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RESEARCH ARTICLE

Genetic variability and character association study on cooking quality attributing traits and DUS characters of rice genotypes in Southern Odisha

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Abstract

Rice (*Oryza sativa* L.) is a staple food crop of global importance, with grain quality traits playing a crucial role in consumer preference. Distinctness, Uniformity and Stability (DUS) testing, alongside the evaluation of cooking quality parameters to assess the extent of genetic variability and to determine character association study among cooking attributing traits. So, a study was conducted during the *Kharif* season (2024-25) at the Post Graduate Research Farm of Centurion University of Technology and Management, Odisha, to evaluate 45 rice genotypes for DUS and cooking quality traits using Randomised Complete Block Design with three replications. Analysis of variances revealed significant variance for kernel length, kernel length after cooking, seed protein content and amylose content. High heritability and high genetic advance as a percentage of the mean (GAM) were noted for all the characters, indicating the presence of additive gene action. Path coefficient analysis revealed that kernel length had the highest positive direct effect on kernel linear elongation ratio, while kernel length after cooking showed a very high negative effect. Positive correlations between kernel linear elongation ratio and seed protein content, amylose content and kernel length affirm their influence. Ketki Joha and Shilkote recorded with maximum kernel breadth and kernel breadth after cooking, respectively. Highest protein content exhibited by Bygon manjira, amylose content raised high for PB1886, kernel linear elongation ratio shown by Nefbi julsi. Kernel length and amylose content emerged as the pivotal, highly heritable traits defining rice cooking quality, offering clear prospects for breeding premium grain quality.

Keywords: analysis of variance; correlation; DUS test; kernel linear elongation ratio; path; rice

Introduction

Rice is classified in the genus *Oryza* (2n=24). It falls under the Poaceae family, which is a monocot crop plant and the *Oryzoideae* subfamily. The two species of rice that are cultivated today are *O. sativa*, cultivated in Asia and *O. Glaberrima*, cultivated in Africa, with the first being the most widely used. Rice is the cultivated rice plant classified into two primary subspecies: indica and japonica. Indica rice has long, thin grains and is mostly found growing in tropical and some sub-tropical areas. It is less sticky compared to japonica when cooked and is widely used in Southeast Asia and South Asia and in parts of Africa (1). Genetic characterisation would lead to a system that records and stores useful data that can easily be retrieved and shared with others, ultimately aiding in the planning of breeding programs (2). The DUS law is the core identification standard for a particular variety that declares it distinct from any other variety and gives a legal description that can be used at all levels of identification of varieties (3). Since most of the germplasm require evaluation for their valuable traits, these traits could be a great source of raw materials for the breeders to carry out their varietal improvement program (4).

Thus, the goal of the present study is the characterisation of varieties, especially farmers' varieties, traditional varieties and landraces, following the DUS criterion. Therefore, characterisation of 45 rice genotypes was carried out according to DUS guidelines. The rise in consumer demand for rice with quality standards means that consumer-preferred rice with the required grain properties fulfils the demand of the world. Rice grain quality is a multidimensional property covering all properties and traits of the grain (5). The quality trait of rice grain is a complex trait that encompasses all those properties and characteristics of rice or rice products that are in line with consumer needs and preferences. Qualities like viz. kernel length, kernel breadth, cooked kernel length, cooked kernel breadth, protein content (%) and amylose content (AC) are crucial in determining the cooking quality of rice considered under the present study. Earlier reports have studied genetic variability for the above quality traits, but there is still unexplored genetic variability in landraces that is of utmost importance in selecting potential parents to obtain maximum heterosis and superior recombinants concerning quality components (6).

Genetic parameters such as genotypic coefficient of variation and phenotypic coefficient of variation can very well help scrutinize the degree of variability in genotypes. On the other hand, heritability accompanied by high genetic advance helps one know the extent of the environment affecting genotype expression and, therefore, character reliability. Correlation can indicate how grain quality relates to its components (7). Therefore, the present experiment was carried out to evaluate the genetic variability, character associations and distinctness, uniformity and stability (DUS) characteristics of rice genotypes in Southern Odisha with special emphasis on cooking quality attributing traits.

Materials and Methods

Experimental site

The current research was conducted during the kharif season of 2024-2025, at the Post Graduate Research farm of M.S. Swaminathan School of Agriculture, Centurion University of Technology and Management (CUTM), Paralakhemundi, Odisha. The location of the station is at a longitude of 84.14195° E and latitude of 18.80027° N, with an altitude of 91 m above the mean sea level. The region in which the experiment was carried out comes under the north-eastern ghat zone of Odisha.

Experimental materials

Forty-five rice genotypes were obtained from Uttar Banga Krishi Vishwavidyalaya, Pundibari, Coochbehar, West Bengal. Table 1 presents a comprehensive list of the genotypes. The study was carried out over the kharif season of 2024. The experimental site soil is characterised by sandy loam texture, optimal drainage and pH of 6.3.

Experimental layout

A Randomised Block Design (RBD) experiment with three replications was carried out to evaluate 45 genotypes for DUS and cooking qualitative traits. Each plot measured 2 m ×1.5 m with a spacing between plots and plant to plant and row to row spacing were 15 cm and 20 cm, respectively. Nitrogen (N), phosphorus (P) and potassium (K) were applied at 60:40:40 kg acre$^{-1,}$ respectively. The entire dose of P and K, along with half of the N, was applied as a basal dose during land preparation. Twenty-fourths of the N was used as a second top dressing 22 days later. Intercultural operations and crop protection measures were implemented as needed.

Observation recorded

DUS characterisation was performed on fifteen randomly selected plants per genotype per replication. The flag leaf colour accounts for a variable phenotype, including a very visual assessment of flag leaf colours, which was determined by the visualisation of the uppermost leaf colour of the rice plant. Basal leaf sheath colour, found by the colour of the rice plant's sheath (the leaf base that encircles the stem), can vary among genotypes. Assessment of lemma and palea colour was carried out at the flowering stage, where these structures can be evaluated visually. While certain traditional or wild rice varieties possess awns that

Table 1. List of rice genotypes

Sr. No.	Name of genotype	Origin	Biological status
1	Br -I sub - II	Bihar	Elite line
2	Paro chakhao sail	Assam	Traditional cultivar
3	Aghani bora	Assam	Released variety
4	Kanchen foe	Assam	Traditional cultivar
5	Disha	Manipur	Elite line
6	Maniram	Others	Released variety
7	Mulga bhoru	Assam	Released variety
8	Dhan sail	Assam	Unknown
9	Banga bandhu red	Assam	Elite line
10	Godhi aki	Odisha	Landraces
11	Ranjit	Assam	Released variety
12	Bahadur	Assam	Released variety
13	Dhalamukh Sali	Unknown	Unknown
14	Nefbi julsi	Assam	Traditional cultivar
15	Diphalu	Assam	Released variety
16	Padum Sali	Assam	Traditional cultivar
17	Mallifulo	West Bengal	Released variety
18	PB 1886	Haryana	Released variety
19	PB 1121	Haryana	Released variety
20	Dehradun Gandheswari	West Bengal	Released variety
21	Shilkote	Unknown	Unknown
22	Gamraho	Unknown	Unknown
23	Jaldhyapa	West Bengal	Released variety
24	Jugal	West Bengal	Released variety
25	Lal basmati	Punjab	Released variety
26	Sial bhomra	Odisha	Released variety
27	Satyrajan	Assam	Released variety
28	Chakho sempak	Manipur	Elite line
29	Gopal bhog	West Bengal	Released variety
30	Pual Sali	Assam	Traditional cultivar
31	Moti saru	Assam	Landraces
32	Piolee	Unknown	Released variety
33	Banga bandhu White	Assam	Elite line
34	Jalkwari	Assam	Released variety
35	Mouriphourin Knganhi	Manipur	Elite line
36	Ketki joha	Assam	Released variety
37	Shanti bhog	Assam	Elite line
38	Hati Sali	Assam	Traditional cultivar
39	Badsha bhog	West Bengal	Elite line
40	Sitabhog	West Bengal	Elite line
41	Kalamani Sali	Odisha	Released variety
42	Kati Sali	Assam	Landraces
43	Bygonmanjira	West Bengal	West Bengal
44	RNR 15048	Telangana	Released variety
45	Pooja	Odisha	Released variety

aid seed dispersal, almost every high-yield, modified version lacks the feature, even at the expense of the end-quality rice harvested being awnless. Fragrance-based aroma concentrations were classified into three levels: mild, medium and strong. Gelatinisation temperature reflects the point at which starch granules absorb water, swell and lose crystallinity during cooking and is classified as low, low intermediate, intermediate or high. The alkali spreading value (ASV) of whole kernel milled rice, when treated with dilute alkali, indicates the starch gelatinisation temperature, which is partially influenced by amylose content (8). Protein content was estimated using the method, which involves the reaction of protein with Folin-Ciocalteu reagent (9). Absorbance was measured at 660 nm using a spectrophotometer with bovine serum albumin as the standard. Amylose content was determined using an ethanol-NaOH extraction followed by iodine colorimetry, with absorbance measured at 720 nm using a spectrophotometer. Samples were classified as waxy, very low, low, intermediate or high based on a standard curve corresponding to 1 %-30 % amylose content. Kernel length and kernel breadth, as well as kernel length after cooking and kernel breadth after cooking, were measured using vernier callipers (10). All measurements were recorded in millimetres (mm). The kernel linear elongation ratio was calculated by dividing the kernel length after cooking by the kernel length before cooking. Cooking quality characters were assessed by randomly selecting ten plants from each plot in every replication. Grains from the selected plants were bulked and observations were recorded on twenty grains sampled from the composite lot.

Statistical analysis

A randomised block design was used to analyse the average data from three replications, enabling the determination of significant variance among genotypes in field conditions. Frequency distribution for all the characters was computed and presented in Table 2. The variance analysis and test of significance were calculated as per the method after (11). The magnitude of GCV and PCV values was characterised as low (less than 10 %), moderate (10 %-20 %) and high (more than 20 %) (12). Heritability was estimated and they classified the heritability as low (below 30 %), moderate (30 %-60 %) and high (more than 60 %), range of genetic advance as percent of the mean was classified as low (<10 %), moderate (10 %-20 %) and high (>20 %) (13). A range of paths was carried out as suggested after (14). Statistical computations were carried out using the WINDOSTAT version 9.3 package.

Results and Discussion

DUS characterization

Flag leaf colour has shown that 43 genotypes were green, while 3 genotypes are yellowish (Fig. 1). Basal leaf sheath exhibited 43 genotypes are green in colour and the purple line represents 3 genotypes (Fig. 2). Lemma and palea exhibited gold and gold furrows and on a straw background by 39 genotypes, while 3 genotypes showed brown spots on straw, while black straw by 3 genotypes showed black straw (Fig. 3). Awn was present in 6 genotypes and absent in 39 genotypes (Fig. 4). 20 genotypes were exhibited with mild aroma, whereas, 19 genotypes were found with medium and 2 genotypes revealed presence of high aroma (Fig. 5). Based on ASV values, gelatinization temperature performed low-alkali digestion are 18 genotypes and intermediate -alkali digestion are 25 genotypes (Fig. 6). Earlier study reported for yield and quality attributing traits found with significant morphological variation (15).

Agro-morphological characterisation of rice genotypes

Similar results were also observed, with green being the colour of the basal leaf sheath in 36 genotypes (16). The traits lemma and palea have exhibited 17 % landraces were straw colour, 3 % landraces had golden lemma and palea with golden furrows on straw background, 15 % landraces had observed with brown furrows on straw, whereas 22 % of landraces were brown colour, 13 % of landraces were blackish purple in colour. The presence of awn was recorded in some of these landraces (17). Awns were present in 12 % of the landraces, while lemma and palea colour

Table 2. Frequency distribution for DUS characterisation

Sr. No.	Characteristics	States	Note	Number of genotypes	Frequency distribution (%)
1	Flag leaf colour	Green	1	1,2,3,4,5,6,7,9,10,11,12,13,14,15,16,17,18,19,21,22,23,25,26,27,28,29,30,31,32,33,34,35,36,37,38,39,40,41,42,43,44,45	95.5
		Yellowish	2	8,20,24	6.6
2	Basal leaf sheath colour	Green	1	1,2,3,4,5,6,7,8,9,11,12,13,14,15,16,17,18,19,20,21,22,23,24,26,27,28,29,30,31,32,33,34,35,36,37,38,39,40,41,42,43,44,45	95.5
		Purple line	2	10,25,30	6.6
3	Lemma and palea colour	Gold and gold furrows on a straw background	1	1,2,3,5,6,8,9,11,12,13,14,15,16,17,18,19,20,21,22,23,24,25,27,29,30,32,33,34,35,37,38,39,40,41,42,43,44,45	86.6
		Brown spot on straw	2	4,7,26	6.6
		Black straw	3	36,28,10	6.6
4	Awn in panicle	Absent	1	1,2,3,4,5,6,7,8,9,10,11,12,13,14,15,16,17,20,21,22,23,25,26,27,29,30,31,32,33,34,35,39,40,41,42,43,44,45	86.6
		Present	2	18,19,25,28,36,38	13.3
5	Aroma	Mild	1	1,11,21,22,23,24,25,26,27,28,29,36,37,38,39,40,44,45	44.2
		Medium	2	2,3,4,5,6,7,8,9,10,12,13,14,16,30,31,32,33,34,35	42.2
		strong	3	41,42,43,17,18,19	13.3
6	Gelatinization temperature	Low alkali digestion	1	1,2,3,13,14,19,21,22,23,24,28,29,32,35,37,38,41,43	40
		Intermediate alkali digestion	2	4,5,6,7,8,9,10,11,12,15,16,17,18,25,26,30,31,44,45,33,34,36,39,40,42	55.5
		High alkali digestion	3	20,27	4.4

Note: The number of the genotype names is as mentioned in Table 1.

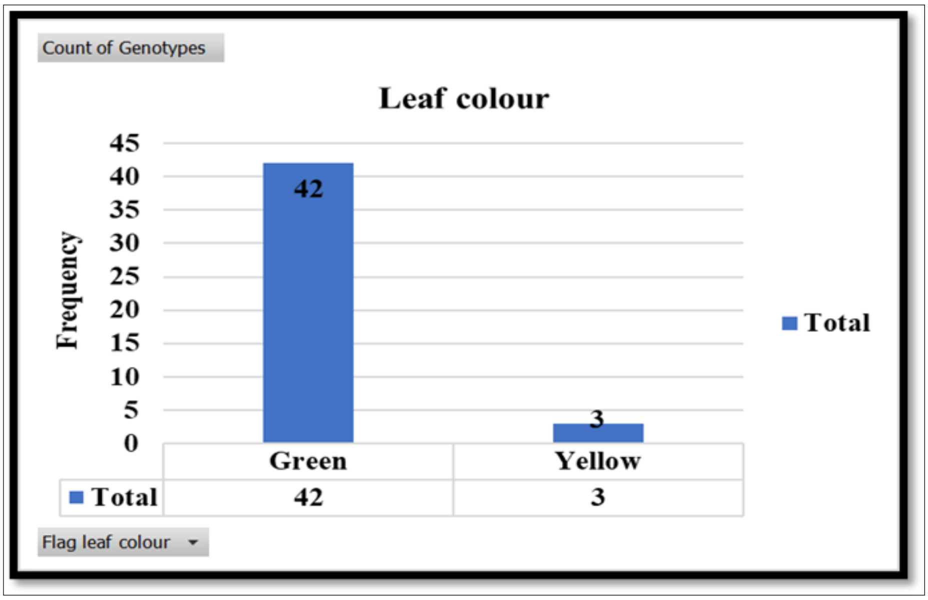

Fig. 1. Leaf colour of rice genotypes.

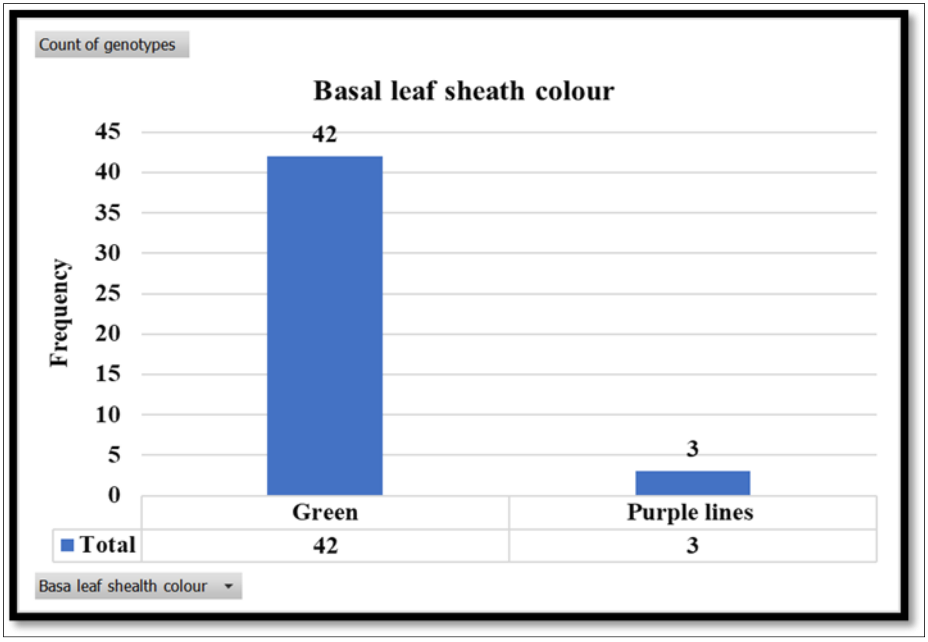

Fig. 2. Basal leaf sheath colour of rice genotypes.

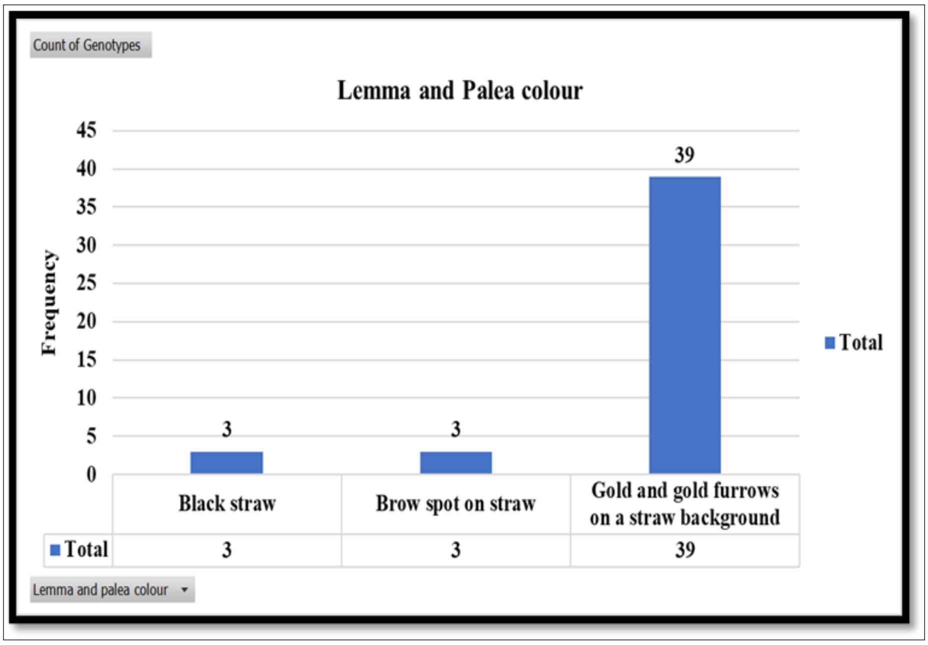

Fig. 3. Lemma and palea colour of rice genotypes.

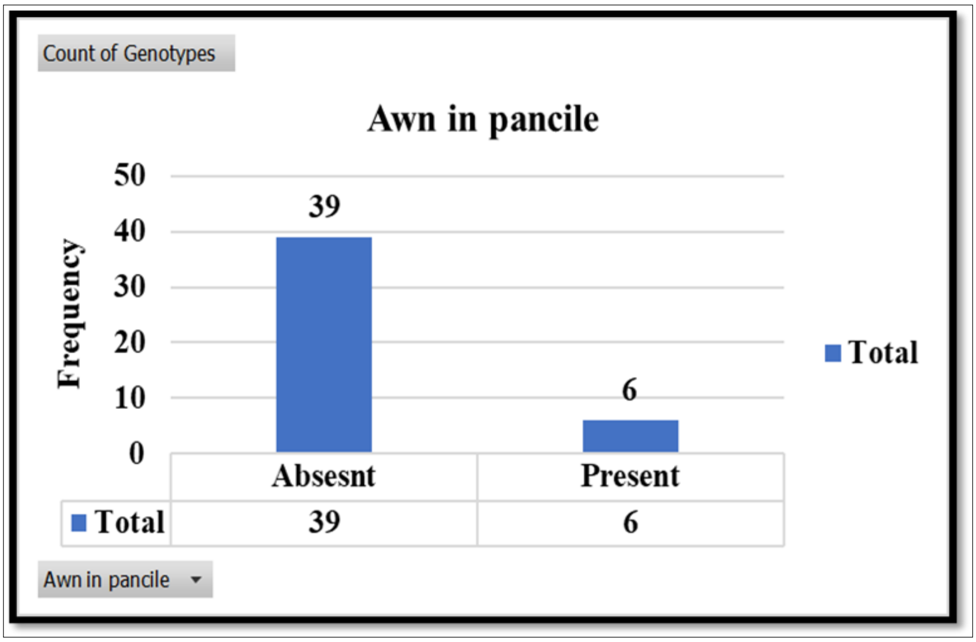

Fig. 4. Awn in panicle in rice genotypes.

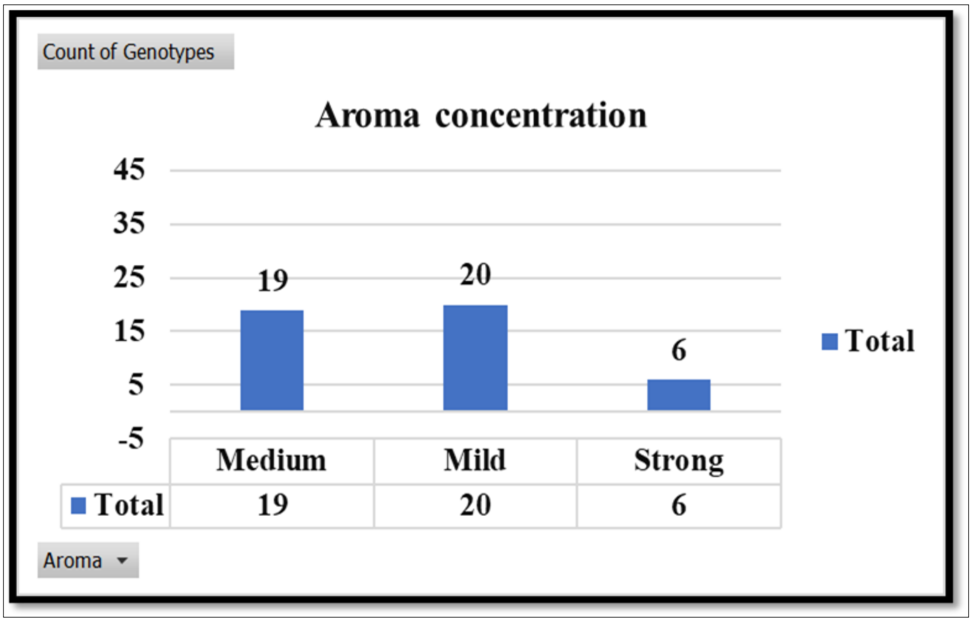

Fig. 5. Aroma concentration in rice genotypes.

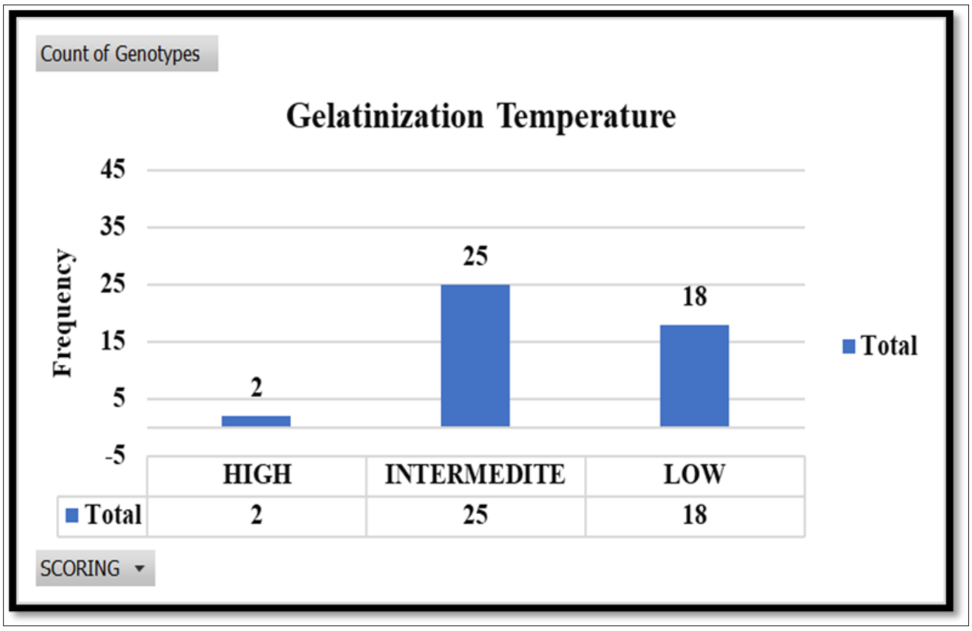

Fig. 6. Gelatinisation temperature of rice genotypes.

exhibited in maximum number of expression states, ranking ninth among the recorded traits (18). Out of 25 studied landraces, 71.50 % had green basal leaf sheath, 12.51 % had green with purple line, 12 % had light purple and 3.94 % had purple. DUS characterisation on rice landraces revealed that 60 % of landraces had awnless. However, 40 % of the studied landraces were found with partly awned (19). Decorticated grain aroma of the varieties studied showed distinct categories into classes of low, medium and high aroma (20). The study report gelatinisation temperature measured by alkali spreading value with low frequency of entries 12, medium frequency of entries 90 and high frequency of entries 83 (21). An earlier study on weedy rice based on agro-morphological traits and DUS characterisation explored the existence of variation for the crop improvement programme (22).

Genetic variability Study

Analysis of variance revealed significant genetic variability for most traits, including kernel length, kernel length after cooking, seed protein content and amylose content, which are important for grain quality improvement (Table 3). Similar finding was reported for analysis of variance results using the following treatment exhibited a significant difference at 5 % in the traits, which are kernel length (0.932), kernel breadth (0.052), kernel length after cooking (1.811), kernel breadth after cooking (0.313), for quality traits in rice (23). The genotypes differ significantly at a 5 % level in the characters, namely, kernel length (0.444), Kernel length after cooking (0.817), kernel breadth after cooking (0.122), kernel linear elongation ratio (0.009) (24). Research indicates that wide genetic diversity in starch physicochemical parameters, such as apparent amylose content (25). The present investigation means performance of cooking quality and biochemical parameters of rice study revealed that kernel length showed the highest mean for PB1121 (8.96), while Ketki Joha exhibited the lowest (2.52). Kernel breadth exhibited high values for Ketki Joha (3.56) and also performed low by RNR 15048 (1.63). Kernel length after cooking was raised the highest by PB1121 (11.07) and Bygon Manjira (4.67) exhibited the lowest. Kernel breadth after cooking exhibited the highest by Shilkote (3.17) and lowest by dish (1.84). The highest protein content was exhibited by Bygon manjira (8.24), while Jaldhyapa (2.45) expressed the lowest. Amylose content was raised highly for PB1886 (20.46) also lowered by Dehradun Gandheswari (5.61). The kernel linear elongation ratio is the highest value shown by Nefbi Julsi (1.29), while Ketki Joha (0.41) exhibited the lowest value (Table 4).

The present study revealed exceptionally high heritability for kernel length (94.70 %), kernel breadth (89.70 %), kernel length after cooking (91.90 %), kernel breadth after cooking (87.00 %), seed protein content (97.60 %), amylose content (96.90 %) and kernel linear elongation ratio (85.10 %), alongside higher phenotypic coefficient of variance (PCV) over genotypic coefficients of variation (GCV) noted for all these traits indicates presence environmental influences upon these traits. These parameters were paired with a high genetic advance as percentage of mean (GAM) for (63.58 %) seed protein content and (63.58 %) for amylose content, kernel length (40.08 %) and kernel length after cooking (36.81 %) presented in Table 5. Additive gene action occurs when alleles at a locus contribute equally and cumulatively to a phenotype, resulting in a continuous range of trait expression. Traits governed by additive gene action are ideal targets for direct selection and breeding, as their genetic improvement is predictable and cumulative across the generations (26). In confirmation with the present study, earlier reported in traditional scented rice characters viz. protein content, amylose content and kernel elongation ratio, revealed additive gene action due to high heritability and genetic advance as percentage of mean (27).

Earlier report in confirmation with present investigation revealed kernel length after cooking, kernel breadth after cooking and amylose content exhibited high heritability coupled with moderate to high genetic advance as percentage of mean indicates predominance of additive gene action (28). The characters such as kernel length, kernel breadth, L/B ratio, water uptake, amylose content, elongation ratio had generally low to moderate estimates for phenotypic coefficient of variation as well as genotypic coefficient of variation, high heritability and low to high estimates of genetic advance pointing out that these traits can be improved through combined exploitation of both additive and nonadditive components by employing breeding procedures like biparental mating, diallel selective mating system (29). High heritability in kernel length, kernel breadth and kernel length after cooking coupled with moderate genetic advance, which suggests that controlling these traits involves additive gene action (30).

Character association study

The correlation matrix exhibited highly significant positive associations at both genotypic and phenotypic correlation level shown in Fig. 7-8. kernel linear elongation ratio revealed significant positive correlation with kernel length ($r_g = 0.417$; $r_p = 0.393$), seed protein content ($r_g = 0.237$; $r_p = 0.199$) on the contrary, significant negative correlations were observed for kernel breadth ($r_g = -0.287$; $r_p = -0.229$), kernel length after cooking ($r_g = -0.287$; $r_p = -0.272$). Kernel length recorded a highly significant positive correlation with kernel length after cooking ($r_g = 0.765$; $r_p = 0.729$) while significant negative associations were observed with kernel breadth ($r_g = -0.596$; $r_p = -0.555$) and kernel breadth after cooking ($r_g = -0.277$; $r_p = -0.262$). The trait kernel breadth was significantly and positively correlated with kernel breadth after

Table 3. Analysis of variance for different characters in rice genotypes

Source of variance	Replication	Genotype	Error
Degree of freedom	(r-1) = 2	(g-1) = 44	(r-1) (g-1) =88
Kernel length (mm)	2.07	3.77*	0.07
Kernel Breadth (mm)	0.57	0.37	0.01
Kernel length after cooking (mm)	4.67**	4.88**	0.14
Kernel breadth after cooking (mm)	0.86	0.31	0.01
Seed protein content (%)	2.70**	8.67**	0.07
Amylose content (%)	19.00**	55.35**	0.59
Kernel linear elongation ratio	0.0004	0.05	0.002

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

Table 4. Mean performance of rice genotypes with respect to cooking quality attributing characters

Genotypes	KL	KB	KLAC	KBAC	PRO	AMYL	KLER
Br -I sub - II	5.34	2.51	6.30	2.56	3.84	13.52	0.85
Paro chakhao sail	3.75	2.73	4.74	2.58	4.64	6.69	0.79
Aghani bora	4.35	1.88	6.54	1.98	5.92	6.93	0.70
Kanchen foe	5.58	2.47	5.90	2.48	3.29	8.92	0.95
Disha	6.24	1.95	7.06	1.84	4.86	5.86	0.88
Maniram	4.97	2.57	5.35	2.52	3.68	8.02	0.93
Mulga bhoru	5.37	2.38	6.01	2.10	6.58	17.76	0.90
Dhan sail	5.26	2.37	5.69	2.40	6.65	20.31	0.92
Banga bandhu red	5.35	2.47	5.48	2.48	4.35	9.99	0.98
Godhi aki	6.34	2.35	6.21	2.19	3.76	17.29	1.02
Ranjit	5.53	2.26	5.88	2.29	7.69	12.79	0.94
Bahadur	5.63	2.47	6.21	2.78	6.93	21.77	0.91
Dhalamukh Sali	3.85	2.65	4.75	2.65	6.75	20.17	0.81
Nefbi julsi	6.30	2.62	4.86	2.92	7.62	19.88	1.29
Diphalu	5.46	2.16	6.49	2.77	6.94	13.10	0.84
Padum Sali	6.01	2.48	6.93	2.99	6.91	12.99	0.87
Mallifulo	8.13	1.93	8.70	2.26	5.46	10.88	0.93
PB 1886	7.87	1.77	9.94	1.88	8.03	20.46	0.79
PB 1121	8.96	1.96	11.07	2.02	7.70	8.99	0.81
Dehradun Gandheswari	5.83	2.41	6.77	2.83	7.37	5.61	0.86
Shilkote	5.47	2.78	7.44	3.17	4.06	14.64	0.74
Gamraho	5.16	2.45	7.60	2.66	6.31	8.57	0.68
Jaldhyapa	5.71	2.91	7.48	3.00	2.45	11.89	0.77
Jugal	5.50	2.87	7.35	2.90	4.82	12.57	0.75
Lal basmati	6.90	1.72	8.33	2.73	3.88	14.32	0.83
Sial bhomra	5.46	2.29	6.80	2.63	6.61	17.40	0.80
Satyrajan	5.41	2.04	6.39	2.39	5.35	17.06	0.84
Chakhao sempak	5.73	2.35	6.20	2.22	3.93	14.59	0.93
Gopal bhog	4.97	2.23	6.93	2.35	5.29	14.31	0.72
Pual Sali	5.20	2.57	6.98	2.90	6.99	12.93	0.75
Moti saru	5.74	2.50	7.09	2.46	3.82	7.98	0.81
Piolee	5.52	2.16	6.68	2.55	9.79	8.76	0.83
Banga bandhu White	5.01	2.53	7.00	2.66	3.35	9.08	0.72
Jalkwari	5.48	2.58	6.99	2.68	4.36	18.03	0.78
Mouriphourin Knganhi	5.52	2.33	6.39	2.49	3.84	17.30	0.87
Ketki joha	2.52	3.56	6.22	2.69	3.70	18.38	0.41
Shanti bhog	5.56	2.17	6.15	2.22	5.94	13.87	0.91
Hati Sali	5.26	2.57	6.64	2.79	3.90	16.59	0.79
Badsabhog	4.64	2.31	5.99	2.33	5.74	15.39	0.78
Sitabhog	7.87	2.25	9.02	2.63	4.94	13.51	0.87
Kalamula Sali	5.48	2.58	8.39	2.84	2.89	18.48	0.66
Kati Sali	4.98	2.91	6.02	2.77	4.85	13.87	0.83
Bygon manjira	3.83	2.64	4.67	2.86	8.24	13.56	0.82
RNR 15048 (c)	5.41	1.63	7.03	1.93	3.54	14.38	0.77
Pooja (c)	5.68	2.23	6.63	2.28	6.36	13.63	0.86
Mean	5.56	2.39	6.74	2.52	5.42	13.62	0.83
C.V.	4.73	4.91	5.54	4.82	4.90	5.64	5.60
S.E.M	0.15	0.07	0.22	0.07	0.15	0.44	0.03
C.D. (5 %)	0.43	0.19	0.61	0.20	0.43	1.25	0.08
C.D. (1 %)	0.56	0.25	0.80	0.26	0.57	1.65	0.10

C - check genotypes, KL - Kernel length (mm), KB - Kernel breadth, KLAC - Kernel length after cooking (mm), KBAC - Kernel Breadth after cooking (mm), KER - Kernel linear elongation ratio, PRO - Seed protein content (%), AMYL - Amylose content (%)

Table 5. Studies on different genetic parameters for cooking quality attributing traits in rice genotypes

Sr. No.	Characters	Grand mean	Range		Coefficient of variation		Heritability (Broad sense) (%)	Genetic advance	Genetic advance as a % of the mean (%)
			Minimum	Maximum	GCV (%)	PCV (%)			
1	Kernel length (mm)	5.55	2.51	8.95	19.99	20.54	94.70	2.22	40.08
2	Kernel breadth (mm)	2.39	1.63	3.56	14.51	15.31	89.70	0.67	28.31
3	Kernel length after cooking (mm)	6.74	4.66	11.07	18.64	19.44	91.90	2.48	36.81
4	Kernel breadth after cooking (mm)	2.52	1.84	3.17	12.48	13.38	87.00	0.60	23.99
5	Seed protein content (%)	5.42	2.44	9.78	31.24	31.62	97.60	3.44	63.58
6	Amylose content (%)	13.62	5.61	21.76	31.36	31.86	96.90	8.66	63.58
7	Kernel linear elongation ratio	0.833	0.40	1.29	14.65	15.87	85.10	0.23	27.86

PCV: Phenotypic coefficient of variation; GCV: Genotypic coefficient of variation

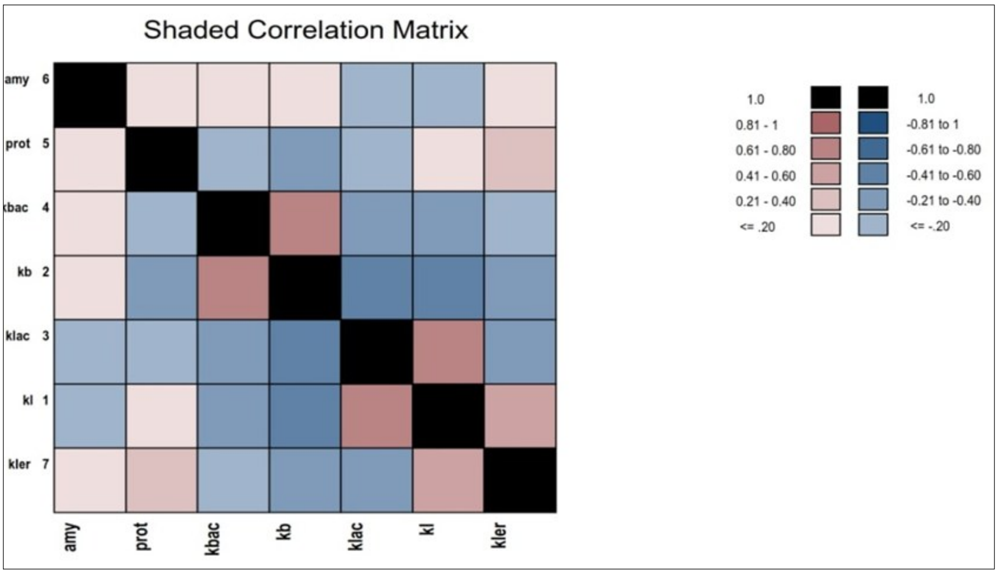

Fig. 7. Genotypic shaded correlation matrix for cooking quality attributing traits in rice.

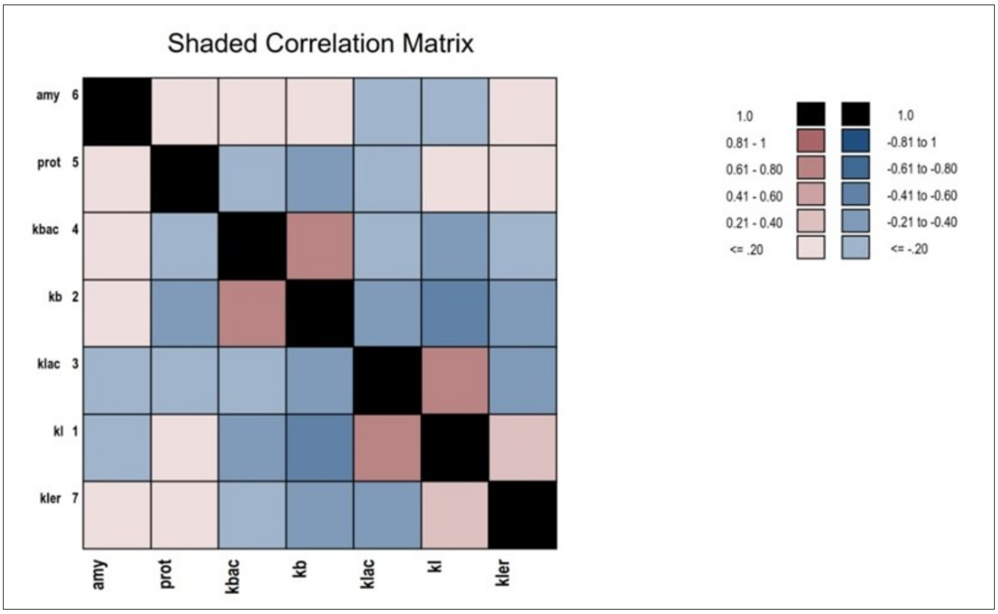

Fig. 8. Phenotypic shaded correlation matrix for cooking quality attributing traits in rice.

cooking (r_g= 0.690; r_p= 0.606), while kernel length after cooking (r_g= - 0.417; r_p = -0.381), seed protein content (r_g= -0.263; r_p= -0. 259), this was a significant and negative association. The character kernel length after cooking exhibited this was a significant and negative association with kernel breadth after cooking (-0.200). The trait seed protein content was significantly and positively correlated with kernel linear elongation ratio (r_g= 0.237; r_p = 0.199) presented in Table 6. This indicates that any selection for kernel length after cooking would also improve the linear elongation ratio, in the shaded matrix in yet this would negatively impact kernel breadth after cooking, which is desirable for improving these quality traits. This was in agreement with the results of

Table 6. Studies on genotypic and phenotypic correlation between cooking quality and biochemical character in rice genotypes

Characters		KB	KLAC	KBAC	PRO	AMYL	KLER
KL	G	-0.596**	0.765**	-0.277**	0.145	-0.048	0.417**
	P	-0.555**	0.729**	-0.262**	0.137	-0.054	0.393**
KB	G		-0.417**	0.690**	-0.263**	0.13	-0.287**
	P		-0.381**	0.606**	-0.259**	0.124	-0.229**
KLAC	G			-0.200*	-0.010	-0.088	-0.287**
	P			-0.161	-0.007	-0.079	-0.272**
KBAC	G				-0.083	0.119	-0.105
	P				-0.081	0.109	-0.114
PRO	G					0.065	0.237**
	P					0.066	0.199*
AMYL	G						0.075
	P						0.060

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 (%), AMYL - Amylose content (%), KLER - Kernel linear elongation ratio.

kernel length depicts a significant positive association with the L:B ratio (r_p= 0.691; r_g= 0.710), with kernel length after cooking (r_p= 0.596; r_g= 0.641). Kernel breadth had a significant negative association with the L:B ratio (31). Study revealed kernel breadth after cooking has been carried out in a very excellent way and is found to have a strong positive correlation with kernel expansion ratio, but is found with a highly significant negative correlation with kernel length after cooking and kernel L:B ratio. A significant negative association exists between kernel length after cooking and kernel L:B ratio. A significant positive association between kernel linear elongation and kernel length after cooking was observed (32).

Path coefficient analysis

The partial regression analysis study revealed that the residual effect within a statistically permissible range (Genotypic: 0.364 and Phenotypic: 0.427) presented in Fig. 9-10, respectively. At the genotypic level, kernel length exhibited the highest positive direct effect on kernel linear elongation ratio (1.555) and a significant positive correlation (r_g= 0.417), confirming its pivotal role in determining kernel linear elongation ratio. Phenotypically, it also showed the highest direct effect (1.275) with a positive and significant correlation (r_p = 0.393). This means that selecting for increased kernel length will directly and substantially improve the kernel linear elongation ratio. Kernel breadth revealed a negligible positive direct effect upon KLER (0.007) at the genotypic level. The same was also observed with a negligible positive direct effect with KLER, which also exhibited significant negative correlation with KLER at both genotypic (r_g= -0.287) and phenotypic (r_p= -0.229) levels. Kernel length after cooking has revealed a negative direct effect on KLER at both the genotypic (-1.469) and phenotypic (-1.191) level, which also observed significant negative correlation with KLER at both genotypic (r_g= -0.287) and phenotypic level (r_p= -0.272). Kernel breadth after cooking had a genotypically negligible positive direct effect on kernel linear elongation ratio (0.024). Seed protein had revealed a negligible negative direct effect upon KLER (-0.002) at the genotypic level and exhibited a negligible positive direct effect upon KLER (0.019) at the phenotypic level. The same character also showed a significant positive association with KLER at both the genotypic (r_g= 0.237) and phenotypic (r_p= 0.199) level. Amylose content, on the other hand, revealed a negligible positive direct effect of 0.017 at the genotypic and 0.030 at the phenotypic level. While kernel length revealed a very high negative direct effect via kernel length after cooking (-1.125) on KLER at the genotypic level and the same has been observed at the phenotypic level (-0.870). Kernel breadth exhibited a positive direct effect upon KLER via kernel length after cooking at genotypic (0.612) and phenotypic level (0.455) presented in Table 7, which indicates that improving these indirectly attributing characters will lead to improvement of grain cooking quality of rice. The direct path coefficient quantifies the unmediated effect of an independent variable on the dependent variable, controlling for other variables. The path coefficient studies showed that kernel length after cooking exerts a significant, positive direct effect on grain yield, where the kernel linear elongation ratio also adds to such improvement. Water uptake ratio also exerts a direct positive effect (33). Path analysis study revealed length-breadth ratio of cooked kernels had a significant positive correlation with linear elongation ratio, whereas kernel breadth after cooking had a significant negative correlation with linear elongation ratio (34). Path analysis study revealed that kernel length, alkali spreading value and elongation ratio had a significant positive direct effect on amylose content (35). A study on short-grain aromatic rice genotypes revealed that negative and direct effects were found for amylose content, kernel length after cooking, kernel breadth after cooking and L/B ratio of the cooked kernel.

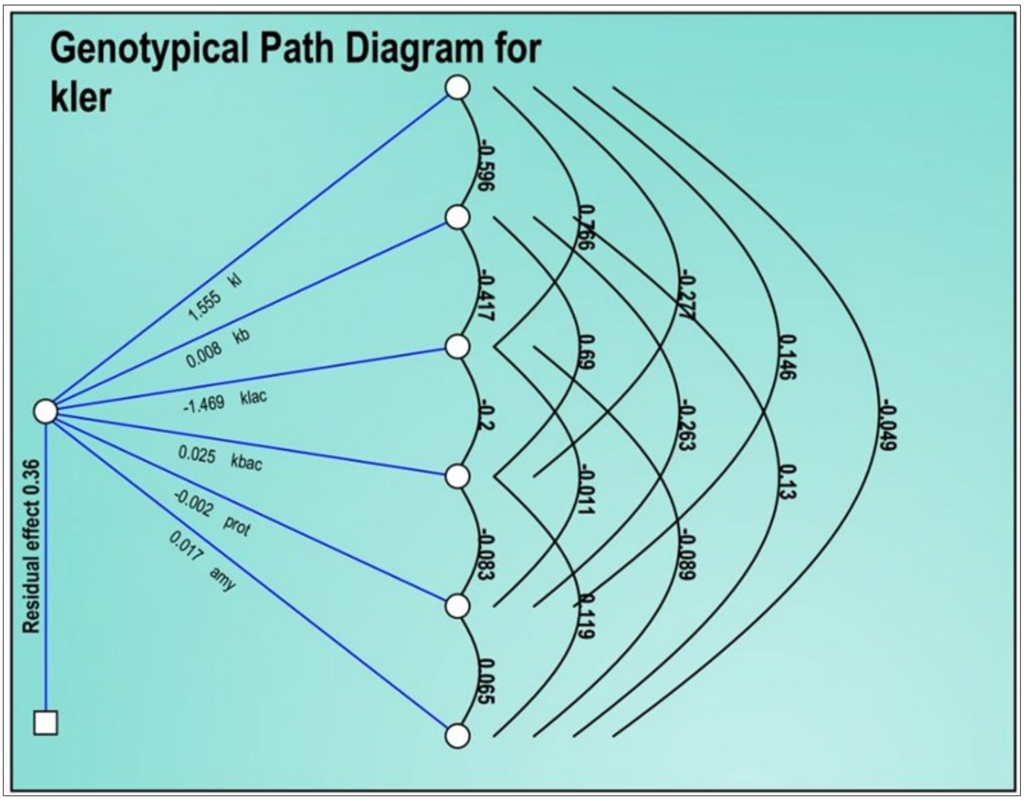

Fig. 9. Genotypic partial regression study of cooking quality attributing traits in rice.

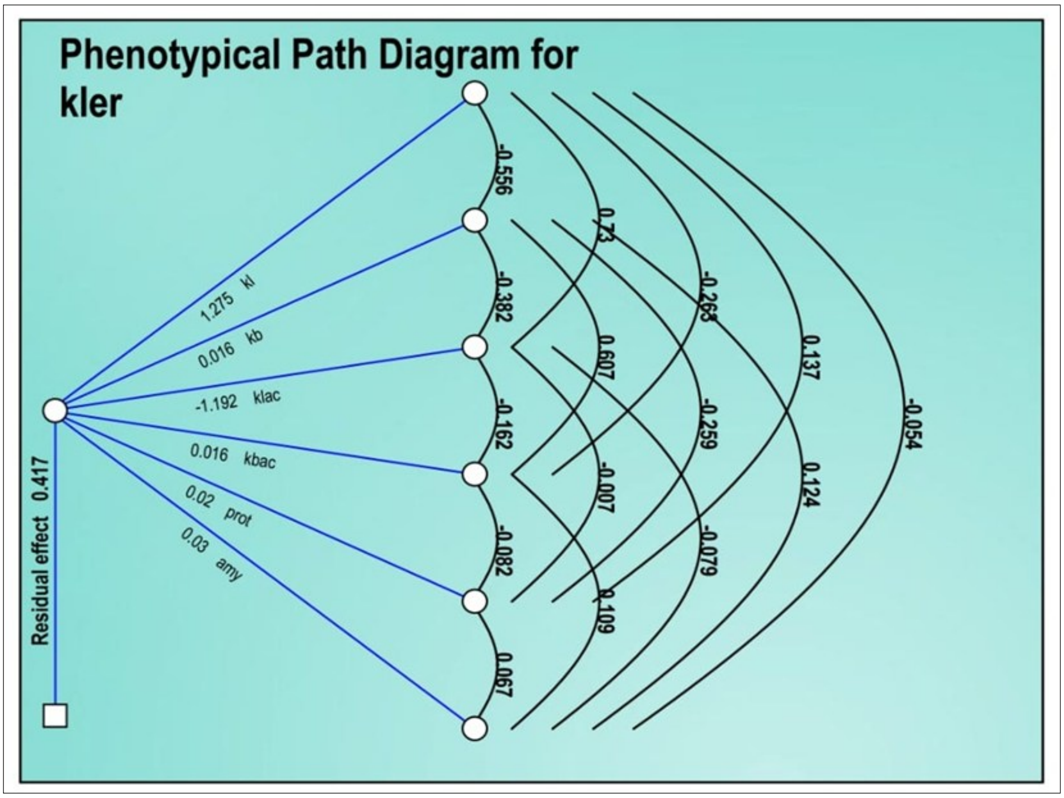

Fig. 10. Phenotypic partial regression study of cooking quality attributing traits in rice.

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

Characters		KL	KB	KLAC	KBAC	PRO	AMYL	KLER
KL	G	**1.555**	-0.004	-1.125	-0.006	-0.0003	-0.0008	0.417**
	P	**1.275**	-0.009	-0.87	-0.004	0.002	-0.001	0.393**
KB	G	-0.927	**0.007**	0.612	0.017	0.0006	0.002	-0.287**
	P	-0.708	**0.016**	0.455	0.009	-0.005	0.003	-0.229**
KLAC	G	1.191	-0.003	**-1.469**	-0.005	0.0001	-0.001	-0.287**
	P	0.930	-0.006	**-1.191**	-0.002	-0.0001	-0.002	-0.272**
KBAC	G	-0.431	0.005	0.294	**0.024**	0.0002	0.002	-0.104
	P	-0.335	0.01	0.192	**0.015**	-0.001	0.003	-0.114
PRO	G	0.226	-0.002	0.015	-0.002	**-0.002**	0.001	0.237**
	P	0.175	-0.004	0.008	-0.001	**0.019**	0.002	0.199
AMYL	G	-0.076	0.001	0.130	0.003	-0.0001	**0.017**	0.075
	P	-0.069	0.002	0.094	0.001	0.001	**0.030**	0.060

Genotypic Residual effect: 0.364; Phenotypic Residual effect: 0.427; KL - Kernel length (mm), KB - Kernel breadth, KLAC - Kernel length after cooking (mm), KBAC - Kernel Breadth after cooking (mm), PRO - Seed Protein content (%), AMYL - Amylose content (%), KLER - Kernel linear elongation ratio G, - Genotype, P- Phenotype

Conclusion

The analysis of variance revealed significant differences. Mean performance indicates kernel length, kernel length after cooking shows the highest by PB1121, PB1886 and Sitabhog. Highest protein content exhibited by Bygon manjira, amylose content raised high for PB1886, kernel linear elongation ratio shown by Nefbi julsi. High heritability coupled with high genetic advance as a percentage of the mean signifies additive gene action. Character association study showed kernel length, kernel breadth, kernel length after cooking and seed protein content exhibited significant positive correlation in both genotypic and phenotypic levels. The partial regression analysis emphasised that kernel length revealed the highest positive direct effect on kernel linear elongation ratio (KLER). Future research can prioritise kernel length, seed protein and amylose content as stable selection indices for quality improvement, supported by molecular tools mediated hybridisation programme between Bygon manjira and Nefbi julsi with PB 1886 and Sitabhog respectively for superior transgressive segregants. Multi-environment validation will be crucial to ensure consistency of these traits in diverse agro-ecological conditions.

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Authors' contributions

AR conceptualised and designed the research, supervised the work and finalised the manuscript. MNPS conducted the field experiments and contributed to drafting the initial manuscript.

GKD evaluated the data and contributed to editing the manuscript. SR performed data evaluation and provided critical comments during revision. VKG assisted in the evaluation of data and interpretation of results. EH revised and edited the manuscript for technical accuracy. PM contributed to improving the structure, language and logical flow of the manuscript. All authors discussed the findings and approved the final version of the manuscript.

Compliance with ethical standards

Conflict of interest: The authors declare they have no conflict of interest to declare.

Ethical issues: None

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