

## Correlation and path analysis for yield and grain yield attributing quality characters of rice (*Oryza sativa* L.) genotypes under irrigated condition

### ABSTRACT

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During the kharif season of 2022, a set of 27 rice genotypes were evaluated for the study of "Correlation and path coefficient analysis for yield and grain yield contributing characters in rice (*Oryza sativa* L.) genotypes" using an RBD with three replications at the research field of Department of Genetics and Plant breeding, Sam Higginbottom University of Agriculture, Technology and Sciences, Naini Allahabad, U.P. Analysis of variance showed significant differences among genotypes for all 13 characters indicating that the material has adequate genetic variability to support the breeding programme for improving the grain yield of rice. Out of 27 rice genotypes evaluated for various characters, four genotypes were found superior for different characters. These four genotypes were found to be better for more than one character. Among the lines SIVA (26.83), KRISHNA (26.19g), RDR-8702 (25.79g) and SS-999 (24.48g) recorded high grain yield per hill. All these genotypes recorded significantly high yield as compared to the check NDR-359 (CHECK) (22.67g). High estimate of heritability coupled with high genetic advance as percent of mean was recorded for spikelets per panicle, biological yield, harvest index, test weight and grain yield per hill. These traits are governed by additive gene effects and therefore, may be improved through direct selection. Grain yield per hill correlated positively and significantly with flag leaf width, biological yield, harvest index, and test weight. Harvest index, biological yield, days to maturity, and number of panicles per hill all had a significant positive direct effect on grain yield per hill at both genotypic and phenotypic levels. Thus, selections for these characters will be proved efficient for the improvement of grain yield of rice.

**keywords:** Rice, Additive gene, Variability, Significance, character Association, path analysis, selection.

### INTRODUCTION

Rice, *Oryza sativa* L. ( $2n=24$ ) belongs to family *Poaceae* (*Graminae*) and two cultivars of the *Oryza* genus, *Oryza sativa* (Asian rice) and *Oryza glaberrima* (African rice), and the rice plant, which is a member of the *Poaceae* (*Graminae*) family, is made up of several species. Rice is short-day autogamous crop, and it requires a hot, humid climate with average temperatures between 21°C and 37°C for the duration of the crop's life cycle. It is grown in a variety of environments and production methods. The only cereal crop which can be produced for an long period of time in standing water is rice. Whole rice is high in complex carbohydrates, vitamins, minerals, and fiber yet low in calories, fat, and sodium. The iconic theme of the International Year of Rice in 2004 was "Rice is Life," signifying the significance of rice as a major meal.

In Asia, rice is the main crop produced for use as a staple food (*Oryza sativa* L.). More than 90% of the world's rice is produced and consumed in Asia, which is home to 60% of all people. For the three billion people, rice accounts for 35–60% of their daily caloric intake. Around 10% of all arable land is dedicated to the cultivation of rice each year, or more than 150 million hectares. Rice is grown throughout the tropical and subtropical parts of the earth. There will be a 26 percent increase in the amount of rice required by the world by the year 2050 AD, or 800 million tons. Rice, the highest-quality grain, contains around 80 percent carbohydrate content and a 7 to 8 percent protein level. (Juliano *et. al.*, 1971).

On approximately 5.70 million acres, rice is cultivated as the primary crop in Uttar Pradesh. The state produces more rice than any other in the country. There is a critical need to increase rice production in Uttar Pradesh given the state's output and productivity, which are respectively 12.27 mt and 2.7 t/ha. Only high producing hybrid types will accomplish this. There are 120 cores of people living in India today; by 2025, there will be more like 150 cores. Consequently, the development of high-yielding cultivars is required.

The genetic improvement of quantitative traits in a crop species is determined by the trait's heritability pattern as well as the kind and degree of variability in current germplasm. The two most important selection factors are heritability and genetic advancement. When estimating the increase under selection, heritability estimates combined with genetic progress are frequently more accurate than heritability estimates alone. Characters are passed on from one generation to the next through heritability. Furthermore, selecting yield-related component qualities for agricultural yield development necessitates a grasp of heredity. The genetic advancement is the difference between the mean genotypic values of the selected population and the original population from which these values were picked. Rather than relying solely on heritability estimates, the genetic gain under selection is assessed using both heredity and genetic advance (Ajmera *et. al.*, 2017).

The degree of association between two variables is quantified by the phenotypic correlation, which is determined by inherited and environmental factors. The correlation coefficient between the characters, on the other hand, does not always imply a cause-and-effect relationship. As a result, path analysis combined with grouping correlation would provide a clearer understanding of the cause-and-effect relationship between various pairs of characters. (**Jayasudha and Sharma, 2010**).

Genetic parameters such as genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) are useful to identify the amount of variability present in germplasm. Heritability along with high genetic advance would be useful tool in estimating the resultant effect in selection of best genotypes for yield and its attributing traits. It helps in determining the influence environment on the expression the genotypic and reliability of characters.

To make the most of these interactions in selection, it is critical to understand the relationship between yield and its individual pieces. Character associations derived from correlation coefficients can aid in assessing the relative impact of multiple component characters on grain yield. Path coefficient research identifies the link between direct and indirect effects. Selection should be based on qualities that affect yield rather than just grain yield per plant. The expression of grain yield per plant is strongly reliant on yield attributing factors. Assessments of genetic association are also useful in understanding and maintaining the scale of relative value of desirable features in the rice breeding plan.

Grain yield has a complicated personality that is determined by its primary components, which are the number of effective tillers, panicle length, number of grains per panicle, and 1000 grain weight. These components are also dependent on various morphological and developmental qualities that are connected, hence the parents chosen for breeding programs should have a wide range of genetic variation for a forementioned morphological and developmental characteristics. Furthermore, knowing the extent of variance due to heritable component could be useful as a reference for picking the improvement in the population.

### **Objectives:**

- 1.To estimate genetic variability, heritability and genetic advance for quantitative traits.
- 2.To study the nature of character association of yield and yield attributing characters.
3. To Study the direct and indirect contribution of yield component parameters for grain yield.

## **MATERIALS AND METHODS**

During the Kharif of 2021, the current study was conducted at the Field Experimentation Center of the Department of Genetics and Plant Breeding, Naini Agricultural Institute, Sam Higginbottom University of Agriculture, Technology, and Sciences, Prayagraj (Allahabad), Uttar Pradesh. The experiment is located at latitude 25.570N and longitude 81.560N, 98 metres above mean sea level. This region's subtropical climate has extremely hot and cold seasons. Temperatures might drop as low as 1°C to 2°C in December and January, especially during the Rabi season.

The 27 rice genotypes were planted in lowland circumstances in kharif-2022 by using a RBD with 3 replications for each genotype. All rice genotypes were nursery sown in kharif 2022 on June 18, and were transplanted into the main field 30 days later, on July 12. A 2-meter-long row was planted with three replications of each genotype. The crop was grown according to the guidelines, with 20 cm between rows and 15 cm between plants. During Kharif 2022, 27 genotypes were grown to investigate the effect of numerous variables on grain yield over time, including heritability, correlation, path analysis, and genetic divergence.

### 3.1 Experimental materials

The experimental material for present investigation comprised of 27 genotypes of rice obtained from Department of Genetics and Plant Breeding, Prayagraj. The details of genotypes are listed in Table 1

**Table-1 List of genotypes used in the Experiment**

SL.No.	Germplasm Name	S. No.	Germplasm Name	S. No	Germplasm Name
1	SAVITRI	10	RGL-11414	19	RDR-8702
2	DULAR	11	RGL-2332	20	RDR-763
3	NL-42	12	SS-999	21	RDR-7555
4	MTU-3626	13	PUSA BASMATI	22	BPT-5204
5	KRISHNA	14	SUMATI	23	WGL-14
6	TRIVENI	15	MTU-1010	24	C0-51
7	SIVA-555	16	RNR-10754	25	ADT-37
8	BPT-01	17	RNR-15048	26	C0-45
9	BPT-02	18	RDR-355	27	NDR-359(CHECK)

### Statistical analysis

1. (ANOVA) Analysis of variance
2. Co-efficient of variation (**Burton and Devane,1953**)
  - a. Genotypic coefficient of variation (**GCV**)
  - b. Phenotypic coefficient of variation (**PCV**)
3. Heritability broad sense (**Burton and Devane,1953**)
4. Genetic advance (**Johnson et al.,1955**)
5. Correlation coefficient analysis (**Al Jibouri et. al.,1958**)
6. Path coefficient analysis (**Dewey and Lu,1959**)

To carry out the analysis, software known as "R-Language" was employed.

## **RESULTS AND DISCUSSION**

ANOVA of the mean squares owing to genotypes revealed highly significant differences ( $=0.01$ ) for all features, indicating a high level of genetic diversity seen among rice genotypes. In Table 2 and Figure 1, which showed a wide range of variation for all traits studied, the mean values, the coefficient of variation (C.V.), standard error of the mean (SEm+), are presented for a range of 27 genotypes for 13 quantitative characters.

- Based on Mean performance, genotype like SIVA-555 (26.83 g) recorded the high grain yield per hill followed by the genotypes KRISHNA (26.19g), RDR-8702 (25.79g) and SS-999 (24.48g). All these genotypes were significantly higher as compared to the check NDR-359(CHECK) (22.67g). Genotypes RNR-15048(9.61g) recorded minimum grain yield per hill followed by the genotype SUMATI (13.41g), NL-42 (13.58g) These genotypes were statistically at par to the character.
- In the present study, the PCV was greater than the matching GCV for each feature, showing that the environment had an effect. The panicle length had the lowest GCV (percentage) value of 8.178 and the highest value of 24.44. (Test weight).
- PCV value which is ranged from a lowest value of 10.22 (panicle length) to the highest value of 25.55(test weight).
- Whereas Kishore *et al.* (2015) reported similar findings with test weight, grain yield per plant. and Parihar *et. al.* (2017) no. of tillers per hill, panicle length, test weight, grain yield per plant.

### **Heritability**

- In the current study, all traits exhibited strong heritability ranging from 92.90 percent to 99.90

percent. The highest heritability was found in test weight (91.50 percent), followed by flag leaf width (89.27 percent), grain number of spikelets per panicle (88.305 percent), days to 50 percent blooming (87.97 percent), and biological yield (82.43 percent).

- The high heritability values found in the current study for the traits under consideration indicated that they were influenced by the environment and aided in the successful selection of traits based on phenotypic expression by employing a straightforward selection approach. The possibility of genetic advancement was also suggested by these high heritability values.
- Similar findings are reported by Aditya *et al.* (2013) and Parihar *et al.* (2017).

#### **Genetic Advance as Percentage of Mean**

- Apart from plant height, flag leaf length, and panicle length, all features in the current study displayed the largest genetic advance as a percentage of the mean. Test weight (48.16) demonstrated the greatest genetic progress as a percentage of the mean, followed by the number of spikelets per panicle (43.55), grain yield per plant (40.69), harvest index (37.61), biological yield (37.46), flag leaf width (36.35), number of tillers per hill (33.32), number of panicles per hill (28.74), days to 50% flowering (28.01), flag leaf length (21.93), and days to maturity (20.12).
- All the studied traits, with the exception of plant height and panicle length, displayed high heritability and high genetic advancement as a percentage mean, indicating that the traits are primarily regulated by additive gene action. Therefore, direct selection of these qualities based on phenotypic expression using a simple selection strategy would be effective as more additive genes will accumulate and lead to further development.
- Similar results were reported for Dinesh *et al.* (2014), Shiva *et al.* (2018), for plant height, biological yield.

#### **Phenotypic Correlation Coefficient**

From Table -4 of the current study the phenotypic relationship between grain production per hill and flag leaf width (0.294\*), biological yield (0.343\*\*), harvest index (0.601\*\*), and test weight (0.410\*\*) was positive and significant. Plant height (0.0010), days until 50% of the flowers are in bloom (0.1356), the number of tillers per hill (0.511), the number of panicles per hill (0.1932), and the number of spikelets per panicle (0.1967) connection reveal positive non-significant features. Negative non-significant connection is seen for the length of the flag leaf (-0.061) and the length of the panicle (-0.087).

- Similar findings are reported by Aditya *et al.* (2013) and Parihar *et al.* (2017).

#### **Genotypic Correlation Coefficient**

Table - 4 correlation between yield and yield-attributing features demonstrated that the genotypic link between grain yield per hill and flag leaf width (0.244\*), test weight (0.410\*\*), biological yield (0.348\*), and harvest index (0.602\*) was substantial and positive. Days to 50% flowering (0.1348), days to maturity (0.140), and tillers per hill (0.1482) all indicated positive but not statistically significant correlations. Number of tillers per hill (-0.1482) and panicle length (-0.0753) reveal a negative but non-significant link. The correlation did not reveal a non-significant negative connection.

- Similar findings are reported by Aditya *et al.* (2013) and Parihar *et al.* (2017).

#### **Phenotypic Path coefficient analysis**

Phenotypic path coefficients are created using the phenotypic correlation coefficient. It distinguishes between evaluations of the direct and indirect effects using the phenotypic correlation coefficients (Dewey and Lu, 1959). A further study of statistics from Table 5 and Figure 2 revealed a positive direct relationship between grain yield per plant and days to maturity (0.2586), plant height (0.582), flag leaf width (0.0365), number of panicles per hill (0.1926), biological yield (0.8243), and harvest index (1.0431). Days to 50% flowering (-0.2192), flag leaf length (-0.0139), number of tillers per hill (-0.1029), panicle length (-0.0978), number of spikelets per panicle (-0.0249), and test weight all showed negative direct effects (-0.0403)

- Similar findings are reported by Aditya *et al.* (2013) and Parihar *et al.* (2017).

#### **Genotypic path coefficient analysis**

Additionally, it was found that the genotypic route coefficient was larger than the phenotypic path coefficient, showing the environment's ability to disguise traits. A detailed analysis of the diagonal values in Table 5 and Figure 3 revealed that there was a positive direct effect on the following variables: days to maturity (0.2571), plant height (0.0557), flag leaf width (0.0353), number of panicles per hill (0.1929), biological yield (0.8228), and harvest index (0.8510). Days to 50% flowering (-0.2178), flag leaf length (-0.0148), number of tillers per hill (-0.1041), panicle length (-0.0953), number of spikelets per panicle (-0.0235), and test weight all indicated negative direct effects (-0.0387).

Similar findings are reported by Aditya *et al.* (2013), Parihar *et al.* (2017) and Rashmi *et al.* (2017),

#### **Cooking Quality:**

The result of quality assessment of 27 genotypes, BPT-5204 is higher and CO-51 is lower in hulling percentage, SUMATI is higher and RDR-7555 is lower in L/B ratio, BPT-5204 is

higher and BPT-02 is lower in kernel elongation ratio, RGL 2332 is higher in and SUMATI is lower in head rice recovery, ADT 37 is higher and WGL 14 is lower in gel consistency and CO 45 is lower and DULAR is lower in amylose content.

## CONCLUSION

According to the results of the experiment, 26 rice genotypes tested, SIVA-555 had the highest grain yield per hill, followed by RDR-355, RDR-8702, SS-999, RGL-2332, and KRISHNA. TRIVENI had the shortest days to 50% blooming and the longest days to maturity. Number of spikelets per panicle, biological yield, harvest index, test weight, and grain yield per hill all had high PCV, GCV, heritability, and genetic advance as a percentage of mean. The relationship between the grain yield per hill and the flag leaf width, test weight, biological yield, and harvest index was positive and statistically significant. High positive direct effect measured by harvest index, biological yield, days to maturity, and number of panicles per hill on grain yield per hill at both genotypic and phenotypic levels. Genotypes **SUMATI, BPT-5204, RGL 2332, ADT 37, and CO 45** showed better cooking quality, hulling percent, kernel elongation, L/B ratio, head rice recovery, gel consistency, and amylose content. The cultivation and selection processes for crop development may consider these genotypes and those characteristics.

**Table:2 Analysis of Variance (ANOVA) among 27 rice germplasm for 13 quantitative parameters**

Parameters	MSS		
	Treatment	Replication	Error
<b>Degree of Freedom</b>	26	<b>2</b>	52
Days to 50% Flowering	5.1480	640.513**	27.93
Days to Maturity	3.0120	642.554**	55.102
Plant Height	48.6280	428.838**	43.453
Flag Leaf Length	8.8520	51.774**	4.437
Flag Leaf Width	0.0060	0.115**	0.004
Number of Total Tillers	1.30	8.511**	0.524
Number of Productive Tillers	1.1130	6.343**	0.539
Panicle Length	3.3650	15.747**	2.49
Biomass	428.5380	5101.152**	215.68
Harvest Index	14.0490	187.753**	12.451
Test Weight	15.9910	366.532**	25.198
Number of Grains per Plant	0.4130	43.726**	1.312
Grain Yield (gm)	11.0950	61.268**	5.21

\*\* Significant at P<0.01 and \* Significant at P<0.05

**Table:3 Genetic Parameters analysis for 13 Quantitative Characters for Rice Germplasm**

<b>Trait</b>	<b>GCV%</b>	<b>PCV%</b>	<b>H<sup>2</sup></b>	<b>GA% of Mean</b>
Days to 50% Flowering	14.499	15.459	87.968	28.014
Days to Maturity	11.055	12.514	78.04	20.118
Plant Height	9.601	11.107	74.724	17.097
Flag Leaf Length	12.052	13.641	78.052	21.933
Flag Leaf Width	18.678	19.768	89.27	36.353
Number of Total Tillers	17.695	19.358	83.562	33.322
Number of Productive Tillers	15.776	17.837	78.224	28.743
Panicle Length	8.178	10.225	63.962	13.473
Biomass	22.496	23.939	88.305	43.547
Harvest Index	20.026	22.057	82.435	37.456
Number of Grains per Plant	20.18	22.303	81.869	37.614
Test Weight	24.442	25.551	91.505	48.164
Grain yield	22.337	25.26	78.196	40.69

**GCV:** Genotypic Coefficient of Variation, **PCV:** Phenotypic Coefficient of Variation, **H<sup>2</sup>:** Heritability, **GA % of Mean:** Genetic Advance at percent of mean

**Table:4Correlation Coefficient Analysis**

Parameters		DF50	DM	PH	FLL	FLW	NTT	NPT	PL	BM	H.I.	NGPP	TW	GY
DF50	P	1.0000	0.976**	0.2059	-0.2180	0.417**	-0.0835	-0.1107	0.0145	0.271*	0.362**	-0.2067	-0.269*	0.1356
	G	1.0000	0.976**	0.2069	-0.2145	0.417**	-0.0806	-0.1075	0.0134	0.271*	0.360**	-0.2065	-0.269*	0.1348
DM	P		1.0000	0.1991	-0.2169	0.359*	-0.0956	-0.1294	0.0225	0.252*	0.351*	-0.2009	-0.284*	0.1405
	G		1.0000	0.1995	-0.2141	0.359**	-0.0933	-0.1268	0.0219	0.252*	0.351*	-0.2005	-0.284*	0.1400
PH	P			1.0000	0.0297	0.1753	0.0180	-0.0167	0.553**	0.0118	0.439**	-0.355*	0.0454	0.0016
	G			1.0000	0.0384	0.1794	0.0257	-0.0084	0.540**	0.0102	0.433**	-0.356*	0.0434	-0.0030
FLL	P				1.0000	0.1198	0.0805	0.1195	0.1116	0.0241	0.0854	-0.1106	0.0820	-0.0612
	G				1.0000	0.1252	0.0897	0.1285	0.1016	0.0226	0.0805	-0.1129	0.0794	-0.0654
FLW	P					1.0000	0.420**	0.367**	0.0844	0.260*	0.365**	-0.0945	0.297*	0.249*
	G					1.0000	0.423**	0.370**	0.0782	0.257*	0.360**	-0.0963	0.295*	0.244*
NTH	P						1.0000	0.977**	0.1403	-0.1604	0.2088	-0.0840	0.444**	0.1511
	G						1.0000	0.977**	0.1333	-0.1578	0.2054	-0.0846	0.440**	0.1482
NPH	P							1.0000	0.0826	-0.1607	0.235*	-0.0686	0.457**	0.1932
	G							1.0000	0.0766	-0.1574	0.232*	-0.0690	0.453**	0.1905
PL	P								1.0000	-0.1005	0.1806	-0.1693	0.0564	-0.0874
	G								1.0000	-0.0929	0.1867	-0.1622	0.0589	-0.0753
NSPP	P									1.0000	0.296*	-0.0508	-0.482**	0.1967
	G									1.0000	0.300*	-0.0467	-0.479**	0.2030
BY	P										1.0000	-0.503**	0.1194	0.343*
	G										1.0000	-0.497**	0.1208	0.348*
H.I.	P											1.0000	0.292*	0.601**
	G											1.0000	0.293*	0.602**
TW	P												1.0000	0.410**
	G												1.0000	0.410**
GYP	P													1
	G													1

**DF50:** Days to 50% Flowering, **DM:** Days to Maturity, **PH:** Plant Height, **FLL:** Flag Leaf Length, **FLW:** Flag Leaf Width, **NTT:** Number of tillers per hill, **NPT:** Number of panicles per hill, **PL:** Panicle Length, **NSPP:** Number of spikelets per panicle, **BY:** Biological Yield, **H.I:** Harvest Index **TW:** Test Weight, **GYP:** Grain Yield per Plant, **P:** Phenotypic, **G:** Genotypic

**Table:5 Path Coefficient Analysis**

Parameter s		DF50	DM	PH	FLL	FLW	NTH	NPH	PL	NSPP	BY	H.I.	TW
<b>DF50</b>	P	<b>-0.2192</b>	-0.2138	-0.0451	0.0478	-0.0914	0.0183	0.0243	-0.0032	-0.0595	-0.0792	0.0453	0.0589
	G	<b>-0.2178</b>	-0.2125	-0.0451	0.0467	-0.0909	0.0176	0.0234	-0.0029	-0.0590	-0.0785	0.0450	0.0586
<b>DM</b>	P	0.2523	<b>0.2586</b>	0.0515	-0.0561	0.0928	-0.0247	-0.0335	0.0058	0.0651	0.0909	-0.0520	-0.0735
	G	0.2508	<b>0.2571</b>	0.0513	-0.0551	0.0923	-0.0240	-0.0326	0.0056	0.0647	0.0901	-0.0516	-0.0731
<b>PH</b>	P	0.0120	0.0116	<b>0.0582</b>	0.0017	0.0102	0.0010	-0.0010	0.0322	0.0007	0.0256	-0.0206	0.0026
	G	0.0115	0.0111	<b>0.0557</b>	0.0021	0.0100	0.0014	-0.0005	0.0301	0.0006	0.0241	-0.0198	0.0024
<b>FLL</b>	P	0.0030	0.0030	-0.0004	<b>-0.0139</b>	-0.0017	-0.0011	-0.0017	-0.0016	-0.0003	-0.0012	0.0015	-0.0011
	G	0.0032	0.0032	-0.0006	<b>-0.0148</b>	-0.0019	-0.0013	-0.0019	-0.0015	-0.0003	-0.0012	0.0017	-0.0012
<b>FLW</b>	P	0.0152	0.0131	0.0064	0.0044	<b>0.0365</b>	0.0153	0.0134	0.0031	0.0095	0.0133	-0.0034	0.0108
	G	0.0147	0.0127	0.0063	0.0044	<b>0.0353</b>	0.0149	0.0131	0.0028	0.0091	0.0127	-0.0034	0.0104
<b>NTH</b>	P	0.0152	0.0131	0.0064	0.0044	0.0365	<b>0.0153</b>	0.0134	0.0031	0.0095	0.0133	-0.0034	0.0108
	G	0.0084	0.0097	-0.0027	-0.0093	-0.0440	<b>-0.1041</b>	-0.1017	-0.0139	0.0164	-0.0214	0.0088	-0.0458
<b>NPH</b>	P	-0.0213	-0.0249	-0.0032	0.0230	0.0707	0.1882	<b>0.1926</b>	0.0159	-0.0309	0.0452	-0.0132	0.0881
	G	-0.0207	-0.0245	-0.0016	0.0248	0.0713	0.1886	<b>0.1929</b>	0.0148	-0.0304	0.0447	-0.0133	0.0875
<b>PL</b>	P	-0.0014	-0.0022	-0.0540	-0.0109	-0.0082	-0.0137	-0.0081	<b>-0.0978</b>	0.0098	-0.0177	0.0165	-0.0055
	G	-0.0013	-0.0021	-0.0515	-0.0097	-0.0074	-0.0127	-0.0073	<b>-0.0953</b>	0.0089	-0.0178	0.0155	-0.0056
<b>NSPP</b>	P	-0.0068	-0.0063	-0.0003	-0.0006	-0.0065	0.0040	0.0040	0.0025	<b>-0.0249</b>	-0.0074	0.0013	0.0120
	G	-0.0064	-0.0059	-0.0002	-0.0005	-0.0061	0.0037	0.0037	0.0022	<b>-0.0235</b>	-0.0071	0.0011	0.0113
<b>BY</b>	P	0.2980	0.2897	0.3621	0.0704	0.3006	0.1721	0.1936	0.1488	0.2442	<b>0.8243</b>	-0.4144	0.0984
	G	0.2964	0.2884	0.3562	0.0663	0.2965	0.1690	0.1906	0.1536	0.2466	<b>0.8228</b>	-0.4088	0.0994
<b>H.I.</b>	P	-0.2156	-0.2096	-0.3698	-0.1154	-0.0986	-0.0876	-0.0715	-0.1765	-0.0529	-0.5244	<b>1.0431</b>	0.3049
	G	-0.2145	-0.2083	-0.3692	-0.1172	-0.1000	-0.0879	-0.0717	-0.1684	-0.0485	-0.5161	<b>0.8510</b>	0.3044
<b>TW</b>	P	0.0108	0.0115	-0.0018	-0.0033	-0.0120	-0.0179	-0.0184	-0.0023	0.0194	-0.0048	-0.0118	<b>-0.0403</b>
	G	0.0104	0.0110	-0.0017	-0.0031	-0.0114	-0.0170	-0.0175	-0.0023	0.0185	-0.0047	-0.0113	<b>-0.0387</b>
<b>GYP</b>	P	0.1356	0.1405	0.0016	-0.0612	0.249*	0.1511	0.1932	-0.0874	0.1967	0.343*	0.601**	0.410**
	G	0.1348	0.1400	-0.0030	-0.0654	0.244*	0.1482	0.1905	-0.0753	0.2030	0.348*	0.602**	0.410**

**DF50:** Days to 50% Flowering, **DM:** Days to Maturity, **PH:** Plant Height, **FLL:** Flag Leaf Length, **FLW:** Flag Leaf Width, **NTT:** Number of tillers per hill, **NPT:** Number of panicles per hill, **PL:** Panicle Length, **NSPP:** Number of spikelets per panicle, **BY:** Biological Yield, **H.I.:** Harvest Index **TW:** Test Weight, **GYP:** Grain Yield per Plant, **P:** Phenotypic, **G:** Genotypic

**TABLE: 6 MEAN PERFORMANCE OF 26 RICE GENOTYPES FOR 12 QUALITATIVE PARAMETERS DURING *KHARIF* 2022.**

Serial no	GENOTYPES	KLBC	KWBC	KLAC	KWAC	HP	L/B RATIO	KER	HRR%	GC	ASV	AC	GRAIN TYPE
1	SAVITRI	6.58	1.83	6.88	2.47	50.4	3.60	1.05	66.9	35	4	25.5	LONG SLENDER
2	DULAR	5.95	2.47	6.83	2.71	72	2.41	1.15	59.48	55.67	3	16.1	SHORT BOLD
3	NL_42	7.06	1.94	7.31	2.51	70.45	3.64	1.04	61.45	72.45	6	24.4	LONG SLENDER
4	MTU_3626	6.14	2.27	6.98	2.45	65.2	2.70	1.14	54.84	39.92	5	22.23	LONG BOLD
5	KRISHNA	5.73	1.78	7.41	2.52	62.25	3.22	1.29	64.25	74.33	4	16.63	SHORT SLENDER
6	TRIVENI	5.62	1.71	6.41	2.42	60.1	3.29	1.14	51.12	65	4	22.8	SHORT SLENDER
7	SIVA 555	5.38	1.57	6.45	2.16	67.85	3.43	1.20	57.85	23	5	25.9	SHORT SLENDER
8	BPT-01	5.15	1.58	6.21	2.24	52.7	3.26	1.21	46.8	51.22	4	20.2	SHORT SLENDER
9	BPT-02	5.22	1.38	5.11	2.14	70.7	3.78	0.98	68.2	52.69	4	24.2	SHORT SLENDER
10	RGL 11414	6.21	2.26	6.87	2.61	58.45	2.75	1.11	49.1	50.1	5	21.2	LONG BOLD
11	RGL 2332	6.25	1.98	7.98	2.45	81.2	3.16	1.28	72.75	68	5	20.1	LONG SLENDER
12	SS 999	5.81	1.72	6.46	3.09	66.9	3.38	1.11	56.7	22.7	4	22.7	SHORT SLENDER
13	PUSA BASMATI	7.55	1.45	9.28	2.25	57.8	5.21	1.23	45.65	93.85	6	25.1	LONG SLENDER
14	SUMATI	6.79	1.24	7.47	2.56	20.25	5.48	1.10	30.51	41.5	5	20.1	LONG SLENDER
15	MTU 1010	6.23	1.59	6.66	2.24	68.45	3.92	1.07	58.2	70	4	23.38	LONG SLENDER
16	RNR 10754	6.46	1.82	6.89	2.35	69.9	3.55	1.07	63.2	40	4	23.57	LONG SLENDER
17	RNR 15048	5.62	1.63	6.27	2.26	64.85	3.45	1.12	57.9	22	5	20.72	SHORT

													SLENDER
<b>18</b>	<b>RDR 355</b>	6.61	1.71	7.05	2.59	62.5	3.87	1.07	53.18	40.56	5	25.94	LONG SLENDER
<b>19</b>	<b>RDR 8702</b>	6.62	2.18	7.11	2.54	70.7	3.04	1.07	59.25	40	4	23.7	LONG SLENDER
<b>20</b>	<b>RDR 763</b>	5.45	1.54	6.75	2.17	71	3.54	1.24	63.37	46	6	21.1	SHORT SLENDER
<b>21</b>	<b>RDR 7555</b>	5.03	2.67	5.81	2.89	81.35	1.88	1.16	70.58	65	5	18.76	SHORT BOLD
<b>22</b>	<b>BPT 5204</b>	5.17	1.47	7.08	2.81	85.35	3.52	1.37	72	25	4	24.61	SHORT SLENDER
<b>23</b>	<b>WGL 14</b>	5.34	1.45	6.4	2.34	81.7	3.68	1.20	67.6	22	4	24.99	SHORT SLENDER
<b>24</b>	<b>CO 51</b>	5.77	1.81	7.17	2.89	39	3.19	1.24	63.2	84	2	21.6	SHORT SLENDER
<b>25</b>	<b>ADT 37</b>	4.81	2.46	6.48	2.84	68	1.96	1.35	68.25	96.5	5	23.65	SHORT BOLD
<b>26</b>	<b>CO 45</b>	5.72	1.78	6.65	2.32	66	3.21	1.16	55.05	92	4	33.5	SHORT SLENDER
<b>27</b>	<b>NDR-359</b>	7.17	2.23	9.63	3.6	92	3.05	1.34	52.50	41	4	27.01	LONG SLENDER
<b>RANGE</b>	<b>MAX</b>	7.55	2.67	9.63	3.6	92	5.48	1.37	72.75	96.5	2	33.5	-
	<b>MIN</b>	4.81	1.24	5.11	2.14	20.25	1.88	0.98	30.51	22	6	16.1	-

**KLBC**- kernel length before cooking, **KWBC**- kernel width before cook **KLAC**- kernel length after cooking, **KWAC**-kernel width after cooking, **HP**-hulling percentage, **L/B** – length/ breadth, **KER**-kernel elongation ratio, **HRR**- head rice recovery, **GC**- gel consistency, **ASC**- alkali spreading value, **AC**-amylose content.

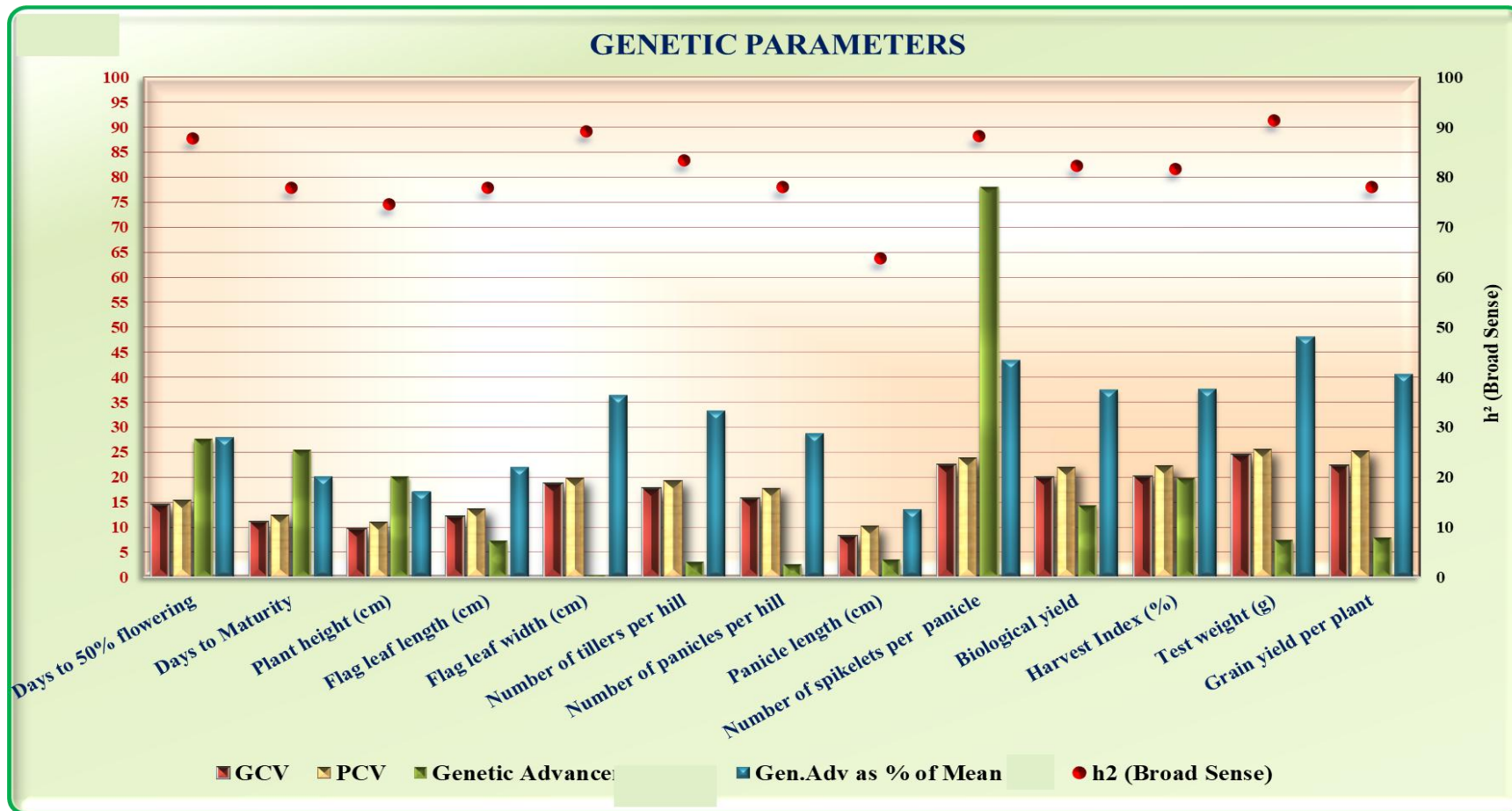


Figure:1 Histogram for rice genotypes displays GCV, PCV, Genetic progress, and Heritability for Quantitative Characters.

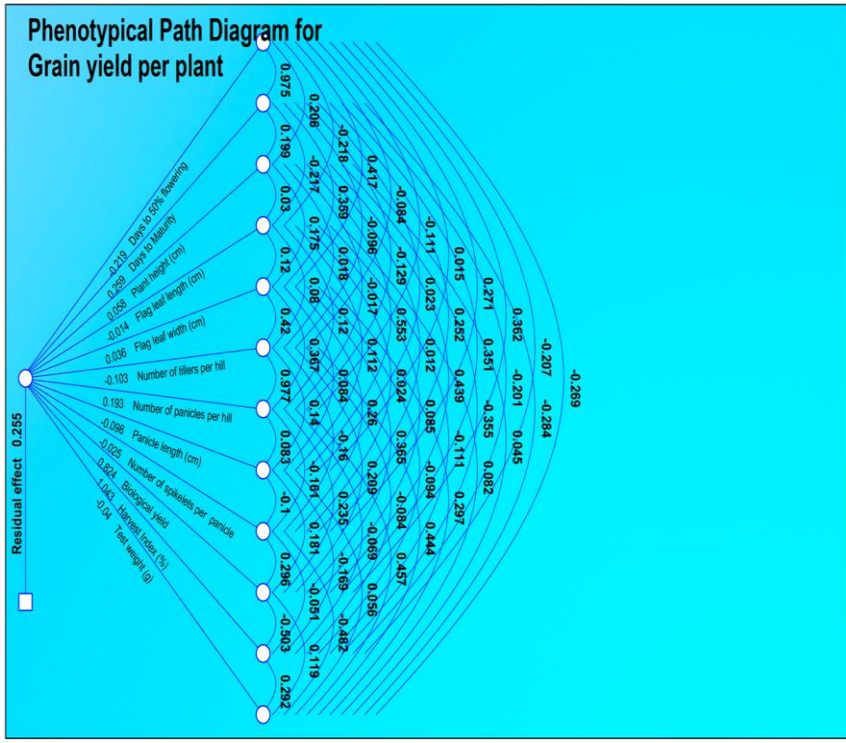


Figure:2 Phenotypical Path Diagram

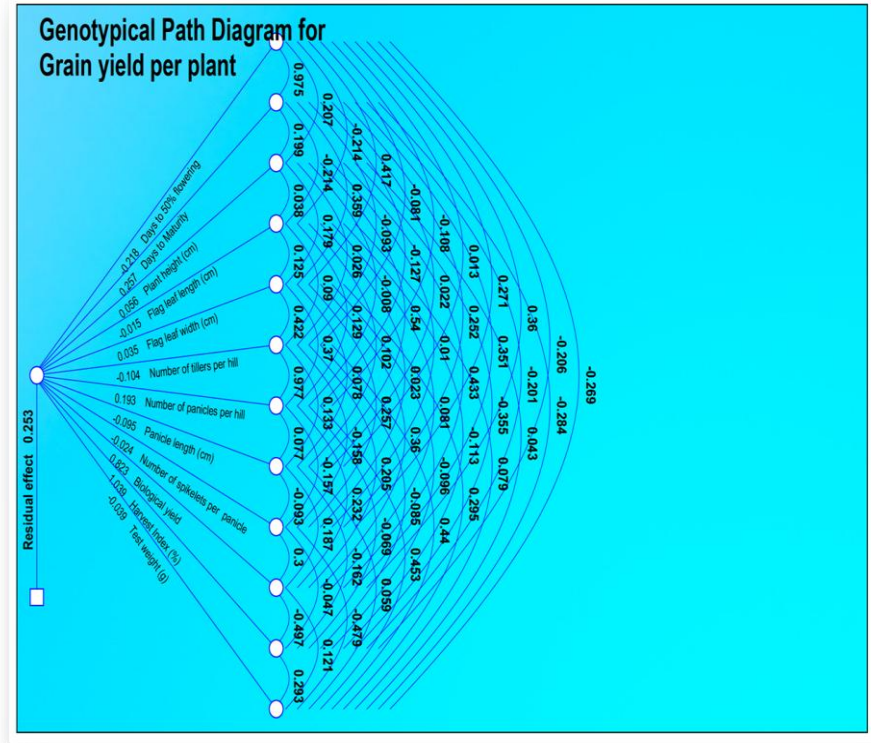


Figure:3 Genotypical Path Diagram

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