboratory-based trait analysis like amylose content, gelatinization temperature and other rice quality attributing traits are the main cost drivers are field operations (40 %), laboratory tests (25 %) and processing (20 %). Regardless of these indications, the choice of genotypes with superior cooking quality traits possesses high economic value through increased market value, consumer acceptance and breeding efficiency. Cost-saving selection is facilitated through emphasis on heritable, correlated traits. The method is therefore scientifically sound and economically justifiable for high-value rice breeding programs.

The primary cost drivers for this study are field operations (40 %), lab testing (25 %) and processing (20 %). Modest material and energy inputs are required for field trials, post-harvest processing and lab-based trait analysis, including amylose content, gelatinization temperature and other rice quality attributing traits. Due to increased market value, consumer preference and breeding efficiency, choosing genotypes with superior cooking quality traits offers significant economic potential despite these inputs. Cost-effective selection is made possible by concentrating on correlated, heritable traits. For high-value rice breeding programs, the strategy is therefore both economically feasible and scientifically sound.

Results and Discussion

New developments in artificial intelligence (AI) have greatly improved capacity for evaluating the economic consequences of innovation in various fields. Of particular importance to industrial and managerial decision-makers, priority has now switched toward models that are not merely technically strong but also interpretable in terms of economic consequence. In this sense, AI-powered simulations like those in digital twin platforms and predictive analytics provide a realistic framework for assessing innovation potential under actual-world restrictions. Current research illustrates how the selection of a minimal number of high-impact characteristics like amylose composition and gelatinization temperature can inform effective genotype selection. This approach reflects the industrial imperative of focusing on a few high-leverage markers when measuring innovation. In making such methodological connections, we highlight the worth of economically meaningful, decision-making models in all the industries (14, 15).

Analysis of variance among quality attributing traits

Analysis of variance established significant variation across genotypes for all the studied traits, reflecting scope for improvement through selection. The results are consistent with (16) and (17), who also established significant trait-wise variations among rice genotypes (Table 2).

Mean performance and variability study among rice genotypes

Mean performance among the rice genotypes for seven quality and biochemical attributing traits showed ample amount of variation indicates scope of improvement (Table 3 and Fig. 1). The statistical attributes such as coefficient of variation least significant differences and error mean sum of square were presented in Fig. 2. Study on characters such as kernel width ranged from 1.70 mm (Pusa Basmati) to 2.70 mm (Hathi Pajar) (Fig. 3). Noted with marginal difference between genotypic and phenotypic coefficients of variation (GCV = 7 %, PCV = 9 %) (Table 4 and Fig. 4) indicated little influence of environment additionally high heritability (61 %) and moderate genetic advance (12 %) confirmed additive gene action. Kernel length showed

Table 2. Analysis of variance for different characters in rice genotypes

Source of variance	Replication	Genotype	Error
Kernel length (mm)	0.09	0.74**	0.04
Kernel Breadth (mm)	0.065	0.11**	0.02
Kernel length after cooking (mm)	2.78	5.93**	0.07
Kernel breadth after cooking (mm)	0.03	0.54**	0.04
Seed protein (mg g^{-1})	0.76	4.41**	0.18
Amylose content (mg g^{-1})	1.15	36.98**	0.17
Kernel linear elongation ratio	0.06	0.09**	0.004

Significance at 5 % level*, Significance at 1 % level**

Table 3. Mean performance of rice genotypes for cooking and biochemical attributes

Sl. no.	Genotypes	KL	KB	KLAC	KBAC	PRO	AMYL	KLER
1	Kamalabhog	5.30	2.30	6.70	3.20	3.90	12.40	1.25
2	Durgasal	5.40	2.10	7.10	3.40	3.60	24.30	1.32
3	Vutmuri	5.10	2.50	6.40	3.10	4.50	16.04	1.24
4	Ratansal	5.00	2.40	6.80	3.00	5.20	22.20	1.33
5	Sitasal	5.80	2.00	7.40	3.40	3.60	23.11	1.25
6	Kataribhog	6.00	2.30	8.40	3.10	6.40	13.90	1.34
7	Malati	5.70	2.40	8.10	3.80	4.70	16.04	1.50
8	Badshahbhog	5.90	2.60	6.90	3.50	5.30	13.53	1.21
9	Tulai Panji	4.80	1.90	5.60	3.80	7.40	15.62	1.19
10	Abita	5.40	2.20	5.40	2.70	8.00	22.92	1.03
11	MTU1075	5.00	2.12	7.30	3.20	4.60	22.37	1.42
12	PRS101	4.30	2.20	7.10	3.70	6.40	19.68	1.65
13	MTU1153	5.80	1.70	8.30	3.60	4.60	12.34	1.41
14	Sukumar	5.70	2.50	8.10	2.50	3.60	15.14	1.41
15	Barsha	5.80	2.30	6.50	3.20	5.70	14.88	1.12
16	Binni	6.70	1.90	8.30	3.80	7.40	16.12	1.31
17	Bidhansuruchi	6.10	1.70	6.50	3.30	4.70	13.66	1.12
18	Gobindobhog	5.20	2.50	7.00	3.10	6.80	19.29	1.36
19	Babui	5.70	2.40	7.40	3.80	3.60	17.66	1.35
20	TN1	6.20	2.03	7.90	3.60	6.30	14.81	1.35
21	Kalma	5.50	2.40	6.80	3.80	5.70	18.68	1.20
22	Hathi Pajar	5.80	2.70	6.60	4.00	6.80	12.86	1.26
23	Pokshali	5.30	2.25	7.40	3.70	5.40	17.82	1.36
24	Sonalu	6.00	2.30	8.30	3.20	4.70	14.77	1.42
25	IR36	6.50	2.25	8.30	3.40	4.80	12.90	1.29
26	Pratiksha	5.70	2.50	8.50	3.70	4.00	14.63	1.61
27	Dudheshwar	5.40	2.21	7.10	3.40	3.80	16.71	1.34
28	Indrabam	4.90	2.70	7.30	3.90	4.10	15.51	1.43
29	Pusa Basmati	7.60	1.70	14.80	2.00	2.90	21.11	2.08
30	Mugi	5.00	2.30	6.00	3.40	5.20	10.28	1.24
31	B1B3	5.90	2.00	7.80	3.00	6.90	19.25	1.35
32	Dhanurban	5.40	2.10	8.20	3.20	7.10	16.77	1.50
33	Ananya	5.30	2.10	7.20	3.40	5.20	18.90	1.36
34	Kanakchur	5.80	2.50	7.30	3.10	5.70	18.13	1.29
35	Swarna	5.80	2.30	7.60	2.70	3.80	17.87	1.35
36	POO7SD	5.10	2.32	8.20	3.40	8.10	11.60	1.61
37	Satabdi	5.90	2.14	7.60	3.20	4.70	12.80	1.21
38	Santoshi	6.50	2.40	8.30	2.70	4.30	11.00	1.29
39	Kabirajsal	4.90	2.10	6.90	2.80	3.70	16.60	1.52
40	IR64	6.10	2.30	7.50	2.80	7.70	12.88	1.27
41	MTU1010	5.30	2.00	7.20	2.50	7.30	15.67	1.41
42 ©	Pooja	5.60	2.30	7.30	2.80	5.80	17.04	1.31
43 ©	RNR 15048	5.30	2.10	8.10	2.80	5.70	21.11	1.58
	Mean	5.62	2.23	7.52	3.25	5.34	16.53	1.36
	C.V (%)	3.48	6.23	3.67	6.12	7.72	2.49	4.65
	S.Em(±)	0.09	0.04	0.21	0.07	0.21	0.54	0.03
	LSD 5 %	0.32	0.23	0.45	0.31	0.68	0.67	0.11
	LSD 1 %	0.43	0.30	0.59	0.42	0.91	0.89	0.14

KL -Kernel length (mm), KB - Kernel breadth, KLAC - Kernel length after cooking (mm), KBAC – Kernel Breadth after cooking (mm), PRO - Seed Protein content (mg/g), AMYL - Amylose content (mg/g), KLER - Kernel elongation ratio, © - Check

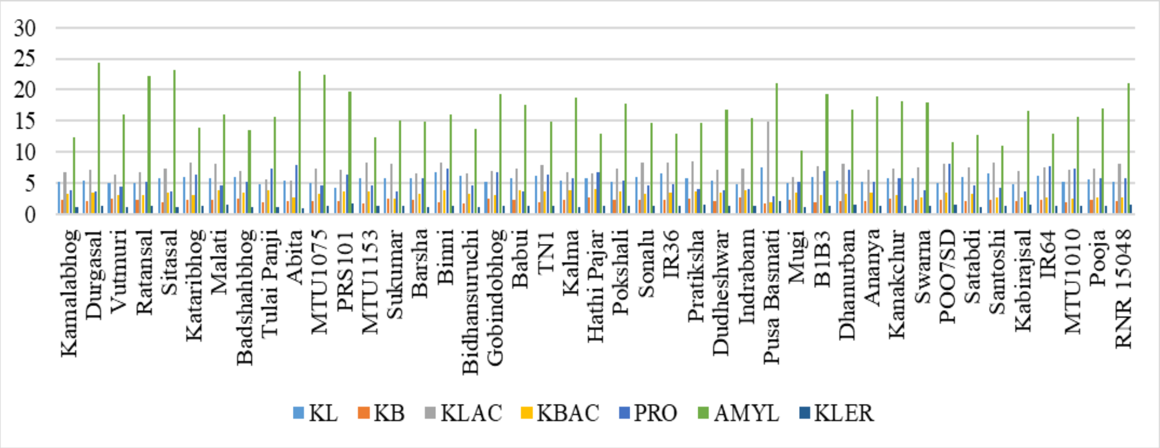

Fig. 1. Mean performance of rice genotypes.

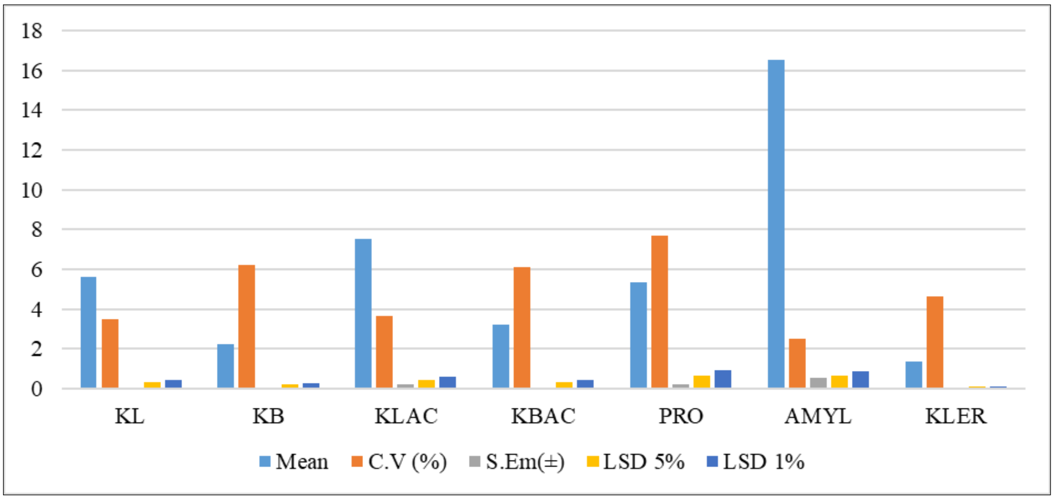

Fig. 2. Genetic data of rice genotypes.

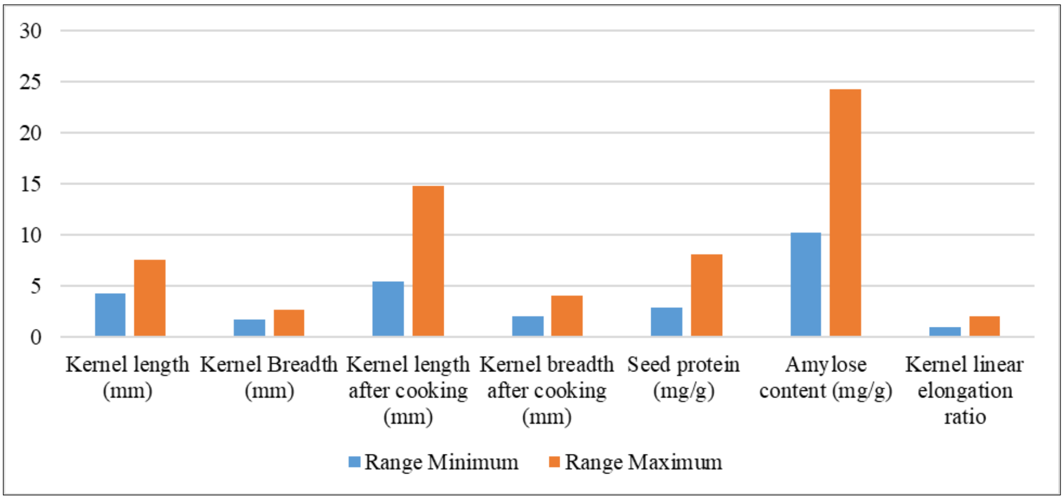

Fig. 3. Mean range of cooking and biochemical characters.

Table 4. Mean, range, variability, heritability (b.s), genetic advance as percent of mean for cooking and biochemical attributing traits among rice genotypes

S. No.	Characters	Grand Mean	Range		Coefficient of variation		Heritability (Broad sense) (%)	Genetic Advance as percent of mean (%)
			Minimum	Maximum	GCV (%)	PCV (%)		
1	Kernel length (mm)	5.62	4.30	7.60	8	9	85	16
2	Kernel Breadth (mm)	2.23	1.70	2.70	7	9	61	12
3	Kernel length after cooking (mm)	7.52	5.40	14.80	18	18	96	36
4	Kernel breadth after cooking (mm)	3.25	2.00	4.10	12	13	81	23
5	Seed protein (mg/g)	5.34	2.90	8.10	21	22	88	42
6	Amylose content (mg/g)	16.53	10.28	24.30	20	21	98	42
7	Kernel linear elongation ratio	1.36	1.03	2.08	12	13	86	23

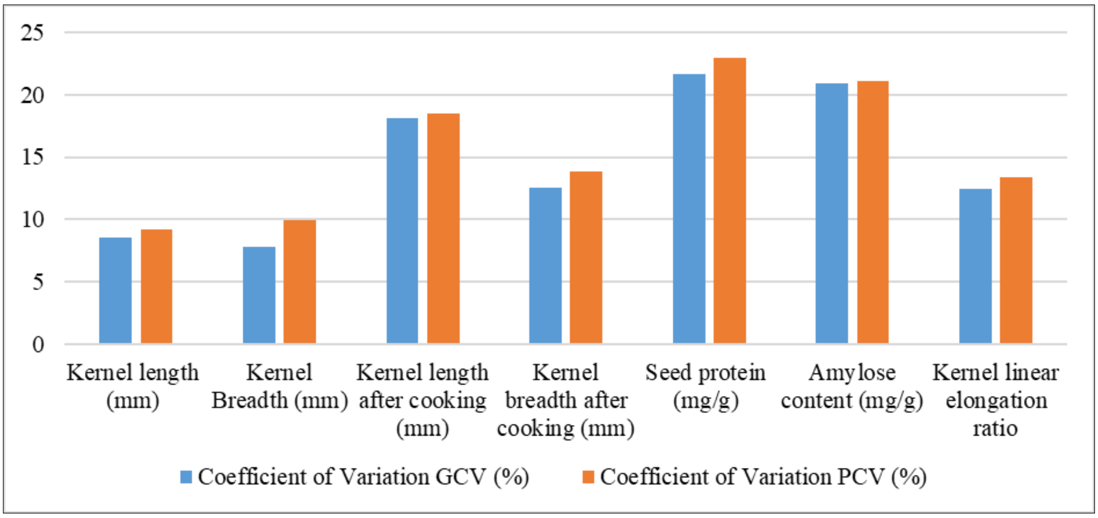

Fig. 4. Coefficient of variation for studied characters.

considerable variation between genotypes, ranged from 4.30 mm in PRS101 to 7.60 mm for Pusa Basmati. Marginal difference between genotypic (8 %) and phenotypic (9 %) coefficients of variation suggested negligible environmental impact on kernel length. Most importantly, high heritability (85 %) along with moderate genetic advance (16 %) implied that additive gene action largely controls the trait which is seen in pointing towards scope for effective selection in breeding. The results are consistent with previous studies (18), reported to have obtained similar results. Length of cooked kernel also significantly differed amongst the studied genotypes, from 5.40 mm (Abita) to 14.80 mm (Pusa Basmati). The narrow difference between phenotypic and genotypic coefficients of variation (PCV = 18 %, GCV = 18 %) indicated very little of environmental impact. High heritability (96 %) and high genetic advance (36 %) (Fig. 5 & 6) indicated additive gene action, in agreement with (19). Kernel breadth after cooking varied from 2.00 mm (Pusa Basmati) to 4.00 mm (Hathi Pajar) in the studied genotypes. The small margin between phenotypic (13 %) and genotypic (12 %) coefficients of variation indicated little environmental impact. High heritability (81 %) and high genetic advance (23 %) revealed additive gene action and direct selection would be rewarded. The same result in accordance with (20). Seed protein content, another important nutritional parameter, differed widely among genotypes, ranging from 2 % (Pusa Basmati) to 8 % (POO7SD). The marginal difference between genotypic (21 %) and phenotypic (22 %) coefficients of variation reflected minimal environmental influence. High heritability (88 %) and high genetic advance (42 %) reflected additive gene action hence direct selection would be useful for improvement of same character. Amylose content was greatly variable among genotypes, varying from 10 % (Mugi) to 24 % (Durgasal) character exhibited with marginal differences between genotypic (20 %) and phenotypic (21 %) coefficients of variation suggested negligible environmental impact on amylose content. However, high heritability (98 %) coupled with high genetic advance (42 %) indicated that additive gene action largely regulates this trait and suggests potential for effective selection in breeding. This agrees with previous paper, who also obtained similar results, citing the significance of genetic influence in defining amylose content (21). Kernel linear elongation ratio (KLER) exhibited significant variation among genotypes, ranging from 1.03 (Abita) to 2.08 (Pusa Basmati) indicating the potential for desirable cooking characteristics. The coefficient of variation (4 %) fell within statistically permissible limits, suggesting relatively consistency for the expression of trait. Furthermore, the minimal difference exhibited between phenotypic (13 %) and genotypic (12 %) coefficients of variation implied minimal environmental influence on KLER. High heritability (86 %) coupled with high genetic advance (23 %) indicated that additive gene action predominantly governs this trait, suggesting that direct selection would be an effective breeding strategy for improving KLER. These findings are consistent with (22), who reported similar results in rice genotypes, highlighting the importance of genetic factors in determining KLER.

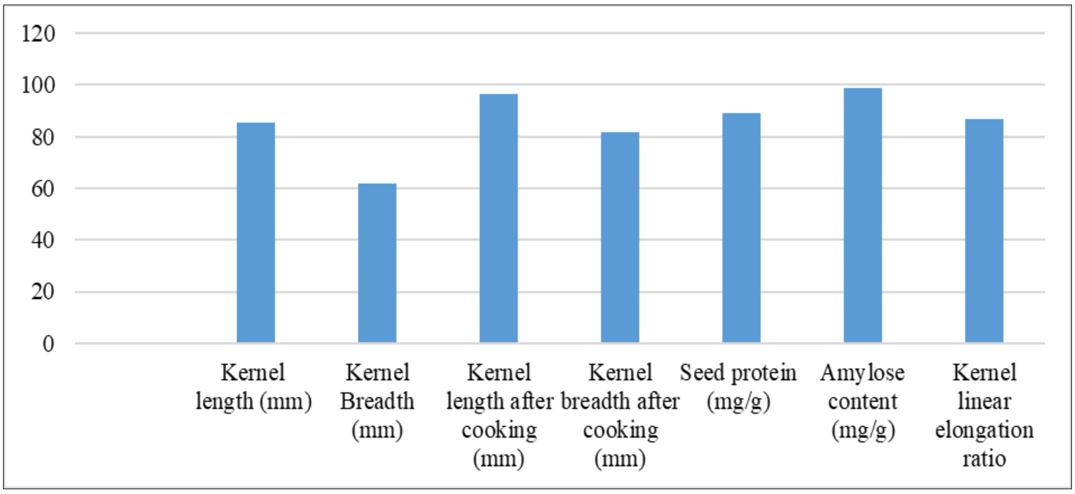

Fig. 5. Heritability (broad sense) for studied characters.

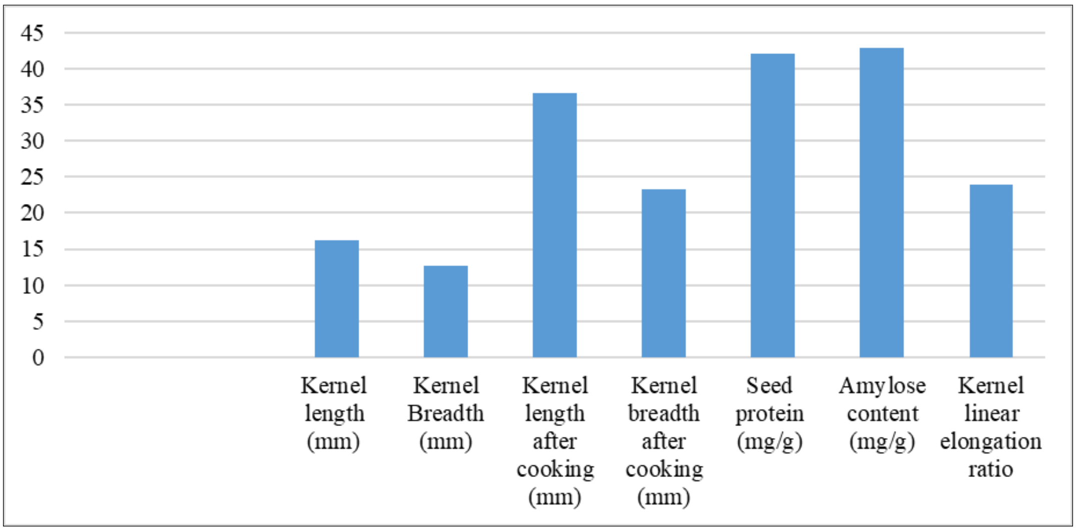

Fig. 6. Genetic advance as percent of mean for studied characters.

Genotypic and phenotypic character association study

The genotypic (Table 5) correlation coefficients (Fig. 7) among seven cooking and biochemical quality attributing traits in rice genotypes revealed significant associations, providing valuable insights into the relationships between these traits. Kernel length after cooking showed a very high significant positive correlation with kernel linear elongation ratio (KLER), (0.839**) indicating a robust relationship. Which suggests that genotypes with longer kernel length after cooking tend to exhibit higher kernel linear elongation ratios, a desirable trait in rice breeding programs. Conversely, kernel breadth after cooking (-0.287*) and seed protein content (-0.311*) exhibited high significant negative correlations with kernel linear elongation ratio, indicating that genotypes with broader kernels or higher seed protein content may have lower kernel elongation ratios. These findings have implications for breeding strategies, as selection for one trait may influence others. Kernel length displayed significant negative correlations with kernel breadth and kernel breadth after cooking, but a positive correlation with kernel length after cooking. This suggests that genotypes with longer kernels tend to have narrower kernels breadth and longer kernel length after cooking. Additionally, kernel length after cooking had significant negative correlations with kernel breadth after cooking and seed protein, indicating that genotypes with longer kernel length after cooking may have narrower kernels breadth and lower seed protein content. These findings are consistent with previous studies (23, 24), which reported stronger genotypic correlations indicating inherent associations among traits. Similarly, (25) found positive correlations between kernel length and kernel length after cooking, as well as between kernel breadth and kernel breadth after cooking. These studies highlight the importance of understanding trait relationships in rice breeding programs. On the other hand at phenotypic level kernel length after cooking (0.816**) exhibited very high significant positive correlation with KLER on the contrary kernel breadth after cooking (-0.241*) and seed protein content (-0.285*) revealed significant negative association with KLER indicates scope of improvement for the aforementioned traits (Table 6). The correlation analysis provides valuable information for breeding programs aimed at improving cooking and biochemical quality traits in rice. By understanding the relationships between traits, breeders can develop targeted selection strategies to enhance desirable traits while minimizing undesirable effects on other traits as explained in (26).

Table 5. Studies on genotypic correlation coefficient among cooking quality and biochemical attributing characters in rice genotypes

Characters	KB	KLAC	KBAC	PRO	AMYL	KLER
KL	-0.389**	0.665**	-0.289*	-0.178	-0.122	0.166
KB		-0.369*	0.290*	0.100	-0.218	-0.185
KLAC			-0.399**	-0.340*	0.097	0.839**
KBAC				0.191	-0.207	-0.287*
PRO					-0.068	-0.311*
AMYL						0.176

Significance at 5 % level *, Significance at 1 % level **

KL- Kernel length (mm), KB - Kernel breadth, KLAC - Kernel length after cooking (mm), KBAC - Kernel Breadth after cooking (mm), PRO - Seed Protein Content (mg/g), AMYL - Amylose content (mg/g), KLER - Kernel elongation ratio

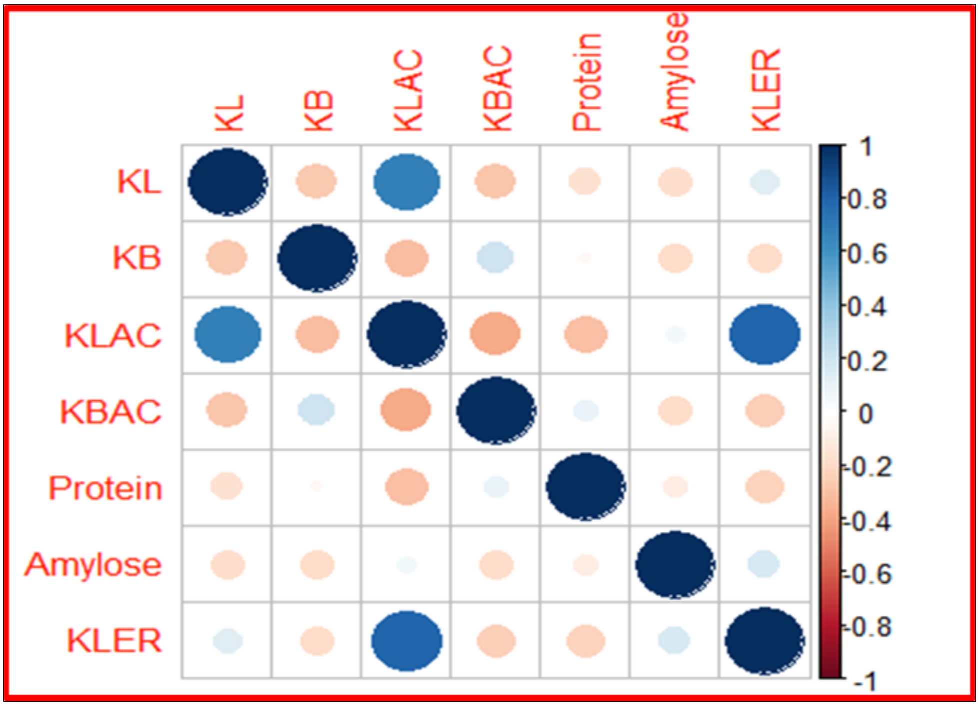

Fig. 7. Genotypic correlation coefficient for cooking quality and biochemical attributing traits in rice.

Kernel length (mm), KB - Kernel breadth, KLAC - Kernel length after cooking (mm), KBAC - Kernel Breadth after cooking (mm), PRO - Seed Protein Content (mg/g), AMYL - Amylose content (mg/g), KLER - Kernel elongation ratio

Table 6. Studies on phenotypic correlation coefficient among cooking quality and biochemical attributing character in rice genotypes

Characters	KB	KLAC	KBAC	PRO	AMYL	KLER
KL	-0.314*	0.607**	-0.253*	-0.154	-0.116	0.049
KB		-0.259*	0.185	0.040	-0.174	-0.078
KLAC			-0.359**	-0.324*	0.094	0.816**
KBAC				0.151	-0.176	-0.241*
PRO					-0.060	-0.285*
AMYL						0.164

Significance at 5 % level; * Significance at 1 % level **

KL - Kernel length (mm), KB - Kernel breadth, KLAC - Kernel length after cooking (mm), KBAC - Kernel Breadth after cooking (mm), PRO - Seed Protein Content (mg/g), AMYL- Amylose content (mg/g), KLER - Kernel linear elongation ratio

Genotypic and phenotypic partial regression study

The path coefficient analysis was carried out to explain the direct and indirect influences of seven cooking and biochemical quality characteristics on kernel linear elongation ratio (KLER), a key factor determining rice quality. The rate of scale for partial regression coefficient direct and indirect effect suggested after (27). At the genotypic level (Table 7), the findings indicated that kernel length after cooking was a strong positive direct influence (1.335) on KLER, corroborating its significant positive correlation as it was seen in (28). This implies that genotypes with longer kernel length when cooked have a tendency to have greater KLER, which is a beneficial character in rice breeding programs. At phenotypic level kernel length (-0.707) and amylose content (-0.030) negatively influenced KLER directly, implying that these characteristics may have a negative effect on kernel elongation ratio. Kernel length also possessed a high positive indirect effect on KLER through kernel length after cooking (0.888), implying that the effect of kernel length on KLER is mediated by kernel length after cooking. On the other hand, kernel breadth possessed a high negative indirect effect (-0.493) on KLER through kernel length after cooking, implying that kernels with large breadths may have a negative effect on KLER. At the phenotypic level, the trends were also similar, kernel length after cooking exerting a significant positive direct effect (1.267) on KLER. The traits kernel breadth (0.022), kernel breadth after cooking (0.021) and seed protein (0.009) recorded minimal positive direct effects on KLER (29). Nevertheless, kernel length (-0.707) and amylose content (-0.030) exhibited minimal negative direct effects on KLER (Table 8). However, kernel length also exhibited very high positive indirect effect upon KLER through kernel length after cooking (KLAC-0.888) which indicates selection of KLAC leads to improvement of KLER under present investigation. The results of this study have important implications for breeding programs that seek to enhance rice quality traits. By knowing the direct and indirect effects of different traits on KLER, breeders can formulate specific selection strategies to improve favourable traits without detrimental effects on other traits. These findings are in line with earlier studies, which documented high correlation between cooked kernel length-to-breadth ratio and linear elongation ratio in rice (30). The incorporation of biochemical and cooking quality characteristics in present set of rice germplasm helps to explored, with its unique genetic variability; this has been

Table 7. Genotypic path coefficient analysis showing the direct (diagonal) and indirect (off-diagonal) effects of cooking quality and biochemical attributes in rice genotypes

Characters	KL	KB	KLAC	KBAC	PRO	AMYL	KLER
KL	**-0.711**	-0.006	0.888	-0.008	-0.001	0.004	0.166
KB	0.277	**0.015**	-0.493	0.008	0.001	0.007	-0.185
KLAC	-0.473	-0.006	**1.335**	-0.011	-0.002	-0.003	0.839**
KBAC	0.205	0.004	-0.533	**0.029**	0.001	0.006	-0.287*
PRO	0.127	0.001	-0.453	0.005	**0.007**	0.002	-0.311*
AMYL	0.087	-0.003	0.129	-0.006	0.000	**-0.031**	0.176

Residual effect: 0.016

Note: KL - Kernel length (mm), KB - Kernel breadth, KLAC - Kernel length after cooking (mm), KBAC - Kernel Breadth after cooking(mm), PRO - Seed Protein content (mg/g), AMYL - Amylose content (mg/g), KLER - Kernel elongation ratio

Table 8. Phenotypic path coefficient analysis showing the direct (diagonal) and indirect (off-diagonal) effects of cooking quality and biochemical attributes in rice genotypes

Characters	KL	KB	KLAC	KBAC	PRO	AMYL	KLER
KL	**-0.707**	-0.007	0.770	-0.005	-0.001	0.003	0.049
KB	0.222	**0.022**	-0.326	0.004	0.000	0.005	-0.078
KLAC	-0.431	-0.006	**1.267**	-0.007	-0.003	-0.003	0.816**
KBAC	0.180	0.004	-0.453	**0.021**	0.001	0.005	-0.241*
PRO	0.109	0.001	-0.411	0.003	**0.009**	0.002	-0.285*
AMYL	0.082	-0.004	0.119	-0.004	-0.001	**-0.030**	0.164

Residual effect: 0.0163

Note: KL - Kernel length (mm), KB - Kernel breadth, KLAC - Kernel length after cooking (mm), KBAC - Kernel Breadth after cooking(mm), PRO - Seed Protein content (mg/g), AMYL - Amylose content (mg/g), KLER - Kernel elongation ratio explored by this research by integrating biochemical markers such as amylose content with the cooking characteristics such as gelatinization temperature and kernel parameters. This integrative analysis maximizes breeding efficiency through the detection of trait correlations and valuable genotypes, as well as facilitating conservation and sustainable use of precious regional genetic resources. In contrast to studies on monogenic traits, this method goes beyond and aligning breeding efforts more closely with consumer preferences and regional specificity (31, 32). Emerging computing technologies now allow to Streamline intricate agricultural procedures, such as crop cultivation with cumulative data of genotypic, phenotypic and environmental characteristics, digital twins can simulate how rice genotypes behave under different climatic conditions, forecasting not just agronomic results but also techno-economic effects such as yield efficiency, energy consumption, processing quality and market value which reflect the whole value chain, from breeding and production to processing and commercialization which contributes to economic value creation in the whole eco-system of rice industry (33). It is pertinent to underscore that recent advancements in artificial intelligence have substantially improved our ability to estimate the impacts of emerging concepts and innovations within economy-specific contexts. Methodologically, these approaches mirror the rigorous trait-dissection strategies used in agricultural genomics; for instance, genetic variability and character-association analyses in rice breeding studies employ correlation and path-coefficient models to identify promising genotypes based on cooking quality traits.

Frequency distributing among rice genotypes for gelatinization temperature

Present study revealed substantial variation in gelatinization temperature (GT) amongst the rice genotypes, assessed through alkali spreading values (Fig. 8) as it was done in (23) GT significantly influences cooking and eating quality, associating with starch properties, particularly amylopectin structure. The genotypes were categorized into three GT groups: low, intermediate and high, based on alkali spreading scores (3-7). The majority (39 %) exhibited intermediate GT (score 5), including diverse cultivars like Kamalabhog and MTU1075. This prevalence suggests intermediate GT may represent an optimal balance between cooking time and texture, preferred by many consumers. Genotypes with score 6 (27 %) included landraces like Durgasal and Badshahbhog, known for aromatic and palatable properties. Combined, scores 5 and 6 represented 67 % of genotypes, highlighting intermediate GT's dominance. Low GT genotypes (scores 3-4) comprised 25 %, with improved varieties like Abita and IR36. Only Pusa Basmati exhibited extremely low GT (score 3), underscoring its rarity. High GT genotypes (score 7, 6 %) included Binni and Pokshali, requiring longer cooking times (Table 9).

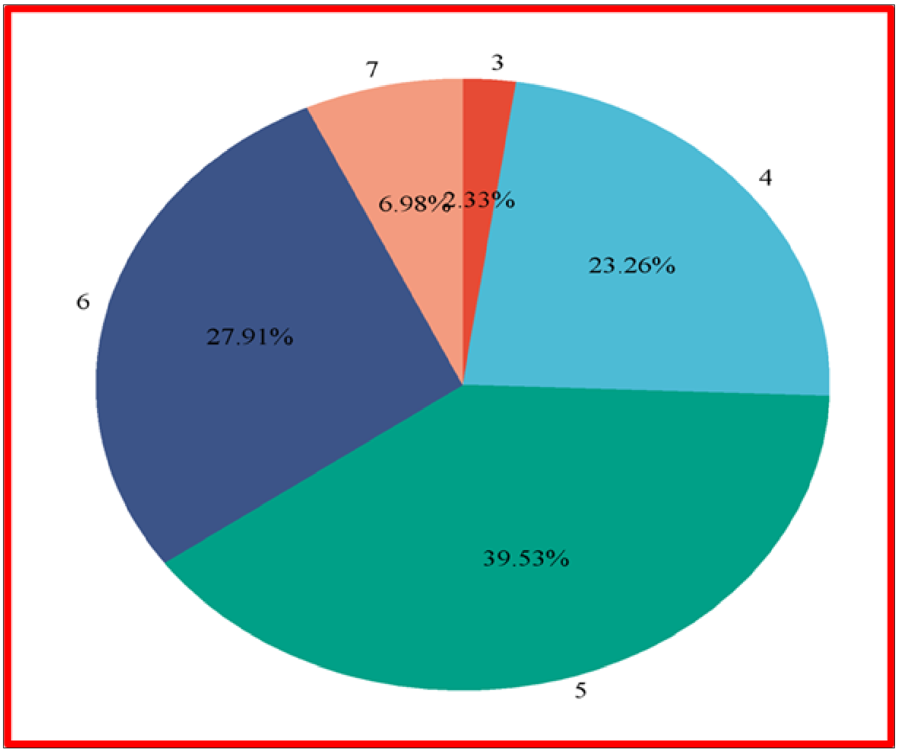

Fig. 8. Alkali spreading value rating for rice genotypes.

Table 9. Frequency distribution of rice genotypes for gelatinization temperature

Characteristics	State of Alkali spreading	Note	Genotypes	Frequency distribution (%)
Gelatinization temperature	Low	3	Pusa basmati	2
	Low	4	Abita, MTU1153, Bidhansuruchi, IR36, B1B3, Dhanurban, Swarna, POO7SD, IR64, MTU1010	23
	Intermediate	5	Kamalbhog, Vutmuri, Ratansal, Kataribhog, Tulai Panji, MTU1075, PRS101, Barsha, Babui, Sonalu, Pratiksha, Indrabam, Mugi, Ananya, Satabdi, Pooja, RNR 15048	40
	Intermediate	6	Durgasal, Sitasal, Malati, Badshahbhog, Sukumar, Gobindobhog, TN1, Kalma, Hathi Pajar, Santoshi, Kabirajsal, Dudheswar	28
	High	7	Binni, Pokshali, Kanakchur	7

Conclusion

Analysis of variance indicated significant differences among genotypes for various cooking and biochemical traits, reflecting genetic variability. Phenotypic coefficients of variation exceeded genotypic ones, suggesting environmental influence. Kernel length after cooking showed a strong positive correlation and direct effect on kernel linear elongation ratio. In contrast, kernel breadth after cooking and seed protein content were negatively correlated. Thus, selecting for kernel length after cooking may effectively enhance kernel linear elongation ratio. Additionally, research informs rice breeders by facilitating effective selection of improved genotypes with cooking quality attributing traits. Farmers, millers and consumers benefit from improved and consistent rice varieties, whereas policymakers can use these findings to encourage quality-improving cultivars that enhance food security and economic advancement.

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Authors' contributions

The research was conceptualized and designed by VKG. AD conducted the field experiments. VKG and AR evaluated the data. AD and VKG drafted the manuscript. AKB, RC, PM, NS, V and VK edited the manuscript. The findings of the final manuscript were discussed, read and approved by all the authors.

Compliance with ethical standards

Conflict of interest: The authors claim they are not aware of any conflicts of interest that would have seemed to have an impact on the work they described in this manuscript.

Ethical issues: None

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