Plant Archives Vol. 24, No. 1, 2024 pp. 157-162

e-ISSN:2581-6063 (online), ISSN:0972-5210



**Plant Archives** 

Journal homepage: http://www.plantarchives.org DOI Url : https://doi.org/10.51470/PLANTARCHIVES.2024.v24.no.1.023

# EXPLORING GENETIC VARIABILITY, CORRELATION AND PATH ANALYSIS FOR YIELD AND ITS COMPONENT TRAITS IN RICE (ORYZA SATIVA L.)

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The present investigation was carried out with 72 germplasm lines and three checks of rice (Oryza sativa L.) were grown at Crop Research Station, Masodha Ayodhya conducted in the Genetics and Plant Breeding Farm, Acharya Narendra Deva University of Agriculture and Technology, Kumarganj, Ayodhya (U.P.) during Kharif June 2022- February 2023. Data on 10 characters, including grain yield per plant focused on assessing genetic variability, studying correlation and path coefficient analysis with genetic diversity within the germplasm collections. The analysis of variance (ANOVA) highlighted the substantial impact of blockinduced variation on various grain yield-contributing traits and seed quality parameters. Genotype variations were significant across all traits, emphasizing the potential for diverse utilization in selection and hybridization programs. The study identified substantial genetic variability, with high broad-sense heritability (>80%) in ABSTRACT traits such as days to maturity, number of productive tillers, biological yield, harvest index, and grain yield per plant. Correlation coefficients revealed strong positive associations between grain yield per plant and harvest index, as well as days to maturity. Significant negative correlations were observed with days to 50% flowering, flag leaf area, biological yield and 1000-grain weight. Path coefficient analysis highlighted the influential role of harvest index in positively affecting grain yield per plant, while days to 50% flowering exhibited a highly negative impact.

Key words : Heritability, Genetic advance, GCV, PCV, Correlation, Path coefficient.

# Introduction

Rice (*Oryza sativa* L.) is a short-day, C3 plant that is cultivated primarily in Asian agroecosystems. It belongs to the family Poaceae (Graminae) and is an annual, semiaquatic, and self-pollinating crop. There are two main domesticated species of rice: Asian rice (*Oryza sativa* L.) and African rice (*Oryza glaberrima* Steud.), both possessing the genome AA (2n = 24) (Hoyos *et al.*, 2020). The data for the current 2022-23 *kharif* season reveals that out of the total 3.59 million hectares under kharif crops, paddy was cultivated on 3.13 million hectares (Anonymous, 2023). In India, it accounts for 20-25% of agricultural production and ensures food security for over half of the population (Wang, 2022). Rice production in

India constitutes 55% of the total cereal production, with 116.48 million tons of rice being produced in the year 2018-19 from approximately 44.16 million hectares of planted rice land (AGRISTAT, 2019). Rice is one of the chief cereals consumed across the world. Rice proteins are known for having amino corrosive substances and are uniquely wealthy in lysine content (RathnaPriya *et al.*, 2019). India ranks first in the area of rice production and also first in rice export. The interest in food is consistently extending with the increment of populace, making a yearly increment of 3% for each years popular rice (Sujarwo *et al.*, 2022).

Variation among the varieties for the economical yield and associated traits is the foundation of any selection program in breeding (Begna, 2021). The heritable variability within the population or intermating resource can be concluded by genetic diversity. This helps to succeed in the subject of plant breeding by projecting genetic variation and keen information about the concerned traits in the given resource. The information about the gene exchange to offspring's can be evaluated using heritability. Heritability provides information about the capability of a trait that can be transmitted to possible generations (Hansen and Pélabon, 2021). Heritability estimates thus helps to predict the expression of traits in further generations. A combination of genetic advance and heritability is helpful for proper selection is said by (Johnson et al., 1955). High heritability coupled with high genetic advance results helps breeder to select preferable estimations in breeding programme. The path coefficient analysis predicts the direct and indirect effects of source variables to the expressing variable. The nature of effect like direct or indirect effect of yield and its characteristics

**Table 1 :** List of 72 Germplasms of rice used in investigation.

can be explained through path coefficient analysis (Baye *et al.*, 2020). There after this method can be used in selection techniques which helps to read about specific traits resulting in correlation between grain yield and other traits.

The coefficient of correlation expresses associations between two variables, but it doesn't indicate which variable is reliant on which or which variable is independent. Consequently, it is essential to study the path coefficient. Wright (1921) invented the idea of path analysis, but Dewey and Lu (1959) were the first to apply the method to plant selection. The correlation coefficient is divided into measurements of direct and indirect effects by the path coefficient, which is only a standardized partial regression coefficient. In order to determine the most crucial yield components, path analysis clearly demonstrates the relative relevance of various yield components. Any crop-breeding program's success is dependent on the type and degree of genetic variability available (Swarup et al., 2021). Knowing the type and extent of variability, heritability, and genetic progress in the breeding materials at hand is crucial for developing a successful breeding strategy (Terfa and Gurmu, 2020). Since genetic variation is heritable, any selection programme must take into account its importance.

#### **Materials and Methods**

# **Experimental site**

The current field experiment took place at the Crop Research Station (CRS) in Masodha, while certain laboratory experiments were carried out in the Department of Genetics and Plant Breeding, Narendra Deva University of Agriculture and Technology, Ayodhya (U.P.), India. Geographically, Narendra Nagar is

Geetu-II	Bilaspur	Kalakand	101/5115
Sarye	Yuvraj	K-14	102/5110
Lindhinia-I	Vijets	CH-1039	103/5119
Dilaora Local	Palhari	KMP-41	104/1503
Chingard-I	Padheri	KSR-4111	106/5111
Tarochani	Mangal	T-65	107/5106
Indrajon	Harikesh	KR-103-96	108/5113
Sahdlia	PR-6	GMP-12	109/5114
Darahi	NC-495	CR-209	110/5107
Turahwa	H-118	TN-1	111/5109
Loungchoor	NC-491	KSR	112/5108
Local-chl-Fzd	NC-492	CR-118	113/5127
Kataribhog	T-1242(I)	W-418	Sarjoo-52©
Bans	N-10-B	T-116	NDR-97©
Sirdgarh	Nanital(saryu)	W-496	Narendra Usar Dhan-3 ©
	Geetu-II Sarye Lindhinia-I Dilaora Local Chingard-I Tarochani Indrajon Sahdlia Darahi Turahwa Loungchoor Local-chl-Fzd Kataribhog Bans Sirdgarh	Geetu-IIBilaspurSaryeYuvrajLindhinia-IVijetsDilaora LocalPalhariChingard-IPadheriTarochaniMangalIndrajonHarikeshSahdliaPR-6DarahiNC-495TurahwaH-118LoungchoorNC-491Local-chl-FzdNC-492KataribhogT-1242(I)BansN-10-BSirdgarhNanital(saryu)	Geetu-IIBilaspurKalakandSaryeYuvrajK-14Lindhinia-IVijetsCH-1039Dilaora LocalPalhariKMP-41Chingard-IPadheriKSR-4111TarochaniMangalT-65IndrajonHarikeshKR-103-96SahdliaPR-6GMP-12DarahiNC-495CR-209TurahwaH-118TN-1LoungchoorNC-491KSRLocal-chl-FzdNC-492CR-118KataribhogT-1242(I)W-418BansN-10-BT-116SirdgarhNanital(saryu)W-496

positioned at 26.47°N latitude and 82.12°E longitude, with an elevation of 113 meters above sea level, situated in the Gangetic plains of eastern Uttar Pradesh, India.

#### **Experimental details**

The present investigation utilized 72 rice germplasm lines, in addition to three checks *viz*. Narendra Usar Dhan-3, Sarjoo-52 and NDR-97 tabulated in Table 1. These germplasm lines demonstrated a diverse range of variation in both agronomic and morphological traits. The cultivation of these lines took place during the *Kharif* season of 2022, employing an Augmented Block Design.

#### Statistical analysis

The analysis of variance for various traits in the augmented design followed the methodology outlined by Federer (1956). To assess variability in different traits, the approach recommended by Burton and de Vane

 
 Table 2 : Analysis of variance of augmented block design for 10 characters in rice genotypes.

Characters	Blocks	Checks	Error
	<b>D.F.</b> (7)	<b>D.F.</b> (2)	<b>D.F.</b> (16)
Days to 50% flowering	50.08**	176.84**	3.27
Days to maturity	105.09**	113.12**	4.68
Plant height (cm)	377.28**	4166.21**	20.78
No. of productive tiller/plant	1.96**	3.04**	0.26
Panicle length (cm)	15.29**	44.46**	1.91
Flag leaf area (cm <sup>2</sup> )	202.70**	42.91**	1.24
Biological yield/plant (g)	99.44**	832.69**	3.32
Harvest index (%)	779.48**	189.81**	4.47
1000 grain weight (g)	2.25**	41.33**	0.94
Grain yield/plant (g)	47.31**	184.63**	0.41

\*,\*\*significant at 5% and 1% level, respectively.

(1953) was employed. The heritability in the broad sense ( $h^2b$ ) was calculated using the formula proposed by Hanson *et al.* (1956). The expected genetic advance (GA%) was estimated based on the formula suggested by Johnson *et al.* (1955). The association among different traits at both genotypic and phenotypic levels was determined as per the methodology outlined by Searle (1961). Path coefficient analysis was carried out according to Dewey and Lu (1959).

# **Results and Discussion**

#### Analysis of Variation (ANOVA)

The analysis of variance for the augmented block design, incorporating 72 rice genotypes along with three checks was conducted for 10 different traits, as outlined in Table 2. The results revealed that the mean squares attributed to the block were highly significant for all grain yield-contributing traits and seed quality parameters. Block-induced variation was notably significant for traits such as days to 50% flowering, days to maturity, plant height (cm), number of productive tillers/plants, panicle length (cm), flag leaf area (cm<sup>2</sup>), biological yield/plant (g), harvest index (%), 1000-grain weight (g) and grain yield/plant (g). Similarly, significant differences were observed among the check varieties for all the studied traits, excluding germination (%), where the mean square was non-significant. The variance analysis underscores substantial genotype variations across all traits, suggesting significant diversity among the genotypes. This observed high degree of variability presents opportunities for their utilization in various selection and hybridization programs. Sarker (2020), Nawale et al. (2020), Lakshmi et al. (2021), Rahman et al. (2021), Awadh-Allah et al. (2022) and Heera et al. (2023) have reported comparable findings in studies.

Characters	Mean	R	ange	PCV	GCV	Heritability (%)	GA%
		Min	Max	(%)	(%)	$h^2b$	mean
Days to 50% flowering	99.17	89.00	109.00	2.77	2.09	56.68	3.24
Plant height (cm)	124.18	109.00	139.00	3.23	2.72	70.94	4.72
No. of Productive Tillers/plant	133.34	94.15	192.70	10.46	9.89	89.32	19.25
Panicle length (cm)	10.29	7.20	14.16	8.96	7.49	69.81	12.89
Flag leaf area (cm2)	27.65	21.21	33.00	6.94	4.81	48.13	6.88
Days to maturity	36.45	18.44	60.48	15.35	15.04	96.04	30.37
Biological yield /plant (g)	39.76	28.18	61.11	12.14	11.25	85.77	21.46
Harvest Index (%)	40.73	18.30	91.92	16.31	15.46	89.87	30.20
1000-grain weight (g)	23.16	19.14	26.75	6.26	4.65	55.27	7.12
Grain yield/plant (g)	15.61	9.35	33.23	16.41	15.89	93.69	31.68

Table 3 : Estimates of mean, range, heritability, genetic advance and coefficient for 10 characters in rice germplasm.

# Genetic variability, heritability, genetic advance and coefficient of variance

Heritability and genetic advance in percent of mean were calculated for all the ten characters and are presented in Table 3. High broad-sense heritability estimates (>80%) were observed for days to maturity (96.04%), number of productive tillers per plant (89.32%). biological yield (85.77%), harvest index (89.87%) and grain yield per plant (93.69%). Moderate heritability estimates (60-80%) were noted for plant height (70.94%)and panicle length (69.81%), while lower estimates (<60%) were recorded for days to 50% flowering (56.68%), flag leaf area (48.13%) and 1000-grain weight (55.27%). Genetic advance in percent of mean revealed high estimates (>20%) for days to maturity (30.37%), biological yield/plant (21.46%), harvest index (30.20%) and grain yield per plant (31.68%). Medium genetic advance estimates (10.20%) were demonstrated for number of productive tillers (19.25%) and panicle length (12.89cm), while lower estimates (<10%) were observed for days to 50% flowering (3.24%), plant height (4.72cm), flag leaf area (6.88 cm<sup>2</sup>) and 1000-grain weight (7.12%).

In terms of coefficient of variation, phenotypic values consistently exceeded genotypic values across all traits. Moderate estimates (10.20%) of both GCV and PCV, respectively, were observed for days to maturity (15.04%, 15.35%), biological yield/plant (11.25%, 12.14%), harvest index (15.46%, 16.31%) and grain yield/plant (15.89%, 16.41%). The remaining characters, including days to 50% flowering, plant height, number of productive tillers/ plant, panicle length, and 1000-grain weight, exhibited low estimates only for GCV. Behera *et al.* (2020), Palaniyappan *et al.* (2021) reported similar results.

# **Correlation coefficients**

The estimates of simple correlation coefficients between ten characters are represented in Table 4. The correlation analysis among the ten characters revealed significant associations, particularly highlighting the strong positive correlations between grain yield per plant and harvest index (0.841) as well as days to maturity (0.254). Furthermore, grain yield per plant exhibited significant negative correlations with days to 50% flowering (-0.154), flag leaf area (-0.098), biological yield (-0.078) and 1000grain weight (-0.027). The 1000-grain weight demonstrated significant negative correlations with days to 50% flowering (-0.197), but positive correlations with the number of productive tillers per plant (0.061), flag leaf area (0.096) and biological yield per plant (0.025). Harvest index displayed a highly significant positive

Chousefour	Darre to	Dlout	No of	Daniala	Eloc loof	Diclosical	Ucurroct	1000 anoin	C.m.in
Claracters	Days to maturity	Fiant height (cm)	productive tillers/plant	ramce length (cm)	r lag leat area(cm <sup>2</sup> )	biological yield /plant (g)	Index (%)	weight (g)	yield/plant (g)
Days to 50% flowering	$0.614^{**}$	-0.182	0.173	0.116	-0.256*	0.071	-0.153	-0.197	-0.154
Plant height (cm)		-0.001	0.048	-0.019	-0.265*	0.143	-0.175	-0.041	-0.135
No. of Productive Tillers/plant			0.025	-0.210	0.364**	-0.076	0.186	0.061	0.176
Panicle length (cm)				-0.118	600.0	0:005	0.048	-0.029	0.044
Flag leaf area (cm2)					-0.091	0.095	-0.189	0.096	-0.098
Days to maturity						-0.091	0.254*	-0.018	0.254*
Biological yield /plant (g)							-0.574**	0.025	-0.078
Harvest Index (%)								-0.013	$0.841^{**}$

Characters	Days to	Days to	Plant	No.of	Panicle	Flag leaf	Biological	Harvest	1000-grain	Grain
	50% flowering	maturity	height (cm)	productive tillers/plant	length (cm)	area (cm²)	yield /plant (g)	Index (%)	weight (g)	yield/plant (g)
Days to 50% flowering	-0.0369	0.0066	-0.0022	-0.0005	0.0095	0.0001	0.0430	-0.1825	0.0084	-0.154
Plant height (cm)	-0.0226	0.0108	0.0000	-0.0001	-0.0016	0.0001	0.0866	-0.2096	0.0018	-0.135
No. of Productive Tillers/plant	0.0067	0:0000	0.0120	-0.0001	-0.0172	-0.0001	-0.0457	0.2231	-0.0026	0.176
Panicle length (cm)	-0.0064	0.0005	0.0003	-0.0027	-0.007	0.0000	0.0031	0.0577	0.0013	0.044
Flag leaf area (cm2)	-0.0043	-0.0002	-0.0025	0.0003	0.0819	0.0000	0.0571	-0.2267	-0.0041	-0.098
Days to maturity	0.0094	-0.0029	0.0044	0:0000	-0.0074	-0.0002	-0.0547	0.3043	0.0008	0.254
Biological yield /plant (g)	-0.0026	0.0015	-00000	0:0000	0.0078	0.0000	0.6038	-0.6866	-0.0011	-0.078
Harvest Index (%)	0.0056	-0.0019	0.0022	-0.0001	-0.0155	-0.0001	-0.3465	1.1966	0.0005	0.841
1000-grain weight (g)	0.0073	-0.0004	0.0007	0.0001	0.0079	0.0000	0.0149	-0.0150	-0.0428	-0.027

correlation with biological yield per plant (-0.574). Biological yield per plant showed significant positive correlation with days to 50% flowering (0.071). Flag leaf area exhibited significant positive correlations with the number of productive tillers per plant (-0.364) and highly significant negative correlations with days to 50% flowering (-0.256) and plant height (-0.265). Additionally, days to maturity showed a highly significant correlation with days to 50% flowering (0.614). Other characters did not exhibit highly significant or significant correlations with one another, suggesting their non-significant associations. The observed strong positive correlations between yield and its components align with existing literature on rice. Hence, the selection of these traits for high yield is recommended. Negatively correlated traits for both phenotypic and genotypic correlations, like days 50% Flowering, plant height, flag leaf length, biological yield and thousand seed weight, similar results recorded for plant height by Kondi et al. (2022), flag leaf length by Yadav and Pitha (2022) are not suggested for trait selection to improve the grain yield.

#### Path coefficient analysis

Path coefficient analysis, utilizing the simple correlations among the 10 characters, was conducted to assess the direct and indirect effects on grain yield per plant, as presented in Table 5. Harvest index% exhibited the highest positive direct effect on grain yield per plant (0.841), indicating a substantial positive influence on yield. Conversely, Days to 50% flowering (-0.154) showed a highly negative indirect effect on grain yield. Plant height (-0.135), Number of productive tillers per plant (0.176), and flag leaf area (-0.098) demonstrated significant positive direct effects on grain yield per plant. Days to 50% flowering (-0.154), panicle length (0.044), days to maturity (0.254), biological yield per plant (-0.078) and 1000-grain weight (-0.027) showed considerable negative indirect effects on grain yield per plant. Studies by Beena et al. (2021) and Kondi et al. (2022) identified biological yield and harvest index as important direct and indirect yield-contributing characters. The indirect effects of the remaining characters were deemed too low to be considered significant.

# Conclusion

High heritability coupled with high genetic advance possesses the additive gene action, which prioritizes selection of traits for breeding program. Block-induced variations were notable in grain yield-contributing traits and seed quality parameters. With high broad-sense heritability (>80%) identified in crucial traits, such as days to maturity and harvest index, the research underscores

Residual effect = 0.513

the potential for diverse utilization in breeding programs. Correlation and path coefficient analyses further revealed vital associations, notably the positive influence of harvest index on grain yield per plant. Hence, concluded the selection among the traits is preferred to increase the yield of rice per plant.

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