



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

Amulya Rani Madishetty ^{a++*}, Gaibriyal M. Lal ^{a#}
and Adarsh K. ^{at}

^a Department of Genetic and Plant Breeding, Naini Agricultural Institute, SHUATS, Prayagraj, Uttar Pradesh, India.

Authors' contributions

This work was carried out in collaboration among all authors. All authors read and approved the final manuscript.

Article Information

DOI: 10.9734/IJPSS/2023/v35i203914

Open Peer Review History:

This journal follows the Advanced Open Peer Review policy. Identity of the Reviewers, Editor(s) and additional Reviewers, peer review comments, different versions of the manuscript, comments of the editors, etc are available here: <https://www.sdiarticle5.com/review-history/106957>

Original Research Article

Received: 22/07/2023
Accepted: 28/09/2023
Published: 09/10/2023

ABSTRACT

The study aims to estimate the genetic parameters of 13 yield-attributing traits to study Genetic Variability and Correlation studies for yield and yield-related traits in rice. The investigation comprised of 20 Rice genotypes used for the experiment carried out during *Kharif- 2022* in Randomized Block Design with three replications at the field Experimentation Center, Department of Genetics and Plant Breeding, Sam Higginbottom University of Agriculture Technology and Sciences, Prayagraj (Allahabad), India. The greater value of the 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 on biological yield per plant, Grain yield per plant, and test weight. All of the traits had high heritability, indicating that direct selection

⁺⁺ M.Sc. Scholar;

[#] Associate Professor;

[†] Ph.D. Scholar;

*Corresponding author: E-mail: madishettyamulyaraniar@gmail.com;

of these characters based on phenotypic expression using a simple selection procedure for yield improvement would be more accurate. Grain yield per plant showed a significant and positive association with biological yield, panicle length, no of spikelets per panicle, plant height, test weight, flag leaf width, and days to maturity indicating selection of these characteristics for yield improvement may be rewarding. Both at phenotype and genotype levels Biological yield per plant, panicle length, no of spikelets per panicle, plant height, test weight, days to flowering, days to maturity, and flag leaf width had positive direct effects on grain yield per plant indicating their importance during selection in the yield improvement program. Furthermore, the data gained by this study can be used in future rice breeding programs.

Keywords: Rice; genetic variability; genetic advance; correlation; path coefficient analysis.

1. 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 and a hot and humid climate with an average temperature ranging from 21C to 37C during its entire growth cycle” [1]. 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 and 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” [1].

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 billion Asians” [2]. 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” [3]. Before beginning any breeding program, knowledge of variability is essential for improving the character. 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 agroecological 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 high-yielding genotypes, the choice of parents is vital in breeding programs” [3]. Understanding the nature and magnitude of genetic variation that governs the inheritance of quantitative characteristics, 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 and 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 and genetic

advancement are 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 advances, 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” [4].

“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” [3]. 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 levels 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.

2. MATERIALS AND METHODS

The methodology, materials, and 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

2.1 Statistical Analysis

- Analysis of Variance [5]
- Genetic Variability [6]
- Phenotypic Coefficient Variation
- Genotypic Coefficient Variation
- Heritability (Broad sense) (Burton and Dewane, 1953)
- Genetic Advance [7]
- Correlation Coefficient Analysis [8]
- Path Coefficient Analysis [9]

2.2 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).

2.3 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.

3. RESULTS AND DISCUSSION

3.1 Analysis of Variance

Analysis of variance shows the 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.

3.2 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) and 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). The 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 Kishore et al (2018) and Sandeep et al. [10].

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). The 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 Roy et al. [11].

Chart 1. Experimental details

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)

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 genotypes for quantitative characters

Sl.No.	Characters	Var Environmen tal	ECV	Var Genotypical	GCV	Var Phenotypica l	PCV	h2 (Broad Sense)	Genetic Advanceme nt 5%	Gen.Adv as % of Mean 5%
1	Days to 50% flowering	23.832	5.144	41.25	6.768	65.082	8.501	63.381	10.533	11.099
2	Days to maturity	44.744	5.244	30.387	4.322	75.131	6.796	40.445	7.222	5.662
3	Plant height (cm)	38.867	5.3	102.994	8.627	141.86	10.125	72.602	17.813	15.143
4	Flag leaf length (cm)	5.201	7.42	7.532	8.929	12.733	11.61	59.154	4.348	14.147
5	Flag leaf width (cm)	0.006	6.214	0.027	13.732	0.033	15.072	83.005	0.309	25.772
6	Number of tillers per hill	0.771	8.355	2.5	15.05	3.271	17.213	76.44	2.848	27.105
7	Number of panicles per hill	0.427	6.449	2.059	14.152	2.486	15.552	82.808	2.69	26.53
8	Panicle length (cm)	1.705	5.313	4.281	8.418	5.986	9.954	71.512	3.604	14.664
9	Number of spikelets per panicle	356.961	9.097	1207.764	16.732	1564.725	19.045	77.187	62.897	30.283
10	Biological yield per plant (g)	45.952	11.534	268.799	27.896	314.75	30.187	85.401	31.211	53.106
11	Harvest Index (%)	26.727	11.012	53.822	15.627	80.549	19.117	66.819	12.354	26.314
12	Test weight (g)	4.827	10.798	20.917	22.477	25.744	24.936	81.25	8.492	41.737
13	Grain yield per plant (g)	7.271	9.976	51.946	26.664	59.216	28.469	87.722	13.906	51.446

Table 3. Correlation coefficient analysis of both phenotypic and genotypic levels

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 panicle	Biological yield per plant (g)	Harvest Index (%)	Test weight (g)	Grain yield per plant
1 (P)	Days to 50% flowering	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
(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**

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 panicle	Biological yield per plant (g)	Harvest Index (%)	Test weight (g)	Grain yield per plant
(G)	Panicle length (cm)								10000	0.2289	0.441**	0.2132	0.382*	0.578**
9 (P)	Number of spikelets per panicle									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 panicle	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	-0.0232	-0.0318	-0.0145	-0.0098	-0.0101	-0.0198	-0.0193	0.0305	0.0086	0.0044
(G)	Days to 50% flowering\	-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).

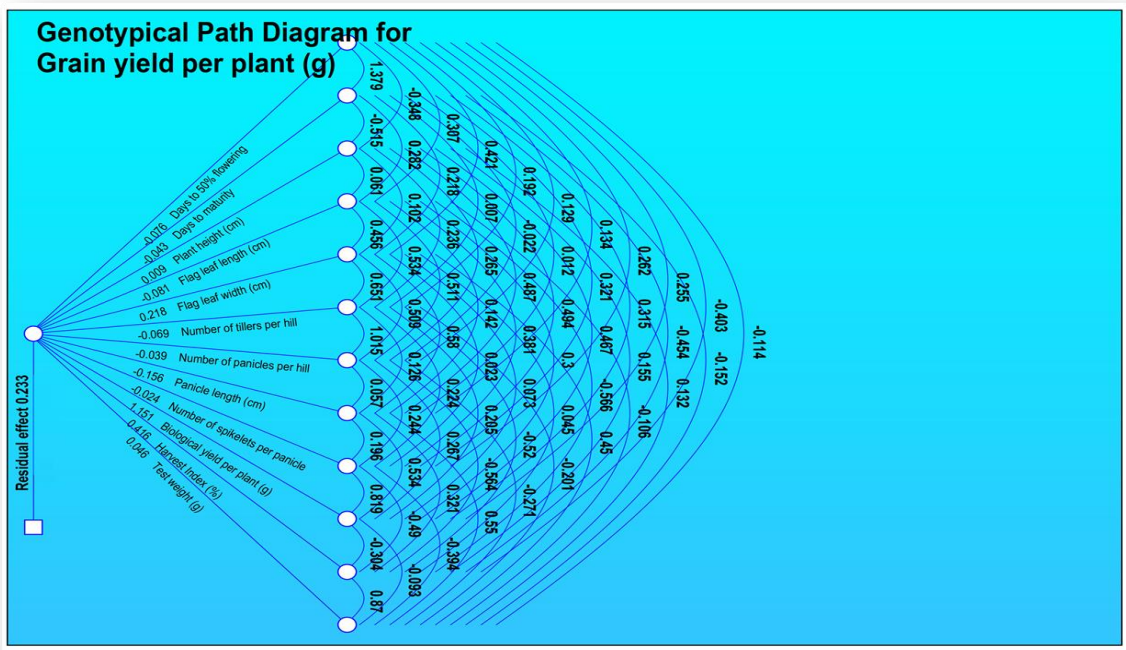


Fig. 1. Genotypic path diagram

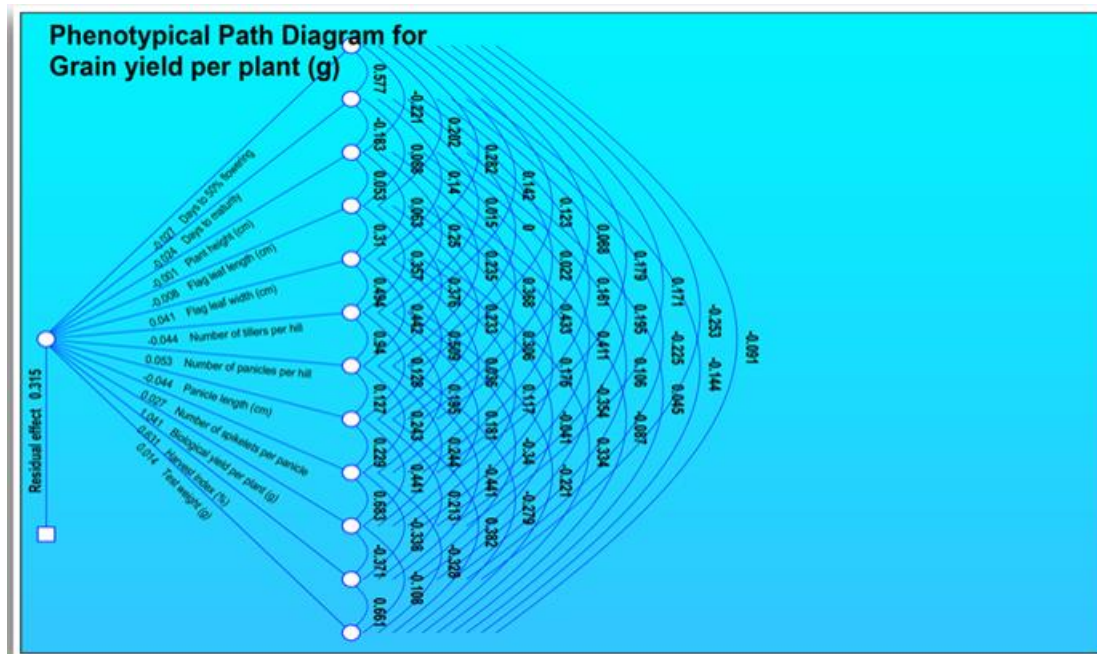


Fig. 2. Phenotypic path diagram

3.3 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)[12].

The 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). The 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 Nandan et al., (2018), and Nuruzzaman et al., (2017)[13].

3.4 Genetic Advance

The estimation of genetic advances helps to understand the types of gene action involved in the expressions. Genetic advances ranged from the number of spikelets per panicle (62.897) to flag leaf width (0.309). The highest genetic advance ranged from the number of spikelets 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). The 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 Lingaiah et al., (2019), and Barik et al., (2020)[14].

3.5 Phenotypic Correlation Coefficient

The genotypic correlation coefficient was compared to know the nature and magnitude of the relationship existing between yield and its component traits as well as the association among the component traits themselves[15].

Grain yield had a 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**), and test weight (0.308**). The traits Plant height (0.2401), flag leaf width (0.1086), and days of maturity (0.280), were non-significant positive correlations 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 the phenotypic level. Similar results were reported by Vijaya et al., (2016), Vincent et al., (2017), and Rashid et al., (2017)[16].

3.6 Genotypic Correlation Coefficient

Grain yield had a 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**), and test weight (0.372*). The traits harvest index (0.2338), flag leaf width (0.1080), days to maturity (0.0308), and days to 50% flowering (0.0044) had a non-significantly positive correlation with grain yield. The traits flag leaf length (-0.0001), number of panicles per hill (-0.0006), and number of tillers per panicle (-0.0384) were non-significantly negative correlations with grain yield at the genotypic level. Similar results were reported by Singh et al., (2018), Srikanth et al., (2017), Srujana et al., (2017)[17].

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[18].

A thought examination of diagonal values revealed a positive direct effect of Biological yield per plant (1.1510), harvest index (0.4162), flag leaf length (0.2183), test weight (0.0463), and plant height (0.0091). Negatively direct effect was shown 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 al., (2020), and Dutt et al., (2020).

3.8 Phenotypic Path Coefficient Analysis

Path coefficient analysis which is worked out from the phenotypic correlation coefficient is referred to as phenotypic path coefficient analysis. It splits the phenotypic correlation coefficient in to the measures of direct and indirect effects[19].

An examination of the yield and yield component phenotypic path coefficient was larger than the

phenotypic path coefficient, demonstrating the environment-making influence. A thought examination of diagonal values revealed a positive direct effect of Biological yield per plant (1.0409), harvest index (0.6310), no of panicles per hill (0.0531), flag leaf 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)[20].

4. CONCLUSION

After examining 20 different types of rice, it has been determined that RNR-1446 is the most effective in producing grain yield per plant, followed by MTU-1271. Biological yield per plant had a high PCV and GCV, while grain yield per plant had high heritability. The number of spikelets per panicle showed high genetic advance, indicating a predominance of additive gene effects. At both genotypic and phenotypic levels, there was a positive and significant correlation between grain yield per plant, biological yield per plant, panicle length, number of spikelets per panicle, plant height, and test weight. In path analysis, grain yield per plant, biological yield per plant, and number of panicles per hill were the most significant factors at both phenotypic and genotypic levels. These traits offer a wide range of variability and may be useful as parents in future hybridization programs to create desirable rice genotypes for improved grain yield..

COMPETING INTERESTS

Authors have declared that no competing interests exist.

REFERENCES

1. Loitongbam B, Kerketta P, Bisen P, Singh BP, Rajan KP, Singh PK. Genetic variability and character association study for yield and its component traits in rice (*Oryza sativa* L.). Journal of Pharmacognosy and Phytochemistry. 2020;9(3):1049-53.
2. Khush GS. What It Will Take to Feed 5.0 Billion Rice Consumers in 2030. Plant Molecular Biology. 2005;59;1-6.
3. Reddy GE, Suresh BG, Sravan T, Reddy PA. Interrelationship and cause-effect analysis of rice genotypes in north east plain zone. The Bioscan. 2013;13;8(4): 1141-4.
4. Kumar A, Kumar H, Gupta V, Khosla G. Correlation and path coefficient analysis for yield and yield component traits in rice (*Oryza sativa* L.). Agricultural Science Digest. 2011;1;31(4).
5. Fisher RA. The Correlation between relative on the supposition of Mendelian Royal Society, Edinburgh. 1918;52:399-403.
6. Burton GW, De Vane EH. Quantitative inheritance in grasses. Proc.6th International Grassland Congress. 1952; 11:277-283.
7. Johnson HW, Robinson HE, Comstock RE. Estimate of genetic and environmental variability in rice (*Oryza sativa* L.). Agronomy Journal. 1955;47:314-318.
8. Al-Jibouri HA, Miller AR and Robinson HF. Genotypic and environmental variances and covariances in upland cotton crosses of interspecific origin. Journal of Agronomy. 1958;50:633-63
9. Dewey Lu, Variability and Path Coefficient Studies for Yield and Yield Related Traits in Rice (*Oryza sativa* L.). International Journal of Agriculture, Environment, and Biotechnology. 1959; 12(4):323-329.
10. Sandeep S, Sujatha M, Subbarao LV, Neeraja CN. Genetic Variability, Heritability and Genetic Advance Studies in Rice (*Oryza sativa* L.). Int.J. Curr. Microbiol. App.Sci. 2018;7(12):3719-3727
11. Aditya JR, Bhartiya A. Genetic variability, correlation and path analysis for quantitative characters in rainfed upland rice of Uttarakhand Hills. Journal of Rice Research. 2013;6:24-34.
12. Abebe T, Alamerew S, Tulu L. Genetic Variability, Heritability and Genetic Advance for Yield and its Related Traits in Rainfed Lowland Rice (*Oryza sativa* L.) Genotypes at Fogera and Pawe, Ethiopia. Advances in Crop Science and Technology. 2017;5:272.
13. Dinkar AK, Kumar RR, Kumar M, Singh SP. Genetic Variability, Correlation, and Path Analysis for Selection in Elite Breeding Materials of Aromatic Rice (*Oryza sativa* L.); 2023.
14. Demeke B, Dejene T, Abebe D. Genetic Variability, heritability and genetic advance of morphological, yield related quality traits

- in upland rice (*Oryza sativa* L.) genotypes at Pawe, northwestern Ethiopia. *Cogent Food & Agriculture*. 2023;31;9(1):2157099.
15. Panse VG, Sukhatme PV. *Statistical methods for agricultural workers*. ICAR New Delhi., 2nd Edn. 1967;381.
 16. Parimala K, Surender R, Prasad H, Sudheer SK, Narender SK. Studies on genetic parameters, correlation, and path analysis in rice (*Oryza sativa* L.). *Journal of Pharmacognosy and Phytochemistry*. 2020;9(1):414-417.
 17. Roy SN. *Some Aspects of Multivariate Analysis*. New York: Wiley; 1957.
 18. Robinson HF, Comstock RE, Harvey PH. Genotypic and phenotypic correlations in corn and their implications in selection. *Agronomy Journal*. 1951;43:282-287.
 19. Singh KS, Suneetha Y, Kumar GV, Rao VS, Raja DS, Srinivas T. Variability, correlation and path studies in colored rice. *International Journal of Conservation Science*. 2020;8(4): 2138-2144.
 20. Lush JL. Heritability of quantitative characters in farm animals. *Hereditas*. 1949;35:356-375.

© 2023 Madishetty et al.; This is an Open Access article distributed under the terms of the Creative Commons Attribution License (<http://creativecommons.org/licenses/by/4.0>), which permits unrestricted use, distribution, and reproduction in any medium, provided the original work is properly cited.

Peer-review history:

The peer review history for this paper can be accessed here:
<https://www.sdiarticle5.com/review-history/106957>