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Genetic Analysis of Backcross Derived Lines for Yield and Yield-attributing Traits in Rice (*Oryza Sativa* L.)

Kadthala Bhargava[1*], M. Sreedhar[1], V. Jhansi Lakshmi[2], Ramya Rathod[3], K. Parimala[4], and S. Vanisri[5]

[1]*College of Agriculture, Professor Jayashankar Telangana Agricultural University (PJTAU), Hyderabad, Telangana, India.*
[2]*ICAR-Indian Institute of Rice Research (IIRR), Hyderabad, Telangana, India.*
[3]*Regional Sugarcane and Rice Research Station (RS&RRS), Rudrur, Nizamabad, Telangana, India.*
[4]*Agricultural Research Institute, Tandur, Vikarabad (dist), Telangana, India.*
[5]*Institute of Biotechnology, Professor Jayashankar Telangana Agricultural University (PJTAU), Hyderabad, Telangana, India.*

ABSTRACT

Rice production faces challenges due to biotic stresses influenced by climate fluctuations. Brown plant hopper (BPH), being a major biotic stress in rice, significantly impacts yield. It is a major insect pest that causes 10%–30% annual yield loss in Asia by direct phloem feeding and transmitting viral diseases like rice ragged stunt virus (RRSV) and rice grassy stunt virus (RGSV). With an objective of BPH resistance integrated with yield, two cross derivatives in BC_2F_1 generation were developed by crossing susceptible, high-yielding, slender grain rice variety, Telangana Sona (TS), with two resistant parents' 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 of94.72% 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, Brown plant hopper (BPH), correlation, genetic variability, genetic advance, heritability, 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 [20]. Wheat, rice, and maize are the primary food crops globally, providing more than 50% of the calories consumed by the human population [13]. Rice, as a crucial staple food, contributes over 20% of the world's dietary energy [11, 14]. 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 [27].

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% [2, 26]. 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 [1, 30]. Therefore, breeding resistant cultivars is the most durable, precise, and environmentally responsible strategy for BPH management to reduce pest incidence and preserve ecological fitness [6].

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 Agricultural University (PJTAU), 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 BC_2F_1 (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.

A crucial aspect of any crop improvement program is conducting a thorough analysis of genetic variability to determine suitable selection strategies [3]. 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

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Corresponding Author: **Kadthala Bhargava*

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[18]. 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 [4]. Heritability measures the phenotypic variation resulting from genetic causes and measures the transmissibility of traits from one generation to the next. On the other hand, genetic advance indicates the proportion of expected genetic gain under selective pressure [25].

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 [23]. This aids in streamlining the selection process and maximizing desired outcomes [21, 15]. The present investigation aimed to assess the genetic variability, correlation, and PCA among the backcross-derived lines (BC_2F_1) of TS///TS//TS/10-3 and TS///TS//TS/M-229.

MATERIAL AND METHODS

Two BC1F1s of TS//TS/10-3 and TS//TS/M229 were backcrossed with the recurrent parent Telangana Sona to develop BC_2F_1 cross material. Genetic variability parameters, correlation, and PCA were evaluated in BC_2F_1 populations from both 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 the Regional Sugarcane and Rice Research Station (RS&RRS), Rudrur, Nizamabad, Telangana. The BC_2F_1 populations of both crosses, TS///TS//TS/10-3 and TS///TS//TS/M229, were evaluated in an augmented block design along with parental checks, Telangana Sona, 10-3, and M229. The experimental material was grown in one row of 3.0 m 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 [22]. PCV and values were calculated based on the method suggested [7] and were categorized as per the classification proposed [32], which includes low (< 10%), medium (10-20%), and high (> 20%) ranges. Heritability and genetic advance were computed as per the standard procedures [12, 16]. The heritability range was classified into low (< 30%), moderate (30%-60%), and high (> 60%) [29]. Similarly, the range of genetic advances as a percentage of 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 [16]. Furthermore, principal component analysis (PCA), biplots were also generated 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 (BC_2F_1) 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 has more variability, and the traits TW, SPY and L/B has less variability in Cross A and all the traits have 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 have 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 little 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 [5, 9]. 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 [24]. 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 [31].

Heritability (h^2 bs) estimates were very high (>90%) for the majority of the traits in both crosses, except KL, KB, and L/B ratio in Cross A (Tables 3 and 4). However, heritability estimates coupled with genetic advances 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, indicating the preponderance of additive genetic variance, which enables the selection of promising lines. The present results were in line with previous findings [9, 33].

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 [10]. 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 [34, 31]. 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 [17].

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 [8]. Selection of traits via PH, PT, KB, DFF, DM, KL, and FG lying in the 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 Aspread 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 [34]. 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 relatively higher contributions (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 the 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 [19].

In the 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 the 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 indicate 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 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.

FUTURE SCOPE OF THE STUDY

The improved lines with best agronomic performance should be advanced to further generations to develop genetically stable, agronomically superior, and environmentally adaptable genotypes infused with resistance against BPH. Based on the field performance, the potential lines may be proposed for varietal release through State and Central variety release procedures.

CONFLICT OF INTEREST

All the authors have declared and confirmed that they have no conflict of interest.

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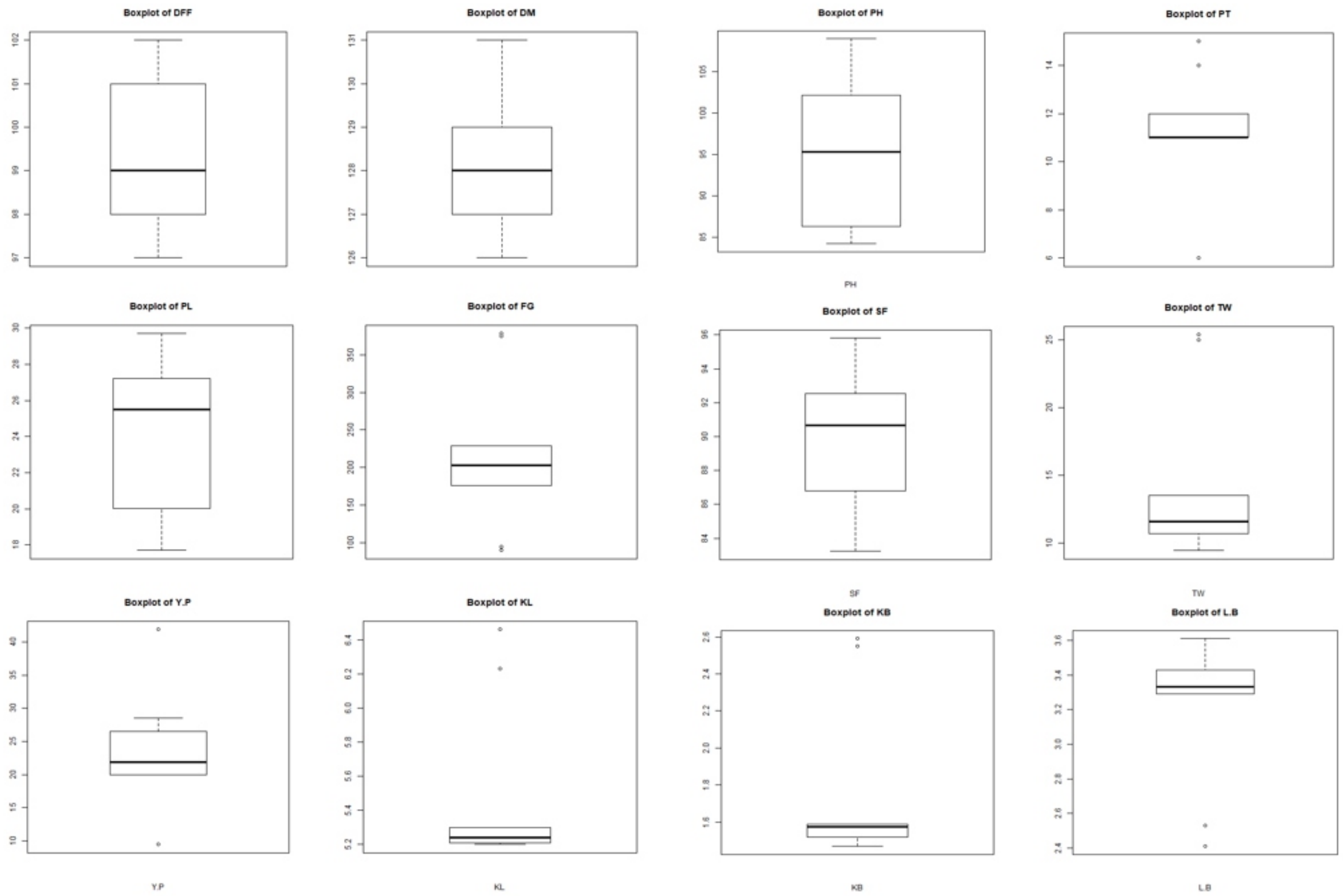

Fig. 1. Box-plots depicting genetic variability for yield traits in backcross derived lines (BC_2F_1) of Cross A

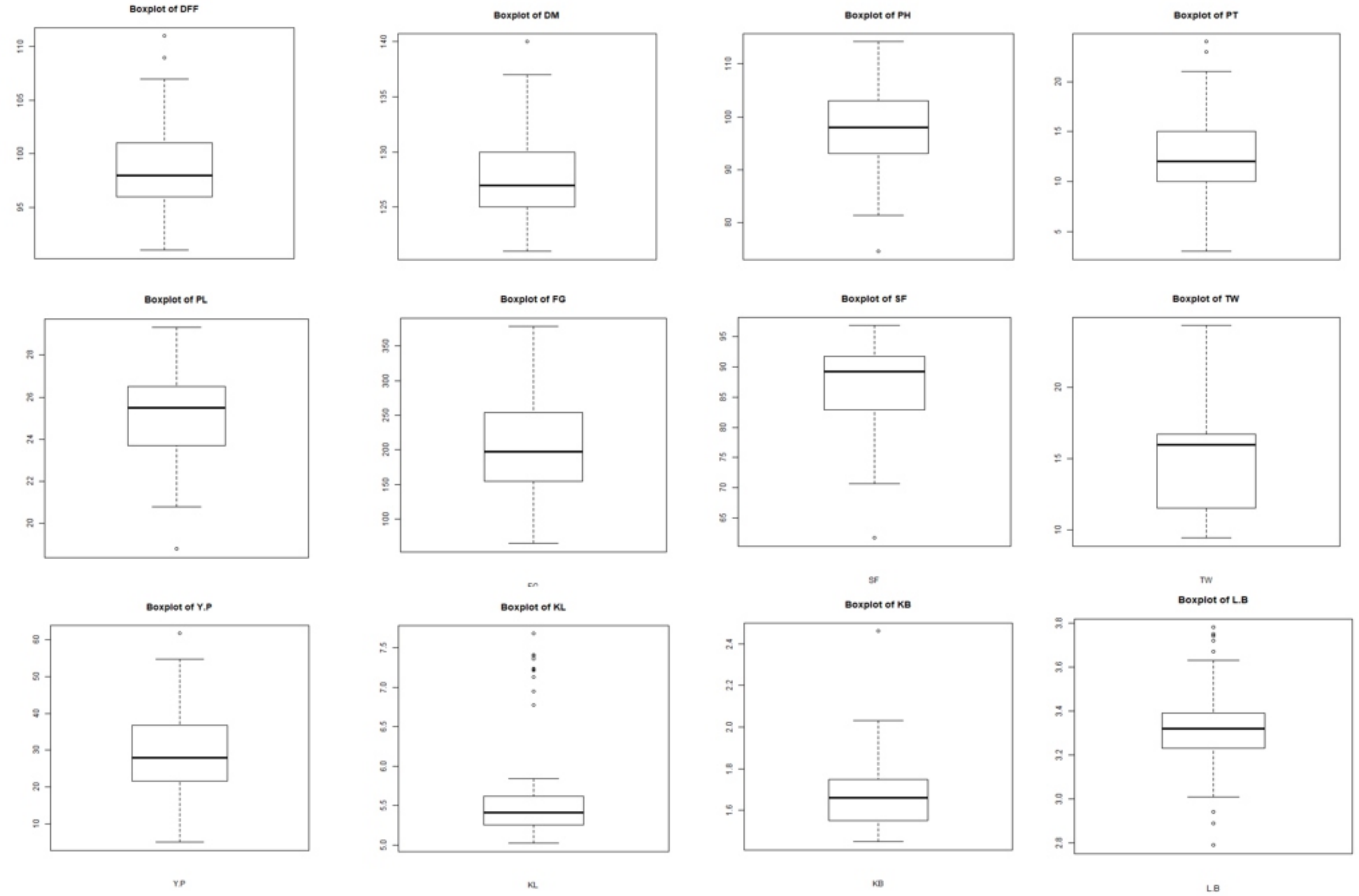

Fig. 2. Box-plots depicting genetic variability for yield traits in backcross derived lines (BC_2F_1) of Cross B

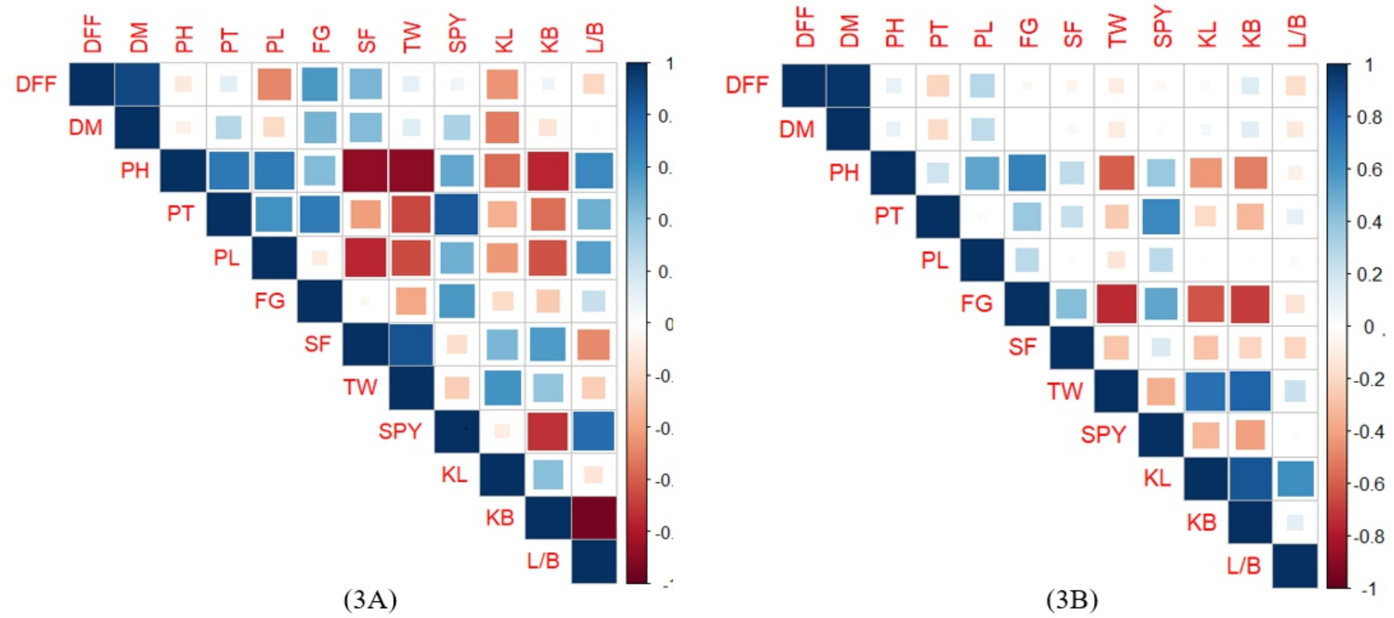

Fig. 3A & 3B. Correlogram depicting association of yield with other traits in backcross derived lines (BC_2F_1) of Cross A and B respectively.

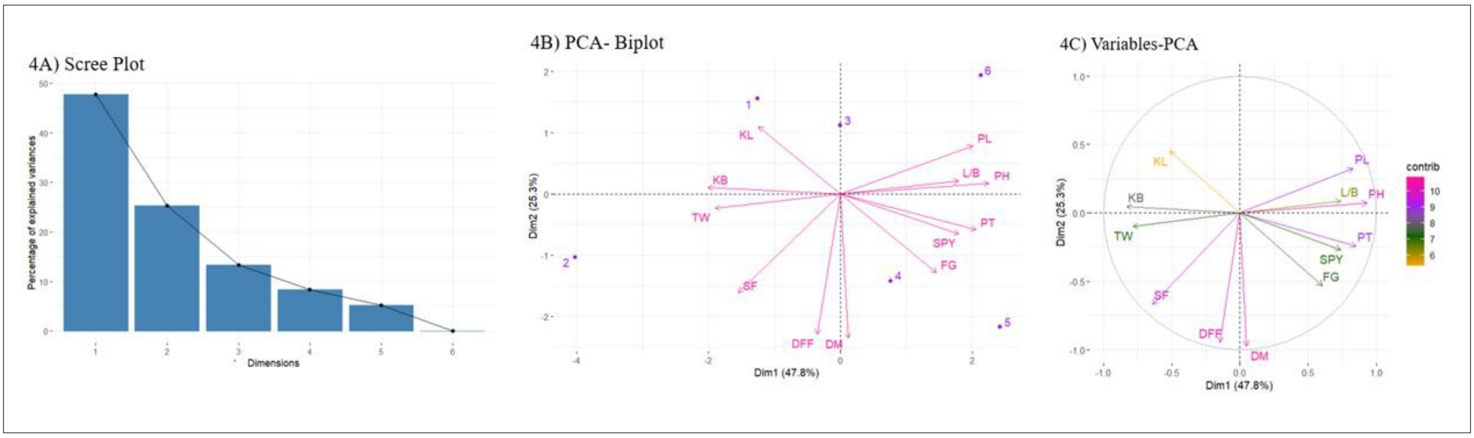

Fig. 4. (A) Scree Plot depicting the contribution of 6 principal components, (B) PCA biplot (C) PCA graph of different traits for first two principal components in backcross derived lines (BC_2F_1) of Cross A

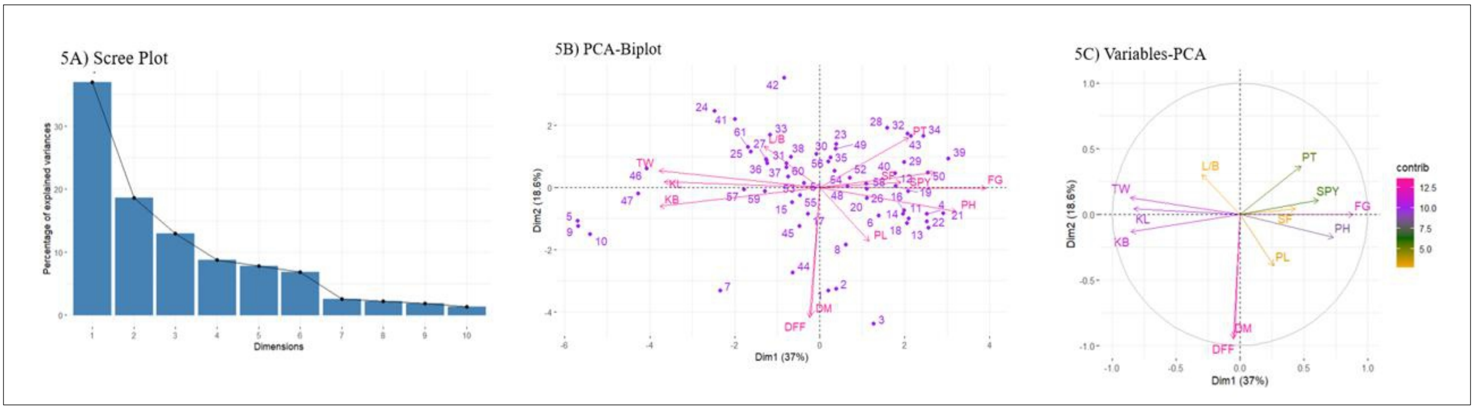

Fig. 5. (A) Scree Plot depicting the contribution of 10 principal components, (B) PCA biplot (C) PCA graph of different traits for first two principal components in backcross derived lines (BC_2F_1) of cross B

Table 1. Analysis of variance for yield and yield attributing traits in backcross derived lines (BC_2F_1) of Cross A

Source	d.f.	DFF	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

**Significanceat5%, **Significanceat1%*

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 (BC_2F_1) of Cross B

Source	d.f.	DFF	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

Significanceat5%,Significanceat1%*

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 (BC_2F_1) of Cross A

S.no	Trait	Mean	Range		PCV	GCV	h2 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 (BC_2F_1) of Cross B

S.no	Trait	Mean	Range		PCV	GCV	h2 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 (BC_2F_1) of Cross A

	DFF	DM	PH	PT	PL	FG	SF%	TW	SPY	KL	KB	L/B
DFF	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 (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 6. Estimates of correlation coefficient for yield contributing traits in backcross derived lines (BC_2F_1) of Cross B

	DFF	DM	PH	PT	PL	FG	SF%	TW	SPY	KL	KB	L/B
DFF	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 (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 7. Eigen values and contribution of variability for the principal component axis in backcross derived lines (BC_2F_1) 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
DFF	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 (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 8. Eigenvalues and contribution of variability for the principal component axis in backcross derived lines (BC_2F_1) 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)

REFERENCES

1. Backus EA, Serrano MS, Ranger CM (2005) Mechanisms of hopperburn: an overview of insect taxonomy, behavior, and physiology. Annual Review of Entomology 50:125-51.

2. Balachiranjeevi CH, Prahalada GD, Mahender A, Jamaloddin M, Sevilla MA, Marfori-Nazarea CM, Vinarao R, Sushanto U, Baehaki SE, Li ZK, Ali J (2019) Identification of a novel locus, BPH38 (t), conferring resistance to brown planthopper (*Nilaparvata lugens* Stal.) using early backcross population in rice (*Oryza sativa* L.). Euphytica 215:1-4.

3. Basavaraj PS, Gireesh C, Bharamappanavara M, Manoj CA, Ishwaryalakshmi LV, Senguttuvel P, Sundaram RM, Subbarao LV, Anantha MS (2022) Genetic analysis of introgression lines of Oryza rufipogon for improvement of low phosphorous tolerance in indica rice. Indian journal of genetics and plant breeding 82(02):135-42.

4. Bello OB, Ige SA, Azeez MA, Afolabi MS, Abdulmaliq SY, Mahamood J (2012) Heritability and genetic advance for grain yield and its component characters in maize (*Zea mays* L.). International Journal of Plant Research 2(5):138-45.

5. Bhargava K, Shivani D, Pushpavalli SN, Sundaram RM, Beulah P, Senguttuvel P (2021) Genetic variability, correlation and path coefficient analysis in segregating population of rice. Electronic Journal of Plant Breeding 12(2):549-55.

6. Brar DS, Virk PS, Jena KK, Khush GS (2009) Breeding for resistance to planthoppers in rice. Planthoppers: new threats to the sustainability of intensive rice production systems in Asia: 401-9.

7. Burton GW, Devane DE (1953) Estimating heritability in tall fescue (Festuca arundinacea) from replicated clonal material 1. Agronomy journal 45(10):478-81.

8. Christina GR, Thirumurugan T, Jeyaprakash P, Rajanbabu V (2021) Principal component analysis of yield and yield related traits in rice (*Oryza sativa* L.) landraces. Electronic Journal of Plant Breeding 12(3):907-11.

9. Devi KR, Hari Y, Chandra BS, Prasad KR (2022) Genetic association, variability and path studies for yield components and quality traits of high yielding rice (*Oryza sativa* L.) genotypes. International Journal of Bio-resource and Stress Management 13(1):81-92.

10. Dixit P, Dubey DK (1984) Path analysis in lentil (*Lens culinaris* Med.). Lentil Experimental News Service.

11. Fahad S, Adnan M, Noor M, Arif M, Alam M, Khan IA, Ullah H, Wahid F, Mian IA, Jamal Y, Basir A(2019) Major constraints for global rice production. In Advances in rice research for abiotic stress tolerance 1-22.

12. Falconer DS (1981) An Introduction of Quantitative Genetics- Second edition. Oliver and Boyd, Edinburgh 312-324.

13. FAO (2016) Save and Grow in practice: maize, rice, wheat A guide to sustainable cereal production.

14. Gadal N, Shrestha J, Poudel MN, Pokharel B (2019) A review on production status and growing environments of rice in Nepal and in the world. Archives of Agriculture and Environmental Science 4(1):83-7.

15. Gireesh C, Husain SM, Shivakumar M, Satpute GK, Kumawat G, Arya M, Agarwal DK, Bhatia VS (2017) Integrating principal component score strategy with power core method for development of core collection in Indian soybean germplasm. Plant Genetic Resources 15(3):230-8.

16. Johnson HW, Robinson HF, Comstock RE (1955) Estimates of genetic and environmental variability in soybeans. Agronomy journal 47(7):314-8.

17. Kasanaboina K, Chandra MY, Krishna L, Parimala G, Jagadeeshwar R (2022) Multivariate analysis based prediction of phenotypic diversity associated with yield and yield component traits in germplasm lines of rice (*Oryza sativa* L.). Electronic Journal of Plant Breeding 13(3):764-71.

18. Kishore NS, Srinivas T, Nagabhushanam U, Pallavi M, Sameera SK (2015) Genetic variability, correlation and path analysis for yield and yield components in promising rice (*Oryza sativa* L.) genotypes. SAARC Journal of Agriculture 13(1):99-108.

19. Lakshmi VI, Sreedhar M, Vanisri S, Anantha MS, Rao LS, Gireesh C (2019) Multivariate analysis and selection criteria for identification of African rice (*Oryza glaberrima*) for genetic improvement of indica rice cultivars. Plant Genetic Resources 17(6):499-505.

20. Mesterhazy A, Olah J, Popp J (2020) Losses in the grain supply chain: Causes and solutions. Sustainability 12(6):2342.

21. Noirot M, Hamon S, Anthony F (1996) The principal component scoring: a new method of constituting a core collection using quantitative data. Genetic Resources and Crop Evolution 43:1-6.

22. Panse VG, Sukhatme PV (1954) Statistical methods for agricultural workers. Statistical methods for agricultural workers.

23. Pearson K. LIII (1901) On lines and planes of closest fit to systems of points in space. The London, Edinburgh, and Dublin philosophical magazine and journal of science 2(11):559-72.

24. Radha T, Satheesh Kumar P, Saravanan K, Suganthi S (2019) Genetic variabilty, association and path analysis for grain yield and quality traits in Rice (*Oryza sativa* L.). Plant Archives 19:2522-6.

25. Ramanujam S, Thirumalachar DK (1967) Genetic variability of certain characters in red pepper (Capsicum annum). Mysore Journal of Agricultural Sciences 1:30-6.

26. Rashid MM, Jahan M, Islam KS (2017) Effects of nitrogen, phosphorous and potassium on host-choice behavior of brown planthopper, *Nilaparvata lugens* (Stål) on rice cultivar. Journal of insect behavior 30:1-5.

27. Rawte S, Saxena RR, Verulkar SB (2021) Analysis of yield stability of rice (*Oryza sativa* L.) landraces under drought conditions with three different approaches. Indian Journal of Genetics and Plant Breeding 81:236-44.

28. Roberts DP, Mattoo AK (2018) Sustainable agriculture-Enhancing environmental benefits, food nutritional quality and building crop resilience to abiotic and biotic stresses. Agriculture 8(1):8.

29. Robinson HF, Comstock RE, Harvey PH (1949) Estimates of heritability and the degree of dominance in corn.

30. Sarao PS, Sahi GK, Neelam K, Mangat GS, Patra BC, Singh K (2016) Donors for resistance to brown planthopper *Nilaparvata lugens* (Stål) from wild rice species. Rice Science 23(4):219-24.

31. Sarker U (2020) Variability, heritability, character association, and path coefficient analysis in advanced breeding lines of rice (*Oryza sativa* L.). Genetika 52(2):711-26.

32. Sivasubramanian S, Madhavamenon P (1973) Genetic analysis of quantitative characters in rice through diallel crosses. Madras Agricultural Journal 60:1097-8.

33. Sudeepthi K, Srinivas TV, Kumar BR, Jyothula DP, Umar SN (2020) Assessment of genetic variability, character association and path analysis for yield and yield component traits in rice (*Oryza sativa* L.). Electronic Journal of Plant Breeding 11(01):144-8.

34. Tiwari DN, Tripathi SR, Tripathi MP, Khatri N, Bastola BR (2019) Genetic variability and correlation coefficients of major traits in early maturing rice under rainfed lowland environments of Nepal. Advances in Agriculture.