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Genetic variability and characters association study for yield and attributing traits in rice (*Oryza sativa* L.) under heat stress condition

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Abstract
Twenty rice genotypes (*Oryza sativa* L.) had been characterized to assess the yield and its attributing characters under heat stress conditions in the present experiment in the *summer* season of 2020 year following a randomized block design with three replications. Statistical analyses carried out to compute variability and correlation study revealed that spikelet fertility has high degree of significant positive association with yield square meter^{-1}. The principal component analysis study revealed that first two PCs accounted for 73.90% of the cumulative variance with eigenvalues of 2.33 and 2.11 for PC1 (Plant height) and PC2 (Panicle length) respectively. Studies on gene action involving parents of contrasting traits and identification of loci of quantitative parameters of significance would enable to identify of elite lines from the present set of genotypes for further improvement in the future.

Keywords: Principal component analysis, character association, rice, heat stress

Introduction
Rice (*Oryza sativa* L.) is the staple food for over half of the world's population. More than 90% of the world, rice is grown and consumed in Asia. Rice contributes nearly 20% of the total calories taken by man. In India, rice is often called ''Prana'' meaning the breath of life. There are an estimated 140,000 varieties of cultivated rice which is in practice worldwide. Lysine contain in rice is very rich 3.8 percent. True protein digestibility and the biological value for rice are also high as compared to the other cereals. Modern rice genotypes have been developed through the hybridization of elite lines. Hybridization program involving genetically diverse parents belonging to different clusters would provide an opportunity for bringing together gene constellations of diverse nature. It has been estimated that during the year 2023, the area, production, and yield of rice in the world were recorded to be about 47 million ha, 134 million tons, and 4.3 Tons/Ha respectively. At the end of fiscal year 2022, India had over 46 million hectares of land area for cultivation of rice. This area had been fluctuating over during the past three years. In fiscal year 2022, rice was the most produced food grain across the South Asian nation. In India, rice is grown in 43.86 million ha, the production level is 104.80 million tones and the productivity is about 2390 kg ha^{-1} [1]. Plants are routinely confronted by a variety of abiotic or biotic stresses, despite many abiotic stresses heat (high temperature) adversely affects plant growth and productivity. Temperatures above 32 ºC negatively affect all stages of rice plant growth and development [2]. In 2003, about 5.18 million tons of rice was lost due to heat waves with temperature above 38 ºC for more than 20 days [3]. High temperature is detrimental to most physiological processes including photosynthesis, grain yield, growth, and stomatal opening.
 Under this present experiment, emphasis has been given to identify genotypes of rice that have a high yield potentiality. Under this investigation, an association of different morphological traits under heat stress condition were assessed with the help of statistical analysis which includes analysis of variance, correlation studies, path analysis, and varietal performance. This morphological study will help in identifying the presence of any relation among these characters with their genetic behavior which will ultimately help in the construction of suitable plant types combining desirable expression of different characters.

Materials and Methods
The study was conducted in the *summer* season of 2020 year. The undersigned experiment was

carried out in the Research cum Instructional Farm, IGKV, Raipur, Chhattisgarh. Twenty rice genotypes were obtained under Heat stress conditions from the Department of Plant Molecular Biology and Biotechnology, IGKV, Raipur presented in Table 1.

Table 1: List of Genotypes

Sl. No.	Genotype	Sl. No.	Genotype
1	IG-103	11	IG-326
2	IG-301	12	IG-227
3	IG-102	13	IG-28
4	IG-308	14	IG-296
5	IG-36	15	IG-290
6	IG-112	16	IG-303
7	IG-19	17	IG-295
8	IG-65	18	IG-300
9	IG-298	19	IG-4
10	IG-35	20	IG-84

The genotypes were tested in the field using randomized block design with 3 replications and plot size was maintained at 2m x 1.5m with spacing of 15 cm distance from plant to plant and 20 cm from row to row and plot to plot distance of 50 cm apart. The soil type is sandy loam with pH 5.74, organic carbon (0.85%) and available N, P_2O_5, and K_2O were 155.85 kg ha^{-1}. (Basal dose used at the time of land preparation. 1st top dressing was carried out 22 days after transplanting). Intercultural operations were carried out as and when necessary. At harvest, a random sample of 5 plants in each plot were taken to measure the following parameters: plant height (cm), panicle length (cm), number of tiller plant^{-1}, Days to 50% flowering, spikelet fertility (%) and yield (g/m^2). Principal component analysis was carried out followed after Clifford and Stephenson, 1975 [4] and Guei *et al*., 2005 [5]. The scree plot was depicted after Cattell, 1966 [6]. OPSTAT was used for statistical analysis.

Results and Discussion
The present experiment revealed that IG-290 (94.7 cm) showed the lowest plant height and IG-84 showed (200.3 cm) the highest. The average panicle length was recorded to be 25.2 cm ranging from 22 cm (IG-290) to 28.6 cm (IG-28). 5.3 average number of tillers/plants were recorded during *Summer*-2020, ranging from 5.33 to 10 with the lowest no. of tillers in IG-84 (5.33) and the highest no. of tillers in IG-300 (10) under heat stress condition. During *Summer* 2020, the mean of Days to 50% Flowering was 101.7 days, the range was from 79 (IG-290) to 132 (IG-298) days. The mean of Spikelet fertility was recorded to be 92.8%, the highest was in IG-103 (95.5%) and lowest was in IG-84 (90.5%). An average yield of 561.9 g/m^2 was recorded during *Summer*-2020, ranging from 496 g/m^2 (IG-84) to 656 g/m^2 (IG-103). The coefficient of variation was found to be within the statistically permissible limit for all the studied parameters for set of 20 rice genotypes. A similar study was also performed [7].
The complicated polygenic characteristic of yield includes many additional contributing component qualities. By examining the relationship between the dependent variable, yield, and its independent factors, correlation analysis can discover the relative importance of different qualities for increasing yield at both the genotypic and phenotypic levels, the correlation coefficients between the grain yield, and each of its five constituents. In the present study, a highly significant and positive correlation was recorded between the panicle length and plant height (0.711**) and between spikelet fertility and yield (0.758**) during *Summer-2020*. A highly significant and positive correlation was recorded between panicle length and plant height (0.720**) and between spikelet fertility and yield (0.771**) and a highly significant and negative correlation was found between number of tiller and plant height (-0.62**) during Summer-2020 (Table 3). For all the studied parameters, genotypic correlations had larger magnitudes than phenotypic correlations. A similar study and finding were also reported [7]. Principal component analysis for rice genotypes assessed for all the morphological characters showed the existence of variability among the genotypes. Two principal component axes were identified with eigen value (^{1}) more than 1 (Fig. 1) contributing cumulatively 73.9% of the total variance. While the first principal component axis with eigen value of 2.33 contributed 38.80% of the total variance the second principal component axis with an eigen value of 2.26 contributed 35.10% of the total variance. The contribution of the remaining principal component axes and the corresponding eigen value as presented in parentheses were (0.88^1) 14.60%, (0.49^1) 8.20%, (0.18^1) 3.0%, and (0.02^1) 0.03% of the total variance respectively (Table 4). Traits such as plant height, spikelet fertility, and yield sq. m^{-1} (0.388 in PC1 and 0.351 in PC2) contributed the most. As far as the relative weight of the respective character corresponding to a principal component axis in the present experiment was concerned, tiller plant^{-1} (-0.508) had negative weightage towards the first principal axis. And the remaining characters had positive weight towards the same axis. In the case of principal component axis 2, panicle length (-0.532), days to 50% flowering (-0.348), and plant height (-0.347) had only negative weight towards the corresponding principal component axis while for principal component axis, 3 all characters but days to 50% flowering (-0.916) had positive weight towards corresponding principal component axis. In the case of principal component axis four all the studied characters had positive weightage towards the corresponding principal component axis. In the case of principal component axis five all characters except yield sq. meter^{-1} (-0.714) had positive weightage towards the corresponding principal component axis presented in (Table 4). The character in first two principal components with high weightage towards total variation can be exploited for further selection and to carry out variability program. Similar studies were also reported by Mahendran *et al*. (2015) [8], Grzesiak *et al*. (2019) [9], Ali *et al*. (2016) [10], Kumar *et al*. (2017) [11], Sandeep *et al*. (2020) [12] and Beena *et al*. (2021) [13].

Table 2: Statistical analysis of average top 20 rice lines for agronomical traits (*Summer-2020)*

S.N.	IGKV S.N.	Height (cm)	Plant Number of length(cm)	Days to 50% tiller	Spikelet Flowering	Yield Fertility (%)	(gm per sq m)
1	IG-103	176.7	25.8	7.0	94	95.5	656
2	IG-301	126.7	22.3	7.0	95	95.1	649
3	IG-102	159.4	25.2	6.7	95	94.7	615
4	IG-308	167.5	25.6	6.0	95	94.6	605
5	IG-36	153.1	26.8	5.3	109	94.2	603
6	IG-112	171.3	24.8	5.3	94	93.8	603
7	IG-19	115.3	22.4	7.3	94	93.4	588
8	IG-65	97.8	22.6	7.0	99	93.0	587
9	IG-298	110.1	23.4	7.0	132	92.7	587
10	IG-35	171.2	26.9	5.7	94	92.5	550
11	IG-326	148.9	27.8	6.7	119	92.5	545
12	IG-227	177.2	27.9	7.7	109	92.3	538
13	IG-28	184.2	28.6	6.0	102	91.8	535
14	IG-296	157.8	27.4	8.3	103	91.7	531
15	IG-290	94.7	22.0	8.7	79	91.7	521
16	IG-303	95.2	25.1	7.7	109	91.7	515
17	IG-295	99.8	25.9	8.3	94	91.6	511
18	IG-300	111.2	22.5	10.0	104	91.6	504
19	IG-4	138.9	24.4	6.0	104	90.8	500
20	IG-84	200.3	26.8	5.3	110	90.5	496
Mean± Sem		142.9±7.4	25.2±0.4	7.0±0.3	101.7±2.4	92.8±0.3	561.9±10.8
Range	Maximum	200.3	28.6	10	132	95.5	656
	Minimum	94.7	22	5.3	79	90.5	496

Table 3: Correlation between five yield attributing traits and yield during *Summer* -2020

	Plant Height	Panicle Length	Number of Tiller	Days to 50% flowering	Spikelet fertility	Yield (gm per sq m)
Plant Height	1.000					
Panicle Length	0.720**	1.000				
Number of Tiller	-0.62**	-0.390	1.000			
Days to 50% flowering	0.056	0.285	-0.129	1.00		
Spikelet fertility	0.146	-0.155	-0.245	-0.242	1.000	
Yield (gm per sq m)	0.140	-0.201	-0.311	-0.164	0.771**	1.000

**Significant at 1% level of significance, * significant at 5% level of significance.

Table 4: Eigen vector and associated variation for principal components in rice genotypes

|	PC1	PC2	PC3	PC4	PC5	PC6
Plant Height	0.496	-0.347	0.276	0.147	-0.731	0.035
Panicle Length	0.297	-0.532	0.133	0.492	0.597	-0.112
Tiller/Plant	-0.508	0.187	0.047	0.795	-0.259	-0.068
Days to 50% Flowering	-0.004	-0.348	-0.916	0.086	-0.163	0.071
Spikelet fertility	0.448	0.473	-0.124	0.281	0.122	0.684
Yield	0.455	0.466	-0.221	0.132	-0.004	-0.714
Eigenvalues	2.33	2.11	0.88	0.49	0.18	0.02
Variance (%)	0.388	0.351	0.146	0.082	0.03	0.003
Cumulative (%)	0.388	0.739	0.885	0.967	0.997	1.00
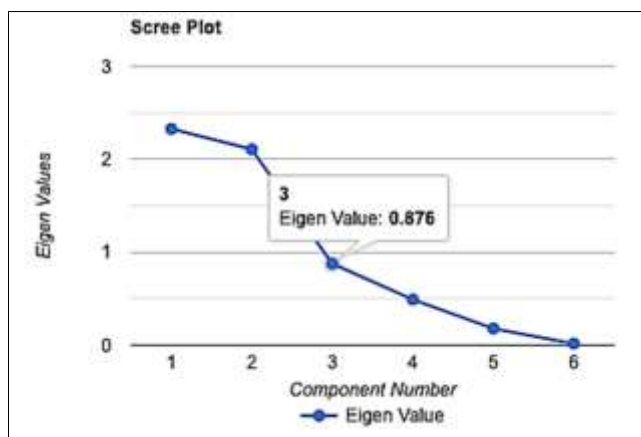
Fig 1: Scree plot for principal component in rice genotypes

Conclusion

Present experiment extracted the important characters responsible for maximum variation under heat stress condition through principal component analysis and correlation study. Utilization of those characters for selection and for further crop improvement programs can give fruitful results in near future. Studies on gene action involving the identified contrasting parents and the same on genetic divergence at the molecular level can make accurate delineations of genetic distance among the genotypes in the future. Identification of loci related to quantitative traits of importance would also aid in the selection of elite lines and their further use in crop improvement programs in rice.

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