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Correlation, path and genetic diversity analysis for yield and yield contributing traits in rice (*Oryza sativa* L.)

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Abstract

The present investigation was conducted to assess the correlation coefficient, path analysis and genetic diversity among 71 rice genotypes including 7 checks for yield traits in randomized block design with two replications during *kharif* 2023. The grain yield per plot was found to be positively correlated with effective tillers/plot, spikelet fertility ratio, biological yield, 1000 grain weight and harvest index. Path analysis result revealed that the biological yield, harvest index, total spikelets/panicle, effective tillers/plot, spikelet fertility ratio, plant height and flag leaf length had a positive direct effect with grain yield. In Principal Component analysis the total variance was partitioned into five PCs contributing maximum total diversity between the genotypes due to various studied traits. It further revealed that nine genotypes were more divergent among the studied genotypes.

Keywords: Correlation coefficient, path analysis, genetic diversity, rice genotypes, yield traits

Introduction

Rice is a member of the genus *Oryza*, the family Poaceae and the subfamily Bambusoideae. There are two cultivated species and 22 wild species. Most cultivable species are diploid ($2n = 24$). Rice is one of the primary carbohydrate sources for half of the world's population. More than 90% of rice is grown and consumed in Asia, where it is a staple diet for most people (Srujana *et al.*, 2017) [12]. Rice is a vital source of food security accounting for more than 40% of food grain production in India. Rice also plays a pivotal role in nutrition, employment, economy, culture and history. Correlation just assesses the relationship between two variables whereas path coefficient analysis evaluates the direct and indirect causes of association (Dewey and Lu, 1959) [3]. Principal component analysis (PCA) is a multivariate technique widely used for data compression, reduction and transformation.

Materials and Methods

The experimental material possesses 71 genotypes including 7 check varieties. The experiment was conducted at the Research and Instructional Farm, Department of Genetics and Plant Breeding, Indira Gandhi Krishi Vishwavidyalaya Raipur, Chhattisgarh during the *Kharif* season of 2023. Data of the quantitative traits were recorded in five randomly tagged plants in each genotype in each replication. The mean data recorded for various biometrical traits were subjected to statistical analysis. Plot-based data was collected for traits such as Days to 50% flowering, effective tiller, grain yield and biological yield.

Results and Discussion

The analysis of variance (ANOVA) revealed that the genotypes differed significantly for all the characters under investigation indicating the existence of variation among the genotypes. The Grain yield/plot (kg) exhibited significant highly positive correlation with traits effective tiller/plot (0.817) followed by biological yield (0.714), harvest index (0.621), test weight (0.543), spikelet fertility ratio (0.242) and significant highly negative correlation with flag leaf length (-0.359). Path coefficient analysis revealed significant positive direct effects between grain yield and biological yield (0.970) followed by harvest index (0.558), total spikelet/panicle (0.363), effective tiller/plot (0.174), spikelet fertility ratio (0.135), plant

height (0.104) and flag leaf length (0.12). A high negative direct effect is shown by character total filled spikelet/panicle (-0.424), days to 50% flowering (-0.343), 1000 grain weight (-0.188) and panicle length (-0.041). Similar findings have been produced by Kishore *et al.* (2018) [7], Parimala *et al.* (2020) [11], Gupta *et al.* (2020) [6], Naik *et al.* (2022) [10], Giri *et al.* (2022) [4], Basavaraj *et al.* (2022) [11] and Vennela *et al.* (2022) [2].

The various yield attributing traits contribute to total variance measured for each variable. In this study, five components showed Eigen values of >1 and showed cumulative variation of 77.5% (Table 3). The first principal component (PC1) contributed 24.46%, while the second principal component (PC2) contributed 21.4%, totaling 45.96% cumulative variation. The outcomes of the current study were consistent with the results of Nachimuthu *et al.* (2014) [9], Gour *et al.* (2017) [5] and Burman *et al.* (2021) [2]. PC2, PC3, PC4, and PC5 accounted for 21.46%, 12.95%, 9.6%, and 9.1% variability, respectively, among the genotype for the traits under study. The important characters of PC1 were the flag leaf length (0.378), no. of

spikelets/panicle (0.325), total filled spikelets/panicle (0.262), days to 50% flowering (0.32) were categorized by the first principal component. Similar findings were reported by Kumari *et al.* (2021) [8]. The second principal component was contributed mostly by biological yield/plot (0.417), total filled spikelets/panicle (0.409) grain yield/plot (0.403) and no. of spikelets/panicle (0.377), effective tillers per plot (0.335), days to 50% flowering (0.333) which explained that PC2 discriminated those genotypes having higher no. of effective tiller/plot and harvest index. Plant height (0.598), panicle length (0.519) were the main traits contributing to PC3 whereas spikelet fertility ratio (0.64) were the main contributing traits for PC4. PC5 was discriminated by biological yield/plot (0.488), 1000 grain weight (0.422) and spikelet fertility ratio (0.406).

The genotype wise biplot diagram of the 71 rice genotypes (scores) across the first two PC axes (Fig. 2) revealed that genotypes the R2733-6-1 (2), Vandana (71), R2723-64-1 (7), R2733-118 (11), R2733-124 (12), R2733-132 (14), R2740-349-1 (40), R2744-17-1 (51), and R2736-119-1 (29) were divergent for the characters under analysis.

Table 1: Genotypic correlation coefficients of yield attributing traits.

TRAITS	DFF	PH	FLL	ET	NSP	PL	NFS	SF	BY	TW	HI	GY
DFF												
PH	0.285**											
FLL	0.436**	0.383**										
ET	0.040	-0.066	-0.420**									
NSP	0.496**	0.044	0.354**	0.016								
PL	0.284**	0.600**	0.204*	0.036	0.176*							
NFS	0.435**	0.056	0.204*	0.095	0.950**	0.133						
SF	-0.244**	0.007	-0.121	0.108	-0.087	-0.117	0.220**					
BY	0.519**	0.123	-0.066	0.345**	0.289**	0.098	0.332**	0.050				
GW	-0.294**	0.095	-0.197*	0.303**	-0.129	-0.001	-0.090	0.164	0.346**			
HI	-0.355**	-0.074	-0.320**	0.739**	-0.145	0.075	-0.047	0.192*	-0.094	0.397**		
GY	0.011	0.030	-0.359**	0.817**	0.007	0.062	0.134	0.242**	0.714**	0.543**	0.621**	

DFF-days to 50% flowering PH-plant height FLL-Flag leaf length NSP-Number of effective tillers/plot NSP-Number of spikelets/panicle, PL-Panicle length, NFS-Number of spikelets/panicles, SFR-Spikelet fertility ratio, BY-Biological yield/plot, 1000 HI-Harvest index, GW-1000 Grain weight

Table 2: Direct and indirect effect of yield attributing trait

TRAITS	DFF	PH	FLL	ET	NSP	PL	NFS	SF	BY	TW	HI	'r' of GY
DFF	-0.34329	0.02984	0.00533	0.00696	0.18026	-0.01166	-0.1847	-0.03298	0.50433	0.05541	-0.19812	0.011
PH	-0.09778	0.10474	0.00468	-0.01159	0.01603	-0.02463	-0.02369	0.00098	0.11988	-0.01789	-0.04111	0.030
FLL	-0.14972	0.04014	0.01222	-0.07332	0.12872	-0.00836	-0.0867	-0.01639	-0.06387	0.03725	-0.17861	-0.359**
ET	-0.0137	-0.00696	-0.00514	0.17442	0.00577	-0.0015	-0.04018	0.01453	0.3349	-0.05716	0.41232	0.817**
NSP	-0.17017	0.00462	0.00433	0.00277	0.36364	-0.00724	-0.40332	-0.01171	0.28056	0.02437	-0.08074	0.007
PL	-0.09745	0.06282	0.00249	0.00636	0.0641	-0.04108	-0.05631	-0.01581	0.09491	0.00015	0.04164	0.062NS
NFS	-0.14942	0.00585	0.0025	0.01652	0.34563	-0.00545	-0.42434	0.02968	0.32244	0.01697	-0.02599	0.134
SF	0.08376	0.00076	-0.00148	0.01875	-0.0315	0.00481	-0.09318	0.13516	0.04849	-0.03096	0.10722	0.242**
BY	-0.1783	0.01293	-0.0008	0.06016	0.10507	-0.00401	-0.14091	0.00675	0.97099	-0.06533	-0.05246	0.714**
GW	0.10078	0.00993	-0.00241	0.05282	-0.04695	0.00003	0.03815	0.02217	0.33608	-0.18874	0.22158	0.543**
HI	0.12186	-0.00772	-0.00391	0.12886	-0.05261	-0.00306	0.01976	0.02597	-0.09128	-0.07494	0.5581	0.621**

Residual Value=0.05

DFF-days to 50% flowering, PH-plant height, FLL-Flag leaf length, NSP-Number of effective tillers/plot, NSP-Number of spikelets/panicle, PL-Panicle length, NFS-Number of spikelets/panicles, SFR-Spikelet fertility ratio, BY-Biological yield/plot, 1000 HI-Harvest index, GW-1000 Grain weight

Table 3: Eigen value, percentage of variance and eigen vector of 71 rice genotypes for yield and grain yield

PC	PC1	PC2	PC3	PC4	PC5
Eigenvalues	2.935	2.576	1.555	1.153	1.092
Proportion	24.461	21.466	12.955	9.608	9.100
Cumulative Proportion	24.461	45.96	58.88	68.49	77.59
TRAITS	PC1	PC2	PC3	PC4	PC5
DFE	0.32	0.333	0.054	-0.315	-0.138
PH	0.172	0.17	0.598	0.25	0.074
FLL	0.378	0.028	0.18	0.035	0.124
ET	-0.321	0.335	-0.028	-0.066	-0.225
NSP	0.325	0.377	-0.345	0.117	-0.123
PL	0.156	0.194	0.519	0.265	-0.28
NFS	0.262	0.409	-0.39	0.301	-0.016
SF	-0.145	0.075	-0.164	0.64	0.406
BY	-0.029	0.417	0.065	-0.427	0.488
TW	-0.305	0.166	0.174	0.112	0.422
HI	-0.403	0.176	0.014	0.185	-0.483
GY	-0.382	0.403	0.069	-0.14	-0.018

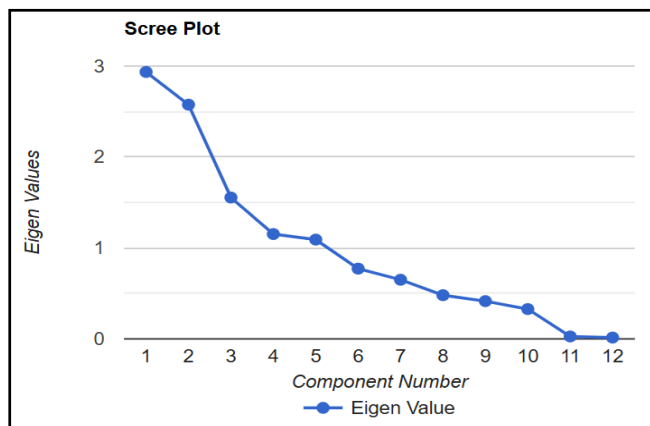


Fig 1: Scree test for component analysis

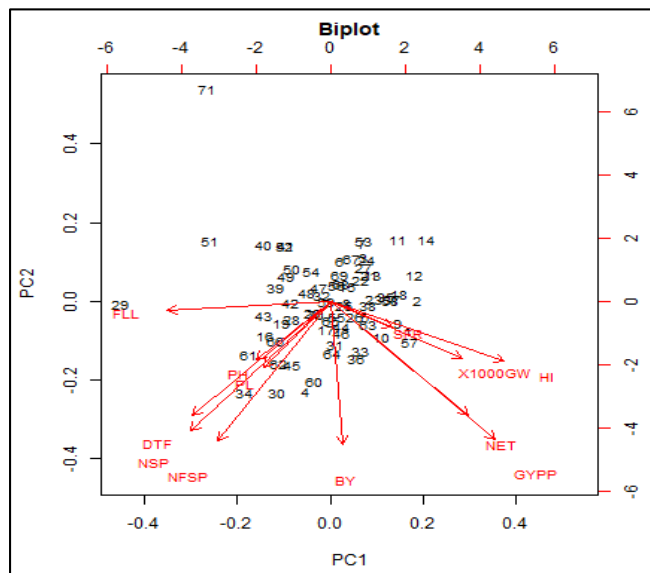


Fig 2: PCA biplot diagram showing the dispersion of rice genotypes across PC1 and PC2

Conclusion

The component character mainly effective tiller/plot (0.817) followed by biological yield (0.714), harvest index (0.621), test weight (0.543), spikelet fertility ratio (0.242) exhibited highly positive correlation with grain yield/plot selection of these characters will increase yield of grain. Positive correlation between useful trait is beneficial because it helps

in improvement of both the characters simultaneously. Conversely, negative correlation prevents the immediate improvement of yield traits. Direct effects of yield contributing characters on grains yield, biological yield showed highest positive direct effect (0.907) on grain yield. From the diversity analysis it can be summarized that the R2733-6-1 (2), Vandana (71), R2723-64-1 (7), R2733-118 (11), R2733-124 (12), R2733-132 (14), R2740-349-1 (40), R2744-17-1 (51), and R2736-119-1 (29), were found to be promising and found to be genetically divergent. Hence, these genotypes could be utilized in the hybridization programme to produce transgressive segregants.

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