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Research Article

GENETIC VARIABILITY AND ASSOCIATION ANALYSIS OF RICE LINES DERIVED FROM BIPARENTAL PROGENY

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Abstract- The sixty-nine advanced rice lines were evaluated for heritability, genetic advance in per cent of mean, character associations and path coefficients. The highest genotypic coefficient of variation (GCV) was found for filled grain per panicle. High heritability with high genetic advance was obtained in filled grains per panicle, grain yield per plant and spikelet fertility percentage which is indicative of additive gene action. The correlation analysis revealed that the grain yield per plant had highly significant association with the effective number of tiller per plant and spikelet fertility. Days to 50 per cent flowering recorded significant correlation with days to maturity at both genotypic and phenotypic level. This implies that selection for these characters would lead to simultaneous improvement of grain yield. The effective tillers per plant, spikelet fertility percentage and filled grain per panicle had the positive direct effect and significant contribution to the grain yield while the grain per panicle had recorded negligible contribution via direct effect to grain yield but high correlation via indirect effect on spikelet fertility percentage. These results showed the positive and significant increase in grain yield whenever there was an increase in these characters. Hence, all the said characters could be considered as main criteria for selection for higher yield as these were mutually and directly associated with grain yield.

Keywords- Variability, Correlation, Heritability, Path coefficients, Rice (*Oryza sativa* L).

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Introduction

Rice is the second largest produce cereal in the world in 158.3-million-hectare area with annual production of about 685.24 million metric tons. Rice is the staple food for over one third of the world's population and more than ~ 95% is produced and consumed in Asian countries. Asia accounts the largest production totalling to about 144.25 million tonnes whereas Africa produces approximately 11.58 million tons [1]. As the demand of rice is increasing day by day, there is a continuous need to produce new varieties with higher yields through various genetic approaches and selection of genotypes. A wide range of genetic variability has been reported for yield traits in the past, but still there exists genetic variability in the genotypes which is of paramount importance in selecting the potential parents as to get maximum heterosis and superior recombinants [2]. Yield is a complex trait, which is highly influenced by the environment, hence direct selection for yield alone limit the selection efficiency and ultimately results in limited success in yield improvement. Enhancement of yield is the major breeding objective in rice breeding programmes and knowledge on the nature and magnitude of the genetic variation governing the inheritance of quantitative traits yield and its components is essential. Therefore, effective improvement in yield may be brought about through selection of yield component characters. Correlation is the measure of mutual relationship between two variables and measures the degree of closeness and the linear relationship between them. Path analysis facilitates the partitioning of correlation coefficients into direct and indirect effects of various traits on yield. Plant Breeder has to find significant correlations among yield and its component traits to predict the superior cross combinations and to select ideal plant type [3]. Therefore, path coefficient analysis is one of the techniques utilized to have an idea of direct and indirect contribution of a trait towards the end product. The present study was undertaken in this context to elucidate information on variability, heritability, genetic advance, character associations and path coefficient in promising rice lines. A good knowledge of genetic resources might also help in identifying desirable lines for future hybridization program.

Material and Methods

Experimental material and plan of work

The study comprised of sixty-nine advance lines derived from the cross HUR 105 and how many IR64 *Sub1* which was carried out during kharif 2016-2017 at Agricultural Research Farm, Institute of Agricultural Sciences, Banaras Hindu University, Varanasi. Each line was grown in three replications. Observations were taken for ten randomly selected plants from each entry for Days to 50% flowering, Days to maturity, Plant height, No. of Effective tillers per plant, Panicle length, Grains per panicle, Fertile spikelet, Test weight, Filled grains per panicle, Spikelet Fertility percentage and Grain yield per plant. The plants were selected from the middle rows to minimise the border effect.

Statistical Analysis

Analysis of variance was carried out by following the procedure of [4] for each of the sixty-nine lines. Phenotypic and Genotypic coefficients of variation were calculated by using the formula given by [5]. The genetic advance, i.e. expected genetic gain resulting from superior plants was estimated by the following formula suggested by [6]. The phenotypic correlation coefficients among the characters were calculated according to the formula suggested by [7]. Path-coefficient analysis was done to partition the total correlation into direct and indirect effects due to the dependent variable [8] suggested this analysis and it was further elaborated by [9].

Results and Discussion

Analysis of variance and genetic parameters

It is evident from the analysis of variance that the treatment differences given to the sixty-nine advance lines were highly significant for the entire quantitative traits [Table-1]. This result is similar to [10, 12]. The extent of variability for character is very important for the improvement of a crop through breeding. The estimates of genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability (h^2) and genetic advance (GA) for different characters have been presented in [Table-2]. Phenotypic coefficient of variation was highest for grain yield per plant (21.09) and lowest was exhibited by panicle length (1.64). The genotypic coefficient of variation filled grains per panicle (16.63) was the highest and lowest value was obtained by days to maturity (1.26). Among the eleven characters studied, grain yield per plant, filled grains per panicle, spikelet fertility percentage and number of effective tillers showed moderate PCV and GCV values, while remaining characters showed low PCV and GCV values. Similar observation was reported by [13,14,15]. It is well known that the heritability (broad sense) helps to estimate the contribution of genotypic variance in phenotypic variance. Heritability estimates were found to be the maximum for filled grains per panicle (75.77%) and lowest was obtained by spikelet fertility (22.39%). Similar results were observed by [16, 17] for the number of filled grains per panicle. For meaningful genetic progress in crop improvement programmes, the selection for characters should be based on the high heritability coupled with the high genetic advance. The highest genetic advance was observed for filled grains per panicle (33.99) and lowest was found in spikelet fertility (0.18). High heritability with high genetic advance was obtained in filled grains per panicle, grain yield per plant and spikelet fertility percentage which is indicative of additive gene action. Similar observations were also obtained by [18, 19] for grain yield per plant.

Table-1 *Analysis of variance (ANOVA).*

		Mean sum of square										
Source	**df**	**DF**	**DM**	**PH**	**NT**	**PL**	**GP**	**SF**	**TW**	**FG**	**SF%**	**GYP**
Replication	2	0.25	18.30	11.76	0.87	0.16	57.43	0.004	5.20	49.89	34.67	18.85
Treatment	68	20.47***	16.77***	67.94***	3.27***	2.72***	541.71***	0.23**	3.82***	1192.99***	248.10***	54.90***
Error	136	7.28	8.01	32.87	1.12	1.11	150.08	0.12	1.91	114.93	68.46	10.01

** Significance at p<0.01.

Days to 50 per cent flowering (DF), Days to maturity (DM), Plant height (PH), No. of Effective tillers per plant (NT), Panicle length (PL), Grains per panicle (GP), Fertile spikelet (SF), Test weight (TW), Filled grains per panicle (FG), Spikelet Fertility percentage (SF%) and Grain yield per plant (GYP).

Table-2 *Variability parameters for eleven traits*

Traits / Parameter		DF	DM	PH	NT	PL	GP	SF	TW	FG	SF%	GYP
Range	**Min**	95.33	129.33	116.70	10.13	22.00	143.43	9.47	18.92	63.60	41.29	9.07
	Max	107.67	141.00	142.67	14.87	26.60	208.90	11.53	27.68	147.60	86.28	39.18
Mean		104.08	135.34	124.11	12.50	24.38	168.90	10.95	23.06	113.93	67.08	23.69
SEM(±)		1.54	1.62	3.28	0.60	0.60	7.02	0.20	0.79	6.14	4.74	1.81
Phenotypic variance		11.68	10.92	44.56	1.84	5.26	280.62	0.16	2.55	474.29	128.34	24.97
Genotypic variance		4.39	2.91	11.69	0.71	0.52	130.54	0.03	0.63	359.35	59.88	14.96
Environmental variance		7.28	8.01	32.87	1.12	1.11	150.08	0.12	1.91	114.93	68.46	10.01
PCV (%)		3.28	2.44	5.37	10.84	1.64	9.91	3.69	6.92	19.11	16.88	21.09
GCV (%)		2.01	1.26	2.75	6.75	3.00	6.76	1.75	3.46	16.63	11.53	16.32
ECV (%)		2.59	2.09	4.62	8.48	4.32	7.25	3.25	6.03	9.41	12.33	13.35
Heritability (%)		37.63	26.65	26.23	38.81	32.59	46.52	22.39	24.95	75.77	46.66	59.90
Genetic advance	**5%**	2.65	1.81	3.60	1.08	0.86	16.05	0.18	0.82	33.99	10.88	6.16
K=2.06	**1%**	3.39	2.32	4.62	1.39	1.10	20.57	0.24	1.05	43.56	13.95	7.90
Genetic advance	**5%**	2.54	1.34	2.90	8.67	3.53	9.50	1.70	3.56	29.83	16.23	26.02
(% of mean)	**1%**	3.26	1.71	3.72	11.11	4.53	12.18	2.18	4.56	38.23	20.08	33.35

Correlation coefficient

The phenotypic and genotypic correlation coefficients between yield and its related characters were estimated and the results are presented in [Table-3]. The correlation analysis revealed that the grain yield per plant had positive and highly signification association with the effective number of tillers per plant and spikelet fertility. Days to 50 per cent flowering recorded significant positive correlation with days to maturity followed by test weight at genotypic and phenotypic level. Day to maturity showed significant negative correlation with filled grains per panicle and spikelet fertility percentage. The filled grains per panicle and fertile spikelet were observed to be highly significant with spikelet fertility percentage. The genotypic correlation coefficients for most of the trait were found to be higher than phenotypic correlation coefficients which indicated that a strong inherent association among themselves and with grain yield per plant. Results are very close to the findings of [20, 21]. The results suggested that effective number of tillers and spikelet fertility may be taken into account in rice breeding programme for high yield and better improvement of the rice variety.

Path analysis

Associations of characters determined by correlation coefficient may not provide an exact picture of the relative importance of direct and indirect influence of each of yield components on grain yield per plant. In order to find out a clear picture of the interrelationship between grain yield and other yield attributes, direct and indirect effects were worked out using path analysis at both genotypic and phenotypic level. The effective tillers per plant (2.26), spikelet fertility percentage (1.07) and filled grains per panicle (0.66) had the positive direct effect and also significant contribution to the grain yield per plant while the trait grains per panicle (-0.93) had recorded negligible contribution via direct effect to grain yield but high correlation via indirect effect on spikelet fertility percentage [Table-4].These findings were in agreement with [22] for effective number of tillers, [23] for spikelet fertility, [24] for filled grains per panicle. These characters could be considered as main criteria for selection of higher yield as they were mutually and directly associated with grain yield. The residual effect (1.37) indicated that there may be few more characters which could have been included for estimation of direct and indirect contribution towards grain yield per plant. The strong positive association of number of effective tillers with grain yield per plant was mainly through its direct effect.

Conclusion

Among the sixty-nine rice lines, the HUR Sub-1-30 recorded highest mean performance for the grain yield per plant followed by HUR Sub-1-20 and HUR Sub1 6. HUR Sub-1-6 also showed highest mean performance in plant height. These lines which show good yields and other yield components would be more suitable for the direct selection and hybridization in order to make the desirable rice improvement programme

Table-3 *Genotypic and phenotypic correlation coefficients among different pairs of yield and yield contributing characters for different genotypes of rice*

Sl no.	Character		Days to 50% flowering	Days to Maturity	Plant Height cm	Effective tillers per plant	Panicle length	Grains per panicle	Fertile spikelet	Test weight	Filled grains per panicle	Spikelet fertility %	Grain yield per plant
1	Days to 50% flowering	Rg	**1**	0.90***	0.39**	0.23	-0.30*	-0.14	-0.47***	0.46***	-0.50***	-0.65***	-0.07
		Rp	1	0.33***	0.05	0.07	-0.13	-0.06	-0.14*	0.24***	-0.22**	-0.21**	-0.05
2	Days to Maturity	Rg		1	0.31*	0.25*	-0.46***	0.01	-0.26*	0.46***	-0.68***	-0.70***	-0.13
		Rp		1	0.17*	0.12	-0.15*	0.03	-0.19**	0.14*	-0.25***	-0.26***	0.02
3	Plant Height (cm)	Rg			1	0.11	-0.53***	-0.09	-0.08	0.33**	-0.57***	-0.51***	0.08
		Rp			1	0.03	-0.09	-0.03	0.02	0.07	-0.19**	-0.21	0.02
4	Effective tillers per plant	Rg				1	-0.35**	0.02	-0.79***	0.01	-0.16	-0.41***	0.53***
		Rp				1	-0.12	0.10	-0.12	0.06	-0.06	-0.12	0.23*
5	Panicle length	Rg					1	0.04	0.38**	-0.45***	0.33**	0.18	-0.13
		Rp					1	0.06	-0.02	-0.11	0.05	0.04	0.02
6	Grains per panicle	Rg						1	0.38**	0.25*	0.57***	-0.05	0.16
		Rp						1	0.02	0.05	0.30***	0.03	0.19
7	Fertile spikelet	Rg							1	-0.15	0.32**	0.43***	-0.03
		Rp							1	-0.00	0.21**	0.22**	-0.15
8	Test weight	Rg								1	-0.19	-0.34**	-0.06
		Rp								1	-0.0955	-0.10	0.00
9	Filled grains per panicle	Rg									1	0.84***	0.26*
		Rp									1	0.53***	0.14
10	Spikelet fertility	Rg										1	0.35**
		Rp										1	0.15
11	Grain yield per plant	Rg											1
		Rp											1

** Significance at p<0.01. **Rg** : Genotypic correlation coefficient, **Rp** : Phenotypic correlation coefficient

Table-4 *Estimate of genotypic matrix of Direct and Indirect effect on grain yield per plant*

Sl no.	Character	Days to 50% flowering	Days to Maturity	Plant Height cm	Effective tillers per plant	Panicle length	Grains per panicle	Fertile spikelet	Test weight	Filled grains per panicle	Spikelet fertility %	Grain yield per plant
1	Days to 50% flowering	**-0.24**	-0.22	-0.09	-0.05	0.07	0.03	0.11	-0.11	0.12	0.15	**-0.07**
2	Days to Maturity	0.87	**0.96**	0.29	0.24	-0.44	0.01	-0.25	0.44	-0.65	-0.67	**-0.13**
3	Plant Height (cm)	0.32	0.25	**0.83**	0.09	-0.45	-0.08	-0.07	0.27	-0.48	-0.43	**0.08**
4	Effective tillers per plant	0.52	0.57	0.26	**2.26**	-0.80	0.05	-1.80	0.03	-0.38	-0.94	**0.53*** **
5	Panicle length	-0.25	-0.38	-0.44	-0.29	**0.82**	0.03	0.32	-0.37	0.27	0.15	**-0.13**
6	Grains per panicle	0.13	-0.01	0.09	-0.02	-0.04	**-0.93**	-0.35	-0.23	-0.53	0.04	**0.16**
7	Fertile spikelet	-0.68	-0.37	-0.12	-1.14	0.55	0.55	**1.43**	-0.21	0.46	0.61	**-0.03**
8	Test weight	0.29	0.28	0.20	0.00	-0.28	0.15	-0.09	**0.61**	-0.12	-0.21	**-0.06**
9	Filled grains per panicle	-0.33	-0.45	-0.38	-0.11	0.22	0.38	0.21	-0.13	**0.66**	0.55	**0.26***
10	Spikelet fertility	-0.70	-0.75	-0.55	-0.44	0.20	-0.05	0.46	-0.37	0.90	**1.07**	**0.35****

Residual Effect = SQRT (1-1.37)

Application of research: Analysis of variance and genetic parameters of rice

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