Trait Association and Path Analysis Studies for Yield Traits in Recombinant Inbred Lines Derived from Cross KP×A-69-1 in Rice (*Oryza sativa* L.)

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ABSTRACT

Studies pertaining to genetic variability, trait association and correlation among yield traits give elementary idea about the amount and direction of genetic association of the traits in the population and devising appropriate breeding methods for further improvement of the crop. This study aimed to estimate coefficients of variability, genetic advance, heritability, trait association and path coefficient analysis among 40 recombinant inbred lines (F_7) derived from biparental cross (KP×A-69-1). These lines were evaluated for yield and its contributing traits in randomised complete block design (RCBD) during *kharif*-2018. High estimates of Genotypic Coefficient of Variations (GCV) and Phenotypic Coefficient of Variations (PCV) were observed for filled grain panicle^{-1} followed by total grain panicle^{-1}, number of effective tillers plant^{-1}, panicle weight and grain yield plant^{-1}. High heritability conjugated with high genetic advance were recorded for plant height and filled grains panicle^{-1}. Panicle weight, filled grain panicle^{-1}, number of effective tillers plant^{-1} and panicle length showed positive and significant ($p ≤ 0.01$) correlation with grain yield plant^{-1}. Path coefficient analysis showed that despite significant and positive correlation of grain yield plant^{-1} with many variables only correlation of panicle weight and number of effective tillers plant^{-1} were verified to have relationship of cause and effect. Overall result gesture towards role of panicle weight, number of effective tillers plant^{-1} and filled grains panicle^{-1} as important variables for use in grain yield plant^{-1} assessment programs as selection indices.

KEYWORDS: Correlation, genetic advance, heritability, path coefficient analysis, rice, yield

Data Availability Statement: Legal restrictions are imposed on the public sharing of raw data. However, authors have full right to transfer or share the data in raw form upon request subject to either meeting the conditions of the original consents and the original research study. Further, access of data needs to meet whether the user complies with the ethical and legal obligations as data controllers to allow for secondary use of the data outside of the original study.

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1. INTRODUCTION

Rice (*Oryza sativa* L.) is a worldwide important cereal crop, and as a most important source of food it accounts for 35–75% of the calorie intake of >3.5 billion humans (Krishnamurthy et al., 2016). The genus *Oryza* (including both cultivated and wild rice species) can grow in diverse climatic conditions and locations from the wettest areas to the driest deserts in the world's geographic distribution extending from 50° N-35° S (Pathak et al., 2018). World's population is increasing and will reach toward 10 billion by 2050, and by then demand for rice will grow faster than other crops. Presently, productivity of rice is increasing at the rate of 1% year⁻¹, which should be increased at the rate of 2.4% to feed the growing population by 2050 (Varshney et al., 2011; Prince et al., 2015; Rejeth et al., 2020). According to FAO, India produced 118.93 mt of milled rice on 45 mha area in the year 2020 (Anonymous, 2020). Uttar Pradesh being key rice producing state has 5.74 mha under rice cultivation, producing 15.52 mt rice during 2020 (Anonymous, 2020). Being a staple food for more than 56% of global population and livelihood source for nearly 40% rural households globally, refining grain yield of this strategic crop has become climacteric (Pathak et al., 2019).

Improvement of yield requires an in-depth knowledge of the magnitude of variation present in the available germplasm, interdependence of quantitative characters with yield, extent of environmental influence on these factors, heritability and genetic gain of the material (Bhargava et al., 2007). Phenotypic coefficient of variation (PCV) provide insight into the role of genotypic as well as environment in the phenotypic expression of the trait while, heritable variability is estimated by the genotypic coefficient of variation (GCV). Other important selection parameters are heritability and genetic advance. During selection, the traits to be taken into consideration are determined by using the estimates of heritability. For predicting the gain under selection and for selecting superior varieties the parameters to be considered are estimates of heritability and genetic advance (Ali et al., 2002; Dey et al., 2021; Vennela et al., 2021). A correlation study provides trustworthy and helpful information about the type, scope, and direction of selection (Zeeshan et al., 2013). The coefficient of correlations aids in determining the level of relationship between two separate traits as well as the level at which these traits are mutually variable (Bocanski et al., 2009; Nagabhushan et al., 2011). Examining this relationship between quantitative traits is an important task of assessing the feasibility of a joint selection of two or more traits instead of selecting the secondary traits as genetic gains for primary traits under consideration (Ezeaku and Muhammad, 2006). Association studies confer an idea about relative contribution of different traits in manifesting yield and magnitude of correlation between yield component and yield and among themselves (Vennela et al., 2021). Consequently, an insight into interrelationships existing amidst yield components is needed, for selection to be effective. Correlation studies alone fails to depict the clear picture with respect to the association among traits. Path analysis determine the yield components, directly or indirectly influencing the yield (Das et al., 2020). The present investigation was undertaken in this context to elucidate information on variability, heritability, genetic advance, character associations and path of effect in forty zinc deficiency tolerant recombinant rice lines (RILs) of F₇ generation. A sound knowledge of genetic resources might also help in identifying promising genotypes for future hybridization program.

2. MATERIALS AND METHODS

The research work was conducted at the research farm of the Institute of Agricultural Sciences, Banaras Hindu University, Varanasi (25.2677° N, 82.9913° E; Altitude - 80.71 m) during the *kharif* (June–November) season of 2018. The field experiment was conducted in randomized complete block design (RCBD) in three replications with a spacing of 10 cm and 15 cm between plants and rows respectively.

2.1. Plant Material and morphological observations

The study comprised of forty F₇ Recombinant Inbred Lines (RILs) derived from the crosses between the two parents Kinandang Patong (high yielding, tropical japonica, sensitive to zinc deficiency tolerance) and A69-1 (indica variety, tolerant to zinc deficiency) by single seed descent method. Recommended package of practices were followed for all the entries in order to raise a good crop. Each F₇ plant was harvested separately and observed for traits like Days to 50% flowering [DF], Days to maturity [DM], Plant height (cm) [PH], Panicle length (cm) [PL], Effective tillers plant⁻¹ [ET], Filled grains panicle⁻¹ [FGP], Unfilled grains panicle⁻¹ [UGP], Total grains panicle⁻¹ [TGP], Spikelet Fertility percentage [SF], Test weight (g) [TW] and Grain yield plant⁻¹ (g) [GYP].

2.2. Statistical analysis of data

The data generated were subjected to analysis of variance (ANOVA) for Randomized Complete Block Design (RCBD) as defined by Panse and Sukhatme (1967). Variability parameter such as mean, range and standard error were calculated as per Singh and Choudhary (1977). Coefficient of variation (such as genotypic and phenotypic variation), heritability and genetic advance were estimated for the different characters as follows. Phenotypic and genotypic coefficient of variation (PCV and GCV) were calculated by the method suggested by Burton and Devane

(1953). PCV and GCV were classified according to Robinson et al. (1966) as follows, 0-10% -Low, 10-20% -Moderate, >20%-High. Heritability is the proportion of genetic variance to the phenotypic variance and expressed in percentage (%). It was calculated by the formula as given by Allard (1990). Heritability percentage was categorized as per scale given by Robinson et al. (1966), as 0-30% -Low, 30-60% -Moderate, >60% -High. The Genetic Advance as percentage of mean was classified as per scale given by Johnson et al. (1955) as 0–10% - Low, 10–20% - Moderate, >20% -High. The correlation coefficients were calculated to determine the degree of association of characters with yield as suggested by Searle (1961). The significance of correlation coefficients was tested against 'r' values given by Fisher and Yates (1963). The path coefficients were obtained according to Dewey and Lu (1959). Grain yield was considered to be dependent variable (effect) which is affected by all other (eleven) independent variables (cause), directly as well as indirectly through other characters. The variation in grain yield unexplained by the traits under consideration was supposed to be contributed by a residual factor which is uncorrelated with other factors.

3. RESULTS AND DISCUSSION

Analysis of variance (ANOVA) for the design of experiment was implied for all the twelve traits studied for appraising 40 treatments. The mean sum of squares due to treatments were found to be significant for all the twelve traits studied (Table 1). Existence of genetic variability is of paramount significance for improvement of any crop. A perusal of GCV and PCV revealed that, GCV and PCV for yield traits were highest for filled grain panicle^{-1} (26.83 and 34.27) followed by total grain panicle^{-1} (20.87 and 27.65) and number of effective tillers plant^{-1} (22.10 and 26.77).

Table 1: Analysis of variance (ANOVA) for twelve (12) yield and yield related traits for 40 Recombinant Inbreds Lines (RILs)

Source of variation	df	Mean sum of squares											
		DF	DM	PH	ET	PL	FGP	UGP	TGP	TW	GYPP	PW	SF%
Replication	2	0.61	6.10	2.73	0.17	11.06	73.95	701.30	1222.33	0.17	23.49	1.78	353.22
Treatment	39	76.97**	87.71**	633.63**	8.61**	34.32**	3065.51**	969.80**	3273.63**	16.03**	27.00**	1.14**	327.00**
Error	78	7.89	8.54	22.67	1.76	4.60	532.84	148.31	658.78	3.43	6.84	0.20	87.89

df: Degree of freedom; DF: Days to 50% flowering; DM: Days to Maturity; PH: Plant height; ET: Number of effective tillers plant^{-1}; PL: Panicle length; FGP: Filled grains panicle^{-1}; UGP: Unfilled grains panicle^{-1}; TGP: Total grains panicle^{-1}; TW: Test weight; GYPP: Grain yield plant^{-1}; PW: Panicle weight; SF %: Spikelet fertility percentage

High GCV and PCV for filled grain panicle^{-1}, total grain panicle^{-1} and number of effective tillers plant^{-1} indicated that selection for these traits would be rewarding. These results are in agreement with Abebe et al. (2017). The GCV and PCV were the lowest for days to maturity (4.45 and 5.11) and days to flowering (5.71 and 6.62). Similarly, Singh et al. (2015) in their studies on 38 germplasm accessions reported highest estimates of GCV and PCV for total grain panicle^{-1} followed by grain yield plot^{-1}, test weight and total number of tillers plant^{-1}, and lowest in spikelet fertility followed by kernel breadth, days to 50% flowering and panicle length. PCV were slightly higher than GCV in case of all the traits, indicating substantial role of environment in the phenotypic expression of these traits. The above results (Table 2) were also evident from the studies of Rashid et al. (2017).

Since mere existence of variability does not guarantee the transmission to the progeny, hence estimates of heritability in broad sense (h^2_{bs}) were also worked out for the traits (Table 2). The parameter contemplates the prospects of phenotype-based selection. The set of the materials studied exhibited moderate to high heritability (broad sense) for all the traits studied as also reported by Fukrei et al. (2011) and Rashid et al. (2017), High heritability does not always guarantee high genetic gain. High heritability combined with high genetic advance is an indicative of additive gene action and selection based on these parameters would be more reliable (Johnson, 1955). Therefore, heritability and genetic advance should be considered together. High heritability conjugated with high genetic advance were recorded for filled grains panicle^{-1}, panicle weight and panicle length. Similar result for these traits was reported by and Fukrei et al. (2011). On the contrary, high heritability and low genetic advance were observed for days to maturity and days to 50% flowering manifesting the preponderance of non-additive gene action and role of genotype×environment interactions in the phenotypic expression of these traits. Similar result was observed by Akinwale et al. (2011) and Singh et al. (2015) for days to maturity.

Trait association studies between yield and yield component are advantageous in selection of desirable plant type for

Table 2: Vvariability parameters for twelve (12) yield and yield related traits among 40 Recombinant Inbreds Lines (RILs)

Traits	DF	DM	PH	ET	PL	FGP
Mean±SE	84.02±1.62	115.57±1.69	110.53±2.75	7.51±0.77	23.42±1.24	108.29±13.33
Range	73.33−94.33	104.33−127.00	83.97−150.43	4.00−13.70	15.47−33.80	55.20−199.67
PCV (%)	6.62	5.11	13.61	26.78	16.27	34.27
GCV (%)	5.71	4.44	12.91	20.10	13.44	26.83
h^2 (%) broad sense	74.50	75.50	90.00	56.40	68.30	61.30
GA as % mean (K=2.06)	10.51	7.96	25.23	31.10	22.87	43.28

Table 2: Continue...

Traits	UGP	TGP	TW	GYPP	PW	SF%
Mean±SE	33.64±7.03	141.47±14.82	23.00±1.07	17.93±1.51	2.68±0.26	76.19±5.41
Range	5.57−88.00	64.93−203.80	16.62−28.43	9.31−23.22	1.44−4.57	51.76−93.49
PCV (%)	61.07	27.65	12.01	20.54	26.76	16.99
GCV (%)	49.19	20.87	8.91	14.46	20.94	11.72
h^2 (%) broad sense	64.90	57.00	55.00	49.60	61.20	47.60
GA as % mean (K=2.06)	81.61	32.44	13.62	20.98	33.76	16.64

effective breeding programme (Das et al., 2020). Yield being complex trait is resultant of multiplicative interaction of different traits referred to as yield components. Hence, genetic architect of yield in rice and other crops is resultant of the balance or overall net effect manifested by various yield components directly or in interaction with one to other. Consequently, identification of significant yield components and information about their association with yield and also with each other is crucial for designing efficient breeding program in order to breed high yielding varieties. Henceforth, correlation coefficient which bestow symmetrical measurement regarding degree of association between two variables or traits assist in elucidating the nature and magnitude of association among yield and yield components. The correlation coefficients with grain yield plant[-1] vis-a-vis other yield components and their all-possible interrelationships are presented in (Figure 1). The grain yield plant[-1] manifested significant positive correlation with panicle weight (0.40**), filled grain panicle[-1] (0.37**), effective tillers plant[-1] (0.32**), panicle length (0.31**), spikelet fertility percentage (0.27**) and plant height (0.25**) (Table 3). This is in consonant with earlier findings on rice with Bhati et al. (2015), Roy et al. (2015) for plant height and filled grains panicle[-1] and Singh et al. (2013) for filled grains panicle[-1]. Total grain panicle[-1] exhibited non-significant but positive correlation with grain yield. These results were in conformity with the previous results of Allam et al. (2015). Similarly, spikelet fertility percentage exhibited significant positive correlation with filled grain panicle[-1] (0.36**), nevertheless, spikelet fertility percentage exhibited negative correlation with unfilled grain panicle[-1] (-0.82**),
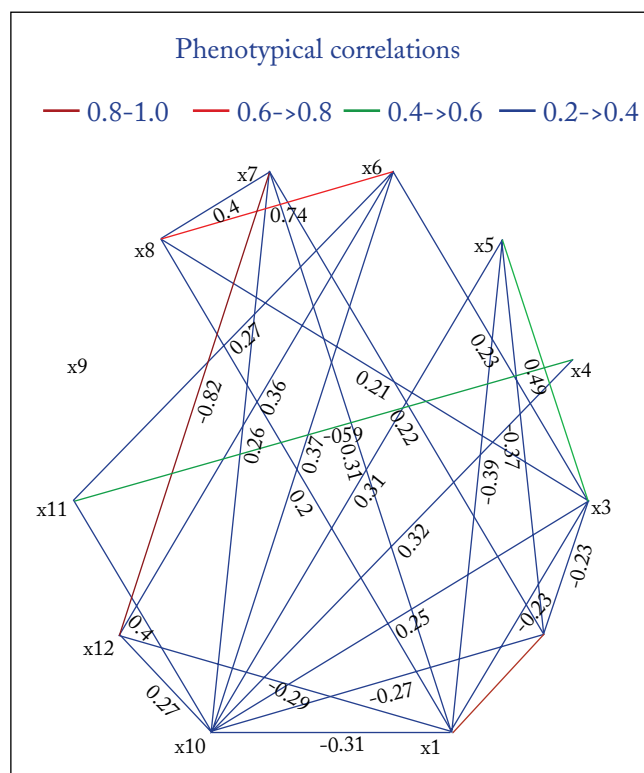

Figure 1: Phenotypic correlations between yield and yield attributing traits

days to 50% flowering (-0. 28%) and days to maturity (-0.18**). Panicle weight showed positive correlation with filled grain panicle[-1] (0.27**). Total grain panicle[-1] showed positive correlation with filled grain panicle[-1] (0.74**), unfilled grain panicle[-1] (0.41**), plant height (0.21*), days to

Table 3: Estimates of phenotypic correlation among yield and yield related traits in rice

Traits	DM	PH	ET	PL	FGP	UGP	TGP	TW	PW	SF%	GYPP
DF	0.89**	-0.23*	-0.18*	0.39**	-0.12	0.31**	0.20*	-0.10	0.11	0.28**	0.31**
DM		-0.25*	0.19*	0.37**	0.11	0.22*	0.16	-0.08	0.18	-0.18*	0.27**
PH			-0.01	0.49**	0.23*	-0.01	0.21*	0.16	0.11	0.04	0.25**
ET				0.16	0.01	0.01	0.01	0.03	0.59**	-0.02	0.32**
PL					0.12	-0.10	0.03	0.15	-0.01	0.13	0.31**
FGP						-0.06	0.74**	-0.18	0.27**	0.36**	0.37**
UGP							0.40**	0.15	-0.09	0.82**	0.26**
TGP								-0.06	0.16	0.01	0.13
TW									0.01	-0.08	-0.02
PW										0.16	0.40**
SF%											0.27**

*: Significant at $p<0.05$; **: Significant at $p<0.01$

flowering (0.20*). Panicle length showed significant positive correlation with days to maturity (0.37**) and plant height (0.49**) while manifested negative correlation with days to flowering (0.39**). Filled grain panicle⁻¹ showed positive correlation with plant height. Plant height manifested significant negative correlation with days to 50% flowering (-0.23*) and days to maturity (-0.25*). Days to 50% flowering manifested significant positive correlation (0.89**) with days to maturity, unfilled grains panicle⁻¹ and highly negative significant phenotypic correlation with the panicle length followed by grain yield panicle⁻¹ and spikelet fertility percentage. The correlation studies provide ample scope for mutual improvement of traits via common selection.

Correlation alone frequently depicts misleading results when more traits are accounted in the correlation study. It might be possible that many of the traits may associate by virtue of mutual association, positive or negative, with other traits. Inclusion of more variables in the correlation studies further complicate their indirect association, thus, perplexing the selections. Under such situations, the path coefficient analysis proves to be an empathic tool for separating direct and indirect cause of association, thus allowing critical analysis of the specific forces operating to produce a given correlation and to appraise the relative proportion of each casual factor. The path coefficient analyses were carried out by using simple correlations between twelve characters to resolve direct and indirect effects of eleven different characters on grain yield plant⁻¹.

Path coefficient analysis taking grain yield a dependent while other traits as independent variable is presented in (Figure 2). Direct and indirect path coefficient values manifest that panicle weight possessed maximum direct effect (0.844**) followed by number of effective tillers plant⁻¹ (0.767**).
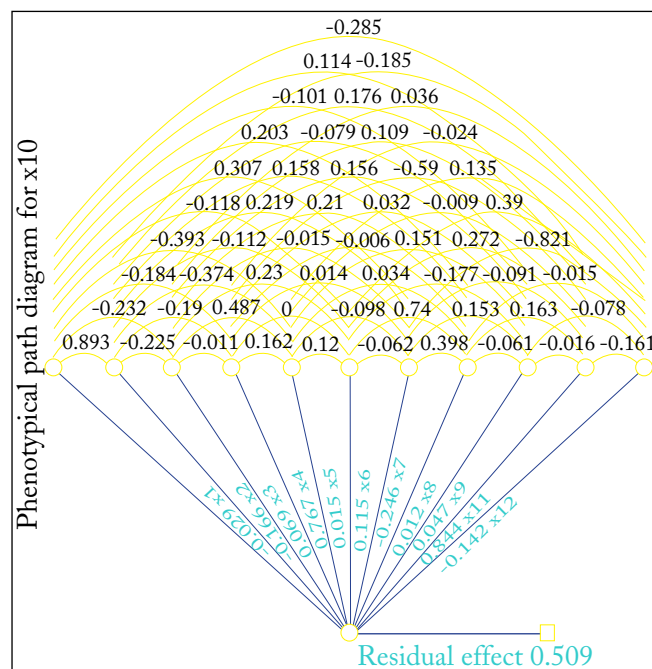

Figure 2: Phenotypic path analysis for different traits (x1: Days to 50% flowering; x2: Days to Maturity; x3: Plant height; x4: Number of effective tillers plant⁻¹; x5: Panicle length; x6: Filled grains panicle⁻¹; x7: Unfilled grains panicle⁻¹; x8: Total grains panicle⁻¹; x9: Test weight; x10: Grain yield plant⁻¹; x11: Panicle weight; x12: Spikelet fertility percentage

Positive direct effects of these traits on grain yield gestures toward their significance in determining yield plant⁻¹. Henceforth, their inclusion in selection targeted to the improvement of grain yield would be rewarding. The other characters viz. plant height, panicle length, filled and total grains panicle⁻¹ also showed positive direct effect but were

found non-significantly correlated with grain yield. These results are in consonant with earlier findings of Chakraborty et al. (2001), Sudeepthi et al. (2020) and Singh et al. (2013) for total grains panicle^{-1}.

Critical analysis of results obtained from character association and path analysis revealed that the panicle weight possessed both positive association and highest positive direct effects at phenotypic level followed by number of effective tillers. Hence, selection for these traits would be fruitful for improvement in yield and component characters. In view of the nature and magnitude of character association and their direct and indirect effects, it can be concluded that simultaneous improvement of grain yield plant^{-1} is possible through manifestation of plant height, number of effective tillers plant^{-1}, panicle weight and number of filled grains panicle^{-1}. Further, the residual effect is 0.509, which is high since the traits contribute only 49.1% to the variability in grain yield plant^{-1}. Therefore, the result calls for inclusion of other traits which have not been studied, to account fully for the variation in grain yield.

4. CONCLUSION

The present study indicated the scope of selection in the improvement of grain yield for the population studied and revealed the role of plant height, number of effective tillers plant^{-1}, panicle weight and number of filled grains panicle^{-1} in devising selection criteria for improving grain yield. It emphasized the need for balanced selection in light of negative correlation of panicle weight with effective tillers plant^{-1} in yield improvement programme in the set of material studied.

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