PLANT SCIENCE TODAY
Vol 13(sp1): 01–07
https://doi.org/10.14719/pst.11755

eISSN 2348-1900

RESEARCH ARTICLE

Genetic analysis and trait associations for yield and quality in the BC_2F_3 generation of rice (*Oryza sativa* L.)

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Received: 12 September 2025; Accepted: 11 December 2025; Available online: Version 1.0: 03 February 2026

Cite this article: Kadthala B, Sreedhar M, Jhansi LV, Ramya R, Parimala K, Pushpavalli SNCVL, Vanisri S. Genetic analysis and trait associations for yield and quality in the BC_2F_3 generation of rice (*Oryza sativa* L.). Plant Science Today. 2026;13(sp1):01–07. https://doi.org/10.14719/pst.11755

Abstract

This study evaluated genetic variation, heritability, genetic advance and trait relationships among yield, yield-related attributes and physical grain quality characteristics in 56 BC_2F_3 progenies derived from a cross between Telangana Sona (TS) and an Assam landrace 10-3. The lines carrying the brown planthopper (BPH) resistance QTL *qbph-1-1* were assessed along with parents and two high-yielding checks (KNM 1638 and JGL 3844) in an alpha lattice design at Regional Sugarcane and Rice Research Station (RR & RRS), Rudrur, Nizamabad, during the Rabi, 2022-23. ANOVA revealed significant variation for agro-morphological and grain quality traits. High genotypic and phenotypic coefficients of variation were recorded for kernel breadth and high heritability coupled with high genetic advance was recorded for panicle length, 1000-seed weight, grain yield per plant and kernel breadth, indicating additive gene action. Grain yield per plant showed significant positive association with number of tillers per plant, number of productive tillers per plant, panicle length and number of filled grains per panicle. Based on superior yield performance relative to the best check, reduced plant height and resemblance to Telangana Sona in maturity and grain traits, 12 BC_2F_3 lines were shortlisted for further physical, chemical and cooking quality analyses. Among them, three lines exhibited favorable cooking and chemical quality parameters, demonstrating grain quality comparable to Telangana Sona. These findings highlight the potential of these lines for further evaluation in advanced yield trials and release.

Keywords: brown planthopper; genetic advance; genetic variation; heritability; Telangana Sona

Introduction

Rice (*Oryza sativa* L.) is the most widely cultivated staple cereal, sustaining more than half of the global population and contributing 60-70 % of daily caloric intake in Asia and Africa (1). Beyond its nutritional significance, rice underpins rural economies and cultural traditions in many regions, particularly in India, where it remains a cornerstone of food and livelihood security (2). With the rising global population, changing climate and increasing land and water scarcity, the dual challenge of improving rice yield and grain quality while ensuring resilience against biotic stresses has never been more urgent. Among insect pests, the brown planthopper (BPH, *Nilaparvata lugens*) poses a persistent threat, capable of causing yield losses exceeding 60 % through direct feeding damage ("hopper burn") and by transmitting viral diseases such as rice ragged stunt virus (RRSV) and rice grassy stunt virus (RGSV) (3, 4). The rapid emergence of virulent BPH biotypes has rendered many resistance sources ineffective, necessitating continuous efforts to introgress durable resistance into high-yielding cultivars. One such widely adopted variety, Telangana Sona, is valued for its short duration, high yield, superior grain quality and low glycemic index, but remains susceptible to BPH. To address this gap, a marker-assisted backcross breeding (MABB) program was initiated at the Institute of Biotechnology (IBT), Professor Jayashankar Telangana Agricultural University (PJTSAU), to introgress the *qbph-1-1* quantitative trait locus (QTL) for BPH resistance from the donor line 10-3 into Telangana Sona (5). Through two backcrosses, 56 BC_2F_3 progenies were developed, combining BPH resistance with the genetic background of Telangana Sona. These populations not only provide novel material for resistance breeding but also serve as a valuable genetic resource for dissecting the inheritance of yield and quality traits under a partially stabilized genetic background.

Since grain yield and quality are complex polygenic traits influenced by multiple genetic and environmental factors, their improvement depends on a detailed understanding of genetic variability, heritability, genetic advance and inter-trait associations. Phenotypic and genotypic coefficients of variation (PCV, GCV), coupled with heritability estimates and expected genetic advance, are critical indicators for gauging selection efficiency. In addition, correlation analyses enable the identification of traits with significant direct or indirect contributions to yield, providing practical guidance for indirect selection strategies. In this study, we evaluate the genetic variation, heritability and genetic advance for yield and quality-related traits and examine their interrelationships within the BC_2F_3 population carrying the *qbph-1-1* QTL. By integrating genetic analysis with trait association studies, this work provides a framework for simultaneously enhancing yield, grain quality and pest resistance in elite rice varieties, ultimately contributing to sustainable rice improvement under pest-prone production environments.

Materials and Methods

The study was conducted at RS&RRS, Rudrur, Nizamabad, Telangana (18°34′ N, 77°52′ E; 404 m above mean sea level) in the Northern Telangana agro-climatic zone. The objective was to assess genetic variability among 56 BC_2F_3 lines derived from Telangana Sona × 10-3, carrying the BPH resistance QTL *qbph-1-1*. Two parental checks (Telangana Sona and 10-3) and two high-yielding varieties (KNM 1638 and JGL 3844) were included for comparison. The experiment followed an Alpha Lattice Design with two replications during Rabi, 2022–23. Twenty-eight-day-old seedlings were transplanted in two rows of 25 hills per replication at 20 × 15 cm spacing, with standard agronomic practices to ensure optimal plant growth and development.

Observations recorded

Phenotypic data were recorded from five randomly selected plants of each BC_2F_3 progeny in both replications for 10 yield-related traits, viz., days to initial flowering (DIF), days to 50 % flowering (DFF), days to maturity (DM), plant height (PH) (cm), number of tillers per plant (TT), number of productive tillers per plant (PT), panicle length (PL) (cm), number of filled grains per panicle (FG), 1000-seed weight (TW) (g) and grain yield per plant (GYP) (g). Additionally, three physical grain quality traits were assessed including kernel length (KL) (mm), kernel breadth (KB) (mm) and kernel length to breadth (L/B) ratio. The recorded data were analyzed using the statistical analysis system (SAS) software, v9.3, according to the Alpha Lattice Design (6, 7).

Statistical analysis

The GCV and PCV were estimated following the standard procedure (8) and the extent of variability was categorized as high (>20 %), moderate (10-20 %) and low (<10 %) (9).

$$GCV = \frac{\text{Genotypic standard deviation}}{\text{Mean}} \times 100$$

$$PCV = \frac{\text{Phenotypic standard deviation}}{\text{Mean}} \times 100$$

Broad-sense heritability (h^2) was estimated using the common formula (10) and the obtained values were categorized as high (> 60 %), moderate (30-60 %) and low (0-30 %) (11).

$$h^2 = \frac{\sigma^2 g}{\sigma^2 p}$$

Where,

h^2 (bs) = heritability in broad sense

$\sigma^2 g$ = genotypic variance

$\sigma^2 p$ = phenotypic variance ($\sigma^2 g + \sigma^2 e$)

$\sigma^2 e$ = environmental variance

Genetic advance as percent of mean was calculated from the heritability estimates as per the standard formula (12) and classified as high (> 20 %), moderate (10-20 %) and low (<10 %).

$$\text{Genetic advance as percent of mean} = \frac{GA}{\text{Grand mean}} \times 100$$

Simple correlation coefficients were computed to evaluate the degree of association among different agronomic traits and their relationship with grain yield in the BC_2F_3 population (13).

$$rP_{xy} = \frac{CoV_{xy}}{\sqrt{Var_x \, . \, Var_y}}$$

Where,

CoV_{xy} = Covariance between the characters x and y

Var_x = Variance of character x

Var_y = Variance of the character y

Based on the statistical analysis for agronomic performance, 12 BC_2F_3 superior lines were identified. These selected lines were further evaluated for physical (hulling (%), milling (%) and head rice recovery (HRR) (%)), cooking (kernel length after cooking (KLAC) (mm), kernel breadth after cooking (KBAC) (mm) and kernel elongation ratio (KER)) and chemical kernel parameters (alkali spreading value (ASV) (14), amylose content (AC) (%) (15) and gel consistency (GC) (mm) (16) to determine the grain quality profile of the selected lines.

Results and Discussion

The recorded phenotypic data on 56 BC_2F_3 progenies, along with the parents (Telangana Sona and 10-3) and two high-yielding checks (KNM 1638 and JGL 3844), were analyzed using an Alpha Lattice Design. Analysis of Variance (ANOVA) revealed significant mean squares for all traits, indicating the presence of substantial genetic variability among the BC_2F_3 progenies, which is a prerequisite for effective selection in breeding programmes (Table 1).

The GCV was slightly lower than the PCV for most traits (Table 2; Fig. 1a, 1b), indicating a minimal environmental influence on trait variability. The narrow difference between PCV and GCV suggests that genetic factors played a dominant role in trait expression. Notably, high PCV and GCV were observed for kernel breadth (KB), reflecting substantial genetic variability and potential for effective selection due to additive gene action. Moderate PCV and GCV were recorded for panicle length (PL), number of filled grains per panicle (FG), 1000-seed weight (TW)

Table 1. Analysis of variance (Alpha Lattice Design) for yield, yield-attributing and quality traits in BC_2F_3 progenies

		Mean sum of squares												
Source of variation	**d.f.**	**DIF**	**DFF**	**DM**	**PH**	**TT**	**PT**	**PL**	**FG**	**TW**	**GYP**	**KL**	**KB**	**L/B**
Replication	1	11.5	5.17	0.91	0.27	0.09	0.48	4.8	7.19	0.15	0.15	0.01	0	0.05
Block/replication	18	1.04	1.54	0.88	7.02	0.17	0.17	1.00	74.72	0.16	0.16	0.01	0.01	0.04
Treatment	59	7.82**	8.75**	10.07**	27**	1.24**	0.92**	7.98**	974.85**	1.32**	1.32**	0.13**	0.12**	0.3**
Error	41	2.11	2.22	0.74	3.96	0.18	0.19	1.56	239.86	0.34	0.34	0.01	0.004	0.03

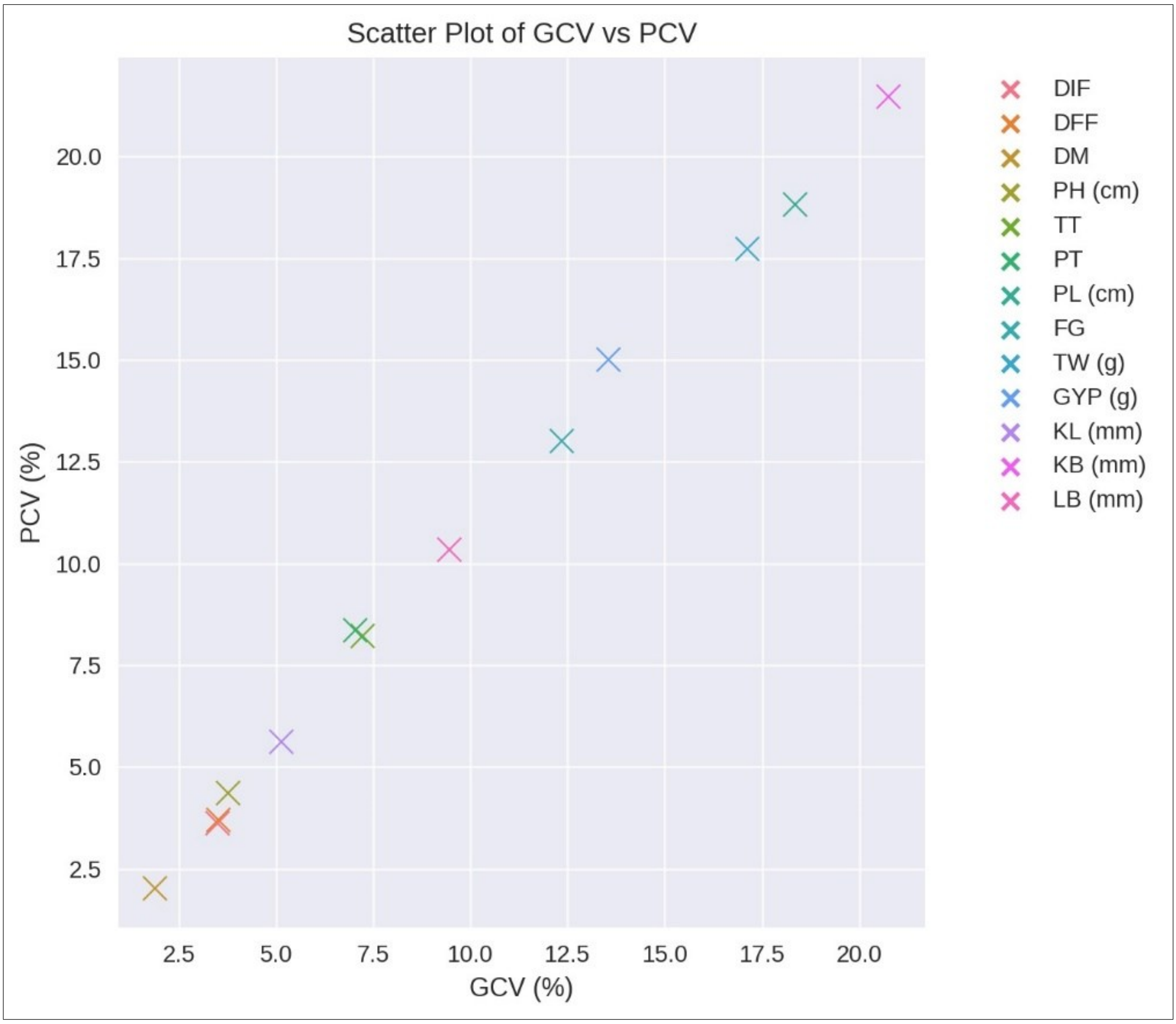
**- Significant at 1 %

DIF- Days to initial flowering, DFF- Days to 50 % flowering, DM- Days to maturity, PH-Plant height (cm), TT- No. of tillers per plant, PT- No. of productive tillers per plant, PL- Panicle length (cm), FG-Number of filled grains per panicle, TW- 1000-seed weight (g), GYP-Grain yield per plant (g), KL- Kernel length (mm), KB- Kernel breadth (mm) and L/B- Kernel length/breadth ratio

Table 2. Estimates of mean and genetic parameters for yield, yield-attributing and quality traits in BC_2F_3 progenies

Trait	Mean	GCV (%)	PCV (%)	h^2 broad sense (%)	GAM
DIF	91.33	3.50	3.62	93.49	6.97
DFF	98.33	3.52	3.70	90.19	6.88
DM	125.28	1.89	2.02	87.73	3.65
PH (cm)	101.39	3.77	4.36	74.92	6.72
TT	10.72	7.23	8.22	77.40	13.11
PT	9.56	7.04	8.36	70.92	12.22
PL (cm)	21.89	18.35	18.82	95.10	36.87
FG	247.36	12.35	13.01	51.94	18.34
TW (g)	11.49	17.12	17.73	93.26	34.06
GYP (g)	26.44	13.55	15.01	81.54	25.21
KL (mm)	5.08	5.14	5.62	83.60	10.68
KB (mm)	1.25	20.75	21.47	93.35	41.29
LB (mm)	4.15	9.46	10.34	83.73	17.84

PCV- Phenotypic coefficient of variation, GCV-Genotypic coefficient of variation, h^2-Heritibility, GAM- Genetic advance as per cent of mean, DIF- Days to initial flowering, DFF- Days to 50 % flowering, DM- Days to maturity, PH- Plant height (cm), TT- No. of tillers per plant, PT- No. of productive tillers per plant, PL- Panicle length (cm), FG-Number of filled grains per panicle, TW- 1000-seed weight (g), GYP- Grain yield per plant (g), KL- Kernel length (mm), KB- Kernel breadth (mm) and L/B- Kernel length/breadth ratio



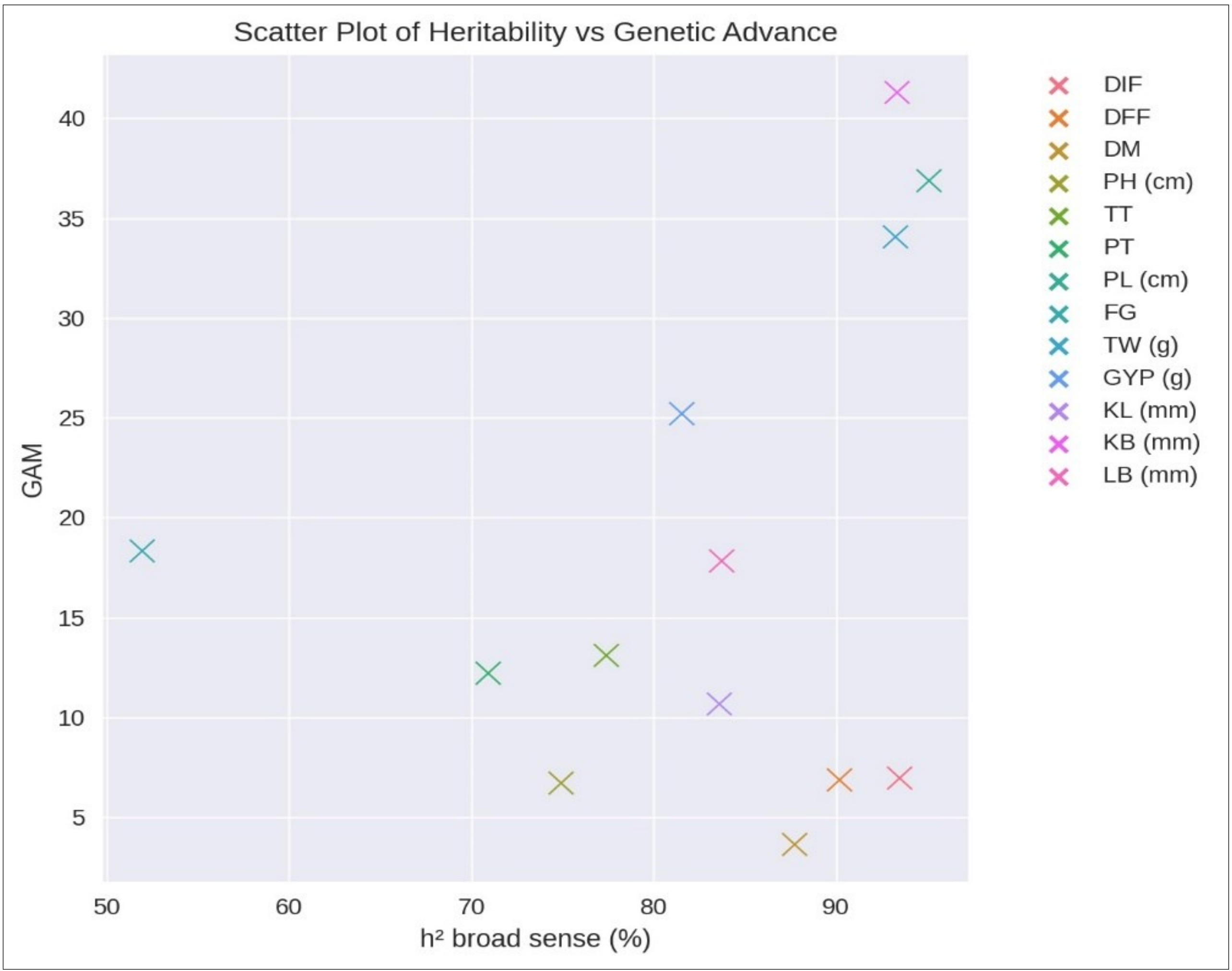


Fig. 1a. PCV and GCV and **1b.** Heritability in broad sense (h^2) and genetic advance as percent of mean for grain yield and its component characters in BC_2F_3 progenies.

and grain yield per plant (GYP), indicating that these traits can be improved through selection in advanced generations. Low PCV and GCV were observed for days to initial flowering (DIF), days to 50 % flowering (DFF), days to maturity (DM), plant height (PH), number of tillers per plant (TT), number of productive tillers per plant (PT), kernel length (KL) and kernel length to breadth ratio (L/B). The low variability in these traits suggests a narrow genetic base for these traits in the present material, implying that broadening diversity through hybridization may be necessary to achieve larger gains. These results are consistent with previous findings (17, 18). Since gene expression is frequently influenced by environmental factors (19), simultaneous consideration of both PCV and GCV is essential for effective selection.

The combined consideration of heritability and genetic advance as a percent of mean provides deeper insight into the nature of gene action controlling these traits. Traits such as panicle length (PL), 1000-seed weight (TW), grain yield per plant (GYP) and kernel breadth (KB) exhibited high heritability coupled with high genetic advance as a percentage of the mean (GAM), indicating their control by additive gene action with minimal environmental influence. Such traits are highly amenable to direct selection and rapid improvement can be expected in early segregating generations. Similar findings were reported for KB, GYP, PL and TW in rice, reinforcing the robustness of these parameters as indicators of selection efficiency (20-23). High heritability with moderate GAM was observed for traits viz., number of tillers per plant (TT), number of productive tillers per plant (PT), kernel length (KL) and kernel length to breadth ratio (L/B). This suggests both additive and non-additive gene action, making improvement through selection possible but requiring careful breeding strategies. Similar results were reported for TT, PT, KL and L/B ratio (24-27). Moderate heritability and GAM for the number of filled grains per panicle (FG) suggest that selective breeding could achieve moderate improvements in this trait.

Given the complex genetic nature of grain yield, direct selection may not be effective without considering its genetic background and associated traits. Correlation analysis helps to identify key traits contributing to yield improvement through indirect selection. The association study results are presented in Table 3 and Fig. 2. Correlation analysis revealed that DIF had a strong positive association with DFF, DM and PH, confirming their interdependence, which is consistent with earlier reports (28). DFF also showed a positive correlation with DM and PH, in agreement with previous studies (24, 29). These relationships suggest that manipulation of flowering time will inevitably affect maturity and plant height, which needs to be considered when designing ideotypes adapted to specific environments. Similarly, DM displayed significant positive correlations with PH, KL and KB, indicating their collective influence on grain development. TT registered a significant positive correlation with PT, PL, FG, TW, GYP and KB (30). PT was positively correlated with FG, PL, TW, GYP, KL and KB, suggesting that direct selection for a higher number of productive tillers per plant may increase the grain yield per plant (22, 31). PL showed a significant positive association with the FG and GYP, suggesting its role in enhancing yield, as also reported in earlier studies (32). FG showed a strong

Table 3. Estimates of correlation coefficient for yield-attributing traits in BC_2F_3 progenies

	DIF	DFF	DM	PH	TT	PT	PL	FG	TW	GYP	KL	KB	L/B
DIF	1.00	0.90**	0.79**	0.37**	-0.63**	-0.43**	-0.46**	-0.40**	0.04	-0.73**	0.12	0.10	-0.07
DFF		1.00	0.83**	0.41**	-0.58**	-0.39**	-0.49**	-0.36**	0.03	-0.72**	0.14	0.12	-0.08
DM			1.00	0.29**	-0.49**	-0.35**	-0.36**	-0.37**	0.15	-0.60**	0.24**	0.24**	-0.18*
PH				1.00	-0.40**	-0.30**	-0.39**	-0.06	-0.51**	-0.39**	-0.22*	-0.18*	0.15
TT					1.00	0.66**	0.49**	0.37**	0.22*	0.65**	0.16	0.25**	-0.25**
PT						1.00	0.21**	0.31**	0.22*	0.45**	0.24**	0.32**	-0.29**
PL							1.00	0.36**	0.13	0.51**	0.05	0.12	-0.18
FG								1.00	-0.27**	0.42**	-0.18*	-0.11	0.05
TW									1.00	-0.09	0.76**	0.72**	-0.58**
GYP										1.00	-0.19*	-0.13	0.07
KL											1.00	0.86**	-0.62**
KB												1.00	-0.92**
L/B													1.00

*-Significant at 5 %, **-Significant at 1 %

DIF- Days to initial flowering, DFF- Days to 50 % flowering, DM- Days to maturity, PH-Plant height (cm), TT- No. of tillers per plant, PT- No. of productive tillers per plant, PL- Panicle length (cm), FG-Number of filled grains per panicle, TW- 1000-seed weight (g), GYP-Grain yield per plant (g), KL- Kernel length (mm), KB- Kernel breadth (mm) and L/B- Kernel length/breadth ratio

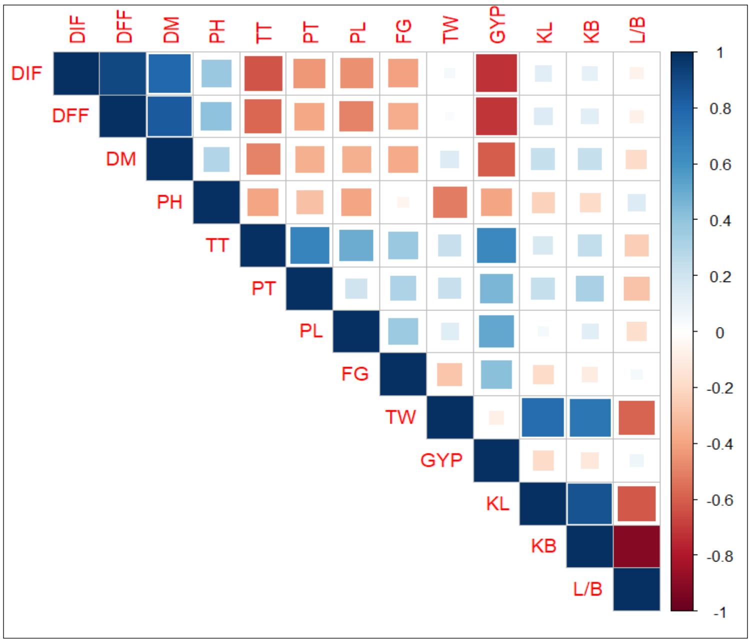


Fig. 2. Correlogram depicting association of grain yield with other traits in BC_2F_3 progenies.

DIF- Days to initial flowering, DFF- Days to 50 % flowering, DM- Days to maturity, PH-Plant height (cm), TT- No. of tillers per plant, PT- No. of productive tillers per plant, PL- Panicle length (cm), FG-Number of filled grains per panicle, TW- 1000 seed weight (g), GYP-Grain yield per plant (g), KL- Kernel length (mm), KB- Kernel breadth (mm) and L/B- Kernel length/breadth ratio

positive correlation with GYP, identifying it as a key trait for yield improvement, in line with previous findings (33). TW had a significant positive correlation with KL and KB, emphasizing its role in grain quality. GYP exhibited a positive association with TT, PT, PL and FG indicating that indirect selection for these traits could enhance yield. Finally, KL and KB were positively correlated, confirming their genetic linkage in grain quality improvement, as similarly reported earlier (34).

Based on agronomic performance (Supplementary Table 1), twelve superior BC_2F_3 progenies, viz., BC_2F_3-3-14, BC_2F_3-3-52, BC_2F_3-3-63, BC_2F_3-3-64, BC_2F_3-3-74, BC_2F_3-3-84, BC_2F_3-3-107, BC_2F_3-3-148, BC_2F_3-3-167, BC_2F_3-3-171, BC_2F_3-3-183 and BC_2F_3-3-219 were selected. These identified lines recorded days to 50 % flowering earlier or on par and plant height less than or on par with the recurrent parent Telangana Sona. The grain yield per plant in these 12 BC_2F_3 lines was higher than that of the recurrent parent and also than the best check variety KNM 1638, which is widely cultivated in Telangana due to its higher yield. These selected lines, along with the recurrent parent Telangana Sona, were assessed for grain quality traits. The detailed results are presented in Table 4.

Hulling percentage ranged from 79.1 % to 82.4 %, with most progenies showing values comparable to Telangana Sona (82.1 %). Milling percentage varied between 53.7 % and 65.6 %, while head rice recovery (HRR) exceeded the 60 % threshold in seven progenies, meeting varietal release standards. KLAC ranged from 6.7-8.3 mm and KBAC from 2.3-2.9 mm, with several lines matching the parent. The kernel elongation ratio (KER) was consistent (1.4-1.6), indicating stability in cooking quality. All lines showed an alkali spreading value of 4.0, suggesting intermediate gelatinization temperature (70-74 °C), favourable for faster cooking. Amylose content ranged from 21.1-27.4 %, with most progenies within the preferred intermediate range (21–25 %). Gel consistency values (22.0 mm) were comparable to the parent, ensuring similar texture and softness. These findings demonstrate the potential of selected BC_2F_3 lines to maintain desirable grain quality traits akin to Telangana Sona. Variations in cooking and chemical traits across lines reflect effective

Table 4. Estimation of cooking and chemical parameters in the best 12 BC_2F_3 introgression progenies

S. No	BC_2F_3 lines	Hulling (%)	Milling (%)	HRR (%)	KLAC (mm)	KBAC (mm)	KER	ASV	AC (%)	GC (mm)
1	BC_2F_3(a)-3-14	79.5	64.5	61.7	6.7	2.7	1.4	4.0	21.1	22.0
2	BC_2F_3(a)-3-52	79.9	53.7	60.9	8.3	2.8	1.6	4.0	26.2	22.0
3	BC_2F_3(a)-3-63	80.8	54.3	60.9	7.9	2.7	1.6	4.0	21.8	22.0
4	BC_2F_3(a)-3-64	79.1	53.7	59.6	7.7	2.3	1.4	4.0	22.6	22.0
5	BC_2F_3(a)-3-74	81.4	62.1	60.8	8.0	2.7	1.6	4.0	24.6	22.0
6	BC_2F_3(a)-3-84	81.6	62.6	59.7	7.9	2.9	1.6	4.0	21.6	22.0
7	BC_2F_3(a)-3-107	80.5	59.7	60.3	7.9	2.7	1.6	4.0	24.5	22.0
8	BC_2F_3(a)-3-148	82.4	65.6	61.4	7.7	2.7	1.5	4.0	22.6	22.0
9	BC_2F_3(a)-3-167	81.4	63.3	56.1	7.9	2.8	1.6	4.0	24.4	22.0
10	BC_2F_3(a)-3-171	82.1	62.6	61.1	7.9	2.7	1.6	4.0	24.6	22.0
11	BC_2F_3(a)-3-183	81.0	63.4	58.5	7.4	2.9	1.5	4.0	27.4	22.0
12	BC_2F_3(a)-3-219	81.7	62.9	59.9	7.5	2.6	1.5	4.0	25.0	22.0
Telangana Sona		82.1	62.3	61.0	7.9	2.7	1.6	4.0	24.6	22.0

HRR-Head rice recovery (%), KLAC- Kernel length after cooking (mm), KBAC- Kernel breadth after cooking (mm) KER-Kernel elongation ratio, ASV-Alkali spreading value, AC-Amylose content (%) and GC-Gel consistency (mm)

introgression. Overall, these lines show promising features for consumer acceptance and varietal advancement.

The evaluation of cooking and chemical quality parameters in the 12 BC_2F_3 progenies demonstrated successful recovery of desirable quality traits. Notably, lines BC_2F_3-3-63, BC_2F_3-3-107 and BC_2F_3-3-171 exhibited complete similarity to the recurrent parent, Telangana Sona, across all assessed cooking and chemical traits, indicating effective introgression of quality genes.

Overall, the convergence of high heritability and GAM for key yield and grain traits, favourable correlation patterns and the successful recovery of high-yielding, BPH-resistant and quality-equivalent lines underscores the effectiveness of the backcross breeding strategy employed. The BC_2F_3 lines identified in this study represent promising candidates for advancement to multi-environment yield trials and potential varietal release, particularly in regions where Telangana Sona is already popular.

Conclusion

This study revealed significant genetic variability among BC_2F_3 progenies of Telangana Sona × 10-3 carrying the *qbph-1-1* QTL. High heritability and genetic advance for panicle length, 1000-seed weight, grain yield and kernel breadth indicate strong additive gene action, making these traits promising targets for selection. The positive associations of grain yield with tiller number, panicle length and filled grains further emphasize the utility of indirect selection for yield improvement. Twelve superior progenies were identified with higher yield and desirable plant architecture than the checks, while three lines combined BPH resistance with grain quality comparable to Telangana Sona. These results highlight the success of MABB in pyramiding resistance without compromising grain quality and the identified lines represent valuable resources for developing high-yielding, BPH-resistant rice cultivars suited to consumer and market preferences.

Acknowledgements

The authors greatly acknowledge Professor Jayashankar Telangana Agricultural University (PJTAU) and ICAR-Indian Institute of Rice Research (ICAR-IIRR) for providing financial support for the work in the manuscript.

Authors' contributions

KB carried out the methodology, curated the data, conducted formal analysis and prepared the original draft. SM and VS contributed to conceptualisation, experimental design, funding acquisition and manuscript review and editing. JLV, RR, PK and PSNCVL supported in the collection of field data and its revision. SM and VS gave final improvements in data reviewing and editing. All authors read and approved the final manuscript.

Compliance with ethical standards

Conflict of interest: Authors do not have any conflict of interest to declare.

Ethical issues: None

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Peer review: Publisher thanks Sectional Editor and the other anonymous reviewers for their contribution to the peer review of this work.

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