

# GENETIC VARIABILITY, HERITABILITY, CORRELATION AND PATH ANALYSIS OF YIELD COMPONENT CHARACTERS IN RICE (*Oryza sativa* L.) GENOTYPES

## ABSTRACT:

The present investigation consists of 22 genotypes of Rice including one check, which were grown under the Field Experiment Centre of the Department of GPB, SHUATS, Prayagraj during kharif 2021 following randomized block design (RBD) with three replications in the field for field improvement. The data was collected on 13 characters to evaluate the analysis of variance, heritability, genetic advance, correlation and path analysis. Under the field conditions, based on the mean performance **NUMALI** followed by **MTU-1155** and **TRIVENI** which were identified as desirable genotypes with highest grain yield per hill. High estimates of PCV, GCV, heritability coupled with high genetic advance as percent of mean were recorded for biological yield, number of tillers per hill and grain yield per hill. Biological yield, number of spikelets per panicle, panicle length and harvest index showed positive and highly significant association with grain yield per hill and recorded high positive direct effect on grain yield per hill at both the genotypic and phenotypic levels. It is significant to mention that results of present study have helped to select better germplasm on the basis of these characters such as biological yield, number of spikelets per panicle, panicle length and harvest index which should be given prior consideration during selection for grain yield improvement in rice.

**Keywords:** Rice, GCV, PCV, Heritability, Genetic advance, correlation and path analysis

## INTRODUCTION:

“Rice, *Oryza sativa* L. (2n=24) belongs to family Poaceae (Graminae) and the genus *Oryza* has two cultivated species namely: *Oryza sativa* (Asian rice) and *Oryza glaberrima* (African rice). About 90% of the world’s rice is grown and consumed by Asians. Asian cultivated rice is the world’s most important food crop and is primary food source for more than one third of the world’s population. Rice accounts for about 35 to 60% of the calories consumed by 3 billion Asians” (Khush, 2005). Inflorescence of rice is known as Panicle. Rice need hot and humid climatic conditions (RH 60%) and the average temperature required throughout the life period of the rice ranges from 21 °C to 37 °C. Rice is a short day and self-pollinated plant which grown under different conditions and production system. It is the world's longest domesticated grain (10,000 years) and the primary source of nutrition for 2.5 billion people. Rice is a semi-aquatic crop of the *poaceae* family. In India, rice is mainly grown in the state. “Rice is life” was the famous theme of the International Rice Year 2004, which denote its overwhelming importance as a food and trade them. The demand for food in most parts of world will be double by the year 2025 and nearly triple by 2050. Rice is mostly a starchy food with amylose and amylopectin fractions (78-79 percent starch). It also provides significant protein and vitamin content. Rice is high in vitamin B (thiamin and nicotinamide), as well as iron (Fe), phosphorus (P), and magnesium (Mg). In comparison to other cereals, milled rice has a low protein content (6-7%). However, it contains a lot of defective amino acids like lysine. In India rice covers more than 30 % of total cultivated area and contributes more than 40 % of total food production. The success of plant breeding depends on the extent of genetic variability present

in a crop. Understanding the nature and magnitude of genetic variation governing the inheritance of quantitative characters like yield and its components is essential for genetic improvement. Heritability is the transmission of characters from one generation to another generation. “Moreover, knowledge of heritability is essential for selection of yield related component traits for crop yield improvement. Heritability along with genetic advance is considerate in estimating the genetic gain under selection than heritability estimates alone” (Ajmera *et al.*, 2017). Genetic advance measures the difference between mean genotypic values of the selected population and the original population from which these were selected. Character association derived by correlation coefficient helps in evaluation of relative influence of various component characters on grain yield. Path coefficient analysis picks out correlation into direct and indirect effects. Path coefficient analysis provides information of influence of each contributing trait to yield directly as well as indirectly and also enables breeders to rank the genetic attributes according to their contribution. With this point of view, the present investigation entitled “**GENETIC VARIABILITY, HERITABILITY, CORRELATION AND PATH ANALYSIS OF YIELD COMPONENTS IN RICE (*Oryza sativa* L.) GENOTYPES**” was studied.

## **MATERIALS AND METHODS:**

The present investigation consists of 22 rice genotypes accessions which were evaluated with the help of randomized block design (RBD) with three replications in the field. Investigation was carried out at Field Experiment Centre of the Branch of Genetics and Plant Breeding (GPB) during the time of kharif-2021, Naini Agriculture Institute, Sam Higginbottom University of Agriculture, Technology & Sciences, Prayagraj (Uttar Pradesh). The experimental materials for present investigation comprised of 22 genotypes viz., BASMATI 370, DRR DHAN, DULAR, FR-13-A, GANTASWARI, GOVINDH, HIM-799, KRISHNA, MTU-3626, MTU-1155, NL-42, NLR-3354, NUMALI, RP-BIO 570, SAKET-4, SAVATRI, SHEETAL, TARAMATHI, TRIVENI, VAJRAM, VARDHAN and including one check variety i.e., NDR-356. The recommended doses of fertilizers N: P: K@ 120:60:60 kg/ha were applied. Total number of irrigations given to the crop is four at different growing stages of the crop. intercultural operation like manual weeding was done in field twice at 20 days after transplanting and at 50 days after transplanting respectively. Crop was harvested at 80% physiological maturity. The harvesting was done variety wise and bundles were prepared with proper labelling, were spread on the threshing floor for 2-3 days sun drying and thereafter threshing was conducted. Current investigation is an effort has been made toward assess the amount of genetic variability, heritability, genetic advance, correlation and path analysis in the rice accessions. Data were recorded on 13 characters viz; Days to 50% flowering, Days to maturity, plant height (cm), flag leaf length (cm), flag leaf width (cm), number of tillers per plant, number of panicles per hill, panicle length (cm), number of spikelets per panicle, biological yield (g), harvest index (%), test weight (g), and grain yield per hill (g).

## **RESULTS AND DISCUSSION**

High estimates of GCV and PCV were recorded for biological yield (27.67 and 29.40) and grain yield per hill (26.69 and 29.35). Moderate estimates of GCV and PCV were recorded in Flag leaf length (18.04 and 19.12), number of tillers per hill (15.76 and 16.98), number of

spikelets per panicle (14.53 and 17.82), Flag leaf width (13.77 and 15.03), Plant height (11.84 and 13.53), Test weight (10.08 and 12.61), Harvest index (10.38 and 15.12). Moderate estimates of PCV were recorded in days to 50% flowering (12.06), panicle length (11.98) and number of panicles per hill (11.09). Low estimates of GCV were observed for days to maturity (5.49) followed by days to 50% flowering (6.67), panicle length (9.58) and number of panicles per hill (6.61). Low estimates of PCV were observed for days to maturity (7.97).

The estimates of heritability from present investigation are presented in (Table 3). In the present study, heritability (broad sense) ranged from 30.57% to 89.09%. The highest heritability (above 60%) was observed for Flag leaf length (89.09%) followed by, biological yield (88.57%), number of tillers per hill (86.21%), flag leaf width (83.96%), grain yield per plant (82.70%), plant height (76.59%), number of spikelets per panicle (66.47), test weight (63.95%) and panicle length (63.91%) respectively. Moderate estimates of heritability (30-60%) were observed for days to maturity (47.27%), harvest index (47.13%), number of panicles per hill (35.60%) and days to 50% flowering (30.58%). All the characters showed high to moderate heritability. None of the characters showed low estimates of heritability (below 10%).

In the present study, high genetic advance (above 20%) was observed for by biological yield (49.70%), followed by number of spikelets per panicle (47.96), plant height (30.18%) and grain yield per plant (23.46%). Moderate (10-20%) values of genetic advance was observed for flag leaf length (16.49%) followed by days to maturity (10.40%). Lowest (below 10%) values of genetic advance was observed for days to 50% flowering (8.00%), harvest index (7.51%), panicle length (4.31%), test weight (3.73%), number of tillers per hill (3.57%), number of panicles per hill (0.92%) and flag leaf width (0.33%).

Highest estimates of genetic advance as per cent mean was recorded for biological yield (53.65%), grain yield per plant (50.00%), flag leaf length (35.09%), number of tillers per hill (30.15%), flag leaf width (25.99%), number of spikelets per panicle (24.40%) and plant height (21.35%). Moderate estimates of genetic advance as per cent mean was recorded for test weight (16.61%), panicle length (15.77%), harvest index (14.68%). Lowest estimates of genetic advance as per cent mean was observed for number of panicles per hill (8.13%), days to maturity (7.78%) and days to 50% flowering (7.59%).

High heritability coupled with high genetic advance as per cent mean was recorded for biological yield (90.51% and 19.59%), grain yield per plant (84.47% and 16.13%), flag leaf length (81.63% and 23.77%), number of tillers per hill (86.75% and 31.05%), flag leaf width (81.74% and 22.36%), number of spikelets per panicle (24.40%) and plant height (90.33% and

17.21%). and number of panicles per hill (71.43% and 21.42%). High heritability coupled with moderate genetic advance as per cent mean was observed in test weight (63.95% and 16.61%) and panicle length (63.91% and 15.77%) in the present investigation.

In the present investigation, at phenotypic level grain yield per hill showed positive significant association with biological yield (0.861\*\*), number of spikelets per panicle (0.343\*) and harvest index (0.326\*). while positive and non-significant association showed with days to 50% flowering (0.1513), plant height (0.0397), panicle length (0.1330) and days to maturity (0.1537). Negative and significant association showed with flag leaf length (-0.287\*) only, where as negative and non-significant association showed with flag leaf width (-0.0015), number of tillers per hill (-0.0317), number of panicles per hill (-0.2272) and test weight (-0.0378).

The correlation among the yield and yield attributing characters revealed that grain yield per hill at genotypic level was positively and significantly associated with days to 50% flowering (0.394\*), days to maturity (-0.348\*), number of spikelets per panicle (0.328\*), biological yield (0.903\*\*) and harvest index (0.369\*). But positively and non-significant correlation was found with panicle length (0.1173) only. Negative and significant association showed with flag leaf length (-0.329\*) and number of panicles per hill (-0.536\*\*), while negative and non-significant correlation were found with flag leaf width (-0.0463), number of tillers per hill (-0.0145) and test weight (-0.1082).

A detailed analysis of phenotypic diagonal values showed positive direct effect of days to 50% flowering, number of tillers per hill, panicle length, number of spikelets per panicle, biological yield and harvest index with grain yield per plant. Negative direct effects were exhibited by days to maturity, plant height, flag leaf length, flag leaf width, number of panicles per hill and test weight.

A detailed analysis of genotypic diagonal values showed positive direct effect of number of panicles per hill, panicle length, test weight, number of spikelets per panicle, biological yield with grain yield per plant. Negative direct effects were exhibited by days to maturity, plant height, flag leaf length, days to 50% flowering, number of tillers per hill, flag leaf width and harvest index.

## **CONCLUSION**

From the present investigation, it is concluded that **NUMALI** was found to be superior followed by **MTU-1155** and **TRIVENI** for higher grain yield per hill. Genotypes **VARDHAN** is earliest for days to 50% flowering and **SAKET-4** is earliest for days to maturity. High PCV,

GCV, heritability and genetic advance as percentage of mean were recorded for biological yield, grain yield per hill, number of tillers per hill and flag leaf length. Biological yield, number of spikelets per panicle, panicle length and harvest index showed positive and highly significant association with grain yield per hill and recorded high positive direct effect on grain yield per hill at both the genotypic and phenotypic level. These characters such as biological yield, number of spikelets per panicle, panicle length and harvest index should be given prior consideration during selection for grain yield improvement in rice.

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**Table 1. Analysis of variance for 13 quantitative characters among 22 genotypes of Rice.**

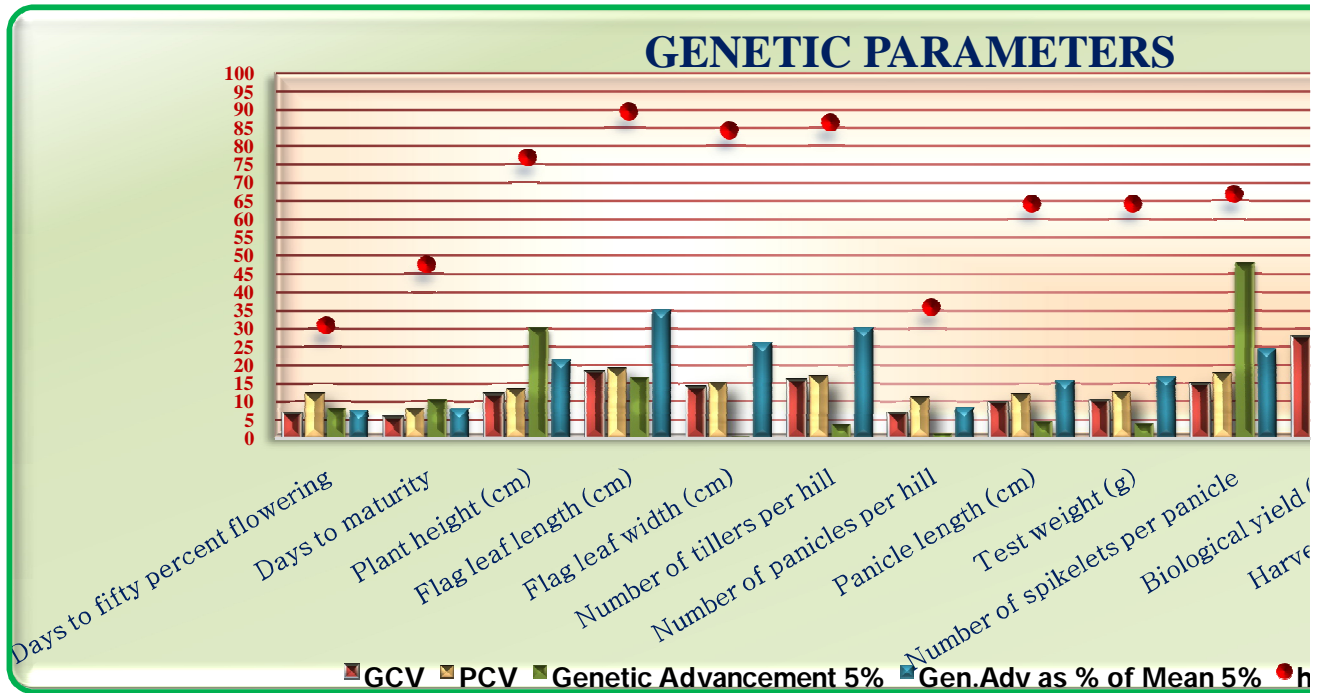
S. No	Features	Mean Sum of Squares		
		Replications (d. f=02)	Treatments (d. f=39)	
1	Days to 50 flowering	335.4240	259.959**	
2	Plant height	193.7490	222.253**	
3	Flag leaf length	170.7890	926.406**	
4	Flag leaf width	10.3540	224.589**	
5	Number of total tillers per hill	0.0110	0.098**	
6	Number of panicles per hill	1.3590	10.999**	
7	Panicle length	2.9960	2.713**	
8	Number of spikelets per panicle	1.3680	25.428**	
9	Days to maturity	5.760	18.298**	

10	<b>Biological yield</b>	114.9470	2857.271**
11	<b>Harvest Index</b>	169.0260	2056.759**
12	<b>Test weight</b>	41.3890	116.184**
13	<b>Grain yield per hill</b>	65.5710	503.265**

**Table 2. Estimates of components of variance and genetic parameters for different characters in rice.**

S. No	Characters	Coefficient of variation		Heritability	Genetic advance	Genetic advance as % of mean (5%)
		GCV	PCV			
1.	<b>Days to 50% flowering</b>	6.67	12.063	30.577	8	7.598
2.	<b>Plant height</b>	5.498	7.996	47.272	10.409	7.787

<b>3.</b>	<b>Flag leaf length</b>	11.845	13.534	76.591	30.181	21.354
<b>4.</b>	<b>Flag leaf width</b>	18.048	19.121	89.094	16.491	35.093
<b>5.</b>	<b>Number of tillers per plant</b>	13.771	15.029	83.958	0.33	25.993
<b>6.</b>	<b>Number of panicle per plant</b>	15.767	16.981	86.21	3.568	30.157
<b>7.</b>	<b>Panicle length</b>	6.617	11.09	35.606	0.923	8.134
<b>8.</b>	<b>Number of spikelets per panicle</b>	9.579	11.982	63.909	4.398	15.775
<b>9.</b>	<b>Days to maturity</b>	10.085	12.611	63.95	3.733	16.614
<b>10.</b>	<b>Biological yield</b>	14.53	17.822	66.474	47.958	24.404
<b>11.</b>	<b>Harvest index</b>	27.673	29.404	88.571	49.705	53.65
<b>12.</b>	<b>Test weight</b>	10.382	15.123	47.127	7.508	14.681
<b>13.</b>	<b>Grain yield per hill</b>	26.693	29.351	82.703	23.46	50.006



**Fig 1. Histogram depicting estimates of GCV, PCV, Heritability and Genetic advance as percent of means for 13 quantitative characters in rice genotypes**



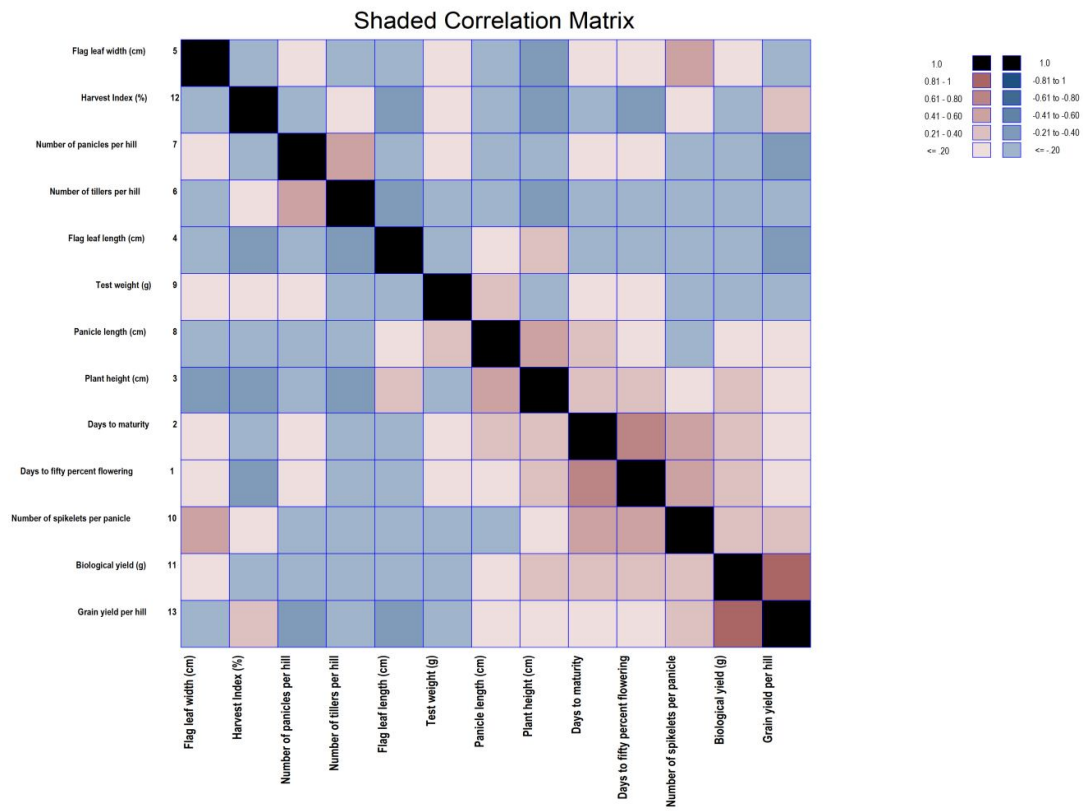


**Table 5. Direct and indirect effects of yield related traits on grain yield in 22 rice genotypes at phenotypic level.**

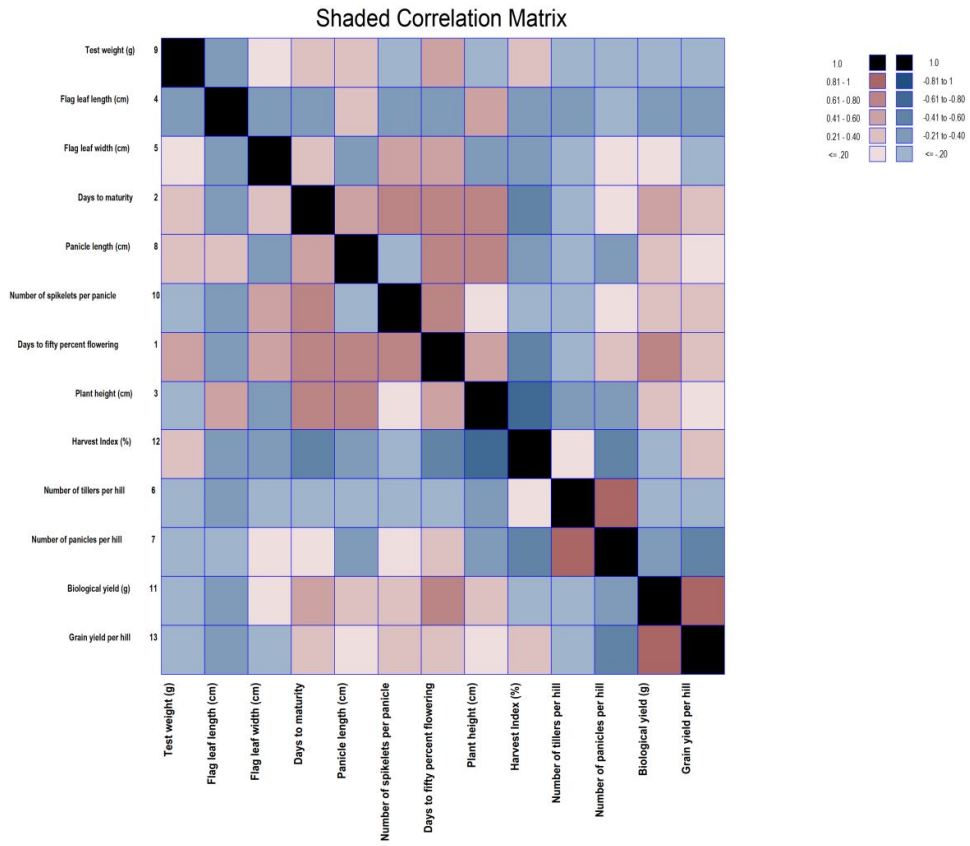
<b>Traits</b>	<b>DF</b>	<b>DM</b>	<b>PH</b>	<b>FL</b>	<b>FW</b>	<b>NTPH</b>	<b>NPPH</b>	<b>PL</b>	<b>TW</b>	<b>NSPP</b>	<b>BY</b>	<b>HI</b>	<b>GYPH</b>
<b>DF</b>	<b>0.0297</b>	0.0180	0.0091	-0.0002	0.0051	-0.0017	0.0021	0.0057	0.0022	0.0130	0.0086	-0.0076	0.1513
<b>DM</b>	-0.0552	<b>-0.0910</b>	-0.0325	0.0108	-0.0160	0.0087	-0.0098	-0.0282	-0.0156	-0.0377	-0.0289	0.0179	0.1537
<b>PH</b>	-0.0173	-0.0202	<b>-0.0567</b>	-0.0226	0.0114	0.0143	0.0001	-0.0282	0.0022	-0.0065	-0.0139	0.0207	0.0397
<b>FL</b>	0.0000	0.0004	-0.0015	<b>-0.0037</b>	0.0007	0.0010	0.0004	-0.0005	0.0005	0.0007	0.0007	0.0009	-0.287*
<b>FW</b>	-0.0113	-0.0115	0.0131	0.0122	<b>-0.0655</b>	0.0006	-0.0062	0.0101	-0.0064	-0.0276	-0.0055	0.0058	-0.0015
<b>NTPH</b>	-0.0012	-0.0020	-0.0052	-0.0059	-0.0002	<b>0.0208</b>	0.0090	-0.0021	-0.0006	-0.0002	-0.0021	0.0014	-0.0317
<b>NPPH</b>	-0.0005	-0.0008	0.0000	0.0008	-0.0007	-0.0032	<b>-0.0074</b>	0.0005	0.0000	0.0000	0.0012	0.0011	-0.2272
<b>PL</b>	0.0127	0.0205	0.0329	0.0089	-0.0102	-0.0067	-0.0042	<b>0.0662</b>	0.0179	-0.0024	0.0120	-0.0074	0.1330
<b>TW</b>	-0.0016	-0.0037	0.0008	0.0031	-0.0021	0.0006	0.0000	-0.0058	<b>-0.0214</b>	0.0022	0.0008	-0.0012	-0.0378
<b>NSPP</b>	0.0377	0.0357	0.0098	-0.0154	0.0363	-0.0010	-0.0004	-0.0031	-0.0087	<b>0.0860</b>	0.0291	0.0010	0.343*
<b>BY</b>	0.2675	0.2925	0.2259	-0.1738	0.0778	-0.0947	-0.1474	0.1664	-0.0328	0.3112	<b>0.9215</b>	-0.1347	0.861**
<b>HI</b>	-0.1091	-0.0842	-0.1560	-0.1012	-0.0380	0.0296	-0.0634	-0.0480	0.0248	0.0048	-0.0626	<b>0.4283</b>	0.326*

**Table 6. Direct and indirect effects of yield component traits on grain yield for 22 rice genotypes at Genotypic level.**

<b>Traits</b>	<b>DF</b>	<b>DM</b>	<b>PH</b>	<b>FL</b>	<b>FW</b>	<b>NTPH</b>	<b>NPPH</b>	<b>PL</b>	<b>TW</b>	<b>NSPP</b>	<b>BY</b>	<b>HI</b>	<b>GYPH</b>
<b>DF</b>	<b>-0.1174</b>	-0.1592	-0.0681	0.0308	-0.0504	0.0199	-0.0286	-0.0768	-0.0489	-0.0802	-0.0776	0.0684	0.394*
<b>DM</b>	-0.6356	<b>-0.4685</b>	-0.2833	0.1192	-0.1436	0.0843	-0.0478	-0.2726	-0.1827	-0.3081	-0.2635	0.2405	0.348*
<b>PH</b>	-0.2744	-0.286	<b>-0.473</b>	-0.2136	0.1254	0.1561	0.1174	-0.3322	0.0675	-0.0773	-0.1429	0.3559	0.0216
<b>FL</b>	0.0114	0.0111	-0.0197	<b>-0.0435</b>	0.009	0.014	0.0085	-0.0088	0.0093	0.0145	0.0095	0.0143	-0.329*
<b>FW</b>	-0.0974	-0.0696	0.0602	0.0468	<b>-0.2269</b>	0.0044	-0.0187	0.0653	-0.018	-0.1306	-0.0179	0.0567	-0.0463
<b>NTPH</b>	0.0401	0.0424	0.0778	0.0758	0.0046	<b>-0.2357</b>	-0.2106	0.0385	0.016	0.0033	0.0244	-0.0286	-0.0145
<b>NPPH</b>	0.0419	0.0175	-0.0427	-0.0335	0.0142	0.1535	<b>0.1718</b>	-0.0428	-0.0028	0.0092	-0.0651	-0.0826	-0.536**
<b>PL</b>	0.3138	0.279	0.3368	0.0972	-0.138	-0.0783	-0.1196	<b>0.4796</b>	0.1798	-0.0039	0.1014	-0.1105	0.1173
<b>TW</b>	0.0217	0.0203	-0.0074	-0.0111	0.0041	-0.0035	-0.0008	0.0195	<b>0.052</b>	-0.0012	-0.0074	0.0129	-0.1082
<b>NSPP</b>	0.3063	0.2948	0.0733	-0.1493	0.258	-0.0063	0.0239	-0.0036	-0.0106	<b>0.4483</b>	0.174	-0.0317	0.328*
<b>BY</b>	0.7713	0.6555	0.3521	-0.2544	0.0922	-0.1205	-0.4414	0.2465	-0.1649	0.4524	<b>0.922</b>	-0.1055	0.903**
<b>HI</b>	0.012	0.0106	0.0155	0.0068	0.0051	-0.0025	0.0099	0.0048	-0.0051	0.0015	0.0019	<b>-0.0206</b>	0.369*



**Fig 2. Phenotypic path diagram for 13 quantitative characters of rice genotypes**



**Fig 3. Genotypical Path diagram for grain yield per hill for 13 Quantitative characters of rice genotypes**