Original Research Article

Genetic Variability and Correlation Studies for Yield and Yield Related Traits in Rice (*Oryza sativa* L.)

ABSTRACT

The present investigation consists of 25 Rice genotypes used for the experiment was conducted during *Kharif- 2019* in Randomized Block Design with three replications at field Experimentation center, Department of genetics and plant Breeding. Sam Higginbottom University of Agriculture Technology and Sciences, Prayagraj (Allahabad). The aim of the present study was to estimate genetic parameters of13 yield attributing traits to study Genetic Variability, heritability, genetic advance and correlation coefficient analysis and path analysis with a view to select better yield attributes in rice. The higher value of phenotypic coefficient of variation (PCV) compared to the corresponding genotypic coefficient of variation (GCV) for all the studied traits indicated that there was an influence of the environment. Grain yield per plant, number of total tillers per hill, number of spikelets per panicle, and number of panicles per hill. High heritability coupled with high genetic advance was observed in all the characters which reflected that the direct selection of these characters based on phenotypic expression by simple selection method for yield improvement would be more reliable. Grain yield per plant showed significant and positive association with days to 50% flowering, plant height, biological yield per plant, number of panicles per hill, number of total tillers per hill, number of spikeles per panicle, days to maturity, harvest index and panicle length indicating selection of these characters for yield improvement may be rewarding. Both at phenotype and genotype level days to 50% flowering, plant height, number of tillers per hill, number of panicles per hill, number of spikelets per panicle, days to maturity, biological yield per plant and harvest index had positive direct effects on grain yield per plant indicating their importance during selection in yield improvement program. Moreover, the information generated from this study, can be exploited in future rice breeding program.

Key words:- Rice, Genetic variability, Genetic advance, Correlation , path coefficient analysis.

INTRODUCTION

The rice plant, scientifically known as Oryza sativa L. (2n=24), is a member of the family Poaceae (Graminae) and the genus oryza includes two main cultivated species: Oryza sativa (Asian rice) and Oryza glaberrima (African rice). Rice is a crop that self-pollinates and requires a short day length, as well as a hot and humid climate with an average temperature ranging from 21C to 37C during its entire growth cycle. It can be cultivated under various conditions and production systems, and is the only cereal crop that can withstand flooded conditions for extended periods. Whole rice is a low-calorie food that is high in complex carbohydrates, vitamins, minerals, and fiber, and contains no fat or sodium. The famous theme of the International Year of Rice in 2004 was "Rice is life," emphasizing the importance of rice as a significant food and commercial item. Did you know that 90% of the world's rice is grown and consumed by Asians? The rice plant, scientifically known as Oryza sativa L. (2n=24), is a member of the family Poaceae (Graminae) and the genus oryza includes two main cultivated species: Oryza sativa (Asian rice) and Oryza glaberrima (African rice). Rice is a crop that self-pollinates and requires a short day length, as well as a hot and humid climate with an average temperature ranging from 21C to 37C during its entire growth cycle. It can be cultivated under various conditions and production systems, and is the only cereal crop that can withstand flooded conditions for extended periods.

Whole rice is a low-calorie food that is high in complex carbohydrates, vitamins, minerals, and fiber, and contains no fat or sodium. The famous theme of the International Year of Rice in 2004 was "Rice is life," emphasizing the importance of rice as a significant food and commercial item. Rice is the world's most important food crop and is the primary food source for more than one third of the world's population. It accounts for about 35 to 60% of the calories consumed by 3 million Asians (Khush, 2005). So, it's no wonder that it's a staple food for a large segment of the world's population.

Rice is considered a model cereal crop due to its small genome size, vast germplasm correlation, and efficient transformation system. Before beginning any breeding program, knowledge of variability is essential for improving the character. In order to improve the genetic quality of crops, it is important to select the proper breeding methodology. Genetic parameters, such as the genotypic coefficient of variation and expected genetic advance as a percentage of the mean, can be helpful in this process. The development of high-yielding rice varieties for different agro-ecological conditions depends on the variability present in the germplasm collection. Variability parameters, such as the coefficient of variation, heritability, and genetic advance, can be used to devise suitable selection strategies for high yield in rice crops. When selecting for high-yielding genotypes, the choice of parents is vital in breeding programs. Understanding the nature and magnitude of genetic variation that governs the inheritance of quantitative characters, like yield and its components, is essential for genetic improvement. A critical analysis of genetic variability present in the germplasm of a crop, and its estimation, is a prerequisite for initiating any crop improvement program, as well as adopting appropriate selection techniques.

Heritability is the transmission of traits from one generation to another. Knowledge of heritability is essential for selecting yield-related component traits for crop yield improvement. Genetic advance measures the difference between the mean genotypic values of the selected population and the original population from which they were selected. Heritability, along with genetic advance, is considered in estimating the genetic gain under selection. Genetic parameters, such as the genotypic coefficient of variance (GCV) and phenotypic coefficient of variation (PCV), can be useful to identify the amount of variability present in germplasm. Heritability, along with genetic advance, can be a useful tool in estimating the resultant effect in the selection of the best genotypes for yield and its attributing traits. It helps in determining the influence of the environment on the expression of the genotypic and reliability of hectares

It is important to understand the relationship between yield and its components for selecting the best crops. Character association, derived by correlation coefficient, helps in evaluating the relative influence of various component characters on grain yield. Path coefficient analysis can distinguish correlation into direct and indirect effects. Selection based on grain yield per plant alone should also consider yield attributing characters. The yield attributing characters play an important role in the expression of grain yield per plant. Thus, the estimates of genetic correlation are also useful in understanding and maintaining the relative importance of desirable traits in rice breeding programs. The estimates of genotypic and phenotypic correlation coefficient of grain yield per plant with its components indicate some interesting relationships, which can help in the formulation of a selection scheme for the improvement of the yielding ability of the genotypes. Accordingly, correlation studies were conducted to find out the association at the genotypic and phenotypic level between different characters, and path analysis studies were conducted to know the direct and indirect effects of various independent traits on grain yield in rice.

. To develop an economically successful variety, breeders need to understand the relationship between yield and the traits that contribute to it. Path coefficient analysis is a useful tool for determining the direct and indirect influence of each trait on yield, allowing breeders to prioritize genetic attributes based on their contribution. To achieve this, our study aimed to:

1) Estimate the genetic variability, heritability, and genetic advance of quantitative traits.
2) Examine the relationships between yield and its contributing traits.
3) Evaluate the direct and indirect effects of yield components on grain yield.

MATERIALS AND METHODS

The methodology, materials, and the techniques adopted in this present experiment entitled, **"Genetic Variability and Correlation studies for Yield and Yield Related Traits in Rice (*Oryza sativa L.*)"**, was carried out at Crop Research Farm of the Department of Genetics and Plant Breeding, Naini Agricultural Institute, Sam Higginbottom University of Agriculture, Technology and Sciences, Prayagraj (U.P.) during *Kharif* season of 2022

STATISTICAL ANALYSIS

- Analysis of Variance (Fisher,1918)
- Genetic Variability (Burton,1952)
- Phenotypic Coefficient Variation
- Genotypic Coefficient Variation
- Heritability(Broad sense) (Burton and Dewane,1953)
- Genetic Advance (Johnson et al., 1955)
- Correlation Coefficient Analysis (AI Jibouri et al.,1958)
- Path Coefficient Analysis (Dewey and Lu,1959)

OBSERVATION RECORDED :-

1. Days to 50% Flowering
2. Days to Maturity
3. Flag Leaf Length(cm)
4. Flag Leaf Width(cm)
5. Plant Height(cm)
6. Number of Total Tillers
7. Panicle Length
8. Number of Grains per Panicle
9. Number of Productive Tillers
10. Test Weight(g)
11. Biomass(g)
12. Harvest Index (%)
13. Grain Yield per Plant(g).

Experimental material:-

The experimental materials used in this study were obtained from the Department of Genetics and Plant Breeding at SHUATS in Prayagraj (formerly known as Allahabad). The following are the details of the experimental materials..

List 1. Name of Genotypes

S.NO	NAME OF GENOTYPES	S.NO	NAME OF GENOTYPES
1	RNR- 1446	11	MTU-2023
2	JGL-24423	12	MTU-1010
3	KSRU-140	13	WGL-44
4	HMT	14	IR-64
5	NLR	15	MTU-1032
6	Durga Paddy	16	MTU-1271
7	NDLR	17	MTU-1064
8	KNM-118	18	BPT-01
9	MTU-1311	19	MTU-1262
10	MTU-1121	20	NDR 359(CHECK)

3.

4. RESULT AND DISCUSSION:

3.1 Analysis of Variance

Analysis of variance shows that mean sum of square values for 13 biometrical traits. The mean sum of square due to the genotypes was significant for all the characters studied at both the 1% and 5% significance levels, suggesting the existence of high genetic variability among the genotypes for all the traits. A high level of variability might be due to diverse sources of material, as well as environmental influences, affecting the phenotypes. The analysis of variance revealed the amount of variation present in the population.. The genotypes contain a considerable amount of genetic variance and will be used for further processing

Phenotypic Coefficient of Variance .

The phenotypic coefficient of variance ranged from Biological yield per plant (30.187) to days to maturity (6.796). The highest phenotypic coefficient of variance was observed for biological yield per plant (30.187), Grain yield per plant (28.469). Moderate phenotypic coefficients of variance were observed for Test weight (24.936), harvest index (19.117), number of spikelets per panicle (19.045), number of tillers per hill (17.213), number of panicles per hill (15.552), flag leaf width (15.072). Lowest phenotypic coefficient of variance was observed for flag leaf length (11.61), plant height (10.125), panicle length (9.954), days of 50% flowering (8.501), Days to maturity (6.796), Similar results were reported by **Mustikarini *et al.*, (2020), Sarker *et al.*, (2020), Devi *et al.* ()2017, Sala and shanthi *et al.* (2016).**

Genotypic coefficient of variance ranged from biological yield per plant (27.896), Grain yield per plant (26.664). Moderate phenotypic coefficient of variance observed for test weight (22.477), numbers of spikelets per panicle

(16.732), harvest index (15.627), number of tillers per hill (15.05), number of panicles per hill (14.152), flag leaf width (13.732). Lowest phenotypic coefficient of variance was observed for flag leaf length (8.929), plant height (8.627), panicle length (8.418), days of 50% flowering (6.768), and days to maturity (4.322). Similar results were reported by **Behera *et al.* (2020), Abilesh *et al.* (2018), Adhithya *et al.* (2013), Umadevi *et al.* (2009).**

3.2 Heritability

The estimates of the genetic coefficient of variation reflect the total amount of genotypic variability transmitted from parents to progeny. This variability is also reflected by heritability, which is the measure of the genetic relationship between parents and progeny and has been widely used to assess the degree to which a character may be transmitted from parent to offspring. High heritability in the broad sense is not enough to make sufficient improvement through selection unless accompanied by the amount of genetic advance. Genetic variation, along with heritability estimates, would give a better idea about the expected efficiency of selection of the estimates of broad-sense heritability for all studied traits, which ranged from grain yield per plant (87.722) to days to maturity (40.445).

Highest heritability was recorded for grain yield per plant (87.722), biological yield per plant (85.401), flag leaf width (83.005), number of panicles per hill (82.808), test weight (81.25), number of spikelets per panicle (77.187), number of tillers per hill (76.44), plant height (72.602). Moderately high heritability was recorded for panicle length (71.512), and harvest index (66.819). Lowest heritability was observed for days to 50 % flowering (63.381), flag leaf length (59.154), and days to maturity (40.445). Similar results were reported by **Kushwaha *et al.* (2020), Seyoun *et al.*, (2012), Saini *et al.* (2013), Hefena *et al.* (2016) and Anis *et al.* (2016).**

3.3 Genetic Advance

The estimation of genetic advances helps to understand the types of gene action involved in the expressions. Genetic advance ranged from number of spikelets per panicle (62.897) to flag leaf width (0.309). Highest genetic advance ranged from the number of spikelet's per panicle (62.897), and biological yield per plant (31.211). Moderately high genetic advance was recorded for plant height (17.813), grain yield per plant (13.906), harvest index (12.354), and days to 50% flowering (10.533). Lowest genetic advance was ranged for test weight (8.492), days to maturity (7.222), flag leaf length (4.348), panicle length (3.604), number of tillers per hill (2.848), number of panicles per hill (2.69). Similar results were reported by **Nithya *et al.* (2020), Badri *et al.* (2018), Prasad *et al.* (2017), and Devi *et al.* (2017).**

3.4 Genetic Advance as Percentage of Mean

Heritability alone provides no identification of the amount of genetic improvement that would result from the selection of individual genotypes. Hence Knowledge about genetic advances coupled with heritability is most useful. Genetic advance is improvement in the mean of selected families over the base population.

Genetic mean as a percentage of mean varied from biological yield per plant (53.106) to days to 50% flowering (11.099). Highest genetic advance as percentage of mean were observed for biological yield per plant (53.106), grain yield per plant (51.446), test weight (41.737), and number of spikelets per panicle (30.283). Moderately high genetic advance as percentage of mean observed for number of tillers per hill (27.105), harvest index (26.314), number of panicles per hill (26.53), flag leaf width (25.772), plant height (15.143). Lowest genetic advance as percentage of mean observed for panicle length (14.664), flag leaf length (14.147), days to 50% flowering (11.099), and days to maturity (5.662). Similar results were reported by **Kumar *et al.* (2020), Ekka *et al.* (2020), Abebe *et al.* (2017), Konate *et al.* (2016), and Jaiswal *et al.* (2007).**

3.5 Phenotypic Correlation Coefficient

The genotypic correlation coefficient was compared to know the nature and magnitude of relationship existing between yield and its component traits as well as the association among the component traits themselves

Grain yield was significant positive correlation with Biological yield per plant (0.803**), panicle length (0.578**), no of spikelets per panicle (0.505**), plant height (0.504**), test weight (0.308**). The traits Plant height (0.2401), flag leaf width (0.1086), days of maturity (0.280), were non- significant positive correlation with grain yield. The traits no of panicles per hill (-0.0032) ,no of tillers per hill (-0.0103), days to 50% flowering (-0.0109),flag leaf length (-0.0416) were non-significant negative correlation with grain yield at phenotypic level. Similar results were reported by **Parimala *et al.,* (2020), Velprabakaran *et al.,* (2020), Akhi *et al.,* (2020), Sameera *et al.,* (2020).**

3.6 Genotypic Correlation Coefficient

Grain yield was significantly positive correlation with Biological yield per plant (0.856**), Panicle length (0.711**), number of spikelets per panicle (0.586**), plant height (0.568**), test weight (0.372*) . The traits harvest index (0.2338), flag leaf width (0.1080), days to maturity (0.0308), days to 50% flowering (0.0044) were non-significantly positive correlation with grain yield. The traits flag leaf length (-0.0001) , number of panicles per hill (-0.0006), number of tillers per panicle (-0.0384) were non-significantly negative correlation with grain yield at genotypic level. Similar results were reported by **Nithya *et al.*, (2020), Singh *et al.*, (2020), Premkumar *et al.*, (2016), Krishnaveni *et al.*, (2013), Moosavi *et al.*, (2015), Yadav *et al.*, (2010)**

3.7 Genotypic Path Coefficient Analysis.

The Genotypic correlation coefficient was computed to know the nature and magnitude of the relationship existing between yield and component traits as well as the association among the components themselves.

An examination of the yield and yield component genotypic path coefficient was larger than the phenotypic path coefficient , demonstrating the environments making influence. A thought examination of diagnoal values revealed positive direct effect of Biological yield per plant (1.1510), harvest index (0.4162), flag leaf length (0.2183), test weight (0.0463), plant height (0.0091).Negatively direct effect was showed by Panicle length (-0.1562), number of spikelets per panicle (-0.0236), number of panicles per hill (-0.0391), Days to maturity (-0.0425), no of tillers per hill (-0.0694), days to 50% flowering (-0.0756. Similar results were reported by **Kumari *et a*l., (2020), and Dutt *el al.,* (2020).**

3.8 Phenotypic path coefficient analysis

Path coefficient analysis which are worked out from phenotypic correlation coefficient are referred to as phenotypic path coefficient analysis. It splits the phenotypic correlation coefficient in to the measures of direct and indirect effects. figure 1 & 2

An examination of the yield and yield component phenotypic path coefficient was larger than the phenotypic path coefficient , demonstrating the environments making influence. A thought examination of diagnoal values revealed positive direct effect of Biological yield per plant (1.0409), harvest index (0.6310), no of panicles per hill (0.0531), flag lef width (0.0411), no of spikelets per panicle (0.0274), test weight (0.0138). Negatively direct effect on plant height (-0.0015), flag leaf length (-0.0081), days to maturity (-0.0236), days to 50% flowering (-0.0273), panicle length (-0.0437), no of tillers per hill (-0.0438).Similar results were reported by **Lakshmi *et al.*, (2020), and Vanisri *et al.,* (2020).**

Table : 1 Shows the Analysis of Variance for 13 Quantitative Characters in 20 Rice Genotypes.

Sl.no	Characters	Mean Sum of Squares (MSS)		
		Replication (df=02)	Treatment (df=19)	Error (df=38)
1	Days to 50% flowering	2.850	147.582**	23.832
2	Days to maturity	12.20	135.904**	44.744
3	Plant height (cm)	32.1790	347.848**	38.867
4	Flag leaf length (cm)	10.380	27.796**	5.201
5	Flag leaf width (cm)	0.0040	0.087**	0.006
6	Number of tillers per hill	1.5360	8.271**	0.771
7	Number of panicles per hill	0.8520	6.603**	0.427
8	Panicle length (cm)	1.3640	14.547**	1.705
9	Number of spikelets per panicle	149.0480	3980.252**	356.961
10	Biological yield per plant (g)	91.8790	852.348**	45.952
11	Harvest Index (%)	46.1010	188.194**	26.727
12	Test weight (g)	12.8840	67.578**	4.827
13	Grain yield per plant (g)	14.5170	163.108**	7.271

Table 2 Estimation of genetic parameters of 20 rice genotype's for quantitative.

Sl.No.	Characters	GCV	PCV	h^2 % (Broad Sense)	Genetic Advancement (5%)	Gen.Adv as % of Mean (5%)
1	Days to 50% flowering	6.768	8.501	63.381	10.533	11.099
2	Days to maturity	4.322	6.796	40.445	7.222	5.662
3	Plant height (cm)	8.627	10.125	72.602	17.813	15.143
4	Flag leaf length (cm)	8.929	11.61	59.154	4.348	14.147
5	Flag leaf width (cm)	13.732	15.072	83.005	0.309	25.772
6	Number of tillers per hill	15.05	17.213	76.44	2.848	27.105
7	Number of panicles per hill	14.152	15.552	82.808	2.69	26.53
8	Panicle length (cm)	8.418	9.954	71.512	3.604	14.664
9	Number of spikelets per panicle	16.732	19.045	77.187	62.897	30.283
10	Biological yield per plant (g)	27.896	30.187	85.401	31.211	53.106
11	Harvest Index (%)	15.627	19.117	66.819	12.354	26.314
12	Test weight (g)	22.477	24.936	81.25	8.492	41.737
13	Grain yield per plant (g)	26.664	28.469	87.722	13.906	51.446

TABLE :3 Correlation Coefficient analysis

S.NO	Traits	Days to 50% flowering	Days to maturity	Plant height (cm)	Flag leaf length (cm)	Flag leaf width (cm)	Number of tillers per hill	Number of panicles per hill	Panicle length (cm)	Number of spikelets per panicl	Biological yield per plant (g)	Harvest Index (%)	Test weight (g)	Grain yield per pl
1 (P)	**Days to 50% f**	1.0000	0.782**	-0.348*	0.307*	0.421**	0.1922	0.1295	0.1335	0.262*	0.255*	-0.403*	-0.1136	0.0044

	lowering													
(G)	Days to 50% flowering	1000	0.573**	-0.214	0.2016	0.282*	0.1419	0.1226	0.0681	0.1795	0.1714	-0.2530	-0.0914	-0.0109
2 (p)	Days to maturity		1.0000	-0.515**	0.283*	0.2178	0.0073	-0.0223	0.0120	0.321*	0.315*	-0.454**	-0.1516	0.0308
(G)	Days to maturity		1000	-0.1830	0.0878	0.1399	0.0146	-0.0002	0.0222	0.1612	0.1950	-0.2247	-0.1436	0.0280
3 (P)	Plant height (cm)			1.0000	0.0615	0.1020	0.2365	0.265*	0.487**	0.494**	0.467**	0.1547	0.1318	0.568**
(G)	Plant height (cm)			10000	0.0531	0.0631	0.2503	0.2353	0.368*	0.433**	0.411*	0.1064	0.0452	0.504**
4 (P)	Flag leaf length (cm)				1.0000	0.456**	0.534**	0.511**	0.1420	0.381*	0.300*	-0.566**	-0.1058	-0.0001
(G)	Flag leaf length(cm)				1000	0.310*	0.357*	0.376*	0.2333	0.306*	0.1761	-0.354*	-0.0873	-0.0416
5 (P)	Flag leaf width (cm)					1.0000	0.651**	0.509**	0.580**	0.0229	0.0726	0.0454	0.450**	0.1080
(G)	Flag leaf width(cm)					1000	0.494**	0.442**	0.509**	0.0365	0.1167	-0.0406	0.334*	0.1086
6 (P)	Number of tillers per hill						1.0000	0.862**	0.1263	0.2242	0.2047	-0.520**	-0.2009	-0.0384
(G)	Number of tillers per hill						1000	0.940**	0.1278	0.1946	0.1814	-0.340*	-0.2214	-0.0103
7 (P)	Number of panicles per hill							1.0000	0.0568	0.2443	0.267*	-0.564**	-0.271*	-0.0006
	Number of panicles per hill							10000	0.1273	0.2428	0.2444	-0.441*	-0.279*	-0.0032
8 (P)	Panicle length (cm)								1.0000	0.1957	0.534**	0.321*	0.550**	0.711**
(G)	Panicle length (cm)								10000	0.2289	0.441**	0.2132	0.382*	0.578**
9 (P)	Number of spikelets per panicl									1.0000	0.819**	-0.490**	-0.394*	0.586**
(G)	Number of spikelets per panicle									10000	0.683**	-0.338*	-0.28*	0.505*
10(P)	Biological yield per plant (g)										1.0000	-0.304*	-0.0934	0.856**
(G)	Biological yield per plants										10000	-0.371*	-0.1082	0.803**
11(P)	Harvest Index (%)											1.0000	0.870**	0.2338
(G)	Harvest index (%)											10000	0.661**	0.2401
12(P)	Test weight (g)												1.0000	0.372*
(G)	Test weight (g)												10000	0.308*

**** 1% level of significance**

*** 5% level of significance**

TABLE :4 Direct and Indirect Effect of Morphological Characters of 13 genotypes.

S.NO	Traits	Days to 50% flowering	Days to maturity	Plant height (cm)	Flag leaf length (cm)	Flag leaf width (cm)	Number of tillers per hill	Number of panicles per hill	Panicle length (cm)	Number of spikelets per panicl	Biological yield per plant (g)	Harvest Index (%)	Test weight (g)	Grain yield per pl
1 (P)	Days to 50% flowering	-0.0756	-0.1042	0.0263	-	-	-0.0145	-0.0098	-0.0101	-0.019	-0.0193	0.0305	0.008	0.0044

					0.0232	0.0318				8			6	
(G)	**Days to 50% flowerin**	-0.0273	-0.0157	0.0060	-0.0055	-0.0077	-0.0039	-0.0033	-0.0019	-0.0049	-0.0047	0.0069	0.0025	-0.0109
2 (P)	**Days to maturity**	-0.0586	-0.0425	0.0219	-0.0120	-0.0093	-0.0003	0.0009	-0.0005	-0.0136	-0.0134	0.0193	0.0064	0.0308
(G)	**Days to maturity**	-0.0136	-0.0236	0.0043	-0.0021	-0.0033	-0.0003	0.0000	-0.0005	-0.0038	-0.0046	0.0053	0.0034	0.0280
3 (P)	**Plant height (cm)**	-0.0032	-0.0047	0.0091	0.0006	0.0009	0.0021	0.0024	0.0044	0.0045	0.0042	0.0014	0.0012	0.568**
(G)	**Plant height (cm)**	0.0003	0.0003	-0.0015	-0.0001	-0.0001	-0.0004	-0.0003	-0.0005	-0.0006	-0.0006	-0.0002	-0.0001	0.504**
4 (P)	**Flag leaf length (cm)**	-0.0250	-0.0230	-0.0050	-0.0814	-0.0371	-0.0434	-0.0416	-0.0116	-0.0310	-0.0244	0.0460	0.0086	-0.0001
(G)	**Flag leaf length (cm)**	-0.0016	-0.0007	-0.0004	-0.0081	-0.0025	-0.0029	-0.0030	-0.0019	-0.0025	-0.0014	0.0029	0.0007	-0.0416
5 (P)	**Flag leaf width (cm)**	0.0920	0.0475	0.0223	0.0994	0.2183	0.1421	0.1111	0.1266	0.0050	0.0158	0.0099	0.0982	0.1080
(G)	**Flag leaf width (cm)**	0.0116	0.0057	0.0026	0.0127	0.0411	0.0203	0.0182	0.0209	0.0015	0.0048	-0.0017	0.0137	0.1086
6 (P)	**Number of tillers per hill**	-0.0133	-0.0005	-0.0164	-0.0371	-0.0452	-0.0694	-0.0705	-0.0088	-0.0156	-0.0142	0.0361	0.0139	-0.0384
(G)	**Number of tillers per hill**	-0.0062	-0.0006	-0.0110	-0.0156	-0.0216	-0.0438	-0.0412	-0.0056	-0.0085	-0.0079	0.0149	0.0097	-0.0103
7 (P)	**Number of panicles per hill**	-0.0051	0.0009	-0.0104	-0.0200	-0.0199	-0.0397	-0.0391	-0.0022	-0.0096	-0.0105	0.0220	0.0106	-0.0006
(G)	**Number of panicles per hill**	0.0065	0.0000	0.0125	0.0200	0.0235	0.0499	0.0531	0.0068	0.0129	0.0130	-0.0234	-0.0148	-0.0032
8 (P)	**Panicle length (cm)**	-0.0209	-0.0019	-0.0761	-0.0222	-0.0906	-0.0197	-0.0089	-0.1562	-0.0306	-0.0834	-0.0502	-0.0859	0.711**
(G)	**Panicle length (cm)**	-0.0030	-0.0010	-0.0161	-0.0102	-0.0222	-0.0056	-0.0056	-0.0437	-0.0100	-0.0193	-0.0093	-0.0167	0.578**
9 (P)	**Number of spikelets per panicle**	-0.0062	-0.0076	-0.0117	-0.0090	-0.0005	-0.0053	-0.0058	-0.0046	-0.0236	-0.0193	0.0116	0.0093	0.586**
(G)	**Number of spikelets per panicle**	0.0049	0.0044	0.0119	0.0084	0.0010	0.0053	0.0066	0.0063	0.0274	0.0187	-0.0093	-0.0090	0.505**
10 (P)	**Biological yield per plant (g)**	0.2933	0.3627	0.5370	0.3451	0.0835	0.2356	0.3078	0.6143	0.9427	1.1510	-0.3494	-0.1075	0.856**
(G)	**Biological yield per plant (g)**	0.1784	0.2030	0.4283	0.1833	0.1215	0.1888	0.2544	0.4586	0.7114	1.0409	-0.3862	-0.1126	0.803**
11 (P)	**Harvest Index (%)**	-0.1678	-0.1890	0.0644	-0.2355	0.0189	-0.2165	-0.2346	0.1338	-0.2041	-0.1264	0.4162	0.3623	0.2338
(G)	**Harvest Index (%)**	-0.1596	-0.1418	0.0671	-0.2232	-0.0256	-0.2147	-0.2781	0.1345	-0.2134	-0.2341	0.6310	0.4172	0.2401
12 (P)	**Test weight (g)**	-0.0053	-0.0070	0.0061	-0.0049	0.0208	-0.0093	-0.0126	0.0255	-0.0182	-0.0043	0.0403	0.0463	0.372*
(G)	**Test weight (g)**	-0.0013	-0.0020	0.0006	-0.0012	0.0046	-0.0031	-0.0039	0.0053	-0.0045	-0.0015	0.0091	0.0138	0.308*

** 1% level of significance

* 5% level of significance

Residual effect = 1.0409(P),1.1510 (G).

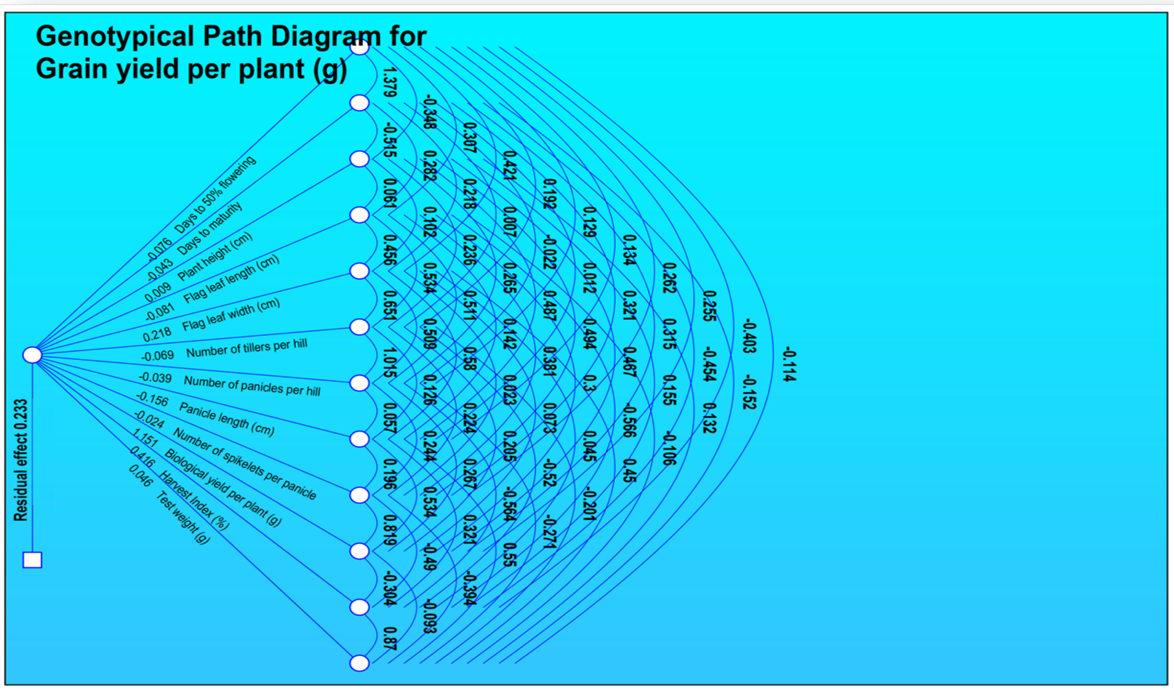

Fig 1 : Genotypic Path Diagram

CONCLUSION

From the present investigation it is concluded that among 20 genotypes of rice, RNR-1446 was found superior followed by MTU-1271 for grain yield per plant over the check (NDR- 359). High PCV, GCV recorded for Biological yield per plant, High Heritability recorded for Grain yield per plant. High Genetic Advance was recorded for Number of spikelets per panicle indicating the predominance of additive gene effects. Correlation at both Genotypic and phenotypic level, Grain yield per Plant showed a a positive significant association with biological yield per plant, Grain yield per plant, Test weight. In path analysis, at both phenotypic and genotypic level were depicted by grain yield per plant, biological yield per yield, no of panicles per hill. These are the characters provide broad spectrum of variability in segregation and may be used as parents in the future hybridization programme to develop desirable genotypes for grain yield improvement in Rice genotypes.

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