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Genetic analysis of high: Temperature stress on rice plant and its traits related to yield

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Abstract

In the present investigation, eighty-seven rice genotypes were assessed for genetic variability and correlations between yield and yield components in summer season. Analysis of variance revealed that existence of significant difference for all the traits under study, indicating the presence of sufficient amount of variability. Highest PCV and GCV were recorded for filled grains per panicle followed by grain yield per plant, total grains per panicle and biological yield per plant. High heritability coupled with high genetic advance as percent of mean was found in days to 50% flowering followed by flag leaf area, total grains per panicle and filled grains per panicle. Grain yield per plant exhibited positive and highly significant correlation with biological yield per plant, filled grain per panicle, tillers per plant, effective tillers per plant, total grains per panicle, spikelet fertility and harvest index. Selection of plants on the basis of these traits would certainly lead to improvement in grain yield.

Keywords: Genetic variability, heritability, PCV, GCV, Genetic advance

Introduction

Rice (*Oryza sativa* L.) is the staple food for over half the world's population. Asian countries produce 89 percent of world's rice and 50% of the population depends on rice for food (FAO, 2016). The optimum temperature for rice cultivation is between 25° C to 35° C, and in temperate regions rice growth is impressed by limited period that favours its growth (Zhao *et al.*, 2012). It has been revealed that 7-8% rice yield decline for each 1°C increase in daytime temperature from 28°C to 34°C (Baker *et al.*, 1992).Rice yields are estimated to be reduced by 41% as a result of high temperature by the end of 21 century. The decline in grain yield and quality of rice grown under heat stress condition has become a trouble for rice cultivation.

Rice cultivation has gradually changed from double season to single season, because the flowering phase *summer* season rice occurs at the period with the high temperature stress that negatively affect the grain yield. During flowering and grain filling phase high temperature leads to heat stress, that result in great decline in spikelet fertility and deterioration in rice quality, which adversely affect the rice yield. Spikelet fertility, grain quality and yield processes in rice are challenged by heat stress.

The basic requirement in plant breeding is the presence of genetic variability in breeding material for selection of diverse parents for use in hybridization programme. For effective genetic improvement knowledge on the nature and magnitude of the genetic variation governing the inheritance of quantitative characters like yield and its components is very essential. Therefore, success on plant breeding activities entirely depends on the existence of genetic variability with respect to desired traits and selection skill of plant breeder. Therefore, assess genetic variability play important role in summer rice cultivation.

Materials and methods

Eighty-seven rice genotypes were evaluated in two replications at Research cum Instructional Farm, Department of Genetics and Plant Breeding, College of Agriculture, Indira Gandhi Krishi Vishwavidyalaya (IGKV), Raipur (C.G.) during *summer* -2017. Each genotype was raised in two rows of five-meter length with a spacing of 20x15cm between and within the rows respectively. Observations were recorded on five randomly selected plants from each replication for thirteen yield and yield contributing traits viz. days to 50% flowering, plant height (cm), tillers/plant, effective tillers/plant, flag leaf area, panicle length (cm), number of filled grains/panicle, total number of grains/panicle, spikelet fertility/panicle (%),100 grain weight (g), grain yield/plant, biological yield/plant and harvest index.

During the crop growth period at the flowering condition 15^{th} to 21^{th} standard meteorological week average maximum temperature was 42.5°C and average minimum temperature was 26.8°C. At this period average rainfall received in 0.6mm. PCV and GCV were calculated following Burton (1951). H² in broad sense and GA were calculated by following Lush (1940) ^[17] and Johnson *et al.* (1955) ^[14], respectively. Correlation coefficient was computed as per the procedure outlined by Karl Pearson (1932) ^[16]

Results and discussion

The analysis of variance showed a wide range of variation and significant differences for all the traits under study, indicating the presence of sufficient amount of variability. Information on the nature and magnitude of genetic variability is of immense significant for initiating any breeding programme. Further the presence of variability in the base material ensures better chances of selection for desirable plant types.

In the present study estimates of phenotypic coefficient of variation (PCV) was greater than the genotypic coefficient of variation (GCV) for all the traits (Table 2), but the difference was relatively small for all traits, it indicating that these characters were less influenced by the environment. Similar

results were finding by Kalyan *et al.* (2017) ^[15] and Pragnya *et al.* (2018) ^[20].

In this study, the highest PCV and GCV was recorded for filled grains per panicle (35.52%, 34.58%), grain yield per plant (31.24%, 28.02%), total grains per panicle (27.24%, 26.59%), biological yield per plant (29.45%, 26.36%), total tillers per plant (28.59%, 24.96%), effective tillers per plant (26.19%, 23.29%) and flag leaf area (23.26%, 23.02%), indicating the presence of considerable genetic variability and less influence of environment on the expression on this traits. Similar findings were also reported by Fukrei *et al.* (2011) ^[13], Sravan *et al.* (2012) ^[25], Pragnya *et al.* (2018) ^[20], Behera *et al.* (2018) ^[8] for grain yield per plant, Babu *et al.* (2012) ^[6] and Dhurai *et al.* (2013) ^[12] Rukmanidevi *et al.* (2016) ^[5] for filled grains per panicle, Ekka *et al.* (2015) ^[12] Sameera *et al.* (2015) ^[22] for effective tillers per plant.

The moderate GCV was found for 100 grain weight (19.29%, 18.57%), spikelet fertility per panicle (19.10%, 17.84%), plant height (14.46%, 12.72%), harvest index (15.65%, 12.63%), and days to 50% flowering (12.68%, 12.58%) and lowest was panicle length (9.79%, 8.00%). Similar findings were reported by Connate *et al.* (2016) for panicle length.

S. No.	Character	Replication (df=1)	Treatment (df=86)	Error (df=86)	
1	Days to 50% flowering	3.89	166.71**	1.28	
2	Plant height (cm)	112.23	357.45**	45.74	
3	Tillers/plant (No.)	3.89	12.86**	1.73	
4	Effective tiller/plant (No.)	3.45	9.63**	1.12	
5	Flag leaf area(cm ²)	1.57	69.47**	0.72	
6	Panicle length (cm)	0.36	7.94**	1.59	
7	Number of filled grains/panicle (No.)	102.33	2598.52**	70.04	
8	Total number of grains/panicle (No.)	72.46	2528.48**	60.36	
9	Spikelet fertility/panicle (%)	72.36	411.17**	28.02	
10	100 grain weight (g)	0.06	0.34**	0.01	
11	Grain yield/plant (g)	12.84	50.51**	5.47	
12	Biological yield/plant (g)	4.36	140.26**	15.49	
13	Harvest index (%)	58	130.64**	27.67	

Table 1: Analysis of Variance (ANOVA) for quantitative traits

* & ** represent significant levels at 5% (6.93) and 1% (1.65) respectively.

Table 2: Genetic parameters of variation for yield and its component traits

S. No.	Character		Range	PCV (%)	GCV (%)	h ² (BS) (%)	GA as % of mean			
1	Days to 50% flowering	72.29	55-97.50	12.68	12.58	98.48	25.66			
2	Plant height (cm)	98.18	75.42-129.17	14.46	12.72	77.31	23.12			
3	Tillers/plant (No.)	9.45	5.50-17.25	28.59	24.96	76.25	44.27			
4	Effective tiller/plant (No.)	8.86	5.50-16	26.19	23.29	79.10	42.06			
5	Flag leaf area(cm ²)	25.47	14.04-45.29	23.26	23.02	97.96	46.94			
6	Panicle length (cm)		17.70-27.17	9.79	8.00	66.67	13.43			
7	Number of filled grains/panicle (No.)	102.82	36.45-181.65	35.52	34.58	94.75	68.71			
8	Total number of grains/panicle (No.)	132.10	47.04-210.80	27.24	26.59	95.34	53.25			
9	Spikelet fertility/panicle (%)	77.59	33.15-97.30	19.10	17.84	87.24	34.18			
10	100 grain weight (g)	2.18	0.97-3.22	19.29	18.57	92.66	36.77			
11	Grain yield/plant (g)	16.94	6.84-26.50	31.24	28.02	80.46	51.58			
12	Biological yield/plant (g)	29.97	14.65-49.15	29.45	26.36	80.11	48.44			
13	Harvest index (%)	56.83	41.32-74.90	15.65	12.63	65.05	20.97			

PCV= Phenotypic coefficient of variation, GCV=Genotypic coefficient of variation, h² (bs)= Heritability in broad sense, GA= Genetic advance

Table 3: Estimation of genotypic and phenotypic correlation coefficient among yield and contributing traits in rice genotypes

		DU	ттр	гтр	FT A	DI	FCD	тср	SE	TW	DVD	ш	CVD
		гп	0.174		FLA 0.020*	PL	rgr	1GP	SF	1 W		ПI	GIP
DFF	g	-0.005	0.174	0.234*	0.230*	0.472**	0.461**	0.523**	0.082	-0.191	0.281**	0.358**	0.012
	р	0.003	0.154	0.215*	0.227*	0.388**	0.447**	0.507**	0.077	-0.176	0.269*	0.333**	0.014
PH	g		-0.487**	-0.415**	0.329**	0.279*	-0.326**	-0.136	-0.405**	0.235*	-0.208	-0.133	-0.163
	р		-0.345**	-0.315**	0.278*	0.195	-0.268*	-0.124	-0.291**	0.195	-0.174	-0.117	-0.133
TTP	g			0.977**	-0.108	0.118	0.555**	0.416**	0.409**	-0.083	0.576**	0.420**	0.482**
	р			0.935**	-0.099	0.055	0.465**	0.358**	0.327**	-0.047	0.538**	0.381**	0.438**
ETP	g				-0.042	0.162	0.579**	0.476**	0.354**	-0.093	0.591**	0.452**	0.470**
	р				-0.036	0.093	0.500**	0.421**	0.289**	-0.056	0.551**	0.422**	0.416**
	g					0.424**	0.109	0.242*	-0.138	0.053	0.015	0.070	-0.039
FLA	р					0.343**	0.105	0.232*	-0.125	0.045	0.012	0.063	-0.040
DI	g						0.193	0.306**	-0.102	-0.014	0.118	0.093	0.093
PL	р						0.139	0.236*	-0.097	-0.004	0.091	0.105	0.036
ECD	g							0.855**	0.591**	-0.349**	0.704**	0.641**	0.483**
FGP	р							0.845**	0.580**	-0.325**	0.671**	0.589**	0.452**
TOP	g								0.090	-0.223*	0.576**	0.541**	0.382**
TGP	р								0.074	-0.204	0.553**	0.499**	0.364**
SF	g									-0.315**	0.456**	0.408**	0.320**
	р									-0.302**	0.418**	0.364**	0.277*
TW	g										0.047	0.007	0.046
	р										0.056	0.017	0.059
BYP	g											0.844**	0.691**
	р											0.834**	0.658**
HI	g												0.219*
	р												0.165

* & ** represent significant levels at 5% and 1% respectively. DFF-Days to 50% flowering, PH-Plant height, TTP-Total tillers per plant, ETP-Effective tillers per plant, FLA-Flag leaf area, PL-Panicle length, FGP-Filled grains per panicle, TGP- Total grains per panicle, TW-Test weight, BYP-Biological yield per plant, HI-Harvest index, GYP-Grain yield per plant

Heritability and genetic advance as percent of mean

Heritability and genetic advance as percent of mean are important selection parameters. Heritability estimates along with genetic advance as percent of mean are more powerful for predicting the genetic gain under selection. From the result, high heritability coupled with high genetic advance as percent of mean was found in days to 50% flowering, flag leaf area, total grains per panicle, filled grain per panicle, test weight, spikelet fertility per plant, grain yield per plant, biological yield per plant, effective tillers per plant, plant height, total tillers per plant, and harvest index, it indicates that these traits are under the influence of additive gene action with least environment influence and simply phenotypic selection would be effective for crop improvement. Similar results were reported by Kalyan *et al.* (2017) ^[15] and Behera *et al.* (2018) ^[8].

High heritability coupled with moderate genetic advance as percent of mean was reported in panicle length indicating importance of both additive and no additive gene action. Sreedhar (2017) reported similar result for panicle length.

Association analysis for yield & yield contributing components

Yield is a complex polygenic traits has a large number of other contributing component traits. Correlation analysis reveals the relationship of dependent variable yield with its independent variables, thus association of various traits would determine their relative significance to improve yield. The correlation coefficients between grain yield and its thirteen component traits and among themselves were estimated at genotypic and phenotypic levels (Table 3). In general, genotypic correlations were higher than phenotypic ones in magnitude for all the characters. A positive correlation between important characters is desirable since it helps in simultaneous improvement of both the characters. A negative correlation may hinder the simultaneous expression of both the characters with high values. In such situation some economic compromise may be made (Simmonds, 1979).

At both genotypic and phenotypic level days to 50% flowering showed positive and highly significant or significant relationship with total grains per panicle, filled grain per panicle, panicle length, harvest index, biological vield per plant, effective tillers per plant and flag leaf area. Plant height exhibited positive and highly significant and significant relationship with total tiller per plant, flag leaf area, and test weight and panicle length. Negative and highly significant relationship was found with filled grains per panicle, spikelet fertility and effective tillers per plant. Effective tiller per plant showed positive and highly significant and significant relationship with total tiller per plant, biological yield per plant, filled grain per panicle, total grain per panicle, and grain yield per plant, harvest index, spikelet fertility and days to fifty percent flowering. Filled grain per panicle exhibited positive and highly significant relationship with total grain per panicle, biological yield per plant, harvest index, effective tiller per plant, spikelet fertility, grain yield per plant, total tiller per plant, days to fifty percent flowering and test weight. Spikelet fertility exhibited highly significant and positive association with filled grain per panicle, biological yield per plant, total tiller per plant, harvest index, effective tiller per plant and grain yield per plant. Grain yield per plant exhibited positive and highly significant correlation with biological yield per plant, filled grain per panicle, total tiller per plant, effective tiller per plant, total grain per panicle, spikelet fertilityandharvest index. So, they may be used as selection criteria to improve the grain yield in rice. This indicated that simultaneous selection of all these characters was important for yield improvement. So, they may use as a selection criteria to improve the grain yield in rice. Similar findings were reported by Alam et al. (2014)^[3], Singh et al., (2018)^[24] for filled grain per panicle, effective tiller per plant. Rangare et al., (2012) ^[21-25] for harvest index and biological yield per plant; Sarawgi et al., (2014)^[23], Mustafa and Elsheikh (2007) ^[18] for panicle length; Dhurai et al., (2016) ^[10] for plant height, flag leaf area and panicle length. Basavaraja et al., (2011)^[7] reported that productive tillers per plant showed significant positive correlation with grain yield. The genetic architecture of grain yield is based on the balance or overall net effect produced by various yield components interacting with one another. Based on the studies on genetic variability and correlation analysis, it may be concluded that biological yield per plant, filled grain per panicle, total tiller per plant, effective tiller per plant, total grain per panicle, spikelet fertility and harvest index exhibited positive direct effect on grain yield per plant coupled with significant positive association with grain yield per plant. Hence, utmost importance should be given to these characters during selection for single plant yield improvement. Selection of plants on the basis of these traits would certainly lead to improvement in grain yield.

Breeding heat-tolerant rice is one of the strategies used to mitigate the effects of climate change,

Particularly in high temperature regions where the majority of rice is grown. The screening and selection strategies that we developed (in the absence of a controlled growth chamber) for breeding under heat prone conditions could differentiate the genotypes and plant populations (new cross combinations) according to heat tolerance traits. Further studies on combining ability traits should be performed to address this issue.

References

- 1. Adhikari BN, Pokhrel BB, Shrestha J. Evaluation and development of finger millet (*Eleusine coracana* L.) genotypes for cultivation in high hills of Nepal. Fmg. & Mngmt. 2018; 3(1):37-46.
- 2. Aditya JP, Bhartiya A. Genetic variability, correlation and path analysis for quantitative characters in rainfed upland rice of Uttarakhand hills. Journal of Rice Research. 2013; 6(2):24-34.
- Alam MS, Islam MM, Hassan L, Begum SN, Gupta R. Study of correlation, magnitude of genetic diversity and selection indices in popular rice (*Oryza sativa* L.) Landraces of Bangladesh, International Journal of Innovation and Applied Studies. 2014; 8(3):1329-1338.
- Baker JT, Allen Jr LH, Boote KJ. Temperature effects on rice at elevated CO2 concentration. J Exp Bot. 43: 959– 964.Bangladesh. Int. J. of Innovation and Applied Studies. 1992; 8(3):1329-1338.
- Rukmanidevi K, Parimala K, Venkanna V, Lingaiah N, Hari Y, Satishchandra B *et al.* Estimation of variability for grain yield and quality traits in rice (*Oryza sativa* L.). Int. J. Pure App. Biosci. 2016; 4(2):250-255.
- 6. Babu VR, Shreya K, Dangi KS. Usharani G, Shankar AS. Correlation and path analysis studies in popular rice hybrids of India. International Journal of Science and Research Publication. 2012; 2(3):1-5.
- Basavaraja T, Gangaprasad S, Dhusyantha Kumar BM, Shilaja Hittlamani. Correlation and path analysis of yield and yield attributes in local rice cultivars (*Oryza sativa* L.). Electronic journal of plant breeding. 2011; 2(4):523-526.
- 8. Behera B, Sahu S, Kar RK, Pandey RK. Studies on genetic variability for some metric traits in slender grain rice genotypes. J. Appl. & Nat. Sci. 2018; 10(1):375-378.

- 9. Burton GW, Devane EH. Estimating heritability in tall fescue (*Festuca arundinaceae*) from replicated clonal material. Agronomy Journal. 1952; 45:478-481.
- 10. Dhurai SY, Reddy DM, Ravi S. Correlation and path analysis for yield and quality characters in rice (*Oryza sativa* L.). Rice Genomics and Genetics. 2016; 7(4):1-6.
- 11. Dhurai SY, Bhati PK, Saroj SK. Studies on genetic variability for yield and quality characters in rice (*Oryza Sativa* L.) Under integrated fertilizer management. The Bioscane. 2014; 9(2):745-748.
- Ekka RE, Sarawgi AK, Kanwar RR. Genetic variability and inter -relationship analysis for various yield attributing and quality traits in traditional germplasm of rice (*Oryza sativa* L.). Plant Archives. 2015; 15(2):637-645.
- 13. Fukrei PK, Kumar A, Tyagi W, Pattanayak A. Genetic Variability in Yield and its Components in Upland Rice Grown in Acid Soils of North East India. Journal of Rice Research. 2011; 4(1):4-7.
- 14. Johnson HW, Robinson HF, Comstock RE. Estimation of genetic and environmental variability in soybeans. Agronomy Journals. 1955; 47:314-318.
- Kalyan B, Radha Krishna KV, Subba Rao LV. Correlation Coefficient Analysis for Yield and its Components in Rice (*Oryza sativa* L.) Genotypes. International Journal of Current Microbiology and Applied Sciences. 2017; 6(7):2425-2430.
- 16. Karl Pearson. Tables for statisticians and biometricians, Stat. J. Biometrics, 1932.
- 17. Lush JL. Intra-sire correlation and regression of offspring on dams as a method of estimating heritability of characters. Proc. Ame. Soc. Anim. Prod. 1940; 33:293-301.
- 18. Mustafa MA, Elsheikh MAY. Variability, correlation and path coefficient analysis for yield and its components in rice. Afican. Crop Science Journal. 2007; 15:143-189.
- 19. Panse VG, Sukhatme PV. Statistical methods for agricultural workers. ICAR New Delhi, 1967, 381.
- Pragnya K, Radha K, Krishna VLV, Subba Rao, Suneetha K. Estimation of Genetic Variability Parameters in Soft Rice (*Oryza sativa* L.) Genotypes. Int. J. Curr. Microbiol. App. Sci. 2018; 7(06):2029-2042.
- Rangare NR, Krupakar A, Ravichandra K, Shukla AK, Mishra AK. Estimation of characters association and direct and indirect effects of yield contributing traits on grain yield in exotic and Indian rice germ-plasm. International Journal of Agriculture Sciences. 2012; 2(1):54-61.
- 22. Sameera S, Srinivas T, Rajesh AP, Jayalaxmi V, Nirmala PJ. Genetic variability studies for yield and yield components in rice (*Oryza Sativa* L.) El. J. of Pl. Breeding. 2015; 6(1):269-273.
- 23. Sarawgi AK, Parikh M, Sharma B, Sharma D. Phenotypic divergence for agro-morphological traits among dwarf and medium duration rice germplasm and inter-relationship between their quantitative traits. The Bioscane. 2014; 9(4):1677-1681.
- 24. Singh N, Verma OP. Genetic variability, heritability and genetic advance in rice (*Oryza sativa* L.) under salt stressed soil. Journal of Pharmacognosy and Phytochemistry. 2018; 7(3):3114-31.
- 25. Sravan T, Rangare NR, Suresh BG, Kumar SR. Genetic Variability and Character Association in rainfed upland rice (*Oryza sativa* L.). Journal of Rice Research. 2012; 5(1&2):24-29.

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- 26. Sreedhar ST, Reddy D, Ramesha MS. Genotype x environment interaction and stability for yield and its components in hybrid rice cultivars (*Oryza sativa* L.). Int. J. Plant Breeding Genet. 2011; 5:194-208.
- 27. Yogameenakshi P, Nadarajan N, Anbumalarmathi J. Correlation and path analysis on yield and drought tolerant attributes in rice (*Oryza sativa* L.) under drought stress. *Oryza*. 2004; 41(3&4):68-70.
- Zhou L, Zeng Y, Hu G. Characterization and identification of cold tolerant near-isogenic lines in rice. Breeding Science. 2012; 62:196-201.