



Research Article

GENETIC VARIABILITY AND CHARACTER ASSOCIATION OF YIELD AND YIELD RELATED TRAITS IN RICE (*Oryza sativa* L.)

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Abstract: The present investigation was conducted to examine the 17 rice genotypes including one checks to study the genetic parameters, correlation and genetic diversity. The experiment was carried out in Research Farm Genetics & Plant Breeding of AKS University, Satna, M.P., during kharif season, 2021-22 in Randomized Block Design (RBD) with three replications. Analysis of variance showed highly significant differences among 17 rice genotypes for 12 characters studied. The results showed that some traits have moderate to high levels of variability, while others have low levels of variability. ECV had the fastest rate of days to 50% flowering, while PCV had the tallest plants and the highest values in most of the traits that impact the grain yield. The heritability of most of the traits was high, with a minimum of 68.1% and a maximum of 96.8%, indicating that a significant portion of the variation in these traits can be attributed to genetics. The results can be used to prioritize traits in breeding programs and make informed decisions about which traits to focus on for improvement. The study found significant and weak correlations between grain yield per plant and various traits in rice. The study also found that harvest index, biological yield per plant, and days to 50% flowering have the highest positive direct effect on grain yield. The characters that were studied were found to be appropriate for the study due to low residual effects. The study results can be useful for rice breeders in selecting specific traits that positively impact grain yield. The indirect effects of germination percentage showed that total seedling length and root dry weight have a positive effect on grain yield through these traits.

Keywords: Rice, Genetic parameters, Correlation, Path analysis

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Introduction

Rice is a staple food crop that is grown and consumed worldwide. It belongs to the genus *Oryza* of the Gramineae family and has two cultivable species, *Oryza sativa* and *Oryza galberima*, with $2n=24$ chromosomes. *Oryza sativa* is the cultivated diploid species and is divided into three sub-species: indica, japonica, and javanica. Rice provides 80% of the calories for over two billion people in Asia and 1/3 of the calories for nearly one billion people in Africa and Latin America. Globally, rice provides 22% of the world's supply of calories and is also a major source of protein, contributing 17%. Rice occupies 1/3 of the area planted to cereals in developing countries, which is 50% more than the area under wheat. India has the largest area under rice cultivation (40.99 million hectares), constituting 28% of the world's total and ranks second in total production (89.58 million tonnes), after China.

Rice is widely grown under a range of agroclimatic conditions, and its genetic vulnerability has increased due to reduced genetic variability, improved cultural practices, and continuous rice cropping. The productivity of rice in India in 2022 is 42.8%. On the other hand, China is the world's leading rice producer with a production of nearly 125 million tonnes. India is the second largest rice producer, occupying second position after China, with an area of 43.86 million hectares and producing nearly a quarter of Asia's production [2].

Heritability is an important measure in plant breeding as it estimates the heritable portion of phenotypic variance and is used to predict the transmission of characters from parents to their offspring.

Estimates of heritability can be worked out from both in-breeders and out-breeders, and the broad sense heritability can be estimated from parental as well as hybrid populations. Genetic advance is a reliable measure of genetic improvement under selection for polygenic traits, and high values of genetic advance are indicative of additive gene action.

Correlation studies provide information about yield contributing characters and are useful for plant breeders to select elite genotypes from diverse genetic populations. Mass selection has been used to improve grain yield in crops through indirect selection of highly heritable traits associated with yield, and path coefficient analysis helps in indirect selection for genetic improvement of yield. Direct selection is straight selection for yield improvement, while indirect selection is selection for a component trait. [5].

Materials and Methods

The materials used for present investigation comprised of 17 rice genotypes, collected from various Sources and the research was conducted at the Research Farm Genetics & Plant Breeding of AKS University, Satna, M.P during the kharif season of 2022.

All the 17 genotypes were grown in Randomized Block Design (RBD) with 3 replications. In each replication, genotypes were sown in 3 rows of 1-meter length with row to row and plant to plant spacing of 25 cm and 20 cm respectively. Recommended fertilizer in the forms of Urea and DAP was applied to each plot in the shallow furrow depths and mixed with soil at the same time during sowing. The central rows were harvested for grain yield and biomass yield from each plot leaving boarder rows to avoid boarder effects. All other agronomical practices were undertaken uniformly to the entire plot as recommended for rice production in the area during the season.

Results and Discussion

Analysis of Variance (ANOVA)

The results of the ANOVA table indicate that the treatments (rice breeding) have a significant effect on the response variables (days to 50% flowering, plant height,

no. of effective tillers/plant, flag leaf length, flag leaf width, days to maturity, no. of spikelet's/panicle, panicle length, test weight, harvest index, biological yield per plant, and grain yield per plant). The replication and error degrees of freedom (Df) suggest that there was some variability in the response variables due to both the replication and the experimental error [Table-1].

The high values of sum of square for the treatments indicate that the treatments have a significant effect on all the traits. The results of the ANOVA table suggest that the rice breeding treatments have a significant effect on the various traits measured. These results provide important information for rice breeding programs, as they indicate which traits are most affected by breeding and can be targeted for improvement [4, 6].

Table-1 Analysis of Variance of the 12 characters

Characters	Replication Df=2	Treatment Df= 16	Error Df=32
Days to 50% flowering	65.06	359.40**	19.98
Plant height	22.82	257.85**	38.20
No. of effective tillers /plant	125.94	248.52**	61.74
Flag leaf length	33.32	11.144**	1.18
Flag leaf width	41.70	37.05**	11.82
Days to maturity	0.13	0.092**	0.01
No. of spikelet's/panicle	2.73	59.945**	5.71
Panicle length	250.71	393.48**	58.90
Test weight	1.90	12.96**	3.62
Harvest index	0.24	12.98**	3.34
Biological yield per plant	0.28	5.70**	0.79
Grain yield per plant	0.01	0.90**	0.09

Mean Performance of the Genotypes

The mean values of each trait indicate the average of the trait across the genotypes being studied. The minimum and maximum values represent the range of the trait, and the coefficient of variation (C.V.) indicates the variability of the trait as a percentage of the mean. The standard error (S.E.) and critical difference (C.D. 5%) values give an estimate of the precision of the mean and the level of statistical significance of differences in means between groups [Table-2].

The average number of days it takes for 50% of the plants to flower is 80.68, with a range of 60.19 to 97.19 days. The coefficient of variation is 5.54%, indicating a moderate level of variability in this trait. On average, the genotypes mature 96.35 days after planting, with a range of 81 to 109.67 days. The coefficient of variation is 6.41%, indicating moderate variability. The average height of the plants is 94.22 cm with a range of 77.27 to 115.81 cm. The coefficient of variation is 8.34%, indicating a high level of variability. The average number of tillers per plant is 13.82, with a range of 10.36 to 17.27. The coefficient of variation is 7.87%, indicating a moderate level of variability. The average flag leaf length is 30.93 cm, with a range of 25.07 to 38.73 cm. The coefficient of variation is 11.11%, indicating a high level of variability. The average flag leaf width is 1.48 cm, with a range of 1.17 to 1.79 cm. The coefficient of variation is 7.85%, indicating a moderate level of variability. The average test weight is 19.34 g, with a range of 11.73 to 27.66 g. The coefficient of variation is 12.35%, indicating a high level of variability. The average number of spikelets per panicle is 272.21, with a range of 128.31 to 411.44. The coefficient of variation is 7.87%, indicating a moderate level of variability. The average panicle length is 25.77 cm, with a range of 23.07 to 30.13 cm. The coefficient of variation is 7.38%, indicating a moderate level of variability. The average harvest index is 40.19, with a range of 37.80 to 43.73. The coefficient of variation is 4.55%, indicating a low level of variability. The average biological yield per plant is 41.19, with a range of 39.27 to 43.27. The coefficient of variation is 2.16%, indicating a low level of variability. The average grain yield per plant is 16.50 g, with a range of 15.23 to 17.67 g. The coefficient of variation is 1.86%, indicating a low level of variability.

The results show that some traits have moderate to high levels of variability while others have low levels of variability. Traits with moderate variability include flowering time, maturity time, number of tillers per plant, number of spikelets per panicle, panicle length, and flag leaf width. Traits with high variability include height of the plants, flag leaf length, test weight. The harvest index, biological yield per plant, and grain yield per plant show low levels of variability. This information can be used to prioritize traits in breeding programs and make informed decisions about which traits to focus on for improvement. The low variability in harvest index, biological yield, and grain yield suggests that these traits are relatively stable and may be less challenging to improve through breeding efforts. The moderate to

high variability in other traits indicates that more effort may be needed to make meaningful improvements in these areas. The finding was quite like as reported by Rajpoot, *et al.*, (2022) [11] for days to 50% flowering, days to maturity and Ghuttai, *et al.*, (2022) [7] for plant height, grain per spike, spike length. Madakemohekar, *et al.*, (2015) [15], Sabit, *et al.*, (2017) [12], Ahmed, *et al.*, (2018) [1], Shah, *et al.*, (2017) [13] for biological yield per plant and harvest index.

Genetic Variability Parameters

Various traits were evaluated and compared between GCV, PCV and ECV. Days to 50% flowering is an important factor in determining the grain production rate with ECV having the fastest rate compared to GCV and PCV. Plant height can impact the photosynthesis rate and grain production, with PCV having the tallest plants. The number of effective tillers per plant, flag leaf length and width, and no. of spikelets per panicle can all impact the grain yield with PCV having the highest values in all these traits. Days to maturity, test weight, harvest index, biological yield per plant, and grain yield per plant also play a role in determining the overall quality and production of rice, with PCV showing the highest values in all these traits compared to GCV and ECV presented in [Table-3]. The results show that the heritability for most of the traits is high, ranging from 68.1% to 96.8%. The minimum heritability was observed for flag leaf width and the maximum for panicle length. The heritability for grain yield per plant was 89.5%. This indicates that 89.5% of the variation in grain yield per plant can be attributed to genetics. The genetic advance, which is the expected increase in the trait due to selective breeding, was also calculated. The genetic advance was highest for panicle length and lowest for days to maturity. These results suggest that rice breeders can expect to make significant progress in improving the target traits through selective breeding, particularly for traits with high heritability such as panicle length and grain yield per plant. High heritability for days to maturity. Nirmaladevi, *et al.*, (2015) [16], Singh and Singh (2022) [14] high heritability for thousand seed weight. Gelalcha and Hanchinal (2022) [6], Madakemohekar, *et al.*, (2015) [15] high heritability for biological yield per plant [10]. [5], [9] reported for plant height. Kumar and Kerkhi (2017) [9], Singh and Singh (2022) [14] reported high genetic advancement as % of mean for grain yield per plant. Kumar and Kerkhi (2017) [9], Devi (2016) [5], Ravindra, *et al.*, (2012) [17] reported high for harvest index.

Genotypic and phenotypic correlation coefficient Analysis

The genotypic (r_g) and phenotypic (r_p) correlation of grain yield per plant with traits viz., days to 50% flowering is negative and significant ($r_g = -0.541$ and $r_p = -0.441$), days to maturity is negative and significant ($r_g = -0.479$ and $r_p = -0.450$), plant height is negative but weak ($r_g = -0.119$ and $r_p = -0.119$), the number of effective tillers per plant is positive but weak ($r_g = 0.129$ and $r_p = 0.129$), flag leaf length is positive but weak ($r_g = 0.145$ and $r_p = 0.145$), flag leaf width is positive but weak ($r_g = 0.392$ and $r_p = 0.392$), test weight is positive and significant ($r_g = 0.534$ and $r_p = 0.634$), the number of spikelets per panicle is positive and significant but weak ($r_g = 0.431$ and $r_p = 0.441$), panicle length is positive but weak ($r_g = 0.355$ and $r_p = 0.355$), harvest index is positive and significant ($r_g = 0.757$ and $r_p = 0.757$), biological yield per plant is negative but weak ($r_g = -0.163$ and $r_p = -0.153$) presented in [Table-4].

The study found several significant and weak correlations between grain yield per plant and various traits in rice. Some of the significant correlations include: longer flowering time and days to maturity being negatively associated with grain yield, higher test weight being positively associated with grain yield, more spikelet's per panicle and higher harvest index being positively associated with grain yield. Rice breeders can use this information to select for specific traits that positively impact grain yield. [4], [9], [12] also agreed with the similar results.

Path coefficient analysis

The Path coefficient analysis [Table-5] revealed that the characters chosen for the study were very much appropriate as evident from the low amount of residual effect. The portioning of correlation coefficient into direct effects showed that harvest index (1.685) exerted highest positive followed by biological yield per plant (1.183) and days to 50% flowering (0.146). These characters, therefore, are required to be considered during selection for vigour improvement in rice.

Table-2 Means performance of the 17 rice genotypes

Genotypes	DFF	DM	PH	ETPP	FLL	FLW	TW	SPPP	PL	HI	BYP	GYP
HMT	88.52	98.67	77.27	15.09	27.80	1.73	23.07	214.31	26.40	43.73	39.60	17.27
NP-124-8	80.52	87.33	88.07	17.27	34.60	1.57	27.66	252.71	25.33	43.00	41.17	17.67
MTU-1212	90.19	102.33	92.07	14.49	34.80	1.57	19.98	321.57	23.07	38.26	43.14	16.47
JGL-1118	90.19	101.33	87.33	12.83	29.80	1.41	21.99	411.44	24.60	38.06	42.31	16.13
MTU-1010	72.53	97.33	88.00	14.69	29.33	1.25	17.42	275.71	23.60	38.50	42.51	16.33
MTU-1262	79.52	86.67	86.87	13.49	25.07	1.53	14.14	327.04	24.67	38.40	42.64	16.47
JGL-24423	74.52	92.67	90.80	11.09	32.20	1.61	18.97	324.84	26.73	38.13	42.14	16.03
SIDHA -SONNALU	82.52	101.33	108.34	14.36	32.60	1.79	25.85	238.11	26.87	37.90	43.27	16.37
MTU-1032	96.86	105.33	87.80	15.49	30.33	1.38	17.74	293.77	30.13	37.80	40.37	15.23
TRIVENI	60.19	81.00	94.20	13.82	29.13	1.17	15.39	259.44	23.13	38.12	42.54	16.17
NLR	64.86	86.33	100.14	10.36	30.73	1.71	17.63	258.77	26.93	41.56	40.27	16.63
JGL3828	67.19	88.00	96.53	10.71	34.93	1.56	13.56	224.91	23.67	41.66	40.84	16.97
RDR1140	71.86	83.33	91.74	13.16	28.80	1.48	22.05	128.31	24.93	41.90	40.97	17.13
WGL18833	79.52	103.33	115.81	13.82	38.73	1.39	11.73	352.11	29.13	41.42	39.87	16.47
RNR-15098	86.86	106.67	97.67	14.19	25.80	1.37	18.60	274.44	26.67	41.36	39.34	16.23
MTU1190	97.19	106.67	102.87	17.03	29.00	1.37	17.94	308.64	24.27	42.30	39.27	16.57
SUJALA	88.53	109.67	96.27	13.09	32.20	1.29	25.14	161.51	28.00	41.03	39.99	16.37
Mean	80.68	96.35	94.22	13.82	30.93	1.48	19.34	272.21	25.77	40.19	41.19	16.50
Min.	60.19	81.00	77.27	10.36	25.07	1.17	11.73	128.31	23.07	37.80	39.27	15.23
Max.	97.19	109.67	115.81	17.27	38.73	1.79	27.66	411.44	30.13	43.73	43.27	17.67
C.V.	5.54	6.41	8.34	7.87	11.11	7.85	12.35	7.87	7.38	4.55	2.16	1.86
S.E.	2.58	3.57	4.54	0.63	1.98	0.07	1.38	12.37	1.10	1.06	0.51	0.18
C.D. 5%	7.43	10.28	13.07	1.81	5.72	0.19	3.97	35.63	3.16	3.04	1.48	0.51

Table-3 Genetic parameters of 12 traits

Traits	GCV	PCV	ECV	Heritability (%)	Genetic Advance	Genetic as percent of mean
Days to 50% flowering	13.184	13.566	5.541	94.40	21.294	26.393
Plant height	8.881	9.622	6.414	85.20	16.269	16.885
No. of effective tillers /plant	8.374	9.66	8.339	75.20	14.092	14.956
Flag leaf length	13.183	13.943	7.867	89.40	3.549	25.675
Flag leaf width	9.374	11.36	11.114	68.10	4.929	15.936
Days to maturity	10.894	11.798	7.845	85.30	0.307	20.722
No. of spikelets/panicle	21.981	23.11	12.355	90.50	8.331	43.071
Panicle length	24.947	25.357	7.87	96.80	137.627	50.558
Test weight	6.849	8.066	7.379	72.10	3.087	11.98
Harvest index	4.461	5.177	4.549	74.30	3.182	7.919
Biological yield per plant	3.106	3.347	2.159	86.10	2.446	5.938
Grain yield per plant	3.139	3.318	1.863	89.50	1.009	6.117

Table-4 Genotypic Correlation Matrix of 12 traits

Traits	Level	DFF	DM	PH	ETPP	FLL	FLW	TW	SPPP	PL	HI	BYP	GYP
DFF	rg	1.000	0.929**	-0.103	0.630**	-0.103	0.032	0.372	0.299	0.412	0.039	-0.287	-0.541*
	rp	1.000	0.822**	-0.102	0.582*	-0.084	0.002	0.330	0.269	0.328	0.020	-0.283	-0.441*
DM	rg		1.000	0.258	0.363	0.228	-0.176	0.179	0.254	0.599*	-0.012	-0.408	-0.479*
	rp		1.000	0.234	0.347	0.102	-0.156	0.168	0.236	0.445*	-0.038	-0.339	-0.450*
PH	rg			1.000	-0.179	0.645**	-0.060	-0.357	0.060	0.370	0.023	-0.182	-0.119
	rp			1.000	-0.116	0.501*	-0.041	-0.273	0.080	0.274	0.043	-0.159	-0.119
ETPP	rg				1.000	-0.060	-0.214	0.385	0.053	0.061	0.178	-0.169	0.129
	rp				1.000	-0.092	-0.203	0.335	0.047	-0.011	0.166	-0.131	0.129
FLL	rg					1.000	0.096	-0.010	0.091	0.285	0.123	0.040	0.145
	rp					1.000	0.151	-0.015	0.092	0.196	0.074	0.051	0.145
FLW	rg						1.000	0.395	-0.124	0.138	0.231	0.125	0.392
	rp						1.000	0.326	-0.094	0.118	0.189	0.111	0.392
TW	rg							1.000	-0.426	-0.004	0.227	0.056	0.534*
	rp							1.000	-0.383	0.072	0.172	0.075	0.334
SPPP	rg								1.000	-0.062	-0.525*	0.255	0.431*
	rp								1.000	-0.034	-0.461*	0.253	0.441*
PL	rg									1.000	0.230	-0.630**	0.355
	rp									1.000	0.084	-0.479*	0.355
HI	rg										1.000	-0.926**	0.757**
	rp										1.000	-0.767**	0.757**
BYP	rg											1.000	-0.163
	rp											1.000	-0.153
GYP	rg												1.000
	rp												1.000

Direct positive effect of some characters indicated that selection of these traits is directly helpful for the improvement of our trait of interest [6, 10]. The indirect effect of germination percentage revealed that the traits total seedling length (2.55) followed by root dry weight (0.5160) exerted positive effect through these traits. First leaf area, shoot length, and root length were indirectly influenced favorably by these two features' total seedling length and root dry weight. This observation highlighted the importance of these two characters for controlling of seedling vigour index in rice. Rajpoot, *et al.*, (2022) [11], Singh and Singh (2022) [14] also agreed with the similar finding. Therefore, the present investigation revealed that total seedling length and root dry weight were the principal vigour determining traits in rice. Hence, these characters should be considered during selection under normal condition in rice.

Conclusion

In conclusion, the study analyzed the relationship between grain yield per plant and various traits in rice using genotypic and phenotypic correlation coefficient and path coefficient analysis. Results showed that grain yield per plant had significant negative correlations with days to 50% flowering and days to maturity, while it had positive correlations with test weight, number of spikelets per panicle, and harvest index.

Path coefficient analysis showed that harvest index, biological yield per plant, and days to 50% flowering had the highest direct positive effects on grain yield per plant. Indirect effects showed that total seedling length and root dry weight were the most important factors determining seedling vigour in rice and should be considered during selection for improving grain yield.

Table-5 Genotypic and phenotypic path matrix of GYP

Traits	Level	DFF	DM	PH	ETPP	FLL	FLW	TW	SPPP	PL	HI	BYP
DFF	G	-0.2057	-0.1912	0.0213	-0.1296	0.0211	-0.0067	-0.0765	-0.0616	-0.0847	-0.0081	0.0591
	P	0.1462	0.1202	-0.0149	0.0851	-0.0122	0.0002	0.0482	0.0393	0.048	0.003	-0.0413
DM	G	0.1519	0.1634	0.0422	0.0593	0.0372	-0.0287	0.0293	0.0416	0.0979	-0.0019	-0.0666
	P	-0.0702	-0.0854	-0.02	-0.0296	-0.0087	0.0133	-0.0143	-0.0201	-0.038	0.0033	0.0289
PH	G	0.0079	-0.0198	-0.0768	0.0138	-0.0496	0.0046	0.0274	-0.0046	-0.0285	-0.0018	0.0139
	P	-0.0007	0.0017	0.0071	-0.0008	0.0036	-0.0003	-0.0019	0.0006	0.002	0.0003	-0.0011
ETPP	G	0.1384	0.0797	-0.0394	0.2197	-0.0131	-0.0469	0.0847	0.0117	0.0134	0.0392	-0.0372
	P	-0.0322	-0.0192	0.0064	-0.0553	0.0051	0.0112	-0.0185	-0.0026	0.0006	-0.0092	0.0072
FLL	G	-0.026	0.0577	0.1635	-0.0151	0.2534	0.0242	-0.0025	0.0231	0.0721	0.0311	0.0101
	P	0.0027	-0.0033	-0.0161	0.003	-0.0321	-0.0048	0.0005	-0.003	-0.0063	-0.0024	-0.0017
FLW	G	0.0138	-0.0745	-0.0255	-0.0906	0.0405	0.4241	0.1676	-0.0528	0.0587	0.0978	0.0528
	P	-0.0001	0.0117	0.0031	0.0153	-0.0113	-0.0751	-0.0245	0.007	-0.0089	-0.0142	-0.0083
TW	G	-0.0316	-0.0152	0.0303	-0.0327	0.0008	-0.0336	-0.0849	0.0362	0.0004	-0.0193	-0.0047
	P	-0.0124	-0.0063	0.0103	-0.0126	0.0006	-0.0123	-0.0376	0.0144	-0.0027	-0.0065	-0.0028
SPPP	G	-0.0286	-0.0244	-0.0058	-0.0051	-0.0087	0.0119	0.0408	-0.0958	0.0059	0.0503	-0.0245
	P	0.0011	0.001	0.0003	0.0002	0.0004	-0.0004	-0.0016	0.0041	-0.0001	-0.0019	0.001
PL	G	-0.294	-0.4279	-0.2645	-0.0436	-0.2033	-0.0988	0.003	0.0441	-0.7142	-0.1641	0.45
	P	0.0248	0.0337	0.0208	-0.0008	0.0148	0.009	0.0055	-0.0026	0.0757	0.0064	-0.0363
HI	G	0.0315	-0.0093	0.0187	0.1431	0.0986	0.185	0.1819	-0.4211	0.1843	0.8024	-0.7434
	P	0.034	-0.0644	0.0722	0.2792	0.1244	0.3192	0.2896	-0.7774	0.1422	1.6849	-1.2917
BYP	G	-0.0011	-0.0015	-0.0007	-0.0006	0.0001	0.0005	0.0002	0.0009	-0.0023	-0.0034	0.0037
	P	-0.3347	-0.4006	-0.1882	-0.155	0.0609	0.1316	0.089	0.2997	-0.567	-0.907	1.1831

Genotypic Path Diagram for GYP

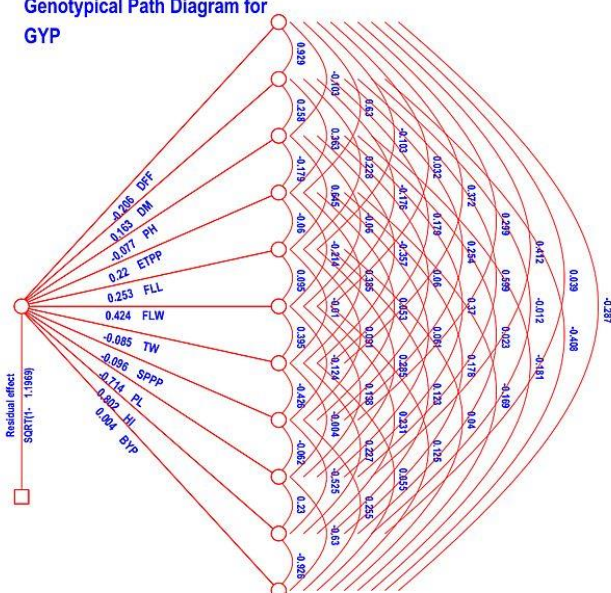


Fig-1 Genotypic path with grain yield per plant

Phenotypic Path Diagram for GYP

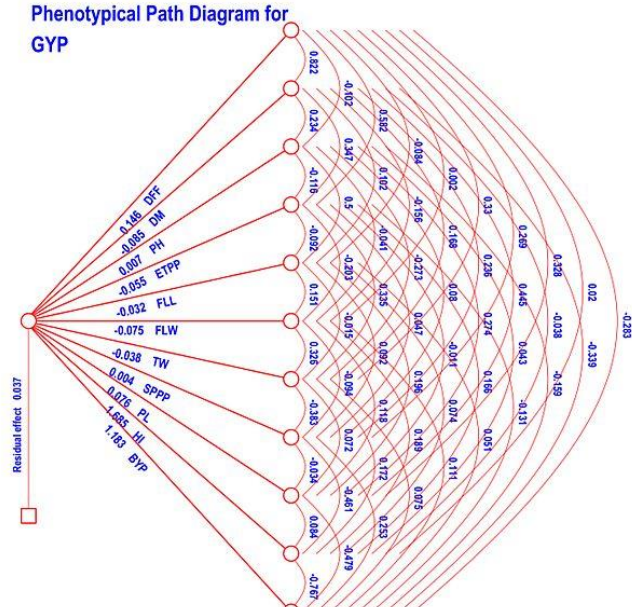


Fig-2 Phenotypic path with grain yield per plant

Application of research: Study on Genetic variability and character association for yield and yield related traits in Rice (*Oryza sativa* L.)

Research Category: Genetic Variability and Correlation

Abbreviations: DFF -Days to 50% flowering, DM- Days to maturity, PH -Plant height, ETPP- No. of effective tillers /plant, FLL- Flag leaf length FLW- Flag leaf width, SPPP- No. of spikelet/panicle, PL- Panicle length, TW- Test weight, HI- Harvest index, BYP- Biological yield per plant, GYP- Grain yield per plant, GCV- Genotypic Coefficient of Variation, PCV- Phenotypic Coefficient of Variation, ECV- Environment Coefficient of Variation h^2 – Heritability, GA- Genetic Advance

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University: AKS University, Satna, 485001, Madhya Pradesh, India
Research project name or number: MSc Thesis

Author Contributions: All authors equally contributed

Author statement: All authors read, reviewed, agreed and approved the final manuscript. Note-All authors agreed that- Written informed consent was obtained from all participants prior to publish / enrolment

Study area / Sample Collection: Agricultural Research farm, AKS University, Satna, 485001, Madhya Pradesh

Cultivar / Variety / Breed name: Rice (*Oryza sativa* L.)

Conflict of Interest: None declared

Ethical approval: This article does not contain any studies with human participants or animals performed by any of the authors.

Ethical Committee Approval Number: Nil

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