Original Research Article

Study on Genetic Variability for Quantitative and Quality Parameters in Rice (*Oryza sativa* L.)

Abstract

The current study investigates twenty genotypes of rice, including one check variety NDR-359, that were raised in the Field Experimentation Centre of the Department of Genetics and Plant Breeding, SHUATS, Prayagraj during *Kharif* 2022 using a Randomized Block Design with three replications.The best genotypes for grain yield per plant were chosen based on the mean performance of genotypes RNR – 1446, followed by MTU - 1121, JGL – 24423, and Rango Komal. All of the qualities under examination had significant differences, according to the analysis of variance. The characters viz., Biological yield, Grain yield ~~her~~ perhill, Number of spikelets per panicle exhibited high Genotypic Coefficient of Variation (GCV) and Phenotypic Coefficient of Variation (PCV). For all the features under study, there were very slight variations between GCV and PCV, indicating that the environment had little to no impact on these individuals. High heritability recorded in Biological yield, Grain yield per hill, Panicle length, Plant height and Days to 50% flowering, whereas moderate heritability observed in Flag leaf width. High heritability coupled with genetic advance as percent mean is recorded in Biological yield, Grain yield per hill, Panicle length and Plant height indicating that simple selection could be effective for improving these characters. Correlation results shown that grain yield per hill exhibited highly and significant~~ly~~ correlation with biological yield and Number of spikelets per panicle. The results of the Path coefficient analysis revealed that both phenotypic and genotypic levels, had positive direct effects on grain yield while compare with parameters like Biological yield, Harvest index %, Number of panicles per hill and Days to 50% flowering. Quality characters *i.e.*, hulling (%), cooking and eating characters i.e., kernel length and breadth before and after cooking, elongation ratio was taken for 19 genotypes. As per mean performance highest maximum grain length was observed in Kasturi, DRRH2, while highest elongation ratio observed in MTU - 1121 and NLR - 40024.

Keywords: GCV, PCV, Heritability, Genetic advance, Correlation

Comment [D1]: MAJOR REVISION:

Whole manuscript is very weak in grammar, its look like copy pasted without any check for meaning of sentences

Comment [D2]: Check for the meaning of sentence, need to reframe it

1. Introduction

Rice, *Oryza sativa* L.(2n=24), a member of the Poaceae family, is a primary source of calories for the world's population, particularly in Asia, where it feeds roughly 1/3 of the world's population. Rice is native to the Himalayan foothills of north-east India and southern China. Rice has cultivated two species: *Oryza sativa* and *Oryza glaberrima*. *Oryza sativa* is extensively cultivated, whereas *Oryza glaberrima* is only grown in west African countries.

Comment [D3]: ???????

Rice contributes to about 60–70% of total calories and one-third of daily protein requirement, and is a great source of complex carbohydrates, which is an important source of the fuel to our body needs. Rice's nutritional value is mostly determined by the amount of protein in milled rice. The amount of protein in milled rice mostly determines the nutritional value of rice. Therefore, quality assessment includes both the physical and chemical characteristics **(Kamalaja *et al*. 2018).**

Comment [D4]: Two same sentences

Knowledge of the genetic variability of yield contributing traits, their interrelationships, and their link to yield is required for an effective breeding programme. Plant breeders can use heritability information to determine the nature of the next generation, make appropriate selections, and measure the extent of genetic improvement achieved through selection **(Pratap *et al*. 2018)**

Comment [D5]: Use scientific term, looks like auto-paraphrased

Path analysis useful to give idea about direct and in direct effects of yield components, while correlation studies give the relationship among plant characters, their degree of linear relationship, path coefficient analysis more clarifies in dividing the two traits into component that measures the direct and indirect effects **(Shreshta *et al*. 2018).**

1.1 Objectives

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It should be In research article format

1. To assess genetic variability among 20 rice genotypes for quantitative and quality characters
2. To assess the correlation between yield and yield attributing traits in Rice
3. To study direct and indirect effects of yield attributing traits on seed yield

2. Materials and Methods

The present experiment was carried out in the Field Experimentation Centre of Department of Genetics and Plant Breeding, Naini Agricultural Institute, Sam Higginbottom University of Agriculture, Technology and Sciences, Allahabad, U.P during *Kharif*, 2022.

The site of experiment is located at 25.57^0 N latitude, 81.51^0 E longitude and 98 meter above the sea level. This region has subtropical climate with extreme of summer and winter, the temperature falls down to as low as 1^0C-2 ^{0}C during winter season especially in the month of December and January. The mercury rises up to 46^0C-48^0C during the summer.The average rainfall in this area is around 1013.4 mm annually with maximally occurring during July to September with few showers and drizzles in winter also.

The 20 assessions of rice genotypes is carried out to perform the experimentconducted in Randomized Block Design with three replications with spacing Row to Row spacing is 20 cm and Plant to Plant spacing is 15 cm. In each replication five randomly selected best competitive plants are examined were recorded on following13 quantitative traits *viz.*, Days to 50% flowering, Plant height (cm), Number of tillers per hill, Number of panicles per hill, Panicle length (cm), Flag leaf length (cm), Flag leaf width (cm), Number of spikelets per panicle, Days to maturity, Biological yield per hill (g), Test weight (g), Grain yield per hill (g) and 7 quality characters *viz.*, Hulling %, Kernal length before cooking (mm), Kernal breadth before cooking (mm), Kernal length after cooking (mm), Kernal breadth after cooking (mm), L/B ratio and Elongation ratio.

The **Panse and Sukhatme (1967)** method were used to analyse the variance in all of the recorded data for the characters under consideration.Additionally, the genetic parameters genotypic coefficient of variation (GCV), Phenotypic coefficient of variation (PCV), Heritability in the broad sense, Genetic advance as percent of mean and correlation analysis was carried out by using the statistical methods. The additional components of variance include Phenotypic variance, Genotypic variance and Environmental Variance.

The Software called "R – Language" was used to perform the analysis mentioned above.

Comment [D7]: Rstudio and also cite properly

Experimental material

The experimental materials for this research were obtained from the SHUATS, Department of Genetics and Plant Breeding in Prayagraj. The details of the experimentalmaterials are mentioned below in table 1.

Table1 : Experimental material

S. No	Genotypes		S. No	Genotypes
1	RNR – 1446		11	NLR – 33057
2	JGL – 24423		12	NLR – 34449
3	MTU – 1311		13	NLR – 40024
4	MTU – 1121		14	NLR – 145
5	DRRH – 2		15	NLR – 40054
6	Kasturi		16	NLR – 30491
7	Deshi Masuri		17	NLR – 33641
8	Rangokomal		18	NLR – 4001
9	NLR – 3354		19	NLR – 33359
10	NLR – 3041		20	NDR – 359 (CHECK)

3. Results and Discussion

3.1 Quality characters:

The preusal of data indicated that out of rice genotypes evaluated for various quality characters, some genotypes were found superior for different characters. These genotypes were found better for more than one character. Among these genotypes NLR-3354 (81%) recorded the highest hulling percentage, Kasturi (4.39) has highest L/B ratio, NLR-40024 (1.31) has highest Elongation ratio. All these genotypes were significantly higher as compared to mean value. Other remaining lines were found better for different quality characters (Table 2). Therefore, these genotypes may be promoted for cultivation as well as in future breeding programmes to develop superior varieties for grain quality characters.

Table 2Mean performance of 19 genotypes for 7 quality parameters in *kharif, 2022*

`S.No	GENOTYPES	Hulling percent	Kernel length before cooking	Kernel breadth before cooking	L/B RATIO	Kernel length after cooking	Kernel breadth after cooking	Elongation ratio
1	RNR-1446	74	6.78	2.10	3.23	7.82	3.20	1.15
2	JGL-24423	79	6.67	2.20	3.04	8.20	2.99	1.23
3	MTU-1311	72	7.12	2.06	3.46	8.28	2.87	1.16
4	MTU-1121	76	5.86	1.88	3.13	7.70	2.69	1.31
5	NLR-3354	81	6.55	1.78	3.68	8.40	2.64	1.29
6	DRRH-2	66	7.27	2.05	3.55	8.38	2.39	1.15
7	Kasturi	62	8.09	1.85	4.39	9.31	2.16	1.15
8	NLR-3041	79	5.40	1.67	3.25	6.96	2.70	1.29
9	Deshi Masuri	67	6.54	2.03	3.23	7.72	2.30	1.18
10	NLR-33057	76	6.36	1.88	3.39	7.23	2.30	1.14
11	NLR-34449	72	5.48	1.60	3.42	6.69	2.59	1.22
12	NLR-40024	78	5.70	1.74	3.31	7.46	2.69	1.31
13	Rango Komal	77	5.98	2.50	2.40	7.18	2.71	1.20
14	NLR-145	76	7.00	1.97	3.61	7.31	2.70	1.05
15	NLR-40054	75	6.53	1.66	3.93	7.87	2.70	1.21
16	NLR-30491	76	5.83	1.80	3.26	6.93	2.54	1.19
17	NLR-33641	73	5.82	2.01	2.94	6.98	2.97	1.20
18	NLR-4001	74	6.06	1.70	3.58	7.07	2.32	1.17
19	NLR-33359	68	6.38	1.88	3.41	7.72	2.74	1.21
	Mean	73.74	6.39	1.91	3.38	7.64	2.64	1.20
	Minimum	62	5.40	1.60	2.40	6.69	2.16	1.05
	Maximum	81	8.09	2.50	4.39	9.31	3.20	1.31

3.2 Analysis of Variance

Analysis of Variance for all parameters recorded in twenty rice genotypes is presented in Table 3 indicating the mean sum of squares due to replications, varieties, and error for thirteen characters studied. The analysis of variance indicated the presence of ample variability in the experiment material and disclosed significant differences among the genotypes for all characters studied.

Analysis of variance revealed that for all 13 quantitative traits shows genotype differences shows highly significant under study at 1% level of significance indicating the presence of genetic differences in the experimental material suggesting the importance of the genetic variability in order to identify the best genetic make-up provide better scope to selection.

Comment [D8]: Check for grammar

Presence of significant differences does not suggest importance of genetic variability, it clearly suggests the opportunity of effective selection

On the basis of mean performance, the highest grain yield per plant was observed for rice genotypes as RNR - 1446 (45.60g), MTU - 1121(36.40g), JGL - 24423(35.67g), Rango Komal (27.87g) and NLR-33641 (26.6g).

3.2.1 Phenotypic and Genotypic variance

The variability estimates such as phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), heritability in broad sense (h^2), genetic advance (GA), genetic advance of mean (GAM) for thirteen traits are explained under the following. For all the traits PCV was higher than GCV indicating that there is environment impact on genotypes. In the present study, Phenotypic coefficient of variation (PCV) was showing highest value for the character Biological yield per hill (g) (39.02), Grain yield per hill (31.55) and Number of tillers per hill (23.32), Number of spikelets per panicle (22.80), Number of panicles per hill (22.78) and Flag leaf length (20.89). while the Genotypic Coefficient of Variation (GCV) was showing highest value for character for Biological yield per hill (g) (38.22), Grain yield per hill (30.24) and Number of spikelets per panicle (21.36), Number of tillers per hill (20.40) and Number of panicles per hill (20.02).

Table 3: Analysis of variance (ANOVA) among 20rice genotypes of 13 quantitative traits.

Sl.No.	Source	Mean Sum of Squares (MSS)		
		Replication	**Treatment**	**Error**
	Degrees of freedom	**2**	**29**	**58**
1	Days to fifty percent flowering	3.9	124.29**	22.9
2	Plant height	9.852	135.126**	47.436
3	Flag leaf length	12.274	56.834**	8.852
4	Flag leaf width	0.021	0.161**	0.02

5	Number of tillers per hill	1.295	11.903**	0.746
6	Number of panicles per hill	0.315	4.822**	0.441
7	Panicle length	0.675	5.625*	2.772
8	Number of spikelets per panicle	450.975	1956.641**	285.973
9	Days to maturity	41.678	120.458*	66.712
10	Biological yield	34.478	234.548**	20.369
11	Harvest Index	12.353	135.377**	6.349
12	Test weight	7.586	8.899**	3.782
13	Grain yield per hill	4.103	42.686**	2.356

** indicates significance at 1% level of significance, * indicates significance at 5% level of significance.

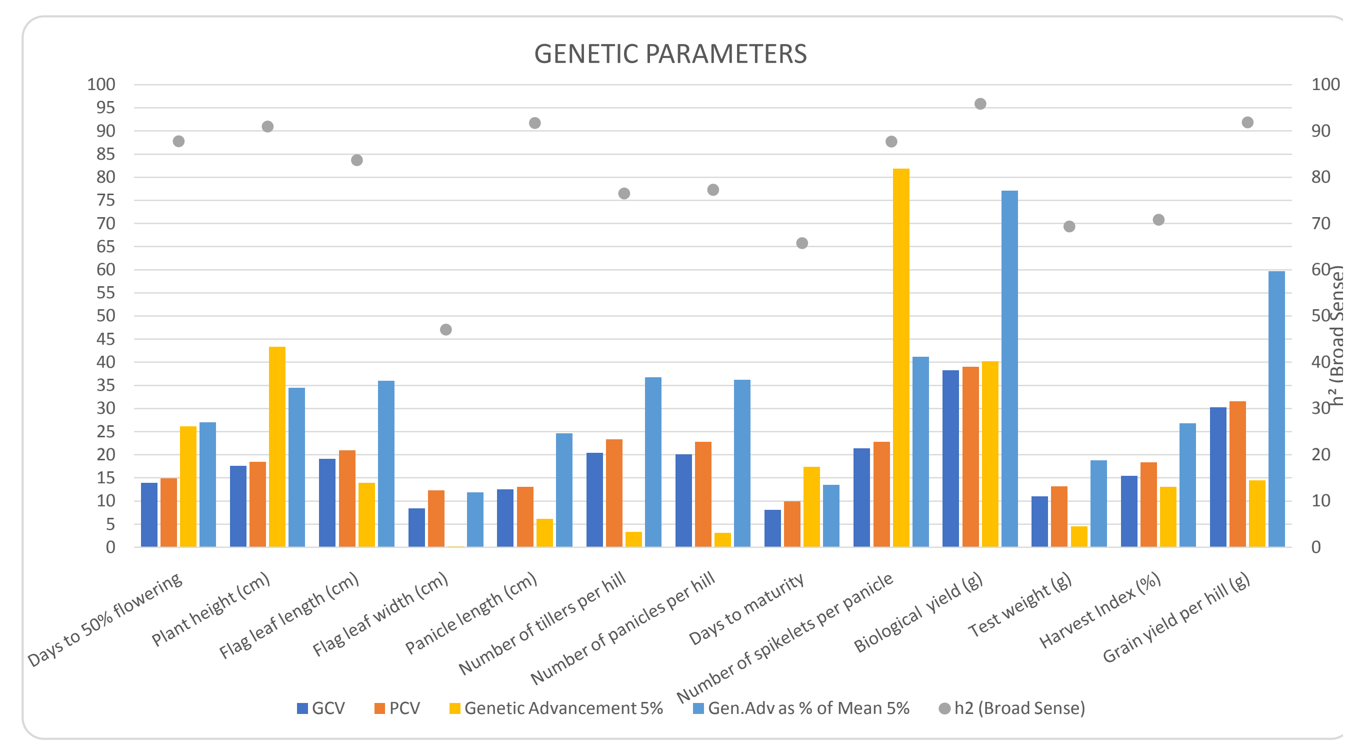
Table 4: Genotypic parameters of 13 quantitative traits in rice genotypes.

Sl.No.	**Characters**	**GCV**	**PCV**	**h^2 (Broad Sense)**	**Genetic Advancement (5%)**	**Gen.Adv as % of Mean (5%)**
1	**Days to 50% flowering**	13.94	14.88	87.81	26.16	26.91
2	**Plant height (cm)**	17.56	18.40	91.00	43.36	34.50
3	**Flag leaf length (cm)**	19.12	20.89	83.76	13.81	36.04
4	**Flag leaf width (cm)**	8.39	12.22	47.08	0.19	11.85
5	**Panicle length (cm)**	12.49	13.03	91.80	6.08	24.65
6	**Number of tillers per hill**	20.40	23.32	76.51	3.34	36.76
7	**Number of panicles per hill**	20.02	22.78	77.26	3.10	36.25
8	**Days to maturity**	8.06	9.93	65.78	17.35	13.46
9	**Number of spikelets per panicle**	21.36	22.80	87.79	81.88	41.23

10	**Biological yield (g)**	38.22	39.02	95.92	40.20	77.10
11	**Test weight (g)**	10.95	13.14	69.38	4.48	18.78
12	**Harvest Index (%)**	15.43	18.34	70.83	13.04	26.76
13	**Grain yield per hill (g)**	30.24	31.55	91.89	14.48	59.72

GCV: Genotypic Coefficientof Variation**, PCV:** PhenotypicCoefficientof Variation**,**h^2 **:**Heritability**,GA% ofMean:**GeneticAdvanceaspercent of mean

Fig 1: Bar diagram depicting GCV, PCV, heritability and genetic advance for 13 quantitative characters in Rice.



3.3 Heritability

- Heritability is showing moderate to high among the characters. These characters show no signs of low heritability. The high heritability and moderate heritability values for the traits under consideration in the current study indicated that they were less and moderate influenced by the environment and aided in the effective selection of features based on phenotypic expression utilising a simple selection approach.
- The estimates of heritability (%) in the broad sense for 13 characters studied, which ranged from 47.08% to 95.92%. High heritability (broad sense) (>60%) was recorded for character Biological yield per hill (95.92), Grain yield per hill (91.89), Panicle length(cm) (91.80), Plant height (91.00), Days to 50% flowering (87.81) Number of spikelets per panicle (87.79), Flag leaf length (83.76) and Moderate heritability (broad sense) (30-60%) was recorded for Flag leaf width (47.08).

Comment [D9]: traits

3.4 Genetic Advance

- Genetic advance for different traits revealed that it varied from 0.19 to 81.88. High genetic advance (above 20%) was observed for Number of spikelets per panicle observed the highest estimates of genetic advance (81.88) among all the quantitative characters followed by Plant height (43.36), Biological yield per hill (40.20), and Days to 50% flowering (26.16). Moderate (10-20%) values of genetic advance were observed for Days to maturity (17.35), Grain yield per hill (14.48), Flag leaf length (13.81), and Harvest index (13.04). Lowest (below 10%) values of genetic advance were observed for Panicle length (6.08), Test weight (4.48), Number of tillers per hill (3.34), Number of panicles per hill (3.10) and Flag leaf width (0.19).

3.5 GeneticAdvance as percentage of Mean

- In the present investigation, genetic advance as % of mean varied from 11.85 to 77.10. High genetic advance as % mean (>20%) was recorded for Biological yield per hill (77.10), Grain yield per hill (59.72), Number of spikelets per panicle (41.23), Number of tillers per hill (36.76), Number of panicles per hill (36.25), Flag leaf length (36.04), Plant height (34.50), Days to 50% flowering (26.91), Harvest index (%) (26.76) and Panicle length (24.65). Moderate genetic advance as % mean (10-20%) was recorded for Test weight (g) (18.78), Days to maturity (13.49) and Flag leaf width (11.85) and no traits has recorded low genetic advance as % mean (<10%).

- All of the traits studied had a high heritability as well as a high genetic advance as a percentage mean, indicating that the characters are predominantly regulated by additive gene action. As a result of the accumulation of more additive genes leading to further improvement, simple selection would be effective of these traits based on phenotypic expression.

Comment [D10]: ???? there are traits with moderate heritability and moderate GAM too

Table 5: Correlation coefficient analysis

Traits		DF 50	PH	FLL	FLW	PL	NTH	NPH	DM	NSPP	BY	TW	HI (%)	GYH
DF 50	P	1.0000	0.505**	0.1799	-0.0202	-0.2130	0.0133	0.0057	0.807**	-0.1897	0.1958	-0.1532	-0.428**	-0.0008
	G	1.0000	0.556**	0.2163	0.0036	-0.1893	0.0545	0.0204	0.745**	-0.2197	0.2024	-0.1534	-0.502**	-0.0091
PH	P		1.0000	0.542**	-0.265*	0.303*	0.1196	0.0474	0.313*	-0.371*	0.477**	-0.2357	-0.645**	0.1059
	G		1.0000	0.617**	-0.436**	0.354*	0.1080	0.0145	0.449**	-0.475**	0.508**	-0.270*	-0.785**	0.1004
FLL	P			1.0000	-0.272*	0.0528	-0.2216	-0.2397	0.1265	-0.314*	-0.0632	0.0340	-0.290*	-0.318*
	G			1.0000	-0.364*	0.0456	-0.2180	-0.255*	0.2238	-0.331*	-0.0564	-0.0244	-0.426**	-0.333*
FLW	P				1.0000	-0.2080	0.276*	0.404*	0.0170	0.487**	0.2287	-0.0491	0.0845	0.351*
	G				1.0000	-0.350*	0.462**	0.635**	0.0113	0.683**	0.343*	-0.1471	0.1305	0.523**
PL	P					1.0000	0.2358	0.1233	-0.359*	-0.2042	0.279*	0.2434	0.0397	0.262*
	G					1.0000	0.267*	0.1207	-0.412*	-0.2111	0.306*	0.294*	-0.0557	0.280*
NTH	P						1.0000	0.960**	-0.1115	0.1035	0.356*	-0.2038	-0.273*	0.278*
	G						1.0000	0.975**	-0.0243	0.0607	0.400*	-0.2169	-0.338*	0.286*
NPH	P							1.0000	-0.1236	0.2491	0.412*	-0.2198	-0.2344	0.378*
	G							1.0000	-0.0235	0.2379	0.472**	-0.2048	-0.319*	0.397*
DM	P								1.0000	-0.272*	0.0842	-0.2067	-0.312*	-0.0925
	G								1.0000	-0.278*	0.0863	-0.301*	-0.467**	-0.0999
NSPP	P									1.0000	0.1874	0.1810	0.2240	0.436**
	G									1.0000	0.2236	0.271*	0.272*	0.476**
BY	P										1.0000	-0.2386	-0.486**	0.840**
	G										1.0000	-0.320*	-0.539**	0.860**
TW	P											1.0000	0.549**	0.0001
	G											1.0000	0.795**	0.0600
HI (%)	P												1.0000	-0.0310
	G												1.0000	-0.0142
GYH	P													1.0000
	G													1.0000

DF 50 : Days to 50% flowering**, PH :** Plant height**,FLL :**Flag leaf length,**FLW :**Flag leaf width, **PL :** Panicle length,**NTH :** Number of tillers per hill,**NPH :**Number of panicles per hill,**DM :** Days to maturity**,NSPP :** Number of spikelets per panicle,**BY :** Biological yield per hill,**TW :** Test weight**, HI(%) :** Harvest index**, GYH :**Grain yield per hill**.**

3.6 Phenotypic Correlation Coefficient

Grain yield shows a positive significant association with Biological yield (0.840**), Number of spikelets per panicle (0.436**), Number of panicles per hill (0.378*), Flag leaf width (0.351*), Number of tillers per hill (0.278*) and Panicle length (0.262*), while positive non-significant association showed with Plant height (0.1059), Test weight (0.0001), The negative significant association showed with Flag leaf length (-0.318*) and negative non-significant association showed with Days to maturity (-0.0925), Harvest index (-0.0310) and Days to 50% flowering (-0.0008).

3.7 Genotypic Correlation Coefficient

Grain yield showed a highly significant positive association with Biological yield (0.860**), Flag leaf width (0.523**), Number of spikelets per panicle (0.476**), Number of panicles per hill (0.397*), Number of tillers per hill (0.286*) and Panicle length (0.280*), while positive non-significant association was showed with Plant height (0.1004), Test weight (0.0600) and negative significant association showed with Flag leaf length (-0.333*) and negative non-significant association showed with Days to maturity (-0.0999), Harvest index (-0.0142) and Days to 50% flowering (-0.0091).

3.8 Phenotypic Path Coefficient Analysis

The phenotypic correlation is used to calculate phenotypic path coefficients. It categorises phenotypic coefficients as direct or indirect impacts on impact measurements**. (Dewey and Lu, 1959)**. A detailed analysis from table 6 and Fig 2, The diagonal values show positive direct effects toBiological yield (1.0207), Harvest index (0.3820), Number of panicles per hill (0.1332), Days to 50% flowering (0.0988), Number of spikelets per panicles (0.0969) and Panicle length (0.0247).Negative direct effects were Number of tillers per hill (-0.1370), Plant height (-0.0895), Flag leaf length (-0.0772), Days to maturity (-0.0658), Flag leaf width (-0.0148) and Test weight (-0.0061)to Grain yield per plant.

3.9 Genotypic Path Coefficient Analysis

An observation of the results on path coefficient for yield and yield components genotypic to be of similar direction and magnitude in general. Further the genotypic path co-efficient were observed to be of higher magnitude, compared to phenotypic path coefficient indicating the masking effect of environment.A detailed analysis from table 6 and fig 3.The diagonal values show positive direct effect toBiological yield (0.7874), Number of panicles per hill (0.6923), Flag leaf width (0.5013), Test weight (0.3148), Days to 50% flowering (0.2892), Plant height (0.1643), Panicle length (0.0637) and Harvest index (0.0201). Negative direct effects were Number of tillers per hill (-0.9682), Days to maturity (-0.4372), Number of spikelets per panicle (-0.3027) and Flag leaf length (-0.2930)to Grain yield per plant.

Comment [D11]: Reframe the sentence, meaning is not clear

Table 6: Path Coefficient Analysis

Traits		DF 50	PH	FLL	FLW	PL	NTH	NPH	DM	NSPP	BY	TW	HI(%)	GYH
DF 50	P	**0.0988**	0.0499	0.0178	-0.0020	-0.0210	0.0013	0.0006	0.0797	-0.0187	0.0193	-0.0151	-0.0423	-0.0008
	G	**0.2892**	0.1607	0.0626	0.0011	-0.0548	0.0158	0.0059	0.2944	-0.0636	0.0586	-0.0444	-0.1451	-0.0091
PH	P	-0.0452	**-0.0895**	-0.0485	0.0237	-0.0271	-0.0107	-0.0042	-0.0280	0.0332	-0.0427	0.0211	0.0577	0.1059
	G	0.0913	**0.1643**	0.1013	-0.0716	0.0581	0.0177	0.0024	0.0737	-0.0781	0.0834	-0.0444	-0.1290	0.1004
FLL	P	-0.0139	-0.0418	**-0.0772**	0.0210	-0.0041	0.0171	0.0185	-0.0098	0.0242	0.0049	-0.0026	0.0224	-0.318*
	G	-0.0634	-0.1808	**-0.2930**	0.1067	-0.0134	0.0639	0.0748	-0.0656	0.0969	0.0165	0.0071	0.1248	-0.333*
FLW	P	0.0003	0.0039	0.0040	**-0.0148**	0.0031	-0.0041	-0.0060	-0.0003	-0.0072	-0.0034	0.0007	-0.0013	0.351*
	G	0.0018	-0.2184	-0.1826	**0.5013**	-0.1756	0.2317	0.3184	0.0056	0.3421	0.1717	-0.0737	0.0654	0.523**
PL	P	-0.0053	0.0075	0.0013	-0.0051	**0.0247**	0.0058	0.0030	-0.0088	-0.0050	0.0069	0.0060	0.0010	0.262*
	G	-0.0121	0.0225	0.0029	-0.0223	**0.0637**	0.0170	0.0077	-0.0262	-0.0134	0.0195	0.0187	-0.0035	0.280*
NTH	P	-0.0018	-0.0164	0.0304	-0.0377	-0.0323	**-0.1370**	-0.1316	0.0153	-0.0142	-0.0487	0.0279	0.0374	0.278*
	G	-0.0527	-0.1045	0.2111	-0.4475	-0.2584	**-0.9682**	-0.9444	0.0236	-0.0587	-0.3875	0.2100	0.3267	0.286*
NPH	P	0.0008	0.0063	-0.0319	0.0538	0.0164	0.1279	**0.1332**	-0.0165	0.0332	0.0549	-0.0293	-0.0312	0.378*
	G	0.0141	0.0100	-0.1770	0.4403	0.0837	0.6762	**0.6932**	-0.0163	0.1649	0.3269	-0.1420	-0.2214	0.397*
DM	P	-0.0531	-0.0206	-0.0083	-0.0011	0.0236	0.0073	0.0081	**-0.0658**	0.0179	-0.0055	0.0136	0.0205	-0.0925
	G	-0.4450	-0.1961	-0.0978	-0.0049	0.1802	0.0106	0.0103	**-0.4372**	0.1217	-0.0377	0.1315	0.2041	-0.0999
NSPP	P	-0.0184	-0.0360	-0.0304	0.0471	-0.0198	0.0100	0.0241	-0.0263	**0.0969**	0.0181	0.0175	0.0217	0.436**
	G	0.0665	0.1439	0.1000	-0.2066	0.0639	-0.0184	-0.0720	0.0842	**-0.3027**	-0.0677	-0.0820	-0.0825	0.476**
BY	P	0.1998	0.4873	-0.0645	0.2334	0.2850	0.3630	0.4204	0.0859	0.1912	**1.0207**	-0.2436	-0.4955	0.840**
	G	0.1594	0.3996	-0.0444	0.2697	0.2411	0.3151	0.3713	0.0680	0.1760	**0.7874**	-0.2518	-0.4242	0.860**
TW	P	0.0009	0.0014	-0.0002	0.0003	-0.0015	0.0012	0.0013	0.0013	-0.0011	0.0014	**-0.0061**	-0.0033	0.0001
	G	-0.0483	-0.0850	-0.0077	-0.0463	0.0926	-0.0683	-0.0645	-0.0947	0.0853	-0.1007	**0.3148**	0.2504	0.0600
HI(%)	P	-0.1636	-0.2462	-0.1108	0.0323	0.0152	-0.1044	-0.0895	-0.1191	0.0856	-0.1855	0.2098	**0.3820**	-0.0310
	G	-0.0101	-0.0158	-0.0086	0.0026	-0.0011	-0.0068	-0.0064	-0.0094	0.0055	-0.0108	0.0160	**0.0201**	-0.0142

DF 50 : Days to 50% flowering**, PH :** Plant height, **FLL :** Flag leaf length,**FLW :** Flag leaf width, **PL :** Panicle length,**NTH :** Number of tillers per hill,**NPH :**Number of panicles per hill,**DM :** Days to maturity**, NSPP :** Number of spikelets per panicle,**BY :** Biological yield per hill,**TW :** Test weight**, HI(%) :** Harvest index**, GYH :** Grain yield per hill**.**

Fig. 2. Genotypic Path Coefficient

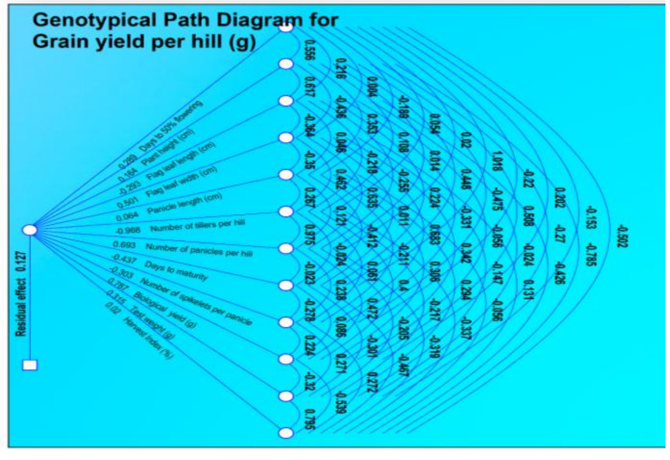
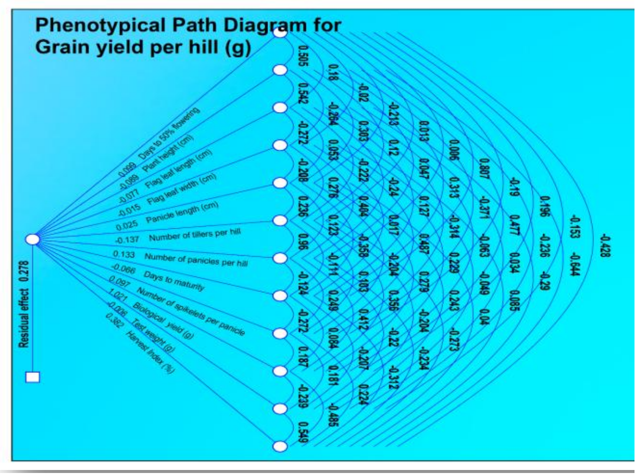


Fig. 3. Phenotypic Path Coefficient



4. Conclusion

From the present investigation, it is concluded that among 20 rice cultivars based on the mean performance **RNR-1446** (45.6g) rice cultivar was found to be superior in grain yield per hill.High PCV, GCV, heritability and genetic advance as percent of mean were recorded least for Flag leaf width to a highest for Biological yield. The high heritability is shown for Biological yield per Hill, Grain yield per hill. All the characters under study showed high heritability coupled with high values of genetic advance as percent mean (except flag leaf width). At both genotypic and phenotypic levels, significant positive correlations were observed for Flag leaf width, Panicle length, Number of tillers per hill, Number of panicles per hill, Number of spikelets per panicle and Biological yield per hill. The results of the path coefficient analysis revealed that both phenotypic and genotypic levels, Days to 50% flowering, Panicle length, Number of panicles per hill, Number of spikelets per panicle, Biological yield per hill, Harvest Index. Selection of plants on these characters would certainly lead to improvement in grain yield. Kasturi and NLR-3354 genotypes had the highest grain length and good cooking qualities. These genotypes can be used in breeding programs aimed at improving the genotype and cooking quality.

Comment [D12]: ????

5. References

Comment [D13]: Cross check the references

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