Original Research Article   https://doi.org/10.20546/ijcmas.2019.807.153

Genotypic and Phenotypic Correlation and Path Analysis of Yield and Yield Contributing Traits in Rice (*Oryza sativa* L.) under Salinity Condition

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A B S T R A C T

The experimental materials consisted of 49 rice genotypes. The experiment was conducted under saline-alkali soil (pH = 8.9; EC = 2.21dSm^{-1}; ESP = 45%) in randomized complete block design with three replications. In each block 49 entries were accommodated. The spacing between rows to row and plant to plant were 20 cm and 15 cm, respectively. Length of row was 5m and 3 rows of each entry were planted in a plot. The nursery was planted after the period of 30 days. The yield and yield contributing traits were utilized for estimation of correlation coefficients. In general, genotypic correlation coefficients were higher than the corresponding phenotypic correlation coefficients suggesting that strong genetic correlation among the yield and yield contributing components of rice. Correlation coefficient analysis showed that grain yield per plant exhibited significant positive correlation with biological yield per plant at both genotypic and phenotypic levels. Path coefficient analysis revealed that highest positive direct effect on grain yield per plant was exerted by biological yield per plant and harvest-index.

Introduction

Rice is the world's most important food and second most widely cultivated cereal in the world and is a staple food for more than half of the world's population. Rice grain yield being a complex trait, depends upon the various yield contributing traits like grains per panicle, panicle length, spikelets fertility, 1000 grain weight, panicle bearing tillers per plant etc. Character association derived by correlation coefficient which is one of the important biometrical tools for formulating selection indices as it reveals the degree and

direction of association between two or more characters. The type and extent of correlation between the yield and other contributing characters helps in estimating the relative effect of the individual traits on yield improvement thereby enable the breeders to identify desirable traits that play a key role in yield improvement. Knowledge about the relationship between a trait with yield and other yield components would be helpful in selecting proper rice genotypes as parents in breeding programmes. Path analysis furnishes the information of influence of each contributing trait to yield directly as well as indirectly and also enables the breeders to rank the genetic attributes according to their contribution.

The present study is aimed at estimating the association between yield and its components for further improvement to derive high yielding rice genotypes with desirable agronomic traits to attain self-sufficiency and meet the future demand resulting from population growth.

Materials and Methods

The research work was done with 49 advance germplasm of rice of IRRI Table 1. The seed was raised on nursery beds and 30 days old seedlings of each entry was transplanted under irrigated system with three replications in a RBD design during *kharif*, 2016 at Genetics & Plant Breeding farm of N.D. University of Agriculture and Technology, Kumarganj, Ayodhya U.P., India. All the recommended package of practices and need based plant protection measures were followed to ensure healthy crop growth. The data was recorded at maturity on 5 random plants for thirteen different quantitative characters viz., days to 50% flowering, plant height (cm), flag leaf area (cm^2), panicle bearing tillers per plant, panicle length (cm), spikelets per panicle, grains per panicle, spikelet fertility (%), 1000-

grains weight (g), L:B ratio, biological yield per plant (g), harvest-index (%) and grain yield per plant(g) except for days to 50% flowering where data was recorded on plot basis during various phenophases of the crop, whereas, random sample was taken to estimate 1000 grain weight (g) for each entry in each replication. The mean data after computing for each trait was subjected to analysis of variance and estimates of correlations and path coefficients were determined to estimate the type and degree of association among the yield and its characters. Genotypic and Phenotypic correlation coefficients for all the possible comparisons were computed.

Estimation of correlations coefficients

The simple correlation coefficient between different characters was estimated according to Searle (1961) as follows:

Correlation coefficient (r) between characters x and y

$$r_{xy} = \frac{Cov.xy}{\sqrt{(Var.x \times var.y)}}$$

Where,

r_{xy} = Correlation coefficient between characters x and y.

Cov. xy = Covariance between characters x and y.

Var.x = Variance for x character.

Var.y = Variance for y character.

The significance of correlation coefficient was tested by comparing at an appropriate level of significance the significant values of (r) at (n-2) degrees of freedom, where 'n' is number of genotypes.

Estimation path coefficient analysis

Path coefficient analysis was carried out according to Dewey and Lu (1959). The equations used are as follows:

$$r_{iy} = P_{iy} + \sum_{j=1}^{13} r_{ij} P_{jy} \quad \text{for } i = 1,2,\ldots\ldots.13.$$

$$r_{iy} = \sum_{j=1}^{13} r_{ij} P_{jy} \quad \text{for } r_{ii} = 1$$

The above equations can be written in the form of matrix:

$[A]_{13\times1} = [B]_{13\times1} [C]_{13\times1}$

Where,

A is column vector of correlations r_{iy},
B is the correlation matrix of r_{ij}, and
C is the column vector of direct effects, P_{iy}
Residual factor was calculated as follows:

$$P_{xy} = \sqrt{1 - R^2}$$

Where,

$$R^2 = \sum_{j} P_{iy} \, r_{iy}$$

The r_{ij}'s i.e. $r_{1.2}$ to $r_{13.14}$ denote correlations between all possible combinations of independent characters and P_{1y} to P_{13y} denote direct effects of various characters on character y.

r_{iy} = Correlation coefficient between i[th] and y character.

Results and Discussion

Analysis of variance revealed highly significant differences among the genotypes for all the traits studied indicating the presence of considerable amount of variability among the genotypes Table 2.

Estimation of correlation co-efficient among the traits

Calculation of correlation between yield and its traits and among the traits plays an important role in selection of desirable genotypes. Genotypic and phenotypic correlations were in perfect agreement with each other and relatively higher magnitude of genotypic correlations indicated the masking effect of the environment Table 3. Similar results were reported by Ratna *et al.,* (2015) and Kalyan *et al.,* (2017). The grain yield per plant exhibited highly significant associates and positive correlation with biological yield per plant (0.70) followed by harvest-index (%) (0.58) and panicle bearing tillers per plant (0.42).

These results clearly indicated that genotypes with more number of productive tillers per hill and bold grains contribute for more grain yield per plant. These results are in agreement with Ratna *et al.,* (2015) Kumar (2015), Kumari *et al.,* (2017), Sumithra *et al.,* (2019) and Sreedhar and Reddy (2019) for productive tillers per plant, Devi *et al.,* (2016) for biological yield per plant. Harvest index showed significant and positive correlation with panicle bearing tillers per plant (0.27).

The physiological trait biological yield per plant possessed positive and highly significant correlation with grains per panicle (0.41) and positive and significant correlation with spikelets per panicle (0.34) followed by plant height (cm) (0.32) which were supported by Kumari *et al.,* (2017). Grain trait spikelet fertility (%) showed positive and high significant correlation with grains per panicle (0.48) and positive and significant association with panicle bearing tillers per plant (0.28).

Table.1 List of genotypes studied

Sl. No.	Genotypes		Sl.No.	Genotypes	
1	IRSSTN-101	IR 13T106	25	IRSSTN-125	IR11T184
2	IRSSTN-102	IR 89331-19-2-1-2-2-1	26	IRSSTN-126	IR11T189
3	IRSSTN-103	IR 89331-36-2-3-3-2-1	27	IRSSTN-127	IR 86385-194-2-1-B
4	IRSSTN-104	IR 90362-B-22-1-1-2-B	28	IRSSTN-128	IR11T205
5	IRSSTN-105	IR 90384-B-25-2-3-3-3	29	IRSSTN-129	IR 11T208
6	IRSSTN-106	IR 90477-36-3-2-B-B	30	IRSSTN-130	IR 11T213
7	IRSSTN-107	IR 91669-25-2-2-AJY 3	31	IRSSTN-131	IR 86385-84-1-1-B
8	IRSSTN-108	IR 91669-25-2-3-AJY 3	32	IRSSTN-132	IR11T230
9	IRSSTN-109	IR 9168-48-1-1-AJY 2	33	IRSSTN-133	IR11T232
10	IRSSTN-110	IR 91682-6-2-1-1	34	IRSSTN-134	IR12T266
11	IRSSTN-111	IR 91683-27-3-2-AJY 2	35	IRSSTN-135	IR12T210
12	IRSSTN-112	IR 91684-20-3-3-3	36	IRSSTN-136	IR13T144
13	IRSSTN-113	IR 91716-60-BAY 1-1	37	IRSSTN-137	IR13T145
14	IRSSTN-114	IR 91716-60-BAY 1-3	38	IRSSTN-138	IR13T147
15	IRSSTN-115	IR 92831-22-BAY 2-1	39	IRSSTN-139	IR13T148
16	IRSSTN-116	IR 92860-26-CUM 1-2-CMU 3-AJY B	40	IRSSTN-140	A 69-1
17	IRSSTN-117	IR 92860-39-CUM-2-1-CMU 2-AJY B	41	IRSSTN-141	CSR 28
18	IRSSTN-118	IR12T193	42	IRSSTN-142	CSR-90-IR-2
19	IRSSTN-119	IR13T141	43	IRSSTN-143 ©	IR 28
20	IRSSTN-120	IR12T127	44	IRSSTN-144	IR 45427-2B-2-2B-1-1
21	IRSSTN-121	IR12T195	45	IRSSTN-145	IR 55179-3B-11-3
22	IRSSTN-122	IR11T171	46	IRSSTN-146	IR 58443-6B-10-3
23	IRSSTN-123	IR12T147	47	IRSSTN-147	IRRI 147
24	IRSSTN-124	IR11T183	48	IRSSTN-148	IR 66946-3R-178-1-1
			49	-	CSR 43

Table.2 Analysis of variance for randomized block design for13 characters in rice genotypes under salinity condition

Characters	Sources of variation		
	Replications	**Treatments**	**Error**
d.f.	2	48	96
Days to 50% flowering	4.76	3520.49**	237.50
Plant height (cm)	35.74	12010.13**	703.76
Flag leaf area (cm^2)	5.87	2684.45**	184.53
Panicle bearing tillers per plant	1.05	285.07**	260.11
Panicle length (cm)	2.17	579.08**	225.68
Spikelets per panicle	23.48	26690.77**	2426.94
Grains per panicle	71.82	23105.41**	1406.41
Spikelet fertility (%)	8.82	3031.70**	421.83
1000- grains weight (g)	0.06	439.38**	3.97
L:B ratio	0.00	22.72**	0.16
Biological yield per plant (g)	0.58	8729.44**	549.96
Harvest-index (%)	1.29	3814.44**	1108.31
Grains yield per plant(g)	8.87	1371.01**	170.74

*, ** Significant at 5% and 1% probability levels, respectively.

Table.3 Estimate of phenotypic (P) genotypic (G) correlation coefficients between 13 characters of rice genotype in salinity condition

Character		Days to 50% flowering	Plant height (cm)	Flag leaf area (cm^2)	Panicle bearing tillers per plant (cm)	Panicle length (cm)	Spikelets per panicle	Grains per panicle	Spikelet fertility (%)	1000-grains weight (g)	L:B ratio	Biological yield per (g)	Harvest index (%)	Grains yield per plant (g)
Days to 50%	P	1.00	0.14	-0.11	0.12	0.00	0.22	0.31	0.26	-0.03	-0.25	0.19	-0.05	0.12
flowering	G	1.00	0.16	-0.13	0.32	-0.03	0.23	0.32	0.29	-0.02	-0.26	0.22	-0.06	0.15
Plant height	P		1.00	0.06	0.02	-0.11	0.17	0.15	0.00	-0.24	0.12	0.32*	-0.10	0.16
(cm)	G		1.00	0.06	-0.13	-0.17	0.22	0.18	0.01	-0.25	0.12	0.35	-0.19	0.17
Flag leaf area	P			1.00	-0.04	0.11	0.10	0.08	0.00	-0.07	-0.08	-0.08	0.03	0.00
(cm^2)	G			1.00	-0.18	0.10	0.08	0.07	0.00	-0.07	-0.08	-0.07	0.01	-0.01
Panicle bearing	P				1.00	0.00	0.17	0.27	0.28*	0.08	-0.08	0.33*	0.27*	0.42**
tillers per plant	G				1.00	-0.04	0.36	0.57	0.64	0.09	-0.15	0.73	0.25	0.79
Panicle length	P					1.00	-0.19	-0.15	0.03	0.23	0.12	-0.20	-0.03	-0.17
(cm)	G					1.00	-0.32	-0.25	0.04	0.31	0.18	-0.24	-0.08	-0.28
Spikelets per	P						1.00	0.90**	0.07	-0.12	-0.19	0.34*	-0.01	0.31*
panicle	G						1.00	0.92	0.13	-0.12	-0.20	0.40	0.01	0.35
Grains per	P							1.00	0.48**	-0.10	-0.19	0.41**	0.04	0.37**
panicle	G							1.00	0.52	-0.09	-0.20	0.46	0.04	0.41
Spikelet	P								1.00	0.01	-0.05	0.25	0.08	0.24
fertility (%)	G								1.00	0.01	-0.05	0.29	0.10	0.29
1000- grains	P									1.00	-0.12	-0.14	0.23	0.04
weight (g)	G									1.00	-0.12	-0.16	0.27	0.03
L:B ratio	P										1.00	-0.03	0.19	0.09
	G										1.00	-0.03	0.23	0.10
Biological yield	P											1.00	-0.12	0.70**
per plant (g)	G											1.00	-0.13	0.76
Harvest-index	P												1.00	0.58**
(%)	G												1.00	0.56
Grains yield	P													1.00
per plant(g)	G													1.00

*, ** Significant at 5% and 1% probability levels, respectively

Table.4 Estimate of phenotypic (P) genotypic (G) direct and indirect (path coefficient) effect of 13 characters on grains yield per plant in rice salinity condition

Character		Days to 50% flowering	Plant height (cm)	Flag leaf area (cm^2)	Panicle bearing tillers per plant (cm)	Panicle length (cm)	Spikelets per panicle	Grains per panicle	Spikelet fertility (%)	1000-grains weight (g)	L:B ratio	Biological yield per plant (g)	Harvest index (%)	Grains yield per plant (g)
Days to 50% flowering	P	**0.02**	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	**0.12**
	G	**-0.04**	-0.01	0.01	-0.01	0.00	-0.01	-0.01	-0.01	0.00	0.01	-0.01	0.00	**0.15**
Plant height (cm)	P	-0.01	**-0.04**	0.00	0.00	0.00	-0.01	-0.01	0.00	0.01	-0.01	-0.01	0.00	**0.16**
	G	0.06	**0.37**	0.02	-0.05	-0.06	0.08	0.07	0.00	-0.09	0.05	0.13	-0.07	**0.17**
Flag leaf area (cm^2)	P	0.00	0.00	**0.04**	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	**0.00**
	G	-0.03	0.01	**0.22**	-0.04	0.02	0.02	0.02	0.00	-0.02	-0.02	-0.02	0.00	**-0.01**
Panicle bearing tillers per plant	P	0.00	0.00	0.00	**-0.04**	0.00	-0.01	-0.01	-0.01	0.00	0.00	-0.01	-0.01	**0.42**
	G	0.39	-0.15	-0.21	**1.20**	-0.05	0.43	0.69	0.77	0.11	-0.18	0.88	0.30	**0.79**
Panicle length (cm)	P	0.00	0.00	0.00	0.00	**0.02**	0.00	0.00	0.00	0.00	0.00	0.00	0.00	**-0.17**
	G	0.01	0.04	-0.03	0.01	**-0.25**	0.08	0.06	-0.01	-0.08	-0.04	0.06	0.02	**-0.28**
Spikelets per panicle	P	0.11	0.09	0.05	0.09	-0.09	**0.49**	0.45	0.03	-0.06	-0.10	0.17	0.00	**0.31**
	G	-0.07	-0.07	-0.02	-0.11	0.09	**-0.30**	-0.28	-0.04	0.03	0.06	-0.12	0.00	**0.35**
Grains per panicle	P	-0.16	-0.08	-0.04	-0.14	0.08	-0.46	**-0.52**	-0.25	0.05	0.10	-0.21	-0.02	**0.37**
	G	0.06	0.04	0.01	0.11	-0.05	0.18	**0.20**	0.10	-0.02	-0.04	0.09	0.01	**0.41**
Spikelet fertility (%)	P	0.05	0.00	0.00	0.06	0.01	0.01	0.10	**0.20**	0.00	-0.01	0.05	0.02	**0.24**
	G	-0.16	-0.01	0.00	-0.35	-0.02	-0.07	-0.28	**-0.54**	-0.01	0.03	-0.16	-0.05	**0.29**
1000- grains weight (g)	P	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	**-0.01**	0.00	0.00	0.00	**0.04**
	G	0.00	-0.01	0.00	0.00	0.01	0.00	0.00	0.00	**0.03**	0.00	-0.01	0.01	**0.03**
L:B ratio	P	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	**-0.01**	0.00	0.00	**0.09**
	G	-0.04	0.02	-0.01	-0.03	0.03	-0.04	-0.03	-0.01	-0.02	**0.17**	0.00	0.04	**0.10**
Biological yield per plant (g)	P	0.15	0.26	-0.06	0.27	-0.17	0.28	0.33	0.20	-0.12	-0.02	**0.81**	-0.09	**0.70**
	G	-0.01	-0.02	0.00	-0.03	0.01	-0.02	-0.02	-0.01	0.01	0.00	**-0.04**	0.01	**0.76**
Harvest-index (%)	P	-0.03	-0.07	0.02	0.19	-0.02	-0.01	0.02	0.06	0.16	0.13	-0.08	**0.69**	**0.58**
	G	-0.02	-0.06	0.00	0.08	-0.02	0.00	0.01	0.03	0.08	0.07	-0.04	**0.30**	**0.56**

Residual effect = 0.2106.
Bold figures indicate the direct effects.

High significant positive correlations at both genotypic and phenotypic levels were recorded for yield contributing trait grains per panicle with spikelets per panicle which was supported by Kumari *et al.,* (2017).

Estimation of path coefficient

The highest positive direct effect on grain yield per plant was exerted by biological yield per plant (0.81) followed by harvest-index (0.69), spikelets per panicle (0.49), spikelet fertility (%) (0.20) and flag leaf area (cm^2) (0.04). The high direct effect of biological yield per plant possessing highly significant positive association with grain yield per plant highlighted the importance of this trait for rice improvement (Table 4).

Direct positive effect of the aforesaid characters on grain yield indicated that selection of these traits is directly helpful for the improvement of yield. Dwivedi *et al.,* (2012), Rai *et al.,* (2014), Devi *et al.,* (2016), Dubey *et al.,* (2018), Sumithra, *et al.,* (2019) and Saha *et al.,* (2019) have also found high direct contribution of biological yield per plant, flag leaf area and harvest-index on grain yield per plant. Thus, biological yield per plant followed by harvest-index emerged as most important direct contributor towards the grain yield.

Maximum positive indirect effects on grain yield per plant exhibited for spikelet per panicle *via* grains per panicle(0.45) followed by, biological yield per plant (g) *via* grains per panicle(0.33), spikelets per panicle (0.28) and panicle bearing tillers per plant (cm) (0.27) and harvest-index (%) via panicle bearing tillers per plant (cm) (0.19) these were also reported by Devi *et al.,* (2016), Dubey *et al.,* (2018) and Saha *et al.,* (2019). High direct effect along with positive and high indirect effects through other traits provides a better chance for a character to be

selected in breeding programs (Gour *et al.,* 2017). Highest negative direct effect on grain yield per plant was exerted by grains per panicle (-0.52) followed by panicle bearing tillers per plant (-0.04), plant height (cm) these results were in conformity with Devi *et al.,* (2016), Saha *et al.,* (2019) and Sumithra *et al.,* (2019).

Negative direct effect of plant height on grain yield per plant indicated that tallness in rice lowers the yield due to high accumulation of photosynthates in vegetative parts as compared to reproductive parts (i.e. seed formation and grain filling) and lodging susceptibility Zahid *et al.,* 2006.

The yield per plant of the selected genotypes can be increased with reduction in plant height. Highest negative indirect effect on grain yield per plant was exerted by grains per panicle via spikelets per panicle (-0.46) followed by spikelet fertility (%) (-0.25) and biological yield per plant (g) (-0.21) results are in agreement with Devi *et al.,* (2016).

The residual effect determines how best the causal factors account for the variability of the resultant factor the yield per plant. In the present study the residual effect was 0.2106 at phenotypic level.

The reason seems to be very low and non-significant correlation of some traits with yield. Besides, some other factors like sampling error, personal error and geographical position which have not been considered here need to be included in this analysis to account fully for the variation in yield.

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