GENETIC VARIABILITY AND PATH ANALYSIS FOR YIELD AND GRAIN YIELD COMPONENT CHARACTERS IN RICE (*Oryza sativa* L.) GENOTYPES

ABSTRACT:

The present investigation consists of 21 genotypes of Rice including one check, which were grown underthe Field Experiment Centre of the Department of GPB, SHUATS, Prayagraj during *Kharif* 2021 following Randomized Block Design with three replications. Analysis of variance among 21 genotypes showed significant difference for all the characters studied. Based on the mean performance, genotypes **NUMALI** followed by **KALINGA** and **MTU-1155** were identified as suitable 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 grain yield per hill, biological yield and flag leaf length indicating that these characters could be used as selection for crop improvement.Biological yieldand harvest indexshowed positive significant association and recorded high positive direct effect on grain yield per hill at both the genotypic and phenotypic levels. These characters such as biological yield, and harvest index should be given prior consideration during selection for grain yield improvement in rice.

Keywords: Rice, Genetic variability, 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 and subfamily of *Oryzoidea*. The rice genus comprises 24 species, 22 of which arewild and 2 of which are grown, i.e.*O. sativa* and *O. glaberrima*. Rice is one of theworld's most important food crops. It absorbs almost 50 % of the total land occupiedby cerealsand accountsfor about one fifth of the global population. Of the twospecies cultivated, *O. Sativa* is grown worldwide. "In West Africa *O. glaberrima* has been cultivated for the last 3500 years. Inflorescence of rice is known as Panicle. Nutritional components include proteinsand micronutrients like Iron and Zinc. The average percentage of proteinin rice grains is 8per cent, Fe is 1.2 mg/100 g and Zn is 0.5 mg/100 g. Malnutrition is a large and growingproblem in the developing world mostly in South and S.E. Asia and Sub Sahara Africa" **(Reddy *et al.*, 2005)**.

"Rice plays acrucial role in the Indian economy being the two-thirds of the population's staple food.The majority of rice produced in Asian countries is in China, India, Indonesia, Bangladesh, Vietnam, Thailand, Myanmar and Pakistan. Asian farmers already account for 87 per cent of the overall production of rice in the world. By 2050, the world's population is anticipated to reach 9.1billion, necessitatinga 70 percent increase in food production" **(Godfray*et al.*, 2010; Hodges *et al.*, 2011; Parfitt *et al.*, 2010).**

The International Rice Research Institute (IRRI 2000) studied "the food problem inrelation to world population, and they predict that 800 million tons of rice will be required in 2025". High yielding varieties is essential in order to meet the food requirement of growing population. The success of plant breeding depends on the extent of genetic variability present in a crop. To formulate an efficient breeding technique, knowledge about the genetic architecture of genotypes is needed. Finding the relative magnitude of additive and non-additive genetic variances, heritability and genetic advantage with respect to breeder-concentrated characters is important. Genetic variability in population segregation, which depends on the level of genetic diversity among genotypes. Efficient and economic crop enhancement scheme refers to obtaining a high yielding variety of superior alleles. The existence of variability is most significant in any breeding programme for effective selection. Genetic parameter can measure the amount of variation present in population *viz.* Phenotypic coefficient of variation and genetic coefficient of variation. "When selection is made based on yield contributing characteristics, heritability and genetic advance are essential selection parameters. Heritability estimates combined with genetic improvement are typically more effective in predicting selection benefit than heritability estimates alone" **(Paul *et al*., 2006).**

Estimates of heritability provide information about a specific genetic attribute to be passed onto the successive generations and directly the breeders to choose the parents toimprove their crops programmes.Correlation coefficient is a statistical measure which is used to find out the degree(strength) anddirectionof relationship betweentwo or more variables.It is represented by**'r'**. A positive value of 'r' shows that the changes of two variables are in the same directions.In the present investigation, correlation coefficient analysis measures the mutual relationship between various plant characters and to determine the component characters on which selection can be used for genetic improvement in yield while selecting the suitable plant type. The direct impact of one variable on another is measured using path coefficient analysis, a standardized regression coefficient. It is a statistical technique that divides the correlation coefficient into its direct and indirect impacts in order to evaluate how much each character contributes to the yield. Since it is impacted by the environment, direct selection for yield is a risky strategy. In order to improve crop production, it is employed in plant breeding programs to ascertain the nature of the relationship between yield and yield components that can be utilized as selection criteria. With this available context information, the present investigation entitled "**GENETIC VARIABILITY AND PATH ANALYSIS FOR YIELD AND GRAIN YIELD COMPONENT CHARACTERS IN RICE (*Oryza sativa* L.) GENOTYPES"** was studied.

MATERIALS AND METHODS:

The experiment comprised of 21 genotypes of rice grown during kharif-2021 collected from the branch of Genetics and Plant Breeding, Sam Higginbottom University of Agriculture, Technology & Sciences, Prayagraj (Uttar Pradesh) in a randomized block design with 3 replications.Current investigation is an effort has been made toward assess the amount of genetic variability and path analysis in the rice accessions.Thirty days old seedlings were transplanted in the experimental site with the spacing of 15 cm between plants and 20 cm between the rows, keeping single seedling per hill. Fertilizer dose of 120 kg N, 60 kg P_20_5 and 40 kg K_20 was applied. The standard agronomic practices were adopted and all recommended package of practices were followed for normal crop growth. Five plants were randomly selected from each replication in each genotype for the analysis of following parameters. 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). The observations were recorded as per the standard procedure and subjected to statistical analysis using mean values of five randomly selected plants.

RESULTS AND DISCUSSION

The results of the analysis of variance showed that there were significant variations among the genotypes examined for each character, showing that there was variability. For every character under study, the analysis of variance revealed genotype differences that were statistically significant ($p<0.05$). The presence of a significant level of diversity may be a result of the materials used being from different sources as well as environmental factors that impact the phenotypes. High estimates of GCV and PCV were recorded for grain yield per hill (28.89 and 0.22) and biological yield (28.11 and 28.88). Moderate estimates of GCV and PCV were recorded in Flag leaf length (16.61and17.81), Harvest index (15.51 and 19.03), Flag leaf width (13.99 and 15.33), Plant height (13.76 and 15.39), Test weight (13.69 and 14.75), number of spikelets per panicle (11.3 and 13.46), days to 50% flowering (11.05 and 12.68) and number of tillers per hill (10.91 and 14.07). Low estimates of GCV and PCV were observed for number of panicles per hill (7.68 and 11.49), panicle length (7.68 and 11,16) and days to maturity(6.27 and 10.16).

The estimates of heritability from present investigation are presented in (Table 4.3). In the present study, heritability (broad sense) ranged from 38.19% to 94.77%. The highest heritability (above60%) was observed for biological yield (94.77%), followed by, grain yield per hill (91.44%), Flag leaf length (86.95%), test weight (86.22%), flag leaf width (83.26%), plant height (79.98%), days to 50%flowering (75.86%), number of spikelets per panicle (70.59), harvest index(66.44%) and number of tillers per hill (60.12%) respectively. Moderate estimates of heritability (30-60%) were observed for days to maturity (38.19%), number of panicles per hill (44.68%) and panicle length(47.38%). 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 (56.06%), followed by number of spikelets per panicle (37.41), plant height(37.38%), grain yield per hill (28.16%) and daysto50%flowering(20.46%). Moderate (10-20%) values of genetic advance were observed for flag leaflength (14.78%) followed by harvest index(13.08%) and days to maturity(10.57%).Lowest (below 10%) values of genetic advance was observed for test weight(6.10%), panicle length(3.07%), number of tillers per hill(1.93%),number of panicles per hill(1.16%) and flag leaf width (0.33%).

Highest estimates of genetic advance as per cent mean was recorded for grain yield per hil (56.92%), biological yield (56.38%), flag leaf length (31.90%), flag leaf width (26.30%), test weight (26.19%), harvest index (26.05%) and plant height

(21.35%). Moderate estimates of genetic advance as per cent mean was recorded for days to 50%flowering (19.82%), number of spikelets per panicle (19.58%), number of tillers per hill (17.43%), panicle length (10.89%) and number of panicles per hill(10.58%). Lowest estimates of geneticadvance as per cent mean was observed for days to maturity (7.99%).

High heritability coupled with high geneticadvanceas per cent meanwas recordedfor biological yield (94.77% and 56.38%), grain yield per hill (91.44% and 56.92%), flag leaf length (86.95% and 31.90%), test weight (63.95% and 16.61%), flag leaf width (81.74% and 22.36%), harvest index (66.44%) and plant height (90.33% and 17.21%). High heritability coupledwith moderate genetic advance as per cent mean was observed in Days to 50% flowering (75.86% and 19.83%), number of spikelets per panicle (70.59% and 19.59%) and number of tillers per hill (60.12% and 17.43%) in the present investigation.

In the present investigation at phenotypic level, grain yield per hill showed positive significant association with biological yield (0.766**) and harvest index (0.480**). while positive and non-significant association showed with flag leaf width (0.1209), test weight (0.0501), number ofspikelets perpanicle(0.0687), panicle length (0.1008) and days to maturity (0.0122). Negative and significant association showed with numberof tillers per hill(-0.286*) and numberof panicles per hill (-0.2982), whereas negative and non-significant association showed with flag leaf length (-0.0631),plant height (-0.0414) and days to50% flowering (-0.1337).

At genotypic level, correlation among the yield and yield attributing characters revealed that grain yield per hill was positively and significantly associated with biological yield (0.832**) and harvest index (0.455**).But positively and non-significant correlation was found with days to maturity (0.0277), number of spikelets per panicle(0.0774), flagleaf width (0.1657), panicle length (0.1674) and test weight (0.0472). Negative and significant association showed with number of tillers per hill (-0.338*) and number of panicles per hill (-0.461**), while negative and non-significant correlation were found with flag leaf length (-0.1312), days to 50% flowering (-0.0929) and plant height (-0.0429).

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

An in-depth investigation of the diagonal data revealed a positive direct relationship among harvest index, biological yield, days to maturity, flag leaf length, number of tillers per hill, number of panicles per hill, and length of panicles. Negative direct effects were exhibited by plant height, days to 50% flowering, test weight, flag leaf width and numberofspikelets per panicle.

CONCLUSION

It is concluded that **NUMALI** was found to be superior followed by **KALINGA**and **MTU-1155**for higher grain yield per hill. Genotypes **POONGAR** is earliest for days to 50% flowering and days to maturity. High PCV, GCV, heritability and genetic advance as percentage of mean were recorded for grain yield per hill, biological yield and flag leaf length. Biological yield and harvest index showed positive significant association and recorded high positive direct effect on grain yield per hill at both the genotypic and phenotypic levels. These characters such as biological yield and harvest index should be given prior consideration and genotypes such as Numali, Kalinga and MTU-1155were found most promising for commercial cultivation under agro-climatic conditions of Prayagraj region and hence it can be useful for further crop improvement programmes during selection for grain yield improvement in rice.

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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.	**Days to 50% flowering**	11.052	12.689	75.859	20.456	11.052
2.	**Plant height**	6.277	10.157	38.197	10.572	6.277
3.	**Flag leaf length**	13.76	15.386	79.989	37.378	13.76
4.	**Flag leaf width**	16.61	17.812	86.95	14.787	16.61
5.	**Number of tillers per plant**	13.993	15.336	83.26	0.337	13.993
6.	**Number of panicle per plant**	10.914	14.075	60.123	1.927	10.914
7.	**Panicle length**	7.687	11.499	44.682	1.161	7.687
8.	**Number of spikelets per panicle**	7.683	11.162	47.378	3.072	7.683
9.	**Days to maturity**	13.696	14.75	86.22	6.105	13.696
10.	**Biological yield**	11.313	13.465	70.589	37.414	11.313
11.	**Harvest index**	28.115	28.88	94.771	56.059	28.115
12.	**Test weight**	15.515	19.034	66.444	13.085	15.515
13.	**Grain yield per hill**	28.898	30.221	91.438	28.159	28.898

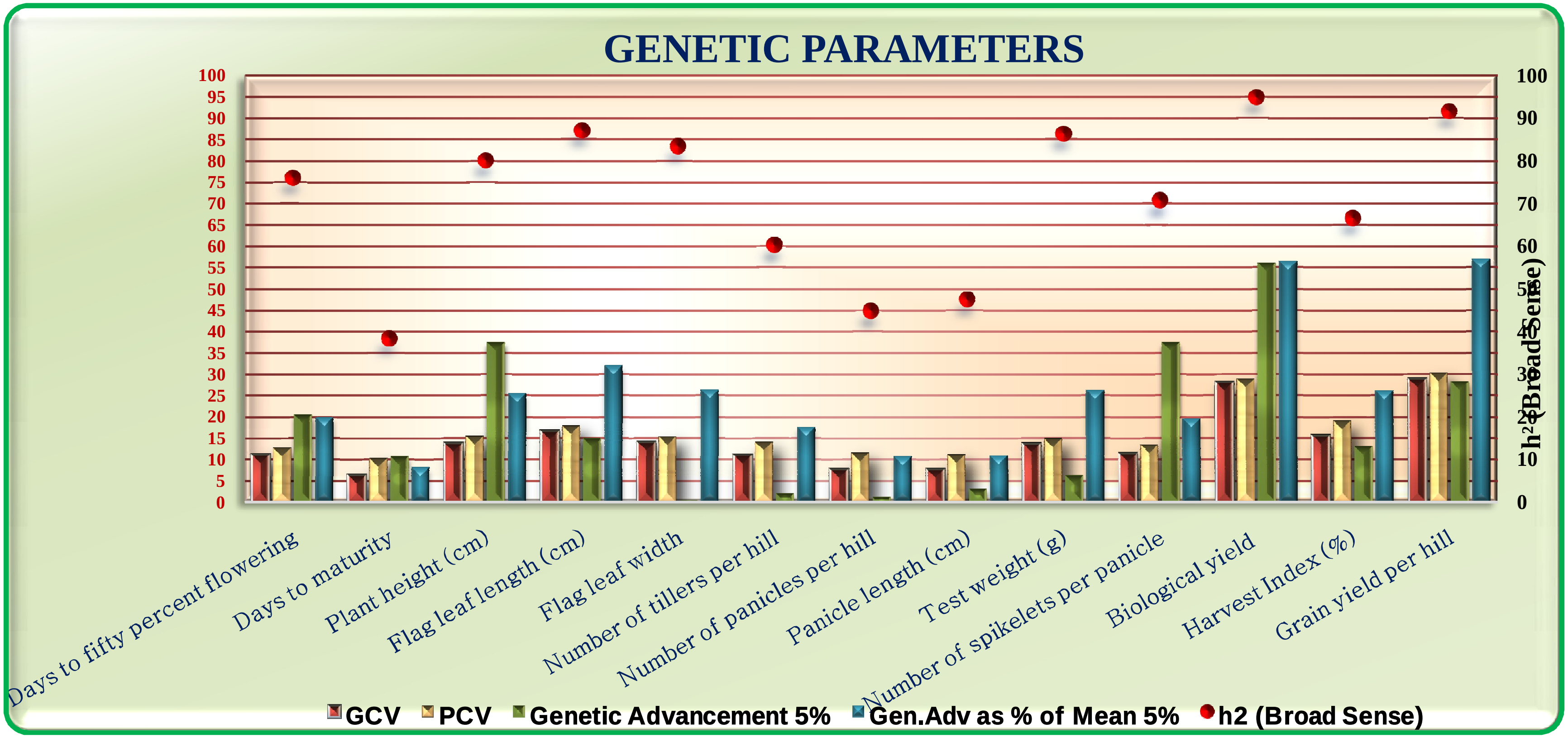

Figure1. Histogram depicting estimates of GCV, PCV, Heritability and Genetic advance as percent of means for 13 quantitative characters in rice genotypes

Table3. Estimation of Phenotypic correlation coefficient for yield and its related traits in 21 rice genotypes.

Traits	Correlation	DF	DM	PH	FL	FW	NTPH	NPPH	PL	TW	NSPP	BY	HI	GYPH
DF	r_p	1.0000	0.713**	0.0883	-0.397*	0.253*	0.340*	0.323*	0.0147	-0.0615	0.335*	0.2308	-0.426**	-0.0631
	r_g	1.0000	0.892**	0.1294	-0.489**	0.253*	0.492**	0.451**	0.1661	-0.0938	0.476**	0.248*	-0.602**	-0.0929
DM	r_p		1.0000	0.1409	-0.352*	0.2091	0.1870	0.1819	0.1509	-0.0968	0.354*	0.2459	-0.343*	0.0122
	r_g		1.0000	0.0937	-0.584**	0.339*	0.518**	0.390*	0.2349	-0.2234	0.593**	0.364*	-0.559**	0.0277
PH	r_p			1.0000	0.0737	-0.484**	-0.1612	-0.1651	0.476**	0.0037	-0.0037	0.275*	-0.447**	-0.0414
	r_g			1.0000	0.1052	-0.543**	-0.290*	-0.2151	0.719**	0.0174	-0.0195	0.315*	-0.586**	-0.0429
FL	r_p				1.0000	-0.1337	-0.283*	-0.2333	-0.1112	-0.1238	-0.356*	-0.2317	0.0638	-0.1337
	r_g				1.0000	-0.2131	-0.381*	-0.324*	-0.1206	-0.1566	-0.507**	-0.274*	0.1598	-0.1312
FW	r_p					1.0000	0.376*	0.1971	-0.249*	-0.1712	0.361*	0.1301	0.0154	0.1209
	r_g					1.0000	0.554**	0.344*	-0.2457	-0.1937	0.407**	0.1532	0.0530	0.1657
NTPH	r_p						1.0000	0.634**	-0.0347	0.1031	0.1119	-0.255*	-0.0369	-0.286*
	r_g						1.0000	0.921**	-0.0458	0.1542	0.1850	-0.312*	-0.1276	-0.338*
NPPH	r_p							1.0000	-0.0113	0.252*	0.0319	-0.290*	-0.0359	-0.298*
	r_g							1.0000	-0.1821	0.311*	0.0272	-0.445**	-0.1121	-0.461**
PL	r_p								1.0000	0.2234	0.0335	0.2037	-0.1031	0.1008
	r_g								1.0000	0.2080	-0.0182	0.333*	-0.2376	0.1674
TW	r_p									1.0000	-0.352*	-0.0797	0.2295	0.0501
	r_g									1.0000	-0.426**	-0.0769	0.2386	0.0472
NSPP	r_p										1.0000	0.302*	-0.297*	0.0687
	r_g										1.0000	0.382*	-0.467**	0.0774
BY	r_p											1.0000	-0.1793	0.766**
	r_g											1.0000	-0.1127	0.832**
HI	r_p												1.0000	0.480**
	r_g												1.0000	0.455**
GYPP	r_p													1.0000

	r_g													1.0000

** And * indicates significance at 1% and 5% level of significance respectively.

DF: Days to 50% flowering, DM: Days to maturity, FL: Flag leaf length (cm), FW: Flag leaf width, PH: Plant height (cm) , NTPH: Number of tillers per plant,NPPH: Number of panicle per plant, PL: Panicle length, NSPP: Number of spikelets per panicle, BY: Biological yield, HI: Harvest index, TW: Test weight, GYPH: Grain yield per hill

Table 4.Directandindirecteffects ofyieldrelatedtraits on grainyieldin21 ricegenotypes atphenotypic level.

Traits	**DF**	**DM**	**PH**	**FL**	**FW**	**NTPH**	**NPPH**	**PL**	**TW**	**NSPP**	**BY**	**HI**	**GYPH**
DF	**0.0203**	0.0144	0.0018	-0.0080	0.0051	0.0069	0.0065	0.0003	-0.0012	0.0068	0.0047	-0.0086	-0.0631
DM	0.0176	**0.0247**	0.0035	-0.0087	0.0052	0.0046	0.0045	0.0037	-0.0024	0.0088	0.0061	-0.0085	0.0122
PH	0.0006	0.0010	**0.0073**	0.0005	-0.0035	-0.0012	-0.0012	0.0035	0.0000	0.0000	0.0020	-0.0033	-0.0414
FL	-0.0091	-0.0081	0.0017	**0.0229**	-0.0031	-0.0065	-0.0053	-0.0025	-0.0028	-0.0082	-0.0053	0.0015	-0.1337

FW	0.0026	0.0022	-0.0050	-0.0014	**0.0103**	0.0039	0.0020	-0.0026	-0.0018	0.0037	0.0013	0.0002	0.1209
NTPH	-0.0168	-0.0092	0.0080	0.0140	-0.0186	**-0.0494**	-0.0313	0.0017	-0.0051	-0.0055	0.0126	0.0018	-0.286*
NPPH	0.0028	0.0016	-0.0014	-0.0020	0.0017	0.0054	**0.0085**	-0.0001	0.0021	0.0003	-0.0025	-0.0003	-0.298*
PL	-0.0001	-0.0011	-0.0034	0.0008	0.0018	0.0002	0.0001	**-0.0072**	-0.0016	-0.0002	-0.0015	0.0007	0.1008
TW	0.0014	0.0022	-0.0001	0.0028	0.0039	-0.0023	-0.0057	-0.0051	**-0.0227**	0.0080	0.0018	-0.0052	0.0501
NSPP	-0.0045	-0.0048	0.0001	0.0048	-0.0049	-0.0015	-0.0004	-0.0005	0.0047	**-0.0135**	-0.0041	0.0040	0.0687
BY	0.2004	0.2135	0.2387	-0.2011	0.1129	-0.2218	-0.2517	0.1769	-0.0692	0.2624	**0.8682**	-0.1557	0.766**
HI	-0.2783	-0.2243	-0.2925	0.0417	0.0100	-0.0241	-0.0235	-0.0674	0.1500	-0.1939	-0.1172	**0.6538**	0.480**

Table 6. Direct and indirect effects of yield component traits on grain yield for 21 rice genotypes at Genotypic level.

Traits	**DF**	**DM**	**PH**	**FL**	**FW**	**NTPH**	**NPPH**	**PL**	**TW**	**NSPP**	**BY**	**HI**	**GYPH**
DF	**-0.0156**	-0.0182	-0.0020	0.0076	-0.0040	-0.0077	-0.0070	-0.0026	0.0015	-0.0074	-0.0039	0.0094	-0.0929
DM	0.0356	**0.0305**	0.0029	-0.0178	0.0103	0.0158	0.0119	0.0072	-0.0068	0.0181	0.0111	-0.0170	0.0277
PH	-0.0121	-0.0087	**-0.0933**	-0.0098	0.0507	0.0270	0.0201	-0.0671	-0.0016	0.0018	-0.0294	0.0547	-0.0429
FL	-0.0317	-0.0379	0.0068	**0.0648**	-0.0138	-0.0247	-0.0210	-0.0078	-0.0101	-0.0329	-0.0177	0.0104	-0.1312
FW	-0.0155	-0.0207	0.0331	0.0130	**-0.0610**	-0.0338	-0.0210	0.0150	0.0118	-0.0248	-0.0093	-0.0032	0.1657
NTPH	0.0083	0.0088	-0.0049	-0.0064	0.0094	**0.0169**	0.0215	-0.0008	0.0026	0.0031	-0.0053	-0.0022	-0.338*
NPPH	0.0131	0.0113	-0.0062	-0.0094	0.0100	0.0368	**0.0290**	-0.0053	0.0090	0.0008	-0.0129	-0.0033	-0.461**
PL	0.0073	0.0103	0.0314	-0.0053	-0.0107	-0.0020	-0.0080	**0.0437**	0.0091	-0.0008	0.0146	-0.0104	0.1674

TW	0.0022	0.0052	-0.0004	0.0037	0.0045	-0.0036	-0.0073	-0.0049	**-0.0234**	0.0100	0.0018	-0.0056	0.0472
NSPP	-0.0026	-0.0033	0.0001	0.0028	-0.0022	-0.0010	-0.0001	0.0001	0.0023	**-0.0055**	-0.0021	0.0026	0.0774
BY	0.2346	0.3442	0.2980	-0.2584	0.1447	-0.2951	-0.4204	0.3148	-0.0726	0.3606	**0.9446**	-0.1064	0.832**
HI	-0.3165	-0.2937	-0.3083	0.0840	0.0279	-0.0671	-0.0590	-0.1249	0.1254	-0.2455	-0.0592	**0.5258**	0.455**

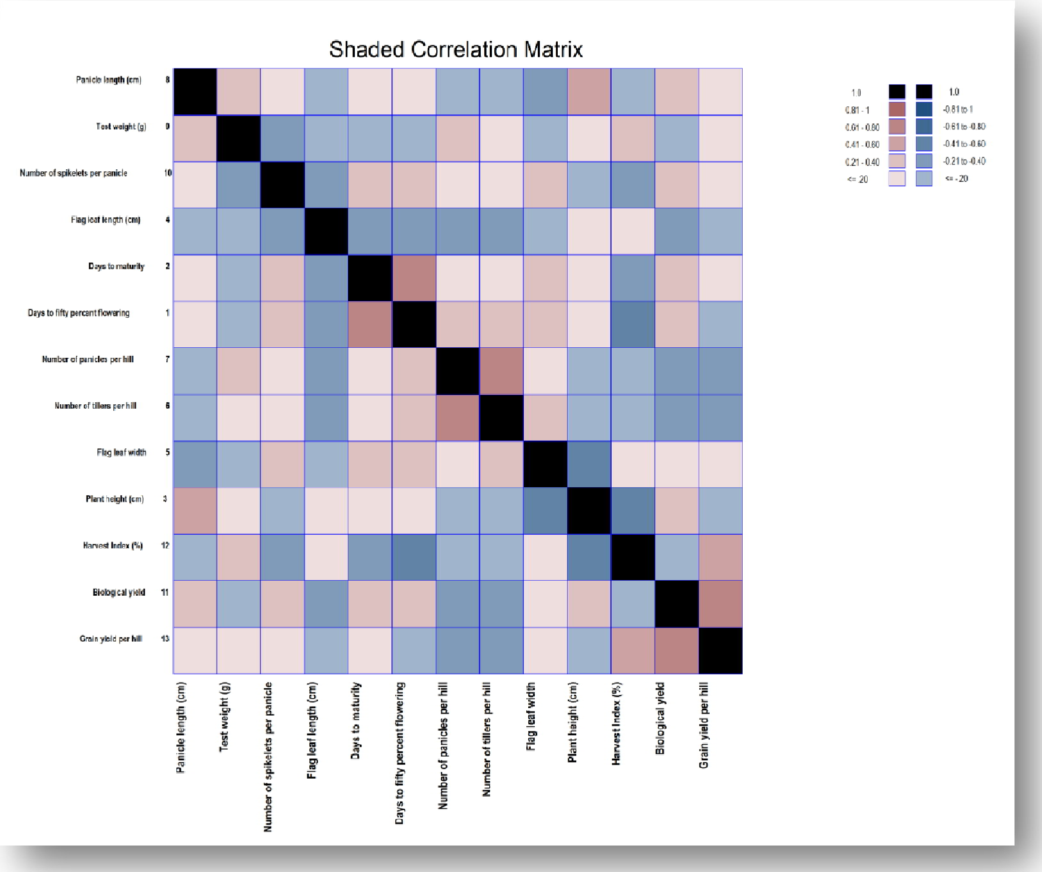

Fig2.Phenotypicpathdiagramfor13quantitativecharactersofricegenotypes

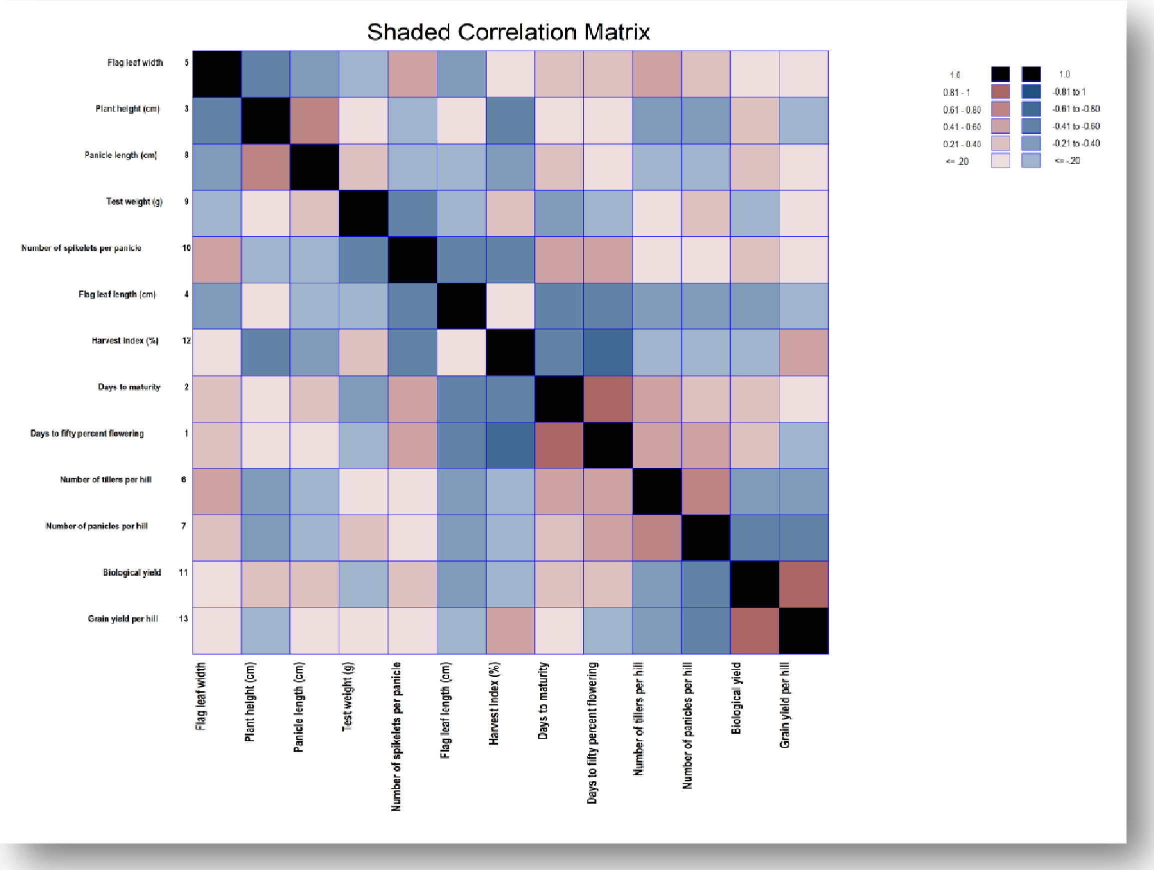

Fig3.GenotypicalPathdiagram for grain yield per hillfor13Quantitativecharacters of rice gentyp