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Genetic variability and correlation studies in backcross inbred lines of rice in direct seeded aerobic conditions.

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ABSTRACT

The research was conducted to evaluate the genetic variability parameters and correlation analysis for ten yield-related traits of stabilized Backcross Inbred Lines (BILs), derived from an aerobic restorer AR-9-18 and YPK 198 under direct seeded aerobic conditions at ICAR-IIRR, Hyderabad during kharif 2022. The results indicated that the productive tiller number showed high PCV and GCV. Productive tiller number, primary branches, grain number per panicle, test grain weight, grain weight per panicle and plant yield exhibited a high heritability and also high genetic advance as per cent of mean which demonstrates simple selection would be effective for improvements of these traits. Correlation studies indicated that plant yield was associated significantly positive with productive tiller number, days to 50 percent flowering, and test grain weight.

INTRODUCTION

Rice is one of the most important stable cereals which is a primary dietary for over half of the world's population. Conventional rice cultivation typically relies on transplanting seedlings which require substantial labor, time and water resources. However, rising problems of water constraints, climate change, and manpower limitations led to the adoption of alternate rice production methods. Direct seeded aerobic rice cultivation is a viable alternative to conventional puddled transplanted rice cultivation systems, offering efficient water and nitrogen use, reduced greenhouse gas emissions, and lower labor demand. However, the performance of the genotypes varies in comparison with the transplanted rice. Therefore, genotypes are evaluated in Direct seeded aerobic conditions and the better-performing lines have been selected in accordance to yield and its related traits.

Yield is a complex dependent trait that is highly influenced by genotype, environment and their interaction. Understanding genetic variability, heritability, genetic advance, and the correlation between yield and its associated traits in the advanced breeding lines is essential for the selection and development of well-adapted rice varieties (Owusu *et al.*, 2021). Generally, environmental influence on genotypes is assessed by phenotypic coefficient of variation (PCV), while the inherent variability is estimated by the genotypic coefficient of variation. Moreover, the estimates of heritability and genetic advance are taken into consideration while predicting genetic gain under selection and for selecting superior rice lines (Bhargava *et al.*, 2021). Correlation analysis is used to determine the relationship between traits, researchers can make an informed decision about selection strategies and identify key traits that can improve overall plant performance. Since yield is influenced by multiple factors, correlation analysis helps breeders understand how secondary traits (e.g., plant height, number of tillers, grain number) contribute to yield improvement. Overall, the present study focuses on evaluating stabilized backcross inbred lines

(BILs) for yield and its related traits under direct seeded aerobic conditions assisted by defined statistical approaches.

MATERIALS AND METHODS:

The present study was carried out at the research farm of ICAR-Indian Institute of Rice Research, Hyderabad, Rajendranagar, Telangana. The experimental materials were comprised of 30 stabilized backcross inbred lines (BILs) along with their parents AR-9-18(A medium tall mid-early aerobic restorer with long bold grain) and YPK 198 (Donor possessing yield enhancing genes Gn1a and OsSpl14 (Bhargava *et al.,* 2021)) along with CR DHAN 201 as check. They have been evaluated for yield and its attributing traits in a Randomized block design (RBD) with three replications under direct seeded aerobic conditions during Kharif 2022 with a spacing of 20 × 15 cm. All the recommended packages of practices were used for growing a proper crop. The phenotypic data for ten agronomic traits such as, Days to fifty percent flowering (DFF), Plant height (PH), Number of productive tillers (PT), Panicle length (PL), Number of primary branches (PB), Grains number per panicle (GPP), Spikelet fertility (SF), Test grain weight (TGW), Grain weight per panicle (GWP), and Single plant yield (SPY) were recorded for five plants in each replication, while for the trait Days to fifty percent flowering it was taken on population basis.

Statistical analysis was performed for the data recorded on ten yield-related traits viz., Phenotypic Coefficient of Variation (PCV), Genotypic Coefficient of Variation (GCV), broad-sense heritability, and genetic advance as a percentage of the mean. The computation of PCV and GCV was performed following the methodology defined by Burton and Dewane (1953). The classification of variation was based on the criteria established by Sivasubramanian and Madhava Menon (1973), categorizing it as high (> 20%), moderate (10–20%), and low (< 10%). Broad-sense heritability (h^2bs) was estimated according to the method confined by Lush (1949) and Hanson et al. (1956), which is expressed as a percentage ratio of genotypic variance to total variance. Robinson et al. (1949) classified heritability estimates as high (> 60%), moderate (30-60%), and low (0-30%). The genetic advance was computed following the guidelines by Johnson et al. (1955) and categorized into high (> 20%), moderate (10–20%), and low (< 10%) classes. Simple correlation coefficients were also calculated using Weber and Moorthy's (1952) formula.

RESULTS AND DISCUSSION:

Analysis of variance:

The analysis of variance (ANOVA) indicated highly significant differences (P < 0.001) among the evaluated rice genotypes for all the biometrical traits (Table 1), highlighting substantial heritable variation among the genotypes for all the traits.

TABLE 1: Analysis of variance (ANOVA) for yield and its related traits

SourceofVariation		Replications	Treatments	Error
d.f		2	32	64
MeanSumof Squares	DFF	1.45	224.37**	3.46
	PH	15.44	225.98**	6.07
	PT	0.279	7.007**	1.109
	PL	0.601	12.193**	0.922
	PB	1.866	14.624**	1.470
	GPP	622.26	4695.00**	157.00
	SF	222.1	158.7**	40.7
	TGW	0.565	27.483**	0.962
	GWP	0.1289	1.9548**	0.344
	SPY	1.31	39.69**	4.96

** Significant at 1% level

DFF- Days to maximum flowering, PH- Height of plant (cm), PT-Productive tiller number, PL-Panicle length(cm), PB- Primary branches, GPP- Grain number per panicle, SF-Fertility of spikelet (%), TGW- Weight of 1000 grains (g), GWP- Grain weight per panicle(g), SPY-Single plant yield(g)

Genetic variability parameters:

The estimates of PCV and GCV are crucial to identifying the effects of environmental influence on genotypes. The Variability parameters observed in this experimental study have been presented in the following table 2. For all the traits studied, PCV values were marginally higher in comparison with GCV values, which indicates that the expression of traits was influenced less by environmental factors (Bhargava *et al.* 2021), and (Kumar*et al.* 2018).

The phenotypic coefficient of variation (PCV) estimates were recorded high for productive tiller number (26.43) and grain weight per panicle (20.91). The traits such as primary branches (18.46), grains per panicle (17.70), spikelet fertility (11.15), test grain weight (13.09), and single plant yield (18.52) exhibited moderate estimates for variability. The PCV estimates observed less variation for the trait days to 50 percent flowering (8.87), plant height (8.83), and panicle length (8.77). The trait productive tiller number (21.13) exhibited a high estimate of genotypic coefficient of variation (GCV). In contrast, traits such as Primary branches (15.97), grains per panicle (16.84), test grain weight (12.41), grain weight per panicle (16.32), and single plant yield (15.50) demonstrated moderate estimates of GCV. Conversely, low GCV estimates were observed for days to 50 percent flowering (8.67), plant height (8.48), panicle length (7.86), and spikelet fertility (7.82).

From the estimates of PCV and GCV the trait productive tiller number (26.43 and 21.13) exhibited higher values, indicating that this trait showed a high degree of variability, so direct selection of this trait would be an asset for crop improvement. Similar results of high PCV and GCV for the above characters were reported by Chacko Arun*et al.* (2023), Pragnya *et al.* (2023), Madhuri *et al.* (2024), Gupta *et al.* (2022), Palaniyappan et al. (2020), Aravind Balaji *et al.* (2022) for productive tiller number. The moderate PCV and GCV values were recorded for Primary branches, grains per panicle, test grain weight and single plant yield. The existence of moderate PCV and GCV were reported by Nath and Kole (2021)for primary branches, Ketan and Sarkar (2014) for the trait grains per panicle, while Saha *et al.* (2019) reported it for the trait test grain weight, Chandramohan*et al.* (2016) and Keerthiraj and Biju (2020) for single plant yield.On the other hand, the traits viz., days to 50 percent flowering, plant height and spikelet fertility recorded low level of PCV and GCV, indicating limited variability. This suggests that selection based on these traits may not provide significant yield improvements as the material studied for the trait is of uniform. Similar results were given by Quadri*et al.* (2023) and Abhilash *et al.* (2018).

Heritability in a broad sense and genetic advance is also an important criterion to take into consideration for selecting the components traits in enhancing yield along with PCV and GCV estimates (Johnson *et al.* 1955). Hanson *et al.* (1956) suggested that broad sense heritability comprises of additive and non-additive components of gene effects. In this study, broad sense heritability was estimated, and it was recorded that almost all the traits studied exhibited high heritability except for spikelet fertility which shows moderate heritability. The traits productive tiller number per plant, primary branches, grains per panicle, test grain weight, grain weight per panicle, and single plant yield exhibited high genetic advance, whereas days to 50 percent flowering, plant height, panicle length, and spikelet fertility exhibited moderate level of genetic advance as percent of mean. From the observed results, the traits that showed high heritability and high genetic advance such as productive tiller number per plant, primary branches, grains per panicle, test grain weight, grain weight per panicle, and single plant yield advocates additive gene action. Similar reports of high heritability and high genetic advance advocating additive gene action were also discussed by Chavan *et al.* (2022), and Dinkar *et al.* (2023) Meanwhile, (Demeke *et al.* 2023) suggested that the traits that recorded high heritability and moderate genetic advance offers limited scope for improvements through direct selection.

TABLE 2: Estimates of PCV, GCV, Heritability and Genetic Advance.

S.No	Characters	Mean	Range		Phenotypic Variance	Genotypic Variance	PCV (%)	GCV (%)	Heritability in broad sense (h2) (%)	Genetic Advance as % of mean
			Min	Max						
1	DFF	98.95	85.56	118.39	77.10	73.63	8.87	8.67	95.51	17.45
2	PH	100.88	84.41	118.28	79.37	73.30	8.83	8.48	92.35	16.80
3	PT	6.67	4.64	10.10	3.03	1.96	26.43	21.13	63.93	34.80
4	PL	24.65	20.59	28.77	4.67	3.75	8.77	7.86	80.29	14.51
5	PB	13.10	8.49	18.00	5.85	4.38	18.46	15.97	74.89	28.48
6	GPP	230.84	143.04	314.80	1669.86	1512.389	17.70	16.84	90.57	33.02
7	SF	80.47	63.57	92.30	80.03	39.32	11.15	7.82	49.14	11.29
8	TGW	23.48	17.87	29.36	9.45	8.49	13.09	12.41	89.82	24.23
9	GWP	4.48	2.35	6.21	0.88	0.53	20.91	16.32	60.95	26.26
10	SPY	22.07	12.33	27.81	16.53	11.57	18.52	15.50	70.03	26.72

DFF- Days to maximum flowering, PH- Height of plant (cm), PT-Productive tiller number, PL-Panicle length(cm), PB-Primary branches, GPP- Grain number per panicle, SF-Fertility of spikelet (%), TGW- Weight of 1000 grains (g), GWP- Grain weight per panicle(g), SPY- Single plant yield(g)

Fig. 1. Bar graph of Phenotypic Coefficient of Variation and Genotypic Coefficient of Variation.

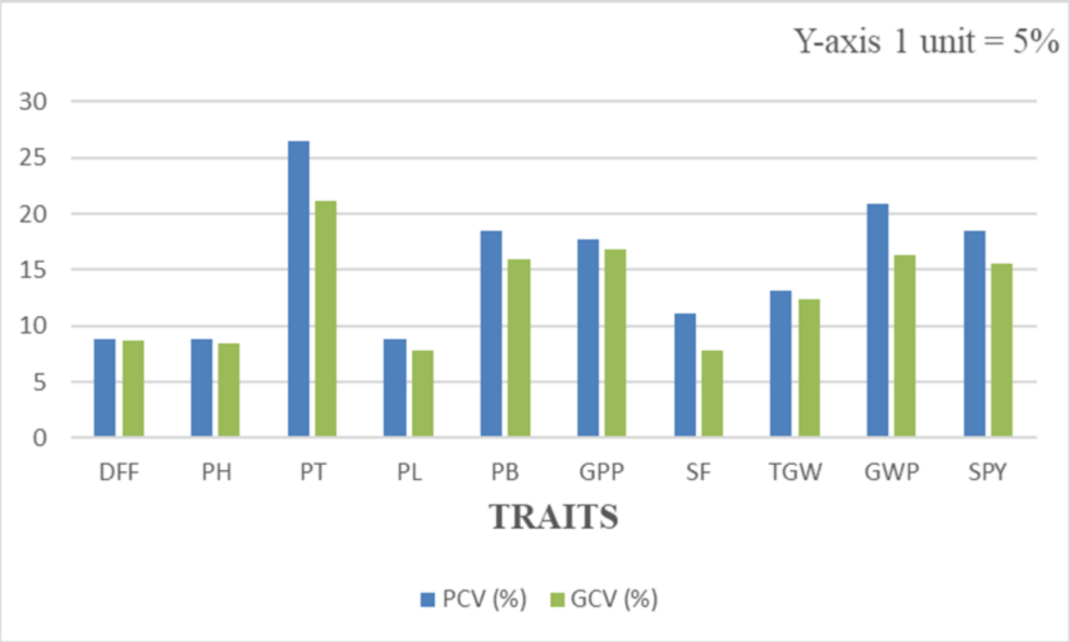
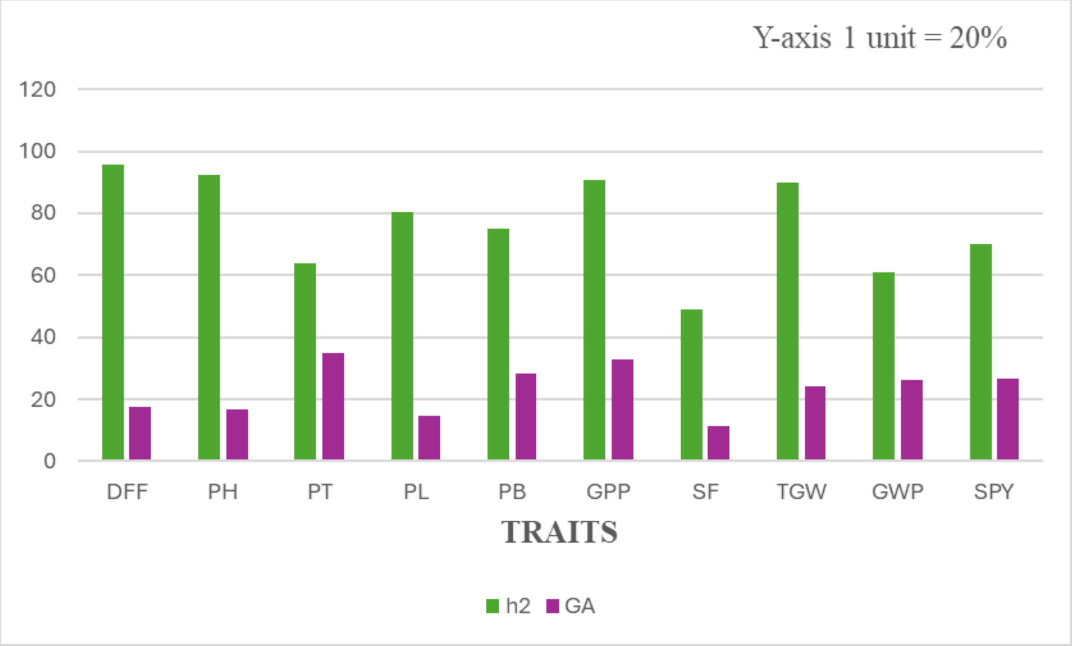


Fig. 1. Bar graph of heritability in broad sense (h^2) and Genetic advance



Correlation analysis:

Correlation analysis provides valuable insights into the nature and extent of relationships among different traits, enabling the identification of component traits that can be targeted to enhance yield. In this study, the correlation coefficients of ten biostatistical traits were presented in table 3.

The correlation analysis results revealed that the trait days to 50 percent flowering showed a significant positive correlation with plant height, panicle length, grains per panicle, and single plant yield and negatively correlated with spikelet fertility.Similarly, plant height showed a significant positive correlation with panicle length, Primary branches, test grain weight, and grain weight per panicle and exhibited negative correlation with number of productive tillers.The trait number of productive tiller showedsignificantpositive association with single plant yield (Manivelan *et al.* 2022), but negative association withPrimary branches, grains per panicle, test grain weight, and grain weight per panicle.

Panicle length exhibited a significantly positive correlation with grains per panicle, test grain weight, and grain weight per panicle. The traits Primary branchesandgrains per paniclehad a significant positive interrelation and also, had a positive influence on grain weight per panicle. However, they showed a negative correlation with the number of productive tillers. Additionally, grains per panicle exhibited a significant negative correlation with spikelet fertility. Test grain weight showed strong positive correlations with grain weight per panicle and single plant yield and a negative association with productive tiller number. Overall, Single plant yield exhibited significant positive correlations with days to 50 percent flowering, productive tiller number, and test grain weight.

Based on the observed results from the correlation analysis revealed that among the yield traits studied, productive tiller number, days to 50 percent flowering, and test grain weight emerged as the most critical traits due to their strong correlation coefficients and significant direct effects on plant yield. Similar research findings have been reported by Limbongan*et al.* (2024), Mandal *et al.* (2023), Kalaivani *et al.* (2023),Sadimantara *et al.* (2023), Thuy *et al.* (2023).However, a negative correlation was observed between productive tiller number and grain number per panicle, indicating that an increase in grain number could result in a reduction in productive tiller number under direct seeded aerobic conditions of evaluated backcross inbred lines. Therefore, selecting lines that balance sufficient grain number with a maximum number of productive tillers would be a strategic approach to improving yield.

Table 3. Correlation analysis among yield and its related traits.

Traits	DFF	PH	PT	PL	PB	GPP	SF	TGW	GWP	SPY
DFF	1 **	0.2753 **	0.0512 NS	0.277 **	-0.1496 NS	0.2396 *	-0.3655 **	-0.0654 NS	0.1453 NS	0.3611 **
PH		1 **	-0.33 **	0.4999 **	0.22 *	0.0999 NS	0.0799 NS	0.2797 **	0.3448 **	0.1533 NS
PT			1 **	-0.1926 NS	-0.4093 **	-0.393 **	-0.1542 NS	-0.2726 **	-0.5306 **	0.3144 **
PL				1 **	-0.0043 NS	0.2648 **	-0.086 NS	0.3238 **	0.3019 **	0.1964 NS
PB					1 **	0.347 **	0.1179 NS	-0.0119 NS	0.483 **	-0.0416 NS
GPP						1 **	-0.2536 *	-0.1855 NS	0.6076 **	0.1562 NS
SF							1 **	0.0745 NS	0.0871 NS	-0.1918 NS
TGW								1 **	0.2296 *	0.2477 *
GWP									1 **	0.1706 NS
SPY										1 **

DFF- Days to maximum flowering, PH- Height of plant (cm), PT-Productive tiller number, PL-Panicle length(cm), PB-Primary branches, GPP- Grain number per panicle, SF-Fertility of spikelet (%), TGW- Weight of 1000 grains (g), GWP- Grain weight per panicle(g), SPY- Single plant yield(g)

CONCLUSION

The present experimental study provides valuable insights into the genetic variability parameters for all the characters studied, along with their association through correlation analysis. PCV and GCV estimates revealed variability among the genotypes and highlighted the potential for selection in increasing the productive tillers. High heritability estimates coupled with high genetic advance for productive tiller number, Primary branches, grains per panicle, test grain weight, grain weight per panicle, and single plant yield advocates that these traits are primarily governed by additive gene action, which turns as a promising target for selection in breeding programme. Correlation analysis pinpoints the traits,productive tiller number, days to 50 percent flowering, and test grain weight are the potential valuables due to their strong correlation coefficients and significant direct effects on plant yield.

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