

# Genetic Analysis of Backcross Derived Lines for Yield and Yield Attributing Traits In Rice (*Oryza sativa* L.)

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## ABSTRACT

Rice production faces challenges due to biotic stresses influenced by climate fluctuations. Brown plant hopper (BPH) being major biotic stress in rice, significantly impacts yield. With an objective of BPH resistance integrated with yield, two cross derivatives in BC2F1 generation were developed by crossing susceptible high-yielding slender grain rice variety, Telangana Sona (TS) with two resistant parent's viz., 10-3 and M229. These backcrosses were studied to investigate genetic variability, correlation, and principal component analysis for yield and yield-related traits. Both crosses exhibited high GCV, PCV, and high heritability coupled with high genetic advance for productive tillers per plant and single plant yield, indicating a preponderance of additive gene action. Correlation analysis demonstrated a significant positive association of single plant yield with plant height, productive tillers per plant, and filled grains per panicle in both crosses. PCA revealed a cumulative variance of 94.72% and 77.23% from plant height, productive tillers per plant, kernel breadth, days to 50 % flowering, days to maturity, kernel length, and filled grains per panicle in TS X 10-3, and filled grains per panicle, 1000 seed weight, kernel breadth, days to 50 % flowering, days to maturity, kernel length/breadth ratio and panicle length in TS X M229 respectively, indicating their substantial contribution to variability. Consequently, the selection of backcross-derived lines based on these traits would be the most appropriate strategy for yield improvement.

**Keywords-** Backcross, correlation, genetic variability, principal component analysis, rice

## INTRODUCTION

Sustaining global food security and meeting the future demands for food and feed necessitate a substantial increase in grain yield [1]. Wheat, rice, and maize are the primary food crops globally, providing more than 50% of the calories consumed by the human population [2]. Rice, as a crucial staple food, contributes over 20% of the world's dietary energy [3, 4]. However, rice production faces persistent challenges from a range of abiotic and biotic factors [5]. Therefore, it is imperative to enhance rice productivity by effectively addressing both abiotic and biotic stresses [6].

The Brown plant hopper (BPH) (*Nilaparvata lugens* Stål) is potential biotic stress that leads to substantial yield losses in rice production. As a phloem-sucking herbivore, BPH has emerged as the most destructive pest of rice in recent years, causing direct damage to plants and resulting in yield losses of up to 80% [7, 8]. Moreover, BPH serves as a carrier for ragged stunt and grassy stunt viral diseases and its infestation leads to hopper burn symptoms, further exacerbating yield losses [9, 10]. Therefore, the breeding of resistant cultivars is the most durable, precise, and environmentally responsible strategy for

BPH management to reduce pest incidence and preserve ecological fitness [11].

Marker-assisted Backcross Breeding (MABB), which involves the utilization of elite varieties as recurrent parents and the incorporation of well-defined QTLs from donor parents, offers a promising approach to combine high yield and stress tolerance in rice. Recognizing the significance of BPH resistance, the Institute of Biotechnology (IBT), Professor Jayashankar Telangana State Agricultural University (PJTSAU), Hyderabad, initiated MABB to introgress BPH resistance into the elite rice cultivar, Telangana Sona. This was achieved through crosses with two BPH-resistant parents, 10-3 and M229, resulting in the development of two BC2F1 (TS//TS//TS/10-3 and TS//TS//TS/M229) backcross populations. To ensure the effectiveness, these lines, were extensively characterized for BPH resistance at both the phenotypic and genotypic levels. However, genetic analysis of backcross-derived lines for yield and yield-attributing traits is necessary to identify superior lines with BPH resistance.

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A crucial aspect of any crop improvement program is conducting a thorough analysis of genetic variability to determine suitable selection strategies [12]. Variability parameters such as range, Phenotypic coefficient of variation (PCV), Genotypic coefficient of variation (GCV), heritability ( $h^2$ (bs)) and genetic advance are usually utilized for efficient exploitation of variability for efficient genetic enhancement [13]. PCV and GCV not only facilitate the comparison of phenotypic and genotypic variation but also serve as tools to assess the effectiveness of selection procedures for improvement [14]. Heritability measures the phenotypic variation resulting from genetic causes and measures the transmissibility of traits from one generation to the other. On the other hand, genetic advance indicates the proportion of expected genetic gain under selective pressure [15].

Correlation studies aid in evaluating the relationship between traits and assist in devising suitable selection strategies for the simultaneous improvement of multiple traits. Principal Component Analysis (PCA) is an indispensable tool in identifying a set of breeding lines that contribute significantly to the overall variability [16]. This aids in streamlining the selection process and maximizing desired outcomes [17, 18]. The present investigation aimed to assess the genetic variability, correlation, and PCA among the backcross-derived lines (BC2F1) of TS//TS//TS/10-3 and TS//TS//TS/M-229.

## MATERIAL AND METHODS

Two BC1F1's of TS//TS/10-3 and TS//TS/M229 were backcrossed with the recurrent parent Telangana Sona to develop BC2F1 cross material. Genetic variability parameters, correlation, and PCA were evaluated in BC2F1 populations from both the crosses for yield and yield-related traits. TS//TS//TS/10-3 was designated as Cross A and TS//TS//TS/M229 as Cross B.

The experiment was conducted at Regional Sugarcane and Rice Research Station (RS&RRS), Rudrur, Nizamabad, Telangana. The BC2F1 populations of both crosses, TS//TS//TS/10-3 and TS//TS//TS/M229, were evaluated in an augmented block design during the Rabi, 2021-22 along with parental checks Telangana Sona, 10-3 and M229. The experimental material was grown in one row of 3.0 m in length with a spacing of 20 x 15 cm following standard agronomic practices to ensure optimal crop growth. Observations were recorded for 12 quantitative traits including days to 50 % flowering (DFF), days to maturity (DM), plant height (PH) (cm), productive tillers per plant (PT), panicle length (PL) (cm), filled grains per panicle (FG), spikelet fertility (SF%), 1000 seed weight (TW) (g), single plant yield (SPY) (g), kernel length (KL) (mm), kernel breadth (KB) (mm) and kernel length/breadth ratio (L/B).

The obtained data were used to compute the averages, which were then subjected to further analysis. Analysis of Variance (ANOVA) was done using R v.4.3.0 software [19]. PCV and GCV values were calculated based on the method suggested [20] and were categorized as per the classification proposed [21], which includes low (< 10%), medium (10-20%), and high (> 20%) ranges. Heritability and genetic advance were computed as per the standard procedures [22, 23]. The heritability range was

classified into low (< 30%), moderate (30%-60%), and high (> 60%) [24]. Similarly, the range of genetic advances as a percentage of the mean (GAM) was grouped into low (< 10%), moderate (10%-20%), and high (> 20%) [23]. Correlation coefficients were calculated to analyze the associations between the traits, utilizing R v.4.3.0 software [23]. Furthermore, principal component analysis (PCA), biplots were also generated in order to visualize the data effectively.

## RESULTS AND DISCUSSION

ANOVA indicated the presence of significant genetic variability among the individuals for the traits studied. For Cross A, significant differences were observed for PH, PL, FG, TW, and KB (Table 1). Similarly, in Cross B, all traits showed significant differences except for SF% and L/B (Table 2). These findings suggested the presence of considerable genetic variability among the backcross-derived lines, highlighting the potential for effective selection strategies.

### 1. Estimation of genetic parameters

Genetic variability is essential for the success of plant breeding programs, allowing breeders to select optimal recombinants from a diverse pool of materials. The genetic variability depicted in the form of box plots (Fig. 1 and 2) showed the frequency distribution for 12 quantitative traits in the backcross derived (BC2F1) lines of TS//TS//TS/10-3 and TS//TS//TS/M-229. The box plot displays the upper, median, and lower quartiles, representing the 75th, 50th, and 25th percentiles of the backcross-derived lines, respectively. The vertical lines demonstrate the variation present in the backcross-derived lines. Additionally, the dots on the plot represent the outliers for each trait. From the box plots, it is clearly seen that the traits DFF, DM, PH, PL, and SF have more variability, and the traits TW, SPY, and L/B has less variability in Cross A and all the traits has variability in Cross B. The traits PT, FG, TW, and SPY have outliers towards the maximum in Cross A, PH has outliers towards the minimum and PT and SPY has outliers towards the maximum in Cross B.

All the traits exhibited a small difference between the PCV and GCV in both the crosses (Tables 3 and 4) indicating very less influence of the environment. Hence, direct selection for these traits would be rewarding. However, traits such as PT and SPY showed high magnitudes of PCV and GCV in Cross A. Similarly, Cross B displayed high GCV and PCV values for PT, FG, TW and SPY. This finding aligns with previous studies for similar traits [25, 26]. Thus, selection based on phenotype holds promise for effectively improving these traits. Moderate estimates of PCV and GCV were observed for PL in Cross A and KL in Cross B. These findings are consistent with previous studies on PL and KL [27]. Low PCV and GCV estimates were observed for DFF, DM, PH, FG, SF%, TW, KL, KB, and L/B in Cross A as well as for DFF, DM, PH, PL, SF%, KB, and L/B in Cross B indicating low variability for these characters offering little scope for the improvement of these traits. Similar findings have been reported [28].

Heritability ( $h^2$  bs) estimates were very high (>90%) for majority of the traits in both the crosses except KL, KB and L/B ratio in Cross A (Tables 3 and 4). However, heritability estimates

coupled with genetic advance are more beneficial in predicting genetic gain under selection than heritability estimates alone since high heritability does not always indicate high genetic gain. High heritability coupled with high GAM was observed for the traits PT, PL and SPY in Cross A and PT, FG, TW, SPY and KL in Cross B. Indicating the preponderance of additive genetic variance, which enables the selection of promising lines. The present results were in line with previous findings [29, 26].

## 2. Correlation analysis

Character association analysis provides valuable insights into the relationship between grain yield and other traits, thus assisting plant breeders in developing effective selection strategies [30]. In the present study, single plant yield showed significant positive correlations with traits DM, PH, PT, PL, and FG in Cross A (Fig. 3A, Table 5) and PH, PT, and FG in Cross B (Fig. 3B, Table 6). While non-significant positive associations were found between single plant yield and DFF in Cross A and PL and SF% in Cross B. Therefore, direct selection based on these correlated traits could be an effective strategy for achieving higher grain yield. These findings are in agreement with previous studies that investigated similar traits in rice [31, 28]. Additionally, significant positive correlations were observed among different pairs of traits in both crosses, indicating their interdependency and potential for simultaneous improvement.

## 3. Principal component analysis (PCA)

PCA conducted on backcross derived lines of Cross A revealed a total of six principal components (Pcs), with the first four PCs being the most informative with eigenvalues 5.73, 3.04, 1.60, and 1.00 respectively. Together, these four PCs accounted for 94.72% of the total variance for all the characters (Table 7). PC1 contributed significantly to the morphological variability, representing 47.77% of the total variance with traits PH, PT, and KB making significant contributions. PC2 predominantly contributed by DFF and DM accounted for 25.30 % of the total variation. PC3 accounted for 13.31% of the overall variation with KL making notable contributions. Furthermore, PC4 accounted for 8.34% of the total variation, with FG being the highest contributor. These traits primarily contribute to divergence and encompass a substantial portion of the observed variability. Comparable cumulative variance with five major principal components was reported in several previous studies [32].

In the scree plot (Fig. 4A), PC1, exhibited the highest variability (47.77 %). while the subsequent PCs showed a decline in variability. This observation was also consistent with the study conducted on 49 rice lines [33]. Selection of traits via PH, PT, KB, DFF, DM, KL, and FG lying in first four PCs would be beneficial in contributing to the overall morphological diversity. The first two principal components biplot including loadings of the various characters along with the backcross derived lines of Cross A spread over is given in Figure 4B. Among these traits, PH exhibits the longest vector length, indicating its significant contribution to the overall divergence followed by PL and DFF (Fig. 4C). The angle between the trait vectors indicates the degree of association with an acute angle representing positive

correlation and a right angle indicating no correlation. Among the 12 traits, PH, PL, L/B, PT, and FG showed a positive correlation with SPY, as earlier reported [31]. Backcross-derived lines positioned close to the trait vector in the same quadrant are likely to exhibit favorable performance for these traits. With respect to the lines in Cross A, 5 and 6 exhibited high PC scores, suggesting their significant contribution to the overall diversity.

The PC analysis in Cross B revealed a total of 12 PCs, with the first four PCs being the most informative. These four PCs exhibited eigenvalues of 4.44, 2.23, 1.55 and 1.05, respectively which together accounted for 77.23% of the total variance for all the characters (Table 8). According to PC1, traits such as FG, TW and KB made a relatively higher contribution (36.96%) to the total morphological variability. PC2 accounted for 18.62% of the total variation with DFF and DM contributing the highest. PC3 accounted for 12.91% of the total variation with L/B ratio and PL contributing maximum variability. PC4 accounted for 8.34% of the total variation with PT and PL making the highest contributions. Comparable cumulative variance with four major principal components was reported previously [34].

In scree plot (Fig. 5A), PC1, displayed the highest variability (36.96 %) which then declined gradually up to 10 PCs. Selection of traits via., FG, TW, KB, DFF, DM, L/B and PL lying in first four PCs would contribute to the total morphological diversity. Figure 5B illustrates the biplot of the first two PCs, representing the loadings of various traits alongside the backcross-derived lines of Cross B and best-performing backcross derived lines for each trait. The trait DFF showed maximum vector length indicating its significant contribution to the overall divergence followed by TW and FG. PH, PT, PL, and FG showed a positive correlation with SPY (Fig. 5C). Lines 42, 44, 9 and 24 in Cross B contributed significantly to the overall diversity, as they registered high PC scores.

## CONCLUSION

The findings of this study highlighted the potential of certain traits, namely PH, PT, FG, and SPY as effective selection criteria for enhancing grain yield in rice as they exhibited high values for PCV, GCV, heritability, and GAM. The substantial PCV and GCV values suggest considerable genetic variability, while the high  $h^2$  (bs) and genetic advance indicated the influence of additive genetic factors in the expression of these traits. Moreover, the positive and significant correlations observed between these traits and grain yield further emphasized their relevance in yield improvement efforts and PCA performed in this study contributed valuable insights into the overall variation present in the backcross-derived lines of both the crosses. Thus, the findings of this study offer practical applications in rice improvement programs, specifically in the development of high-yielding varieties resistant to BPH.

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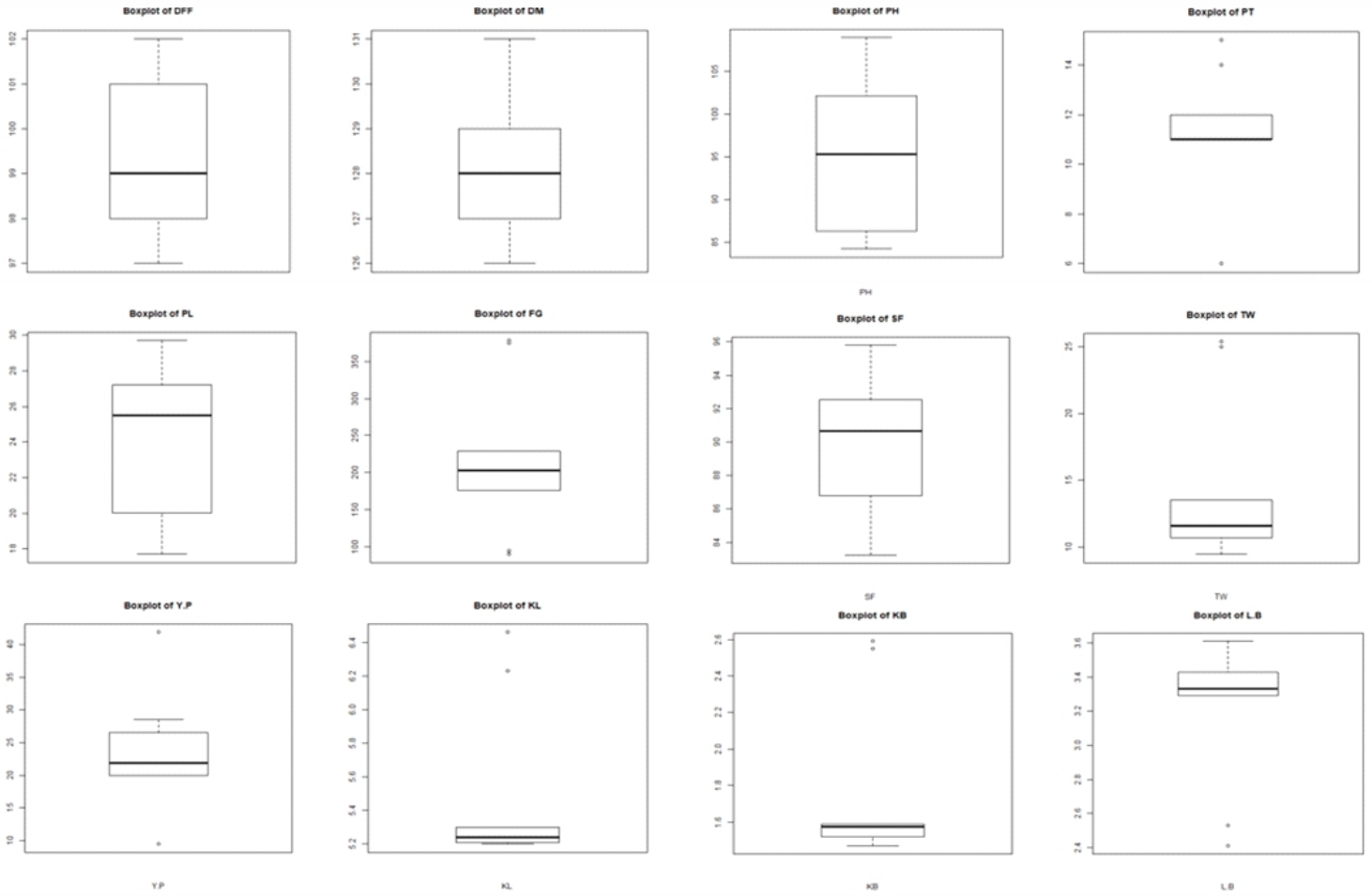


Figure 1. Box-plots depicting genetic variability for yield traits in backcross derived lines (BC2F1) of Cross A

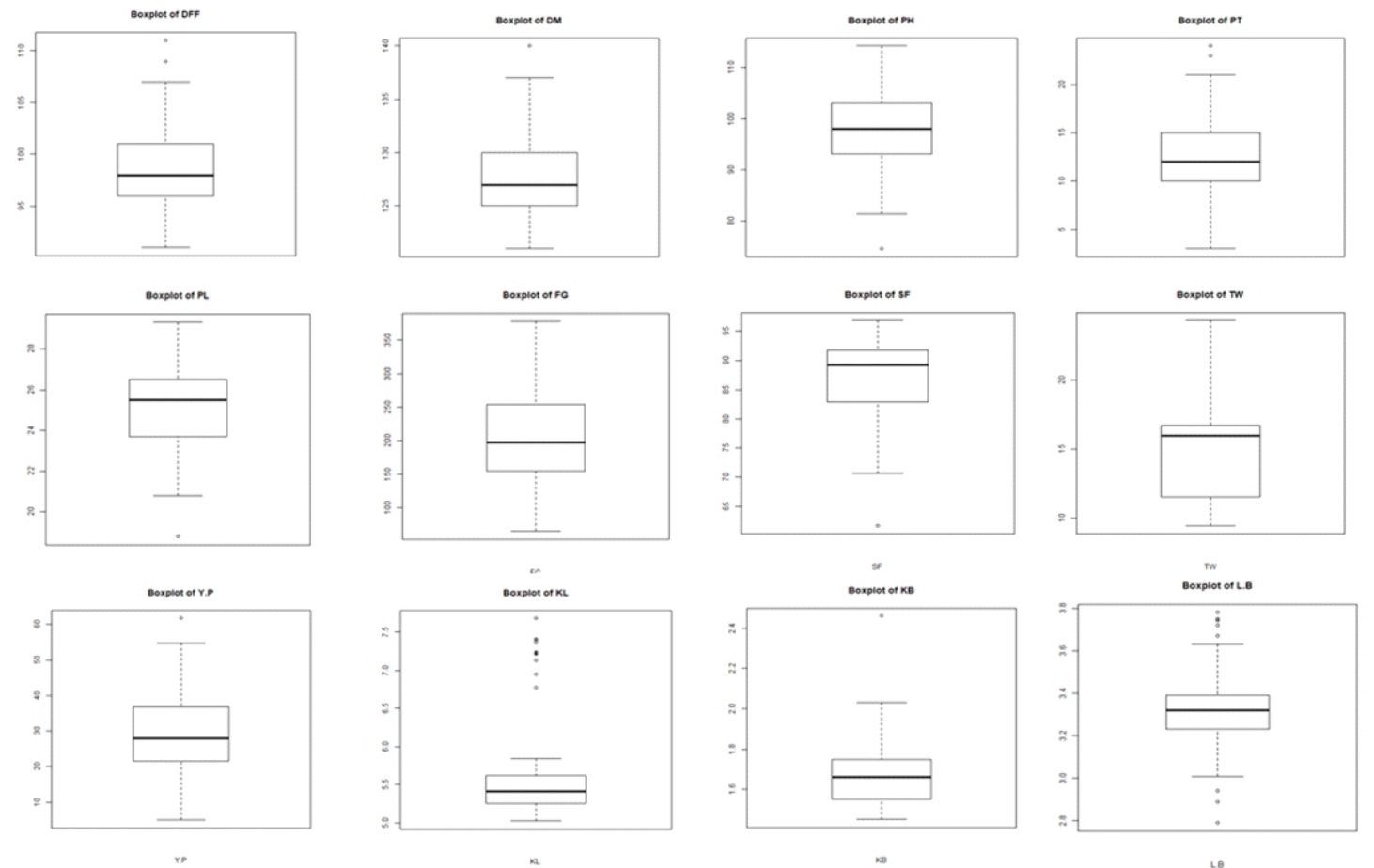


Figure 2. Box-plots depicting genetic variability for yield traits in backcross derived lines (BC2F1) of Cross B



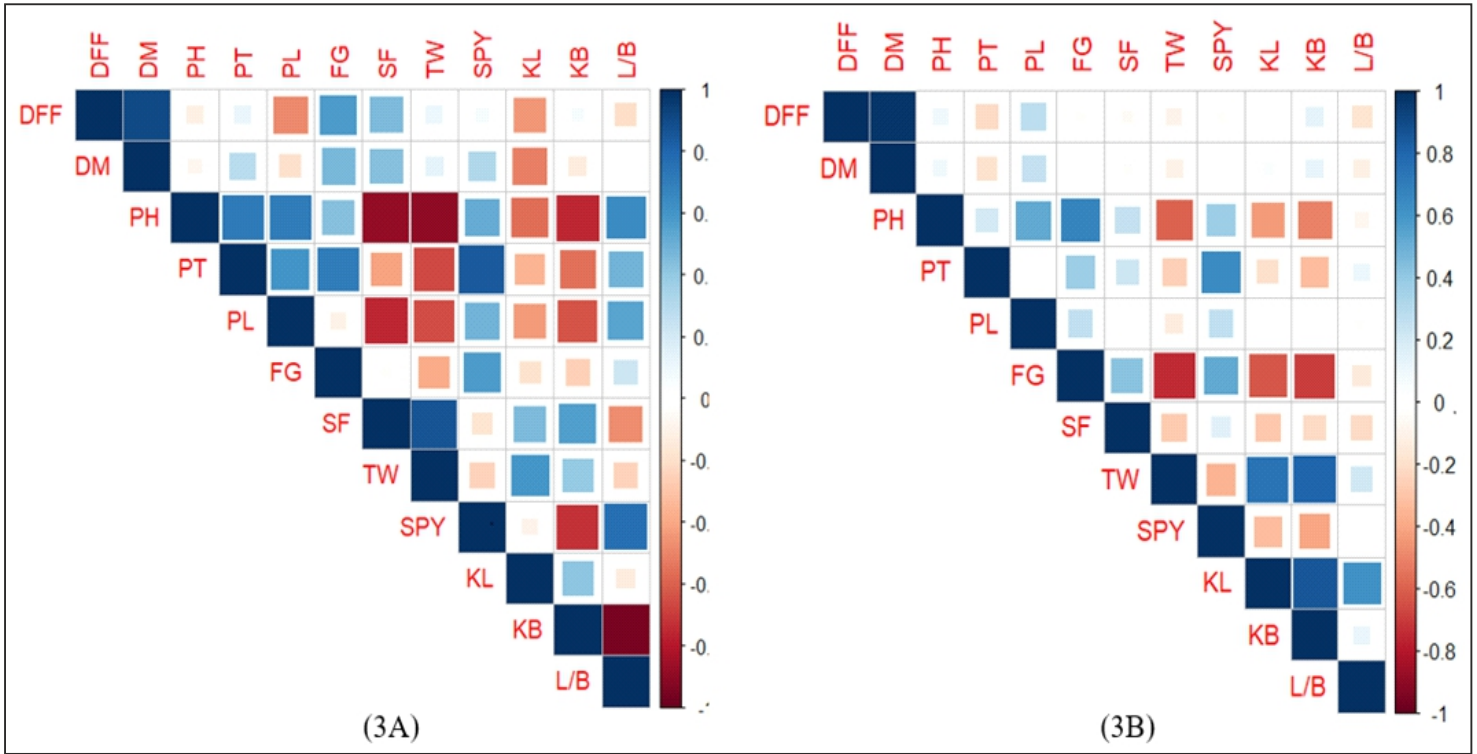


Figure 3A & 3B. Correlogram depicting association of yield with other traits in backcross derived lines (BC2F1) of Cross A and B respectively.

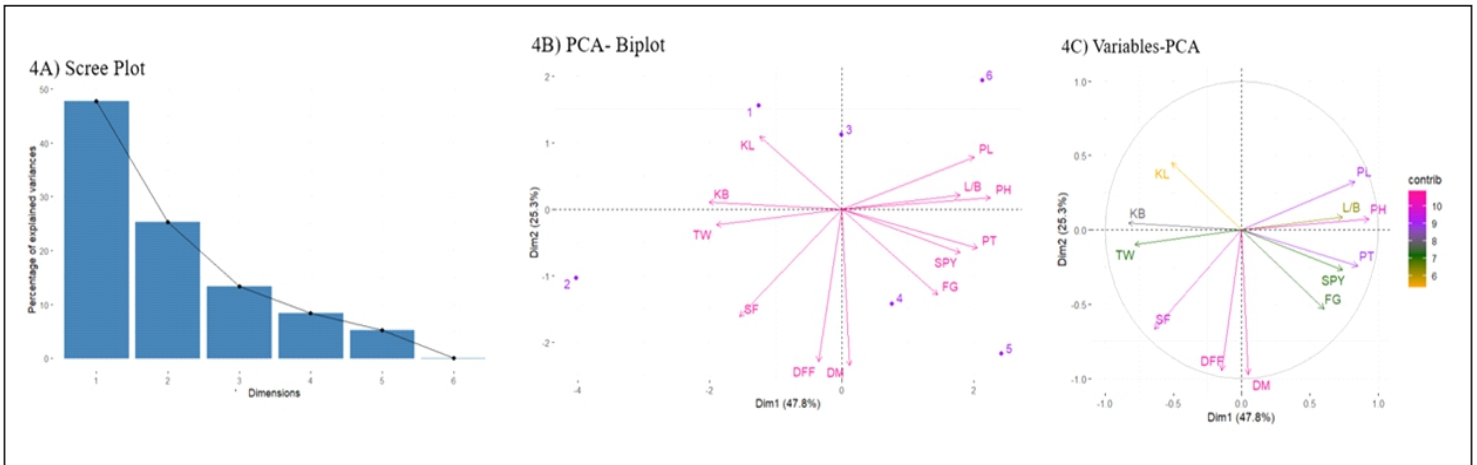


Figure 4. (A) Scree Plot depicting the contribution of 6 principal components, (B) PCA biplot (C) PCA graph of different traits for first two principal components in backcross derived lines (BC2F1) of Cross A

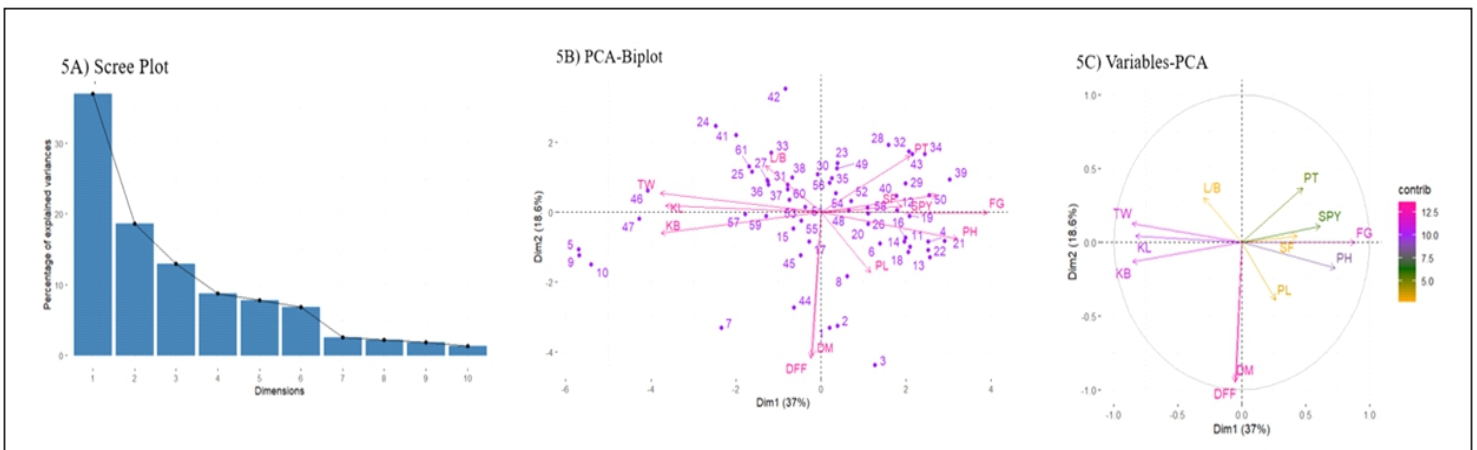


Figure 5. (A) Scree Plot depicting the contribution of 10 principal components, (B) PCA biplot (C) PCA graph of different traits for first two principal components in backcross derived lines (BC2F1) of cross B

**Table 1. Analysis of variance for yield and yield attributing traits in backcross derived lines (BC2F1) of Cross A**

Source	d.f.	DF	DM	PH	PT	PL	FG	SF%	TW	SPY	KL	KB	L/B
Treatment (ignoring Blocks)	7	4.23	6.73	88.32*	7.09	21.78	12134.5*	21.9	46.3*	86.23	0.28	0.24*	0.21
Treatment: Check	1	6.25	20.25	148.72*	0.25	48.09*	80656**	86.12	145.56*	56.1	1.14	1.2*	1.23
Treatment: Test vs. Check	1	7.35	16.02	66.63*	0.02	5.65	2160	10.79	173.98*	0.00054	0.82	0.51*	0.25
Treatment: Test	5	3.2	2.17	80.58*	9.87	19.75	425.1	11.27	0.91	109.51	0.00083	0.00086	0.0034
Block (eliminating Treatments)	1	2.25	0.25	1.68	0.25	0.06	1	9.70E-30	0.37	1	0.01	0.00023	0.0012
Residuals	1	0.25	0.25	0.04	0.25	0.22	16	1	0.05	1	0.02	0.00063	0.01

\*Significance at 5%, \*\*Significance at 1%

Days to 50 % flowering (DFF), Days to maturity (DM), Plant height (PH) (cm), Productive tillers per plant (PT), Panicle length (PL) (cm), Filled grains per panicle (FG), Spikelet fertility (SF%), 1000 seed weight (TW) (g), Single plant yield (SPY)(g), Kernel length (KL) (mm), Kernel breadth (KB) (mm) and Kernel length/breadth ratio (L/B)

**Table 2. Analysis of variance for yield and yield attributing traits in backcross derived lines (BC2F1) of Cross B**

Source	d.f.	DF	DM	PH	PT	PL	FG	SF%	TW	SPY	KL	KB	L/B
Treatment (ignoring Blocks)	62	18.36**	18.26**	63.06**	21.27**	4.22**	6849.29**	70.9**	14.39**	151.06**	0.52**	0.05	0.04
Treatment: Check	1	40.5**	60.5**	72**	6.13**	17.41**	135460.1**	2.6	92.75**	86.26**	7.59**	1.48**	0.45
Treatment: Test vs. Check	1	70.98**	10.62**	8.8*	12.74**	1.27*	8297.43**	338.02**	30.92**	82.17**	4.41**	0.39*	0.04
Treatment: Test	60	17.11**	17.69**	63.82**	21.67**	4.05**	4681.64**	67.59**	12.8**	153.29**	0.34**	0.02	0.03
Block (eliminating Treatments)	3	0.83	4.83*	4.5	0.46	0.47	52.12	0.68	0.1	0.29	0.01	0.03	0.08
Residuals	3	0.17	0.17	0.67	0.13	0.1	66.79	1.22	0.06	0.68	0.01	0.03	0.08

\*Significance at 5%, \*\*Significance at 1%

Days to 50 % flowering (DFF), Days to maturity (DM), Plant height (PH) (cm), Productive tillers per plant (PT), Panicle length (PL) (cm), Filled grains per panicle (FG), Spikelet fertility (SF%), 1000 seed weight (TW) (g), Single plant yield (SPY) (g), Kernel length (KL) (mm), Kernel breadth (KB) (mm) and Kernel length/breadth ratio (L/B)

**Table 3. Estimates of genetic variability parameters in backcross derived lines (BC2F1) of Cross A**

S.no	Trait	Mean	Range		PCV	GCV	h <sup>2</sup> broad sense (%)	GAM
			Min.	Max.				
1	Days to 50% flowering	98.00	96.00	101.00	1.82	1.74	92.19	3.46
2	Days to maturity	126.00	124.00	131.00	1.16	1.09	88.46	2.12
3	Plant height (cm)	95.80	84.85	109.00	9.37	9.37	99.95	19.32
4	Productive tillers per plant	11.00	6.00	15.00	27.77	27.41	97.47	55.83
5	Panicle length (cm)	24.53	17.82	29.82	18.11	18.01	98.9	36.96
6	Filled grains per panicle	212.00	93.00	376.00	9.73	9.54	96.24	19.31
7	Spikelet fertility (%)	89.97	83.74	95.80	3.73	3.56	91.13	7.02
8	1000 seed weight (g)	12.75	9.75	25.17	7.50	7.29	94.46	14.61
9	Single plant yield (g)	23.77	8.99	42.35	44.03	43.83	99.09	90.01
10	Kernel length (mm)	5.37	5.16	6.34	0.54	0.45	26.03	1.23
11	Kernel breadth (mm)	1.68	1.48	2.57	1.75	0.91	27.04	0.97
12	Kernel L/B ratio	3.27	2.47	3.58	1.78	0.95	29.50	1.15

**Table 4. Estimates of genetic variability parameters in backcross derived lines (BC2F1) of Cross B**

S.no	Trait	Mean	Range		PCV	GCV	h <sup>2</sup> broad sense (%)	GAM
			Min.	Max.				
1	Days to 50% flowering	99.00	91.00	111.00	4.21	4.19	99.03	8.61
2	Days to maturity	128.00	121.00	140.00	3.30	3.28	99.06	6.74
3	Plant height (cm)	97.31	74.50	114.20	8.21	8.17	98.96	16.76
4	Productive tillers per plant	13.00	3.00	24.00	36.03	35.93	99.42	73.90
5	Panicle length (cm)	25.32	18.80	29.30	7.95	7.85	97.65	16.01
6	Filled grains per panicle	206.00	65.00	333.00	33.27	33.03	98.57	67.66
7	Spikelet fertility (%)	85.74	61.68	96.85	9.59	9.50	98.2	19.43
8	1000 seed weight (g)	14.55	9.45	24.32	24.60	24.54	99.52	50.50
9	Single plant yield (g)	29.75	4.94	61.73	41.62	41.52	99.56	85.47
10	Kernel length (mm)	5.58	5.02	7.68	10.44	10.35	98.20	21.15
11	Kernel breadth (mm)	1.68	1.50	2.03	7.96	7.69	97.40	9.45
12	Kernel L/B ratio	3.32	3.06	3.78	5.06	4.98	96.50	9.68

**Table 5. Estimates of correlation coefficient for yield attributing traits in backcross derived lines (BC2F1) of Cross A**

	DFE	DM	PH	PT	PL	FG	SF%	TW	SPY	KL	KB	L/B
DFE	1.000	0.905**	-0.112	0.116	-0.481	0.576**	0.455**	0.107	0.067	-0.444	0.062	-0.200
DM		1.000	-0.076	0.280	-0.191	0.465**	0.440**	0.130	0.312**	-0.516	-0.132	-0.013
PH			1.000	0.710**	0.704**	0.439**	-0.888**	-0.893**	0.511**	-0.561	-0.755	0.642**
PT				1.000	0.601**	0.701**	-0.414	-0.660	0.840**	-0.354	-0.551	0.487**
PL					1.000	-0.104	-0.757	-0.653	0.486**	-0.430	-0.632	0.547**
FG						1.000	-0.033	-0.388	0.574**	-0.187	-0.254	0.221
SF%							1.000	0.865**	-0.174	0.450**	0.570**	-0.474
TW								1.000	-0.248	0.598**	0.400**	-0.243
SPY									1.000	-0.090	-0.724	0.761**
KL										1.000	0.415**	-0.138
KB											1.000	-0.958**
L/B												1.000

Days to 50 % flowering (DFE), Days to maturity (DM), Plant height (PH) (cm), Productive tillers per plant (PT), Panicle length (PL) (cm), Filled grains per panicle (FG), Spikelet fertility (SF%), 1000 seed weight (TW) (g), Single plant yield (SPY) (g), Kernel length (KL) (mm), Kernel breadth (KB) (mm) and Kernel length/breadth ratio (L/B)

**Table 6. Estimates of correlation coefficient for yield contributing traits in backcross derived lines (BC2F1) of Cross B**

	DFE	DM	PH	PT	PL	FG	SF%	TW	SPY	KL	KB	L/B
DFE	1.000	0.980**	0.099	-0.210	0.273	-0.031	-0.051	-0.095	-0.032	0.023	0.136	-0.175
DM		1.000	0.093	-0.188	0.256	-0.005	-0.037	-0.107	-0.014	0.049	0.125	-0.111
PH			1.000	0.207	0.530**	0.677**	0.256	-0.593**	0.378**	-0.437**	-0.508**	-0.077
PT				1.000	0.024	0.374**	0.222	-0.257	0.649**	-0.197	-0.322	0.108
PL					1.000	0.262	-0.016	-0.137	0.266	-0.009	-0.004	-0.028
FG						1.000	0.427**	-0.748**	0.524**	-0.629**	-0.699**	-0.149
SF%							1.000	-0.278	0.154	-0.285	-0.212	-0.215
TW								1.000	-0.352**	0.742**	0.802**	0.212
SPY									1.000	-0.328**	-0.406**	-0.014
KL										1.000	0.853**	0.615**
KB											1.000	0.116
L/B												1.000

Days to 50 % flowering (DFE), Days to maturity (DM), Plant height (PH) (cm), Productive tillers per plant (PT), Panicle length (PL) (cm), Filled grains per panicle (FG), Spikelet fertility (SF%), 1000 seed weight (TW) (g), Single plant yield (SPY) (g), Kernel length (KL) (mm), Kernel breadth (KB) (mm) and Kernel length/breadth ratio (L/B)

**Table 7. Eigen values and contribution of variability for the principal component axis in backcross derived lines (BC2F1) of Cross A**

	PC1	PC2	PC3	PC4	PC5	PC6
Eigen value	5.73	3.04	1.60	1.00	0.63	0.00
Variability (%)	47.77	25.30	13.31	8.34	5.28	0.00
Cumulative (%)	47.77	73.07	86.38	94.72	100.00	100.00
DFE	0.37	29.50	3.08	1.77	2.60	0.02
DM	0.04	31.21	0.02	3.01	3.14	37.44
PH	15.15	0.17	1.84	0.08	15.17	2.27
PT	12.61	1.92	0.02	11.61	16.14	0.78
PL	11.98	3.49	1.70	4.46	21.39	1.08
FG	6.31	9.32	0.21	30.19	7.85	0.71
SF%	7.12	14.65	5.38	0.06	9.62	1.86
TW	10.71	0.31	18.18	5.25	5.35	7.30
SPP	9.57	2.38	19.29	2.18	7.81	11.50
KL	4.57	6.74	22.03	17.36	1.21	35.28
KB	12.02	0.07	7.74	15.28	5.07	1.71
L/B	9.55	0.25	20.53	8.75	4.62	0.05

Days to 50 % flowering (DFE), Days to maturity (DM), Plant height (PH) (cm), Productive tillers per plant (PT), Panicle length (PL) (cm), Filled grains per panicle (FG), Spikelet fertility (SF%), 1000 seed weight (TW) (g), Single plant yield (SPY) (g), Kernel length (KL) (mm), Kernel breadth (KB) (mm) and Kernel length/breadth ratio (L/B)

**Table 8. Eigen values and contribution of variability for the principal component axis in backcross derived lines (BC2F1) of Cross B**



	PC1	PC2	PC3	PC4	PC5	PC6	PC7	PC8	PC9	PC10	PC11	PC12
Eigen value	4.44	2.23	1.55	1.05	0.94	0.82	0.30	0.26	0.22	0.16	0.02	0.00
Variability (%)	36.96	18.62	12.91	8.73	7.80	6.84	2.54	2.19	1.85	1.37	0.18	0.01
Cumulative (%)	36.96	55.58	68.50	77.23	85.03	91.86	94.40	96.59	98.45	99.82	99.99	100.00
DFF	0.06	40.44	0.31	5.95	1.13	0.36	0.12	0.03	0.33	0.59	50.67	0.00
DM	0.04	39.03	0.35	7.45	1.83	1.68	0.01	0.00	0.09	0.59	48.92	0.01
PH	12.02	1.38	5.46	15.84	1.29	1.40	7.58	40.92	13.82	0.24	0.05	0.00
PT	5.09	6.01	11.83	28.29	0.04	2.89	42.83	0.43	0.74	1.86	0.00	0.00
PL	1.57	6.89	20.24	22.31	8.42	7.88	0.25	32.01	0.23	0.13	0.06	0.00
FG	17.85	0.00	0.57	0.30	0.23	3.51	6.84	3.77	42.15	24.70	0.06	0.00
SF%	4.22	0.07	1.49	6.89	50.55	26.60	0.85	4.26	4.25	0.80	0.03	0.00
TW	16.62	0.70	1.25	0.44	6.69	3.87	2.33	1.87	13.17	53.00	0.04	0.01
SPY	8.56	0.53	14.99	12.08	0.01	13.43	37.74	1.94	3.15	7.58	0.00	0.00
KL	15.53	0.08	15.29	0.01	1.11	4.54	0.01	2.34	5.65	3.38	0.00	52.08
KB	16.43	0.82	2.24	0.22	14.69	1.13	0.24	9.41	14.33	6.85	0.00	33.62
L/B	1.99	4.05	25.96	0.22	14.02	32.71	1.20	3.01	2.10	0.29	0.17	14.27

Days to 50 % flowering (DFF), Days to maturity (DM), Plant height (PH) (cm), Productive tillers per plant (PT), Panicle length (PL) (cm), Filled grains per panicle (FG), Spikelet fertility (SF%), 1000 seed weight (TW) (g), Single plant yield (SPY) (g), Kernel length (KL) (mm), Kernel breadth (KB) (mm) and Kernel length/breadth ratio (L/B)

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