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Genetic variability, character association and path analysis for yield traits of rice in different water regimes of rice (*Oryza sativa* L.)

Hamsa Poorna Prakash, Suman Rawte, Ritu R Saxena, SB Verulkar and Ravi R Saxena

Abstract
An experiment was conducted with 52 germplasm lines of rice genotypes under three environmental conditions (IR-Irrigated, RF-Rainfed and TSD-Terminal Stage Drought) during *Kharif* 2018 and 2019. Highly significant differences among the genotypes for all thirteen yield traits in three conditions were observed based on pooled data. The highest mean value in IR condition was observed in the trait biological yield. Harvest index and number of filled grains showed high PCV and GCV coupled with high heritability and genetic advance. Harvest index was the only trait to show significant association with grain yield in all the three water regimes. Likewise, biological yield and harvest index reported to have high direct effect on grain yield. Thus, direct the selection of these traits will certainly be rewarding for improving the yield.

Keywords: Rice, PCV and GCV, heritability, genetic advance, correlation, path analysis

Introduction
Rice (*Oryza sativa* L.) is a monocot plant belonging to genus *Oryza* under grass family Poaceae. Rice has the distribution of being the most extensively cultivated crop in the world and important staple food for more than 60% of the world's population. It occupies an important position among food crops under diversified situation. The Asian region produces and consumes around 90% of all rice farmed worldwide. In the world, 85% of the total rice area is in Asia. India is the world's second-largest producer and consumer of rice. Chhattisgarh is renowned as India's "rice bowl," with agriculture providing a living for around 82 percent of the state's inhabitants. Rice is grown on a total of 3.71 million hectares, yielding 7.29 million tons with productivity of 1.96 tons ha^{-1} (Krishi Darshika, 2019) [3]. The critical estimate of nature and magnitude of genetic variability is a prerequisite for any crop improvement program. Variation in population can be attributed to both genetic and environmental factors, as well as the interaction (G x E) between them (Dhavaleshvar *et al*., 2019) [7]. The analysis of genetic parameters namely, phenotypic coefficient of variability (PCV), genotypic coefficient of variability (GCV), heritability and genetic advance for various characters are important pre-requisite for crop improvement (Kishore *et al*., 2015) [13]. Heritability helps to estimate the degree of transmissibility of selected traits (Asante *et al*., 2019) [4]. Heritability of genetic traits is important in determining the response to selection (Tiwari *et al*., 2019) [25]. The broad sense heritability is the ratio of genetic variance to the total variance in the non - segregating population (Dhavaleshvar *et al*., 2019) [7]. Genetic advance also depends on the variation in a population (Asante *et al*., 2019) [4]. High heritability coupled with high genetic advance was reported to be most effective condition for selection of a specific character in a population (Tiwari *et al*., 2019 and Dhavaleshvar *et al*., 2019) [25, 7]. The present study is to estimate genetic variability, heritability and genetic advance among the various quantitative traits of rice genotypes grown under three water stress conditions, irrigated (IR), rainfed (RF) and terminal stage drought (TSD) for the effective selection for successful breeding program (Tiwari *et al*., 2019) [25]. The majority of breeder relevant features are complex, resulting from the interaction of several factors. Understanding the relationship between yield and its components is of importance for making the best use of these relationships in selection. Rice breeding strategy is mostly determined by the degree of related traits, as well as their volume and form of variation (Zahid *et al*., 2006 and Prasad *et al*., 2001) [26, 18]. Correlation coefficient information is usually helpful for breeding program selection. Correlation studies between

yield and its component qualities provide a clearer picture of the relationship between the two. Phenotypic correlation provides the extent to which the two variables are associated and is governed by genotypic and environmental correlation. Path coefficient analysis is a useful method for partitioning direct and indirect matrix correlation (Mohsin *et al*., 2009) [15]. Path analysis also helps in determining the direct and indirect causes of association and formulation of effective breeding strategies for development of better genotypes. The concept of path analysis was first used for plant selection by Dewey and Lu in 1959 [6]. The path coefficient analysis is a standardized partial regression coefficient that divides the correlation coefficient into direct and indirect influence measures. Grafius (1959) [9] suggested that there may not be only one gene for yield per seed, rather for various components, the multiplicative interaction of many genes result in the yield. To enhance the yield productivity, correlation studies between yield and yield components as per requisite to plan a meaningful breeding programme to develop high yielding inbred and hybrids.

Methods and Materials

The experiment was conducted with 52 rice genotypes, including four check varieties at the research farm of Department of Genetics and Plant Breeding, Indira Gandhi Krishi Vishwavidyalaya, Raipur (C.G.) during *Kharif* 2018 and *Kharif* 2019 at Raipur to determine the genetic parameters, correlation and path coefficient in rice considering 13 morphological characters towards yield. This experiment was performed under three different conditions, rainfed (RF) - crop growth entirely depends on the monsoon, irrigated (IR) - controlled condition of crop with all recommended agricultural practices and fertigation; and Terminal Stage Drought (TSD) - in this condition water will be supplied till 21 days of transplanting. In irrigated and TSD condition, twenty-one days old seedlings in both the years were transplanted and in rainfed condition, the seeds were sown directly in the field. Randomized Complete Block with two replications was used in this study having 2 rows with distance of 20 × 20 cm with single plant per hill. The data were pooled across environments and over the years. Thirteen yield attributing traits were evaluated under IR, RF and TSD conditions. The information gathered was subjected to standard statistical procedures. After compiling the data for each character, the data was subjected to the conventional procedure of analysis of variance following Panse and Sukhatme (1967) [17], phenotypic and genotypic coefficient of variation were computed following the methodology outlined by Burton (1952), while the estimates of heritability in broad sense and genetic advance as percent of mean were obtained as per the procedures outlined by Burton and De Vane (1953) and Johnson *et al*. (1955) [11], respectively. The correlation coefficient was calculated Dewey and Lu’s method.

Result and Discussion

The results on analysis of variances (ANOVA) for 13 yield and yield related traits studies are represented in Table 1. The analysis of variance revealed the presence of highly significant differences among all rice accessions for all the yield related traits under all three environmental conditions (IR, RF, and TSD). In all three conditions, indicating the existence of sufficient amount of variation among the genotypes for yield and yield related traits studied in the present experiment. As a result, effective selection is possible.

The estimates of phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV), broad sense heritability (h^2), and genetic advance (GA) are presented in Table 2 indicating the presence of high variability among the varieties**.** Hence, there is a lot of scope for distinct quantitative characters to be chosen for rice improvement. The PCV and GCV provide a measure to compare the variability present in the traits. The magnitude of PCV was higher than the GCV for all 13 traits under all three conditions. PCV and GCV were classified as suggested by Sivasubramanian and Madhavamenon (1973) [23]. PCV and GCV values greater than 20% are considered high, while values between 10% and 20% are considered moderate, and values less than 10% are considered low. Highest value for PCV coupled with GCV were observed in the traits namely, harvest index and number of filled grains in all three conditions. However, number of unfilled grains and total number of grains exhibited high PCV coupled with high GCV only in irrigated condition. Rest all the other traits recorded moderate to low values of PCV coupled with GCV. The present result were closely agree with Prasad *et al*. (2001) [18], Zahid *et al*. (2006) [26], Sahu *et al*. (2017) [19] and Gyawali *et al*. (2018) [10]. For all the characters, the magnitude of PCV were found to be higher than the equivalent GCV, indicating that the environment has an impact on the expression of the trait but has less influence on the traits. As a result, selection only on the basis of phenotype can be helpful in improving features. For majority of the features, however, the differences between PCV and GCV were extremely minor, indicating that environmental variation played a less role in the expression of these traits.

In the selection procedure, broad-sense heritability might be utilized as a predictor (Allard, 1960) [2]. Heritability values more than 70% are regarded as high, whereas values between 70 and 50% to be moderate and values less than 50% are low. In broad-sense heritability, all of the traits showed high heritability in all three conditions except number of tillers. These results are in confirmative with the report of Kishore *et al.* (2015) [13]. The scaling for genetic advance as per cent of mean are categorized as High (>20%), Moderate (10% - 20%) and Low (<10%). High heritability with high genetic advance are exhibited by the traits plant height, flag leaf length, flag leaf width, biological yield, grain yield, harvest index, thousand grain weight, number of filled grains, number of unfilled grains and total number of grains under all three conditions. The two parameters, heritability and genetic advance are helpful for selection to improve grain yield in rice. High heritability coupled with high genetic advance shows additive genetic variance and exhibited by plant height, flag leaf length, biological yield, grain yield per plot, harvest index, thousand grain weight, number of filled grains, number of unfilled grains and total number of grains under all three environmental conditions. However, harvest index and number of filled grains showed high PCV and GCV coupled with high heritability and genetic advance. Similar results were recorder by Tiwari *et al*., 2019 and Dhavaleshvar *et al*., 2019 [25, 7]. High Heritability coupled moderate genetic advance as % of mean depicts the presence of additive and non-additive genetic variance. In the present study, high PCV and GCV coupled with high heritability and genetic advance as per cent of mean indicating the preponderance of additive gene action and therefore scope for improvement of the traits through selection is essential. Similar results were reported earlier by Krishna *et al.* (2009) [14]. Heritability estimates combined with genetic advance are more useful than heritability estimates alone in predicting gain under selection (Johnson *et al*., 1955 and Sinha *et al*., 2004) [11, 22].

The association results for yield attributing traits and their relationship among them are presented in the Table 3. Harvest index is the only trait that is showing significant and positive association with grain yield in all the three water regimes. Number of filled grains and total number of grains showed correlation with grain yield only in irrigated and TSD condition whereas, panicle length exhibited correlation with grain yield in rainfed and TSD condition. The similar results were observed by Nithya *et al*. (2020) [16], Kumar *et al*. (2018) [12]. Phenotypic association is higher than the genotypic association which indicates the correlation between the traits is not only due to genetic effect but also due to favourable interference of the environment. Positive or negative association between any two traits remain same in parental and segregating population that means correlation is due to pleiotropic effect, when it becomes changed in segregating population depicts that correlation is due to linkage only. The results of phenotypic path coefficient for grain yield as dependent trait is showed in the table3. High to very high direct effects was recorded by biological yield and harvest index in all the three conditions. However, number of filled grains and total number of grains recorded high direct effects in irrigated and TSD condition only. Similar results were reported by Singh *et al*. (2018) [21], Babu *et al*. (2012) [5] and Swapnil *et al*. (2020) [24]. Residual effects are fewer at phenotypic level indicate that maximum characters are covered for the estimation of path coefficient analysis except for some traits. Some traits had positive direct effect but were unable to contribute towards grain yield due to some negative indirect effect of other traits. In this study, association between grain yield and the traits like harvest index and biological yield is due to higher heritability and higher genetic advance as per cent of mean. Hence, it shows that the actual relationship between them and direct selection for such character will be effective for grain yield. By withholding irrigation for 25 days, drought stress was produced from the panicle initiation stage. Drought stress is one of the most significant environmental stresses that plants face (Serraj *et al*., 2009) [20]. Drought stress has been proven to impact a variety of physiological processes in plants, as well as induce morphological and physiological responses. This facilitates plant adaptation to a variety of environmental conditions (Nithya *et al*., 2020) [16]. In the study, the grain yield production will be more in irrigated condition when compared to rainfed and TSD conditions. This is because under irrigated condition, there will be no drought stress imposed and proper irrigation facility along with complete agronomical practices will be provided being a controlled environment. Conversely, under rainfed and TSD condition, during the panicle initiation and vegetative growth stages the drought stress will be imposed on them. As a result of this, the grain filling would be reduced and the number of unfilled grains would be more in number.

Table 1: Pooled Analysis of variance of studied traits in 52 rice cultivars under three (irrigation, rainfed and TSD) conditions

Condition	SV	DF	DTF	PH	FLL	FLW	NT	PL	BY
IR	Rep	1	1.163	8.470**	0.345	0.093**	613.041**	9.620**	1,215.610
	Gen	51	180.679**	763.028**	37.315**	0.089**	1,024.880**	18.526**	205854.320**
	Error	51	1.967	2.400	0.485	0.002	196.252	0.431	1,893.510
RF	Rep	1	2.618	0.038	15.292**	0.072**	315.880*	2.236**	868.850**
	Gen	51	107.419**	318.561**	31.473**	0.016**	1,089.370**	10.486**	9,231.320**
	Error	51	2.971	5.413	1.166	0.002	198.754	0.631	371.435
TSD	Rep	1	4.445**	0.868	2.292**	0.001	93.765	0.261	24,103.000**
	Gen	51	110.755**	353.524**	38.216**	0.061**	832.997**	5.294**	8,651.320**
	Error	51	1.778	7.182	1.154	0.002	216.529	0.758	1,070.330

* Significant at 5% and ** Significant at 1% probability level

Condition	SV	DF	GY	HI	TGW	NFG	NUFG	TNG
IR	Rep	1	607.711**	2.313	8.356**	17.188	125.093**	49.542
	Gen	51	2,802.400**	101.221**	41.033**	1,010.370**	152.228**	1564.050**
	Error	51	219.569	1.759	1.263	31.272	25.926	66.157
RF	Rep	1	7.495	8.927*	4.120	2,350.870**	7.383	2,743.630**
	Gen	51	428.334**	65.992**	39.474**	677.353**	81.990**	744.247**
	Error	51	46.997	5.253	2.661	45.500	13.755	60.477
TSD	Rep	1	653.054**	120.271**	0.232	5.594	5.198**	21.576
	Gen	51	865.057**	45.101**	76.889**	454.089**	46.151**	463.231**
	Error	51	53.533	4.550	0.900	27.637	1.834	28.878

* Significant at 5% and ** Significant at 1% probability level

IR = irrigated; RF = rainfed and TSD = terminal stage drought

DTF= days to 50% flowering, PH= plant height (cm), FLL= flag leaf length (cm), FLW= flag leaf width (cm), NT= number of tillers m^2, PL= panicle length (cm), BY= biological yield per plot (g), GY= grain yields per plot (g), HI= harvest index (%), TGW=thousand grain weight (g), NFG= number of filled grains per panicle, NUFG= number of unfilled grains per panicle, TNF= total number of grains per panicle

Table 2: Pooled Mean and variability parameters for thirteen yield and yield attributing traits in three different water regimes during wet season *Kharif* 2018 and 2019

Trait	Parameter	IR	RF	TSD	Trait	IR	RF	TSD
DTF	Mean	107.30	98.23	92.65	GY	283.58	69.93	110.74
	Range	81.75-119.00	74.00-109.75	75.25-104.00		215.40-361.60	43.96-104.95	58.57-150.36
	CV	8.85	7.46	8.03		13.20	20.93	18.78
	PCV	8.90	7.56	8.09		13.70	22.04	19.35

	GCV	8.80	7.35	7.96		12.67	19.74	18.18
	h^2	97.84	94.61	96.84		85.46	80.22	88.34
	GA %	17.95	14.741	16.15		24.13	36.43	35.21
	Mean	130.88	102.30	110.29		18.80	19.99	21.12
	Range	84.20-160.65	68.85-132.65	73.00-132.35		12.87-51.68	8.54-39.29	10.57-34.80
	CV	14.92	12.34	12.05		37.82	28.73	22.48
PH	PCV	14.94	12.44	12.17	HI	38.15	29.85	23.58
	GCV	14.89	12.23	11.93		37.49	27.56	21.31
	h^2	99.37	96.65	96.01		96.58	85.25	81.67
	GA %	30.59	24.77	24.08		75.90	52.43	39.67
	Mean	32.18	30.128	32.34		28.65	22.61	27.43
	Range	23.67-46.63	21.20-39.59	23.19-44.09		20.39-41.06	16.99-37.25	12.57-39.60
	CV	13.42	13.17	13.51		15.80	19.65	22.60
FLL	PCV	13.51	13.40	13.71	TGW	16.04	20.30	22.73
	GCV	13.33	12.92	13.30		15.56	18.97	22.47
	h^2	97.43	92.85	94.13		94.02	87.36	97.68
	GA %	27.11	25.64	26.59		31.08	36.53	45.75
	Mean	1.51	1.335	1.402		98.15	82.69	85.13
	Range	1.08-1.97	1.05-1.50	1.00-1.92		58.47-146.45	48.40-115.49	55.63-124.97
	CV	13.96	6.61	12.49		22.89	22.25	17.70
FLW	PCV	14.09	7.07	12.73	NFG	23.25	22.98	18.23
	GCV	13.83	6.10	12.24		22.54	21.49	17.15
	h^2	96.42	74.52	92.41		93.99	87.41	88.52
	GA %	27.98	10.85	24.24		45.02	41.39	33.24
	Mean	188.29	123.28	173.83		30.47	37.19	24.80
	Range	152.50-242.50	68.75-155	108.75-223.13		17.31-72.71	25.38-56.20	11.68-38.42
	CV	12.02	18.93	11.74		28.62	17.21	19.36
NT	PCV	13.12	20.58	13.17	NUFG	30.96	18.60	19.74
	GCV	10.81	17.11	10.10		26.07	15.70	18.97
	h^2	67.85	69.14	58.73		70.89	71.26	92.35
	GA %	18.34	29.32	15.94		45.22	27.30	37.56
	Mean	25.46	24.40	23.89		128.63	119.87	109.94
	Range	19.30-30.99	18.65-29.40	21.15-27.79		76.40-216.52	85.04-155.43	80.16-153.28
	CV	11.95	9.38	6.81		21.74	16.09	13.84
PL	PCV	12.08	9.66	7.27	TNG	22.19	16.73	14.26
	GCV	11.81	9.09	6.30		21.27	15.42	13.40
	h^2	95.45	88.65	74.96		91.88	84.96	88.26
	GA %	23.76	17.64	11.24		42.01	29.28	25.94
	Mean	1633.00	365.79	540.15				
	Range	705.60-2102.10	189.00-522.60	378.05-659.45				
	CV	19.64	18.57	12.18				
BY	PCV	19.73	18.94	12.90				
	GCV	19.55	18.19	11.39				
	h^2	98.17	92.26	77.98				
	GA %	39.91	36.00	20.73				

CV= coefficient of variation, PCV= phenotypic coefficient of variation, GCV= genotypic coefficient of variation, h^2= broad sense heritability, GA %= genetic advance as percent of mean, DTF= days to 50% flowering, PH= plant height (cm), FLL= flag leaf length (cm), FLW= flag leaf width (cm), NT= number of tillers per m^2, PL= panicle length (cm), BY= biological yield/plot (g), GY= grain yields per plot (g), HI= harvest index (%), TGW=thousand grain weight (g), NFG= number of filled grains per panicle, NUFG= number of unfilled grains per panicle, TNF= total number of grains per panicle

Table 3: Phenotypic Correlation and Direct effect of grain yield and yield attributing traits under different conditions

Traits	Phenotypic Correlation and Phenotypic Path (direct effects) with grain yield					
	Irrigated		Rainfed		TSD	
	Correlation	Path	Correlation	Path	Correlation	Path
DTF	-0.062	-0.128	0.075	-0.012	0.335**	0.030
PH	-0.225*	-0.180	0.153	0.116	-0.032	-0.033
FLL	0.180	0.204	0.150	0.028	-0.099	-0.036
FLW	-0.061	0.047	0.031	0.033	0.011	0.038
NT	0.130	0.007	0.016	-0.083	-0.111	-0.016
PL	-0.136	0.061	0.241*	0.033	-0.231*	-0.053
BY	0.024	1.068	0.099	0.840	0.110	0.642
HI	0.455**	1.236	0.648**	1.190	0.780**	1.088
TGW	0.019	-0.110	-0.082	0.041	-0.114	-0.016
NFG	0.266**	1.813	0.062	-0.096	0.248*	1.355
NUFG	0.158	0.699	-0.228*	-0.072	0.153	0.474
TNG	0.265**	-2.109	-0.021	0.163	0.293**	-1.371
Residual effect		0.299		0.113		0.043

* Significant at 5% and ** Significant at 1% probability level
DTF= days to 50% flowering, PH= plant height (cm), FLL= flag leaf length (cm), FLW= flag leaf width (cm), NT= number of tillers per m^2, PL= panicle length (cm), BY= biological yield per plot (g), GY= grain yields per plot (g), HI= harvest index (%), TGW=thousand grain weight (g), NFG= number of filled grains per panicle, NUFG= number of unfilled grains per panicle, TNF= total number of grains per panicle

Conclusion

Developing rice varieties with high yield is quite essential to combat the hunger of the ever increasing population. Crop improvement can be done by selecting independent traits which directly or indirectly enhance the yield ultimately. Thus, in our study, we found that traits namely, harvest index and number of filled grains showed high PCV and GCV coupled with high heritability and genetic advance. Harvest index was the only trait to show significant association with grain yield in all the three water regimes. Likewise, biological yield and harvest index reported to have high direct effect on grain yield. Thus, direct the selection of these traits will certainly be rewarding for improving the yield.

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