Original Research Article

Studies on Correlation and Path Coefficient for Yield and its Contributing Traits in Rice (*Oryza Sativa* L.)

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ABSTRACT

The current study was conducted at the agriculture research farm of the Department of Genetics and Plant Breeding, School of Agriculture, Lovely Professional University, Punjab during the *kharif* season 2022. A Randomized Block Design (RBD) with three replications were used to study correlation and path including 27 rice germplasm for the thirteen traits studied *viz.* Days to 50% flowering, Plant height (cm), Panicle length (cm), Number of tillers per plant, Number of spikelets per panicle, Flag leaf length (cm), Flag leaf width (cm), Number of filled grains per panicle, Days to maturity, Single plant yield (g), Test weight (g), Biological yield (g) and Harvest Index. Finding reveled that genotypic correlation coefficients were higher than phenotypic correlation coefficients for most of the characters studied indicating slight environmental effects over the traits. Single plant yield had significant positive correlation with harvest index (0.873, 0.976), Test weight (0.686, 0.738), panicle length (0.497, 0.603), number of tillers per plant (0.459, 0.505), days to maturity (0.398, 0.677), number of filled grains per panicle (0.395, 0.461) and days to 50 %flowering (0.253, 0.607) at phenotypic and genotypic level that were found to be helpful in encouraging rapid improvement of yield. Path coefficient analysis indicates that the harvest index (0.735, 0.999) had the highest direct and positive effect on single plant yield followed by biological yield (0.135, 0.459), days to maturity (0.088, 0.317), flag leaf width (0.087, 0.155) at both phenotypic and genotypic level respectively. These results revealed that single plant yield had maximum positive indirect effect through harvest index, biological yield, plant height, number of total tillers and number of filled grains per panicle. Hence, selection for these characters could bring improvement in yield and yield components.

Keywords: Correlation, Path coefficient, Phenotypic, Genotypic, Direct and indirect effect, Single plant yield.

1. 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, semi-aquatic, 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). According to data from the Punjab Agriculture department, paddy cultivation covers approximately 87% of the total area dedicated to kharif crops (grown from June to October) in Punjab. 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 [1]. In India, it accounts for 20-25% of agricultural production and ensures food security for over half of the population. 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 [2].

[3] emphasized that the breeding strategy in rice depends primarily on the extent and degree of correlation between traits, as well as the magnitude and nature of variation. However, it is important to note that selection based solely on correlation, without considering the interactions between component traits, can sometimes lead to misleading results [4]. Path analysis, on the other hand, provides insight into the direct and indirect effects of yield components [5]. Considering these factors, the current experiment was conducted to examine the correlation and path analysis of yield and yield attributing characters, with the aim of improving rice yield through breeding programs.

2. MATERIALS AND METHOD

The current study was conducted at the agriculture research farm of the Department of Genetics and Plant Breeding, School of Agriculture, Lovely Professional University, Punjab during the 2022 season. A Randomized Block Design (RBD) with three replications was employed with recommended cultural, agronomical and plant protection practices followed to ensure a healthy crop stand. Various observations were recorded, including 27 rice germplasm tabulated in (Table 1) for the thirteen traits studied *viz.* Days to 50% flowering, Plant height (cm), Panicle length (cm), Number of tillers per plant, Number of spikelets per panicle, Flag leaf length (cm), Flag leaf width (cm), Number of filled grains per panicle, Days to maturity, Single plant yield (g), Test weight (g), Biological yield (g) and Harvest Index.

The collected data was analyzed using standard statistical procedures as outlined by Panse and Sukhatme [6]. Correlation analysis was performed using the formulae recommended by Falconer [7]. To determine the direct and indirect effects, the correlation coefficients were partitioned using the methodology proposed by Wright [8] and further elaborated by Dewey and Lu [9]. The path coefficients were characterized according to the approach suggested by Lenka and Mishra [10].

Table 1. Total 27 Genotypes of Rice used in present investigation

S. NO.	GENOTYPES	S. NO.	GENOTYPES
1	Haldi Chudi	**14**	Siddha Sanna
2	Taiwan black	**15**	Sanna Jujjulu
3	Java Pula	**16**	Gani
4	Siddha Sannalu	**17**	Nagara
5	Kalajeera	**18**	RNR little
6	Karikalave	**19**	Radha 4
7	HMT paddy	**20**	MTU 7029
8	MTU 1061	**21**	MTU 1166
9	MTU 1064	**22**	PR 118
10	MTU 1318	**23**	PR 111
11	PR 114	**24**	PR 126
12	PR 122	**25**	PR 113
13	Banspatri	**26**	PR 121
		27	PR 128

3. RESULTS AND DISCUSSION

ANOVA demonstrated significant variations across genotypes for each of the thirteen traits studied tabulated in Table 2. All the parameters examined exhibited significant variance at 1 percent level, indicating a substantial range of variability among the germplasm, except for the days to 50 % flowering, which showed significance at the 5 percent level [24]. These findings suggest that selection based on these traits can result in significant improvements, as there is a considerable degree of variability across all the characters. However, it should be noted that the analysis of variance alone could not explain the underlying genetic variability. This becomes apparent when the overall genetic variability and its inheritance in the germplasm are separated from the phenotypic variance, as highlighted by Grafius [11]. Therefore, to better understand the extent of variability for specific features, both the phenotypic and genotypic coefficients of variation must be calculated. Similar findings were reported by [12-15].

Table 2. ANOVA for 13 traits

3.1 Analysis of Correlation

Correlation studies play a crucial role in comprehending the impact of different yield-related traits on overall yield and the interrelationships between these traits. The association between two distinct traits can be attributed to the linkage and pleiotropic effects of genes. Therefore, in order to identify effective selection strategies for enhancing yield, it is important to examine the correlation between yield and its component traits. The phenotypic and genotypic correlation coefficients among the thirteen characters investigated in this study are presented in Table 3 and 4 for phenotypic and genotypic level repectively.

S. No.	Source	Mean Sum of Squares (MSS)		
		Replication	**Treatment**	**Error**
	Degrees of freedom	2	26	52
1	**Days to 50% flowering**	164.9750	95.488*	53.68
2	**Plant height (cm)**	18.8590	537.524**	77.186
3	**Panicle length (cm)**	0.9920	16.682**	2.321
4	**Number of tillers per plant**	2.3380	13.612**	1.099
5	**Number of spikelets per panicle**	63.2290	1893.162**	121.234
6	**Flag leaf length (cm)**	1.4460	48.358**	6.062
7	**Flag leaf width (cm)**	0.0110	0.183**	0.013
8	**Number of filled grains per panicle**	22.9820	1202.643**	143.183
9	**Days to maturity**	11.2960	246.198**	79.716
10	**Single plant yield (g)**	6.9450	112.903**	3.136
11	**Test weight (g)**	1.8750	64.643**	2.427
12	**Biological yield (g)**	1.9120	151.03**	62.353
13	**Harvest Index**	00	0.019**	0.001

Days to 50 % flowering had significant positive correlation with panicle length (0.441, 0.825), harvest index (0.267, 0.587), number of tillers per plant (0.260, 0.685), single plant yield (0.253, 0.607), Test weight (0.235, 0.780) at phenotypic and genotypic level respectively. It also revealed positively correlated with days to maturity (0.993) and number of filled grains per panicle (0.464) at genotypic level.

Plant height had positive significant correlation with flag leaf length (0.287, 0.423), panicle length (0.263, 0.394) at phenotypic and genotypic level respectively. It had negative significant correlation with biological yield (-0.390) followed by number of spikelet's per panicle (-0.272) at genotypic level.

Panicle length had significant positive correlation with days to 50 %flowering (0.441, 0.825), plant height (0.263, 0.394), number of tillers per plant (0.425, 0.490), flag leaf length (0.284, 0.328), number of filled grains per panicle (0.325, 0.463), days to maturity (0.393, 0.585), Test weight (0.465, 0.593), harvest index (0.468, 0.636) and single plant yield (0.497, 0.603) at phenotypic and genotypic level respectively. It had negative significant correlation with biological yield (-0.258) at genotypic level.

Number of tillers per plant had significant positive correlation with days to 50 % flowering (0.260, 0.685), panicle length (0.425, 0.490), number of filled grains per panicle (0.236, 0.375), days to maturity (0.268, 0.451), Test weight (0.279, 0.325), harvest index (0.499, 0.606) and single plant yield (0.459, 0.505) at phenotypic and genotypic level respectively. Whereas, negative significant correlation was observed with biological yield (-0.273, -0.485) at both level.

Number of spikelets per panicle had significant positive correlation with flag leaf length (0.260, 0.273), number of filled grains per panicle (0.234, 0.374). Whereas, negative significant correlation was observed with flag leaf width (-0.237, -0.268) at both phenotypic and genotypic level. Whereas, negative significant correlation was observed with plant height (-0.272) at genotypic level.

Flag leaf length had significant positive correlation with plant height (0.287, 0.423), panicle length (0.284, 0.328), number of spikelet per plant (0.219, 0.273), number of filled grains per panicle (0.355, 0.481), days to maturity (0.239, 0.392) at both phenotypic and genotypic level respectively and harvest index (0.231) at phenotypic only. Whereas, negative significant correlation was observed with biological yield (-0.351) at genotypic level. Flag leaf width had positive non-significant correlation with biological yield (0.200, 0.623) and plant height (0.084, 0.103) at both phenotypic and genotypic level respectively. Whereas, negative significant correlation was observed with number of spikelet's per plant (-0.268), number of filled grains per panicle (-0.307), days to maturity (-0.545), harvest index (-0.295) at genotypic level.

Number of filled grains per panicle had significant positive correlation with single plant yield (0.395, 0.461), harvest Index (0.383, 0.474), flag leaf length (0.355, 0.481), panicle length (0.325, 0.463), Number of tillers per plant (0.236, 0.375), number of spikelets per panicle (0.234, 0.374) at both level whereas days to 50% flowering (0.464) and days to maturity (0.436) at phenotypic level. It had significant negative correlation with flag leaf width (-0.307) at genotypic level.

Days to maturity had significant positive correlation with single plant yield (0.398), followed by panicle length (0.393 0.585), harvest index (0.350, 0.620), Test weight (0.310, 0.528), number of tillers per plant (0.268, 0.451), flag leaf length (0.239, 0.392). It had significant negative correlation with flag leaf width (-0.322). It revealed significant positive correlation with days to 50% flowering (0.993), followed by single plant yield (0.677), number of filled grains per panicle (0.436), number of spikelets per panicle (0.280). It had significant negative correlation with flag leaf width (-0.545) at genotypic level.

Test weight had significant positive correlation with harvest index and single plant yield (0.686, 0.738), followed by panicle length (0.465, 0.593), days to maturity (0.310, 0.528), number of tillers per plant (0.279 0.325), number of filled grains per pa (0.250, 0.291), days to 50% flowering (0.235, 0.780). It also possessed non-significant positive correlation with flag leaf length (0.137). It had non-significant negative correlation with biological yield (-0.130, -0.316) at both phenotypic and genotypic level. It had significant negative correlation with by number of spikelets per panicle (-0.109) at phenotypic level.

Biological yield (g) had negative significant correlation with number of tillers per plant (-0.273) at phenotypic level and positive significant correlation with flag leaf width (cm) (0.623). It had negative significant correlation with harvest index (-0.537), followed by number of tillers per plant (-0.485), plant height (-0.390), flag leaf length (-0.351), Test weight (0.316), panicle length (0.258) at genotypic level.

Harvest Index had positive significant correlation with single plant yield (g) (0.976), followed by Test weight (0.755), panicle length (0.636), days to maturity (0.620), number of tillers per plant (0.606), days to 50% flowering (0.587), number of filled grains per panicle (0.474), flag leaf length (cm) (0.231) at phenotypic level. It had negative significant correlation biological yield (-0.537), followed by number of flag leaf width (-0.295) at genotypic level.

Single plant yield had significant positive correlation with harvest index (0.873, 0.976), Test weight (0.686, 0.738), panicle length (0.497, 0.603), number of tillers per plant (0.459, 0.505), days to maturity (0.398, 0.677), number of filled grains per panicle (0.395, 0.461) and days to 50 %flowering (0.253, 0.607) at phenotypic and genotypic level.

In the present investigation, genotypic correlation coefficients were higher than phenotypic correlation coefficients for most of the characters studied indicating slight environmental effects over the traits. The traits like harvest index, Test weight, panicle length, number of tillers per plant, days to maturity and number of filled grains per panicle which showed significant positive correlation with single plant yield were found to be helpful in encouraging rapid improvement of yield. These results were also supported by the earlier findings of reported test weight had highly significant and positive correlation with plant yield.

3.2 Path coefficient analysis

Simple correlation coefficients indicate association between any two characters but it does not give a complete picture of complex relationship. Therefore, it is essential to have path coefficient analysis in order to get clear picture of association among characters, as it splits the correlation coefficient into the measure of direct and indirect effects of a set of independent variables on the dependent variable through other component traits. The direct and indirect possessions of various characters along with their phenotypic and genotypic path coefficients with grain weight per plant are presented in Figure 2 and 3 and tabulated in Table 5 and 6. In the present investigation, path coefficients were analyzed by taking single plant yield as dependent character and remaining twelve characters viz., days to 50 %flowering, plant height (cm), panicle length (cm), number of tillers per plant, number of spikelets per panicle, flag leaf length (cm), flag leaf width (cm), number of filled grains per panicle, days to maturity, Test weight (g), biological yield (g), harvest index as independent variables.

3.2.1 Direct effect of various characters on single plant yield

In dividing the correlation coefficient into straight and ancillary results, path analysis, which is essentially a generalized partial regression analysis developed by [8] is useful. Path analysis give the complete picture of direct and indirect impact on single plant yield. Therefore, in the present investigation, path coefficient analysis was used in order to obtain the details on the direct and indirect impact on single plant yield by various contributing characters. The critical estimation of path coefficient analysis in which, bold diagonal values represented direct effects indicates that the harvest index (0.735, 0.999) had the highest direct and positive effect on single plant yield followed by biological yield (0.135, 0.459), days to maturity (0.088, 0.317), flag leaf width (0.087, 0.155) at both phenotypic and genotypic level respectively. Whereas, Test weight (0.129), panicle length (0.085) had the highest direct and positive effect on single plant yield at phenotypic level only. Similarly, on the other hands plant height (-0.134) had highest negative straight effect on single plant yield followed by days to 50% flowering (-0.023), flag leaf length (-0.020) at phenotypic level. At genotypic level plant height (0.568), number of grains per tiller (0.158), number of spikelets per panicle (0.112) had the highest direct and positive effect on single plant yield. Similarly, on the other hands panicle length (-0.426) had highest negative straight effect on single plant yield followed by flag leaf length (-0.403), number of tillers per plant (-0.386) and Test weight (-0.215). Therefore, the traits like harvest index, biological yield, Test weight, days to maturity, flag leaf width and panicle length recorded positive direct effect on single plant yield were found to be traits of interest in improving the rice yield. These results were in accordance with the results of [16-18].

3.2.2 Indirect effects of various characters on single plant yield

These results revealed that single plant yield had maximum positive indirect effect through harvest index, biological yield, plant height, number of total tillers and number of filled grains per panicle. Hence, selection for these characters could bring improvement in yield and yield components. [19-20] also observed similar results. Whereas, traits like days to 50% flowering, flag leaf width had highest negative indirect effect on single plant yield and selection of these traits is not recommended during rice breeding. These findings are in accordance with [20-23].

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Table 3. Phenotypic Correlation Matrix for 13 traits in rice

Phenotypic Correlation Matrix													
	DF50%	**PH**	**PL**	**TPP**	**SPP**	**FLL**	**FLW**	**FGP**	**DM**	**TW**	**BY**	**HI**	**SYP**
DF50%	**1.0000**	0.1168	0.441**	0.260*	0.0220	0.0128	-0.0590	0.1987	0.2166	0.235*	-0.0709	0.267*	0.253*
PH		**1.0000**	0.263*	0.1222	-0.1662	0.287*	0.0839	-0.0859	0.0032	0.0496	-0.1897	-0.0209	-0.1495
PL			**1.0000**	0.425**	0.0340	0.284*	-0.1075	0.325*	0.393**	0.465**	-0.0280	0.468**	0.497**
TPP				**1.0000**	-0.0439	-0.0703	-0.0833	0.236*	0.268*	0.279*	-0.273*	0.499**	0.459**
SPP					**1.0000**	0.219*	-0.237*	0.234*	0.1710	-0.1098	0.0544	-0.0015	0.0419
FLL						**1.0000**	-0.1342	0.355*	0.239*	0.1377	-0.0889	0.1898	0.1382
FLW							**1.0000**	-0.2001	-0.322*	-0.0552	0.2004	-0.248*	-0.1403
FGP								**1.0000**	0.2036	0.250*	-0.0789	0.383**	0.395**
DM									**1.0000**	0.310*	-0.0725	0.350*	0.398**
TW										**1.0000**	-0.1306	0.686**	0.686**
BY											**1.0000**	-0.268*	-0.0580
HI												**1.0000**	0.873**
SYP													**1.0000**

DF50%- Days to 50% flowering**, PH-**Plant height**, PL-**Panical length**, TPP-** Tillers per plant**, SPP-** Spikelet per panicle**, FLL-** Flag leaf length**, FLW-** Flag leaf width**, FGP-** Filled grain per panicle**, DM-** Days to maturity**, TW-** Test weight**, BY-** Biological yield**, HI-**Harvest index**, SYP-** Single plant yield

* & ** significance at 5% and 1% probability level respectively

Table 4. Genotypic Correlation Matrix for 13 traits in rice

Genotypic Correlation Matrix

	DF50%	PH	PL	TPP	SPP	FLL	FLW	FGP	DM	TW	BY	HI	SYP
DF50%	**1.0000**	0.1942	0.825**	0.685**	-0.1924	-0.0638	-0.1945	0.464**	0.993**	0.780**	0.0195	0.587**	0.607**
PH		**1.0000**	0.394**	0.1647	-0.272*	0.423**	0.1034	-0.0417	-0.1216	0.0290	-0.390**	-0.0230	-0.1209
PL			**1.0000**	0.490**	0.0251	0.328*	-0.0618	0.463**	0.585**	0.593**	-0.258*	0.636**	0.603**
TPP				**1.0000**	-0.0233	-0.0970	-0.0610	0.375**	0.451**	0.325*	-0.485**	0.606**	0.505**
SPP					**1.0000**	0.273*	-0.268*	0.374**	0.280*	-0.1039	0.1561	0.0092	0.0637
FLL						**1.0000**	-0.1574	0.481**	0.392**	0.1740	-0.351*	0.231*	0.1526
FLW							**1.0000**	-0.307*	-0.545**	-0.0369	0.623**	-0.295*	-0.1524
FGP								**1.0000**	0.436**	0.291*	-0.1008	0.474**	0.461**
DM									**1.0000**	0.528**	0.0314	0.620**	0.677**
TW										**1.0000**	-0.316*	0.755**	0.738**
BY											**1.0000**	-0.537**	-0.0989
HI												**1.0000**	0.976**
SYP													**1.0000**

DF50%- Days to 50% flowering**, PH-**Plant height**, PL-**Panical length**, TPP-** Tillers per plant**, SPP-** Spikelet per panicle**, FLL-** Flag leaf length**, FLW-** Flag leaf width**, FGP-** Filled grain per panicle**, DM-** Days to maturity**, TW-** Test weight**, BY-** Biological yield**, HI-**Harvest index**, SYP-** Single plant yield

* & ** significance at 5% and 1% probability level respectively

Figure 1. Phenotypic Correlation Matrix for 13 traits in rice

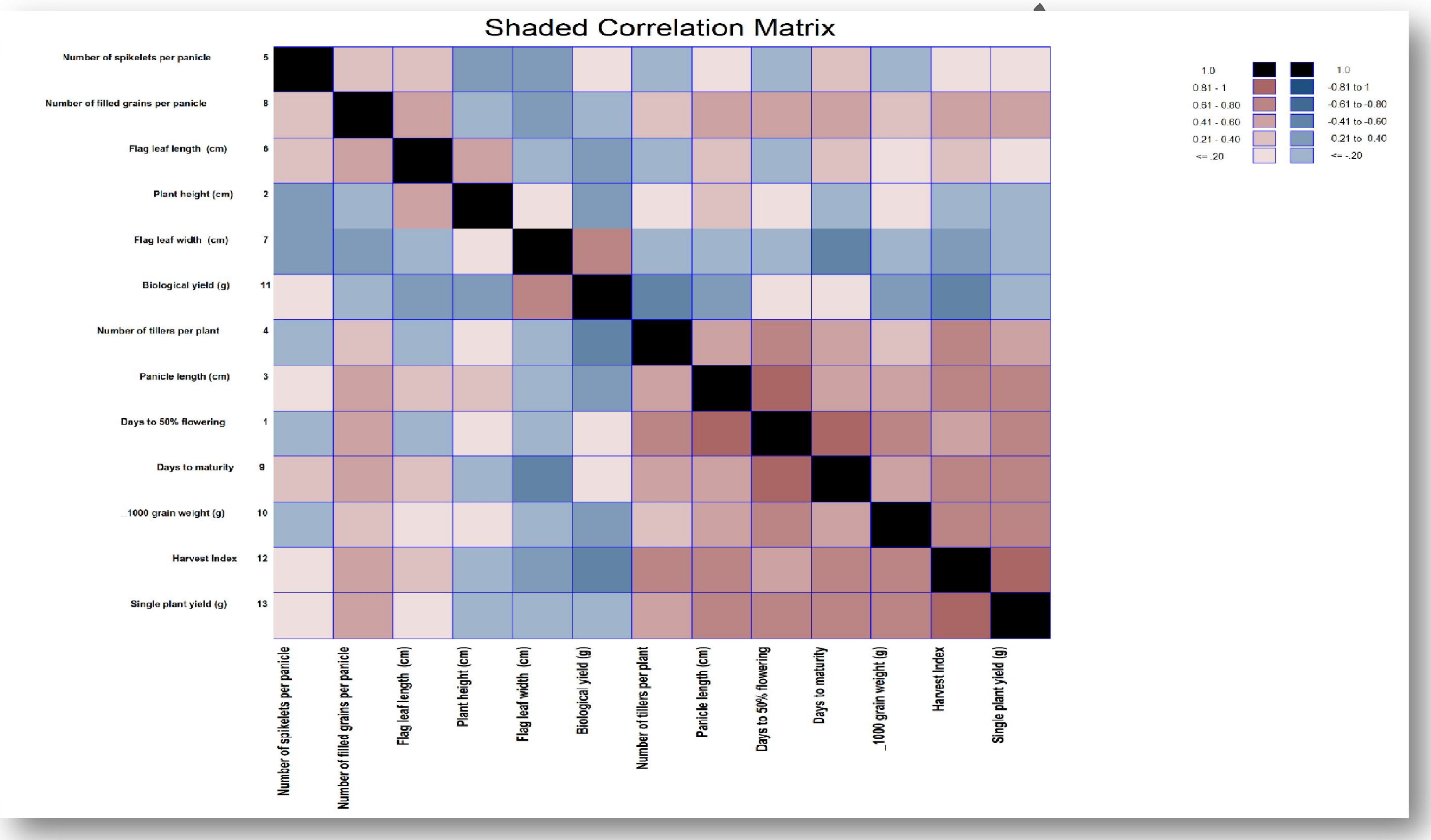

Figure 2. Genotypic Correlation Matrix for 13 traits in rice

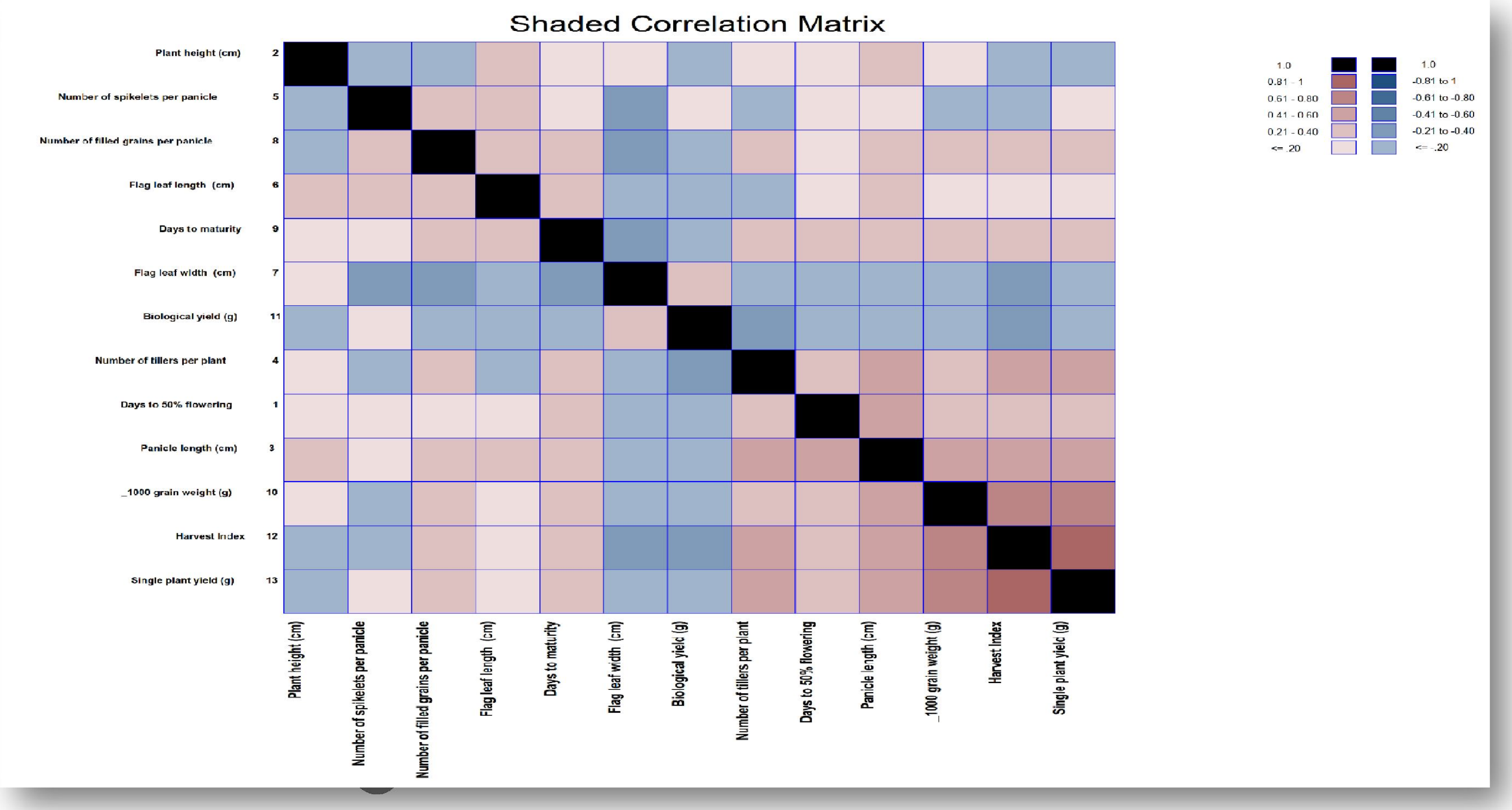

Table 5. Phenotypic Path Matrix Single plant yield for 13 traits in rice

Phenotypic Path matrix of Single plant yield (g)													
	DF50%	**PH**	**PL**	**TPP**	**SPP**	**FLL**	**FLW**	**FGP**	**DM**	**TW**	**BY**	**HI**	**SYP**
DF50%	**-0.0230**	-0.0027	-0.0101	-0.0060	-0.0005	-0.0003	0.0014	-0.0046	-0.0050	-0.0054	0.0016	-0.0061	0.253*
PH	-0.0157	**-0.1343**	-0.0354	-0.0164	0.0223	-0.0386	-0.0113	0.0115	-0.0004	-0.0067	0.0255	0.0028	-0.1495
PL	0.0373	0.0223	**0.0846**	0.0360	0.0029	0.0241	-0.0091	0.0275	0.0332	0.0394	-0.0024	0.0396	0.497**
TPP	0.0136	0.0064	0.0223	**0.0524**	-0.0023	-0.0037	-0.0044	0.0124	0.0140	0.0146	-0.0143	0.0261	0.459**
SPP	0.0006	-0.0044	0.0009	-0.0012	**0.0267**	0.0058	-0.0063	0.0062	0.0046	-0.0029	0.0015	0.0000	0.0419
FLL	-0.0003	-0.0058	-0.0058	0.0014	-0.0044	**-0.0203**	0.0027	-0.0072	-0.0049	-0.0028	0.0018	-0.0039	0.1382
FLW	-0.0051	0.0073	-0.0093	-0.0072	-0.0206	-0.0117	**0.0868**	-0.0174	-0.0279	-0.0048	0.0174	-0.0215	-0.1403
FGP	0.0091	-0.0039	0.0149	0.0109	0.0107	0.0163	-0.0092	**0.0459**	0.0094	0.0115	-0.0036	0.0176	0.395**
DM	0.0191	0.0003	0.0347	0.0237	0.0151	0.0212	-0.0284	0.0180	**0.0884**	0.0274	-0.0064	0.0309	0.398**
TW	0.0303	0.0064	0.0601	0.0360	-0.0142	0.0178	-0.0071	0.0322	0.0400	**0.1291**	-0.0169	0.0886	0.686**
BY	-0.0096	-0.0256	-0.0038	-0.0368	0.0073	-0.0120	0.0270	-0.0106	-0.0098	-0.0176	**0.1349**	-0.0362	-0.0580
HI	0.1964	-0.0154	0.3437	0.3663	-0.0011	0.1395	-0.1824	0.2814	0.2568	0.5043	-0.1971	**0.7349**	0.873**
SYP	0.253*	-0.1495	0.497**	0.459**	0.0419	0.1382	-0.1403	0.395**	0.398**	0.686**	-0.0580	0.873**	**1.0000**

DF50%- Days to 50% flowering**, PH-**Plant height**, PL-**Panical length**, TPP-** Tillers per plant**, SPP-** Spikelet per panicle**, FLL-** Flag leaf length**, FLW-** Flag leaf width**, FGP-** Filled grain per panicle**, DM-** Days to maturity**, TW-** Test weight**, BY-** Biological yield**, HI-**Harvest index**, SYP-** Single plant yield

* & ** significance at 5% and 1% probability level respectively

Figure 3. Phenotypic path diagram for single plant yield

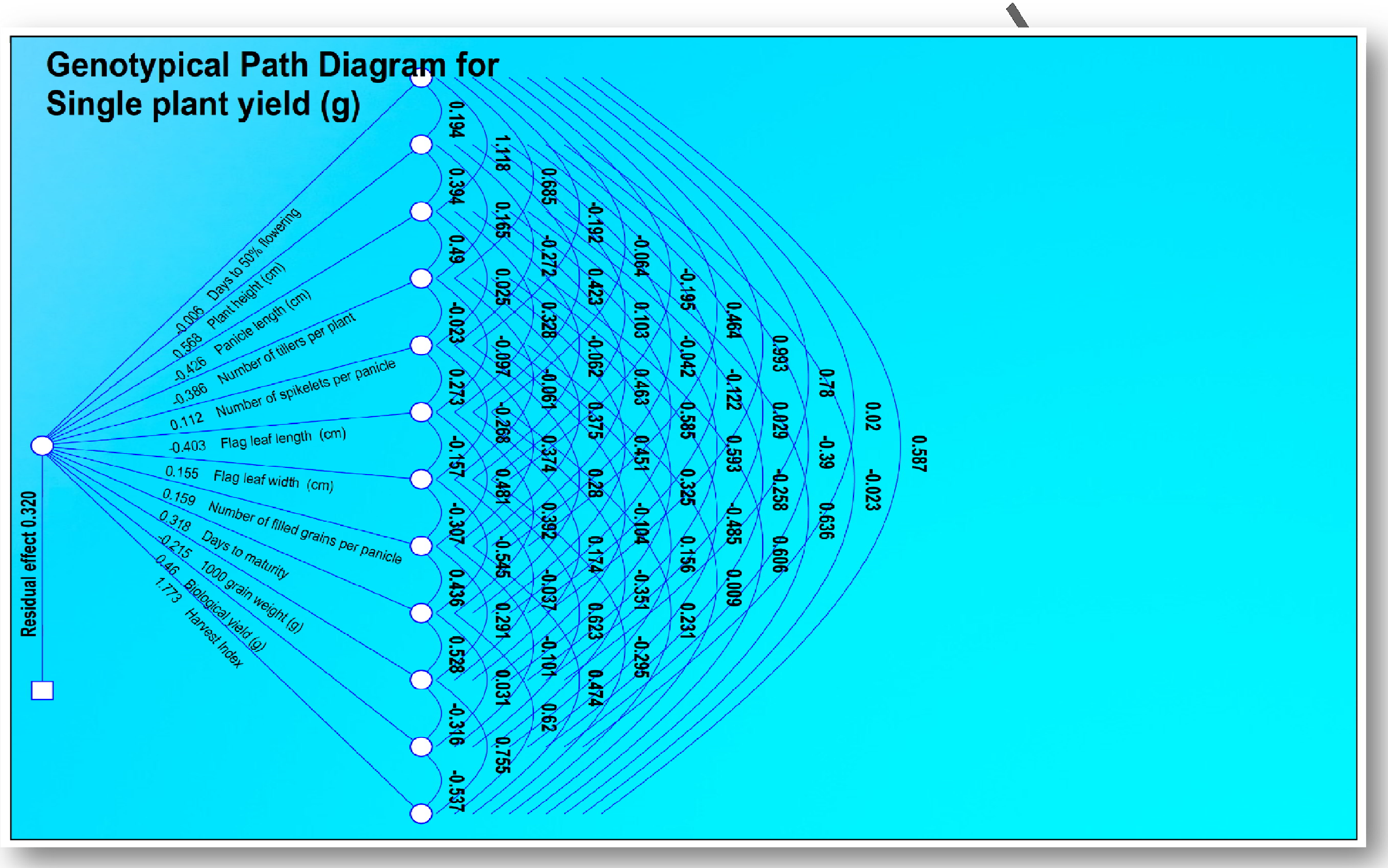

Table 6. Genotypic Path Matrix Single plant yield for 13 traits in rice

Genotypic Path matrix of Single plant yield (g)													
	DF50%	**PH**	**PL**	**TPP**	**SPP**	**FLL**	**FLW**	**FGP**	**DM**	**TW**	**BY**	**HI**	**SYP**
DF50%	**-0.0060**	-0.0012	-0.0067	-0.0041	0.0011	0.0004	0.0012	-0.0028	-0.0059	-0.0047	-0.0001	-0.0035	0.607**
PH	0.1103	**0.5680**	0.2238	0.0935	-0.1547	0.2405	0.0587	-0.0237	-0.0690	0.0165	-0.2213	-0.0131	-0.1209
PL	-0.4761	-0.1679	**-0.4260**	-0.2089	-0.0107	-0.1397	0.0263	-0.1972	-0.2490	-0.2525	0.1100	-0.2708	0.603**
TPP	-0.2643	-0.0635	-0.1892	**-0.3858**	0.0090	0.0374	0.0235	-0.1446	-0.1742	-0.1253	0.1871	-0.2337	0.505**
SPP	-0.0215	-0.0304	0.0028	-0.0026	**0.1116**	0.0304	-0.0299	0.0418	0.0313	-0.0116	0.0174	0.0010	0.0637
FLL	0.0257	-0.1706	-0.1321	0.0391	-0.1099	**-0.4029**	0.0634	-0.1937	-0.1580	-0.0701	0.1414	-0.0929	0.1526
FLW	-0.0302	0.0160	-0.0096	-0.0095	-0.0416	-0.0244	**0.1552**	-0.0477	-0.0846	-0.0057	0.0966	-0.0458	-0.1524
FGP	0.0735	-0.0066	0.0734	0.0594	0.0594	0.0763	-0.0487	**0.1586**	0.0692	0.0461	-0.0160	0.0752	0.461**
DM	0.3153	-0.0386	0.1856	0.1433	0.0889	0.1245	-0.1731	0.1386	**0.3175**	0.1677	0.0100	0.1969	0.677**
TW	-0.1682	-0.0062	-0.1277	-0.0700	0.0224	-0.0375	0.0079	-0.0627	-0.1138	**-0.2155**	0.0681	-0.1627	0.738**
BY	0.0090	-0.1792	-0.1187	-0.2230	0.0718	-0.1613	0.2863	-0.0463	0.0144	-0.1453	**0.4598**	-0.2469	-0.0989
HI	1.0396	-0.0408	1.1269	1.0737	0.0164	0.4088	-0.5232	0.8407	1.0993	1.3383	-0.9518	**1.7726**	0.976**
SYP	0.607**	-0.1209	0.603**	0.505**	0.0637	0.1526	-0.1524	0.461**	0.677**	0.738**	-0.0989	0.976**	**1.0000**

DF50%- Days to 50% flowering**, PH-**Plant height**, PL-**Panical length**, TPP-** Tillers per plant**, SPP-** Spikelet per panicle**, FLL-** Flag leaf length**, FLW-** Flag leaf width**, FGP-** Filled grain per panicle**, DM-** Days to maturity**, TW-** Test weight**, BY-** Biological yield**, HI-**Harvest index**, SYP-** Single plant yield

* & ** significance at 5% and 1% probability level respectively

Figure 4. Phenotypic path diagram for single plant yield