ABSTRACT

Introduction

Rice (*Oryza sativa* L.) occupies a crucial position in the ancient and modern Indian agriculture as well as in the world as it feeds and fulfills the nutritional requirements of 1/3rd of the world's population. Rice is also called as the "Grain of Life", because it is not only the staple food for more than 70 percent of the Indians but also a source of livelihood for about 120-150 million rural households.In order to develop high yielding varieties it is unavoidable for the rice breeders to understand how the grain quality traits are being inherited from their parents to offsprings. Heritability estimates along with genetic advance are generally helpful in predicting the gain under selection than heritability (broad sense) estimates alone (**Shreya *et al.*, 2021**). Therefore, estimates of GCV, PCV, heritability and genetic advance will play an important role in exploiting future research projections of rice improvement. Grain yield is a complex character, which depends on its several components. These components are further dependent for their expression on several morphological traits, which interrelated with each other showing a complex chain of relationship and also highly influenced by the environmental conditions (**Dhurai*et al.*, 2014**). Therefore, the parents selected for the breeding programmeswith objectives to estimate genetic variability, heritability and genetic advance for quantitative traits in rice germplasm, to study the nature of character associations of yield and yield attributing traits by means of correlations coefficients and to assess the direct and indirect effect of yield components on grain yield path coefficient analysis.

Material and Methods

The present experiment was carried out at the field experimentation centre of the Department of Genetics and Plant Breeding, Sam Higginbottom University of Agriculture Technology & Sciences. The site is located at 25.28 N latitude, 81.54 E longitude and 98 meter above the sea level. Itcomes under sub-tropical and semi-arid climate. Lies 102m above sea level. The average annual rainfall is 1042 mm. The present study consists of 20rice lines along with a check (NDR 359) which were collected from Department of Genetic and Plant breeding, SHUATS were grown in *fall*, 2021. The experiment was laid in a randomized block complete design (RCBD) with 21lines in three replications.

Table 1: List of 20 rice genotypes along with a national check

S. No	GENOTYPES	S. No	GENOTYPES
1	NP 124 8	12	DHAN 50
2	RNR 15048	13	RP BIO 226
3	MTU 1001	14	ANKUR POOJA
4	MTU 1010	15	BPT 5204
5	MTU 1064	16	KNM 168
6	MTU 1224	17	BPT 3291
7	PLA 1100	18	NP 9558
8	KNM 118	19	KPH 376
9	KPH 370	20	SIDHASANNALU
10	DHAN 42	21	NDR 359 (CHECK)
11	DHAN 44		

Total thirteentraits have been recorded *viz.*, days to fifty percent flowering, days to maturity, flag leaf length, flag leaf width, plant height, number of total tillers, panicle length, number of spikelet per panicle, number of productive tillers, test weight, biological yield, harvest index and grain yield per plant.

Firstly measure of variability is figured with the aid of Coefficient of variation, which is the ratio of standard deviation of a sample to its mean and expressed in percentage. In the present investigation two types of coefficient of variations were estimated *viz*., phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV).

Coefficient of variation (CV): It is the measure of variability evolved. Coefficient of variation is the ratio of standard deviation of a sample to its mean and expressed in percentage.

CV (%) = Standard deviation / Mean X 100

The formulae used to calculate PCV and GCV were stated by **(Burton, 1952)**

PCV (%) = Phenotypic standard deviation /Grand mean X 100

GCV (%) = Genotypic standard deviation / Grand mean x 100

Heritability calculated by the formula given by**Lush (1949) and Burton and Devane (1953).** CorrelationCoefficientwascalculatedaccordingtotheformulasuggestedby**Miller*et al*(1958)**.Path coefficient analysisisnormally to measures thedirectandindirecteffectsof independentvariablesonthedependentvariables.Thistechnique was firstly used by **Dewey and Lu (1959)**.

Results and Discussion

1. Genetic Variability

1.1 Genotypic Coefficient of Variation (GCV)

Highest estimatesofgenotypiccoefficientofvariation(GCV)wererecordedforgrain yieldperplant(24.65),harvest index (22.30),test weight (21.58), biological yield per plant (19.94) and flag leaf width (17.85).

1.2 Phenotypic Coefficient of Variation (PCV)

High estimates of phenotypic coefficient of variation (PCV) were recordedfor grain yieldperplant(26.76),harvest index (23.20),number of spikelet per plant (22.33), biological yield (21.81), test weight (21.60) andnumber of total tillers (18.74).

ThelargedifferencebetweentheGCVandPCVindicatehighenvironmentalinfluence on the expression of particular traits. Relatively low differences were observedbetween genotypic and phenotypic coefficient of variation for test weight(21.58, 21.60).

1.3 Heritability

Heritability(broad sense) estimated for the thirteen characters were ranged from number ofdays to maturity (55.38) to test weight (99.77). Heritability estimates werehighfortest weight(g) (99.77),plant height (cm) (96.38),harvest index (92.40) flag leaf width (cm) (92.21), grain yield perplant (84.41),biologicalyield (83.51),number of productive tillers (73.40),number of spikelet's per panicle (72.29) andpanicle length (cm) (72.02).Whileitwasmoderatefordays to 50% flowering(57.03) and daystomaturity (55.38).

1.4 Genetic advance

Highgeneticadvance was recorded for number of spikelet per panicle (70.47) followed by plant height (cm) (32.35). While moderategeneticadvance wasrecorded forbiological yield(24.07),harvest index (23.31), days to maturity (16.92) and grain yield per plant (15.56). Low genetic advance was recorded flag leaf width (0.43), number of productive tillers (3.02), number of total tillers (3.15) and panicle length (4.06).

Similar results were reported by **Saha*et al*. (2019)** for number of grains per panicle; **Nithya*et al*. (2020)** for grain yield per plant and productive tillers per plant; **Umarani*et al*. (2017)** and **Sundaram*et al*. (2019)** for zinc and iron content; **Sandeep *et al*. (2018)** for panicle length; **Ameganet *al*. (2020)** for 1000 grain weight; **Maurya*et al*. (2019)** and **Supriya*et al*. (2017)** for L/B ratio and **Singh *et al*. (2020)** and **Sangamithra*et al*. (2018)** for protein content.

2.Correlation

Genotypic correlation for seed yield per plant showed highly significant and positive association with harvest index (0.909**), biological yield (0.805**), 100 seed weight (0.255**), number of pod clusters (0.796**), number of pods per plant (0.797**), number of primary branches (0.521**). It also showed negative but non-significant association with days to fifty percent flowering (-0.0531), days to maturity (-0.1215), plant height (-01588), number of pods per cluster (-0.1466), number of seeds per pod (-0.1407).Seed yield per plant showed significant and positive association with harvest index (0.812**) followed by biological yield (0.721**), number of pods per plant (0.867**), 100 seed weight (0.352*), number of primary branches (0.534*). It also showed negative and highly significant association with days to pod length (-0.485**).negative but non-significant with days to fifty percent flowering (-0.1177), number of seeds per pod (-0.1475), days to maturity (-0.1513). Both the genotypic and phenotypic values are clearly illustrated in Table 1 and 2.

Preliminary studies also revealed the similar results were found in **Mani *et al*. (2018)** and **Maurya*et al*. (2018)**studies, that found significant positive correlation between seed yield and harvest index, similarly**Bagheri*et al*. (2011)**found significant positive correlation between seed yield and biological yield**.**

Table 1: Genotypic correlation among the different traits evaluated in rice during *fall*, 2021

	DTF	DM	PH	FLL	FLW	NTT	NPT	PL	BY	HI	NSP	TW	GYP
DTF	1	0.573**	0.2321	0.1995	0.426**	-0.224	-0.2132	0.0745	0.683**	-0.418**	0.757**	-0.417**	0.1359
DM		1	0.250*	0.1915	0.434**	-0.424**	-0.296*	0.385*	0.398*	-0.522**	0.386*	-0.1306	-0.1565
PH			1	0.583**	0.2424	-0.430**	-0.473**	0.519**	0.134	-0.516**	0.193	0.1013	-0.450**
FLL				1	0.2185	-0.290*	-0.267*	0.176	0.0627	-0.256*	-0.0219	0.1057	-0.249*
FLW					1	-0.1164	-0.1892	0.523**	0.1921	-0.468**	0.280*	0.1093	-0.2428
NTT						1	0.929**	-0.1664	-0.248*	0.2441	0.0082	0.1615	0.0537
NPT							1	-0.284*	-0.1802	0.251*	0.0423	0.0395	0.1203
PL								1	-0.1488	-0.508**	-0.0495	0.1599	-0.601**
BY									1	-0.379*	0.781**	-0.2206	0.419**
HI										1	-0.351*	0.1374	0.670**
NSP											1	-0.484**	0.289*
TW												1	0.0001
GYP													1.00

*** and ** Significant at P<0.05 and P<0.01, respectively**

DTF: Days to 50% flowering, DM: Days to maturity, PH: Plant height (cm), FLL: Flag Leaf Length, FLW: Flag Leaf Width, NTT: No. of Total Tillers, NPT: No. of Productive Tillers, PL: Panicle length, BY: Biological Yield (g), HI: Harvest index (%), NSP: No. of spikelet per panicle, TW: Test Weight (g), GYP: Grain yield per plant (g)

Table 2: Phenotypic correlation among the different traits evaluated in rice during *fall*, 2021

	DTF	DM	PH	FLL	FLW	NTT	NPT	PL	BY	HI	NSP	TW	GYP
DTF	1	0.550**	0.2184	0.1492	0.401*	-0.150	-0.1434	0.0669	0.613**	-0.384*	0.673**	-0.402*	0.1317
DM		1	0.2451	0.1715	0.408**	-0.36*	-0.261*	0.325*	0.357*	-0.491**	0.310*	-0.1315	-0.1411
PH			1	0.530**	0.232	-0.35*	-0.401*	0.416**	0.1311	-0.494**	0.1649	0.0985	-0.403*
FLL				1	0.1696	-0.25*	-0.252*	0.1347	0.0229	-0.2248	-0.0394	0.1006	-0.2428
FLW					1	-0.05	-0.1184	0.442**	0.1665	-0.430**	0.2442	0.1089	-0.2134
NTT						1	0.929**	-0.1876	-0.0818	0.2455	0.1128	0.1359	0.1744
NPT							1	-0.279*	-0.0425	0.255*	0.1192	0.035	0.2182
PL								1	-0.1534	-0.425**	0.0374	0.133	-0.515**
BY									1	-0.351*	0.672**	-0.2026	0.482**
HI										1	-0.268*	0.1306	0.636**
NSP											1	-0.411**	0.292*
TW												1	-0.0016
GYP													1.00

*** and ** Significant at $P<0.05$ and $P<0.01$, respectively**

DTF: Days to 50% flowering, DM: Days to maturity, PH: Plant height (cm), FLL: Flag Leaf Length, FLW: Flag Leaf Width, NTT: No. of Total Tillers, NPT: No. of Productive Tillers, PL: Panicle length, BY: Biological Yield (g), HI: Harvest index (%), NSP: No. of spikelet per panicle, TW: Test Weight (g), GYP: Grain yield per plant (g)

3. Path analysis

The path coefficient analysis suggested by specified the effective measure of direct and indirect causes of association and also depicts the relative importance of each factor involved in contributing to the final product i.e., yield. In order to find out the cause and effect relationship between seed yield and its related characters, path analysis taken in the present investigation. Path coefficient analysis allows separating direct effect and indirect effects through other attributes by partitioning correlation.Path analysis in particular having the direct effect of seed yield on characters such as harvest index followed by biological yield and number of spikelet per panicle in descending order.

Phenotypic path coefficient analysis indicated that, the traits having direct effects on grain yield are understood to be strongly associated with it. The path analysis results showed that positive and direct on grain yield were exhibited by harvest index, biological yield, test weight and flag leaf width. Phenotypic path coefficient analysis indicated that, the traits having direct effects on grain yield are understood to be strongly associated with it. The genotypic path analysis results showed that positive and direct on grain yield were exhibited bynumber of spikelet per panicle,number of productive tillers, harvest index and panicle length.

Table 3: Genotypic direct (in bold) and indirect effects of thirteen traits on seed yield in rice evaluated in *fall*, 2021

	DTF	DM	PH	NPB	NPP	NPC	NCP	PL	NSP	100SW	HI	BYP	SYP
DTF	**0.2338**	0.1341	0.0543	0.0467	0.0996	-0.0525	-0.0499	0.0174	0.1598	-0.0977	0.1771	-0.0976	0.1359
DM	-0.2436	**-0.4249**	-0.1063	-0.0814	-0.1842	0.1803	0.1258	-0.1635	-0.1693	0.2216	-0.1641	0.0555	-0.1565
PH	-0.1453	-0.1566	**-0.6261**	-0.3648	-0.1518	0.2694	0.296	-0.3246	-0.0839	0.3231	-0.1209	-0.0634	-0.450**
FLL	0.0225	0.0216	0.0658	**0.1129**	0.0247	-0.0327	-0.0301	0.0199	0.0071	-0.0289	-0.0025	0.0119	-0.249*
FLW	-0.0804	-0.0818	-0.0457	-0.0412	**-0.1886**	0.0219	0.0357	-0.0986	-0.0362	0.0883	-0.0528	-0.0206	-0.2428
NTT	0.2699	0.5099	0.5171	0.3479	0.1398	**-0.702**	-0.824	0.1999	0.2981	-0.2933	-0.0099	-0.194	0.0537
NPT	-0.1537	-0.2134	-0.3407	-0.1922	-0.1364	0.6693	**0.7207**	-0.2047	-0.1298	0.181	0.0305	0.0284	0.1203
PL	0.0195	0.1008	0.1359	0.0461	0.1371	-0.0436	-0.0744	**0.2621**	-0.039	-0.1331	-0.013	0.0419	-0.601**
BY	0.0732	0.0427	0.0144	0.0067	0.0206	-0.0266	-0.0193	-0.0159	**0.1071**	-0.0406	0.0836	-0.0236	0.419**
HI	-0.2835	-0.354	-0.3503	-0.1736	-0.3179	0.1657	0.1705	-0.3446	-0.2573	**0.6788**	-0.238	0.0933	0.670**
NSP	0.6731	0.3433	0.1716	-0.0195	0.249	0.0073	0.0376	-0.044	0.6944	-0.3118	**0.8889**	-0.4301	0.289*
TW	-0.2498	-0.0781	0.0606	0.0633	0.0654	0.0967	0.0236	0.0957	-0.1321	0.0822	-0.2896	**0.5985**	0.0001

*** and ** Significant at P<0.05 and P<0.01, respectively**

DTF: Days to 50% flowering, DM: Days to maturity, PH: Plant height (cm), FLL: Flag Leaf Length, FLW: Flag Leaf Width, NTT: No. of Total Tillers, NPT: No. of Productive Tillers, PL: Panicle length, BY: Biological Yield (g), HI: Harvest index (%), NSP: No. of spikelet per panicle, TW: Test Weight (g), GYP: Grain yield per plant (g)

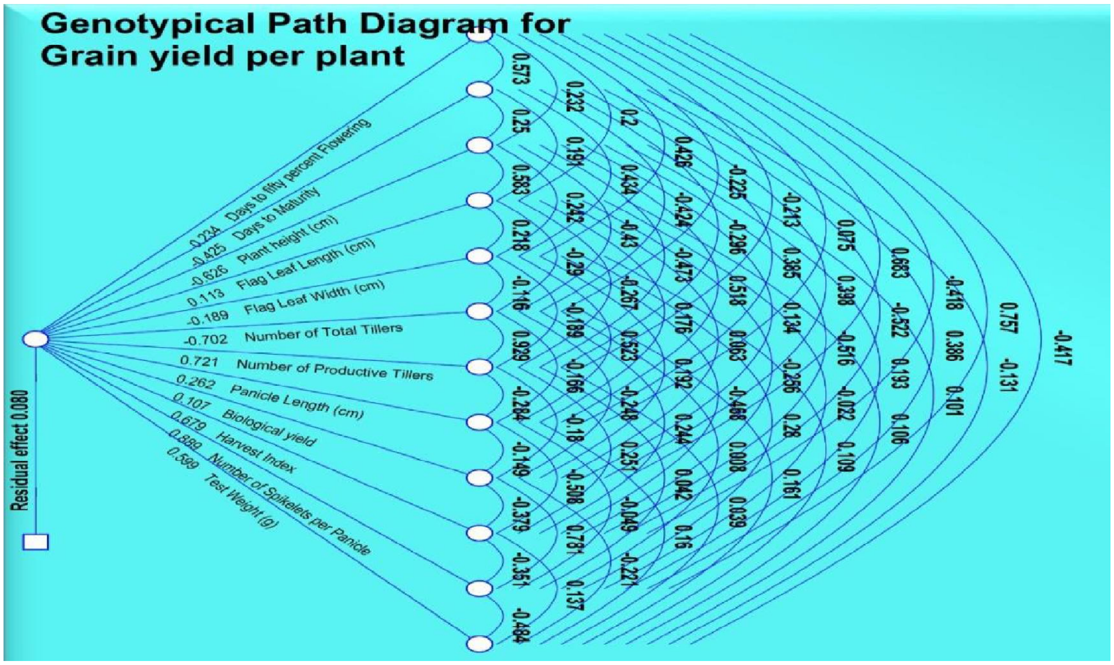
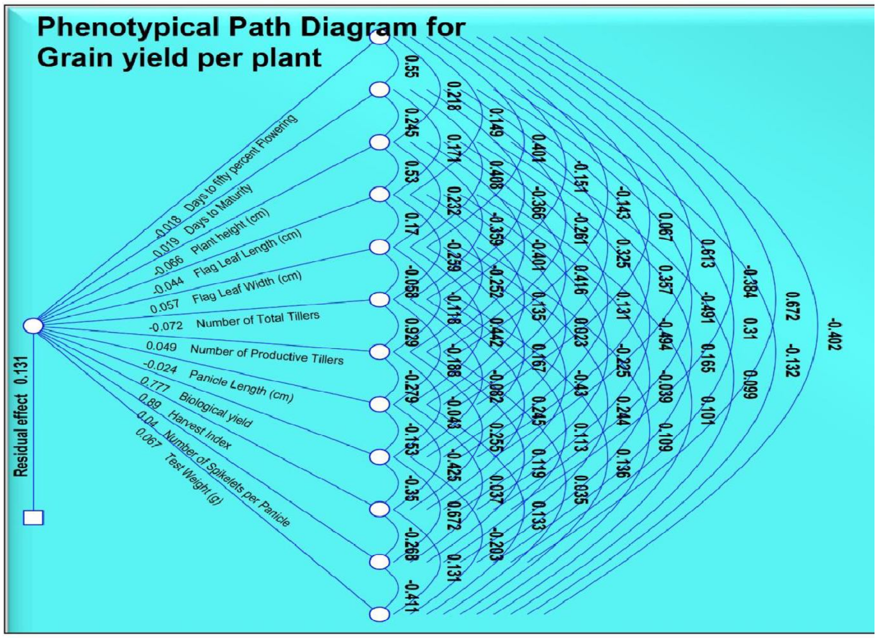


Table 4: Phenotypic direct (in bold) and indirect effects of thirteen traits on seed yield in rice evaluated in *fall*, 2021

	DTF	DM	PH	NPB	NPP	NPC	NCP	PL	NSP	100SW	HI	BYP	SYP
DTF	**-0.0177**	-0.0097	-0.0039	-0.0026	-0.0071	0.0027	0.0025	-0.0012	-0.0109	0.0068	-0.0119	0.0071	0.1317
DM	0.0103	**0.0187**	0.0046	0.0032	0.0077	-0.0069	-0.0049	0.0061	0.0067	-0.0092	0.0058	-0.0025	-0.1411
PH	-0.0143	-0.0161	**-0.0655**	-0.0347	-0.0152	0.0236	0.0263	-0.0273	-0.0086	0.0324	-0.0108	-0.0065	-0.403*
FLL	-0.0066	-0.0076	-0.0235	**-0.0443**	-0.0075	0.0115	0.0112	-0.006	-0.001	0.0099	0.0017	-0.0045	-0.2428
FLW	0.0229	0.0233	0.0132	0.0097	**0.0571**	-0.0033	-0.0068	0.0252	0.0095	-0.0245	0.0139	0.0062	-0.2134
NTT	0.0108	0.0263	0.0259	0.0186	0.0042	**-0.0719**	-0.0668	0.0135	0.0059	-0.0177	-0.0081	-0.0098	0.1744
NPT	-0.0071	-0.0129	-0.0198	-0.0124	-0.0058	0.0458	**0.0493**	-0.0137	-0.0021	0.0126	0.0059	0.0017	0.2182
PL	-0.0016	-0.0078	-0.01	-0.0032	-0.0106	0.0045	0.0067	**-0.024**	0.0037	0.0102	-0.0009	-0.0032	- 0.515**
BY	0.4768	0.2774	0.1019	0.0178	0.1295	-0.0636	-0.0331	-0.1193	**0.7774**	-0.2725	0.5222	-0.1575	0.482**
HI	-0.3418	-0.4365	-0.4394	-0.2	-0.3826	0.2184	0.2266	-0.3784	-0.3118	**0.8897**	-0.2382	0.1162	0.636**
NSP	0.027	0.0125	0.0066	-0.0016	0.0098	0.0045	0.0048	0.0015	0.027	-0.0108	**0.0402**	-0.0165	0.292*
TW	-0.0271	-0.0089	0.0066	0.0068	0.0073	0.0092	0.0024	0.009	-0.0137	0.0088	-0.0277	**0.0675**	-0.0016

*** and ** Significant at P<0.05 and P<0.01, respectively**

DTF: Days to 50% flowering, DM: Days to maturity, PH: Plant height (cm), FLL: Flag Leaf Length, FLW: Flag Leaf Width, NTT: No. of Total Tillers, NPT: No. of Productive Tillers, PL: Panicle length, BY: Biological Yield (g), HI: Harvest index (%), NSP: No. of spikelet per panicle, TW: Test Weight (g), GYP: Grain yield per plant (g)



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