

Genetic Variability Studies on Yield and Physiological Traits in Basmati Rice under Drought Environment (*Oryza sativa* L.)

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ABSTRACT

Thirty eight genotypes of rice were evaluated in Randomized Block Design for 19 physiological and yield related traits to estimate genetic variability, heritability and genetic advance as a percentage of mean. The analysis of variance revealed significant variability for all the 19 traits. Among the characters

studied, the genetic advance as percent of mean along with higher values of heritability, GCV and PCV estimates were maximum for plant height, number of tillers per plant, number of panicles per plant, number of spikelets/panicle, number of filled grains per panicle, number of unfilled grains per panicle, grain yield per plant, harvest Index, SPAD chlorophyll meter reading, total chlorophyll content, specific leaf area and relative membrane injury indicating that the genetic variances for these traits are probably owing to their high additive gene effects. The genotypes Pusa basmati-6, Basmati-564, Pusa basmati-1609, Pant sugandh dhan-15 and Kasturi could be further exploited for development of agronomically superior cultivars of basmati rice as they have shown higher *per se* performance for the desired yield contributing traits. Vallabh basmati-24, Kasturi and Vallabh Nagina⁻¹ could be considered as the best for exploiting the higher yields in drought environment in further breeding programs.

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INTRODUCTION

Rice (*Oryza sativa* L.) is the staple food for more than half of the world population. It belongs to the genus *Oryza*, family Poaceae (Gramineae), tribe *Oryzaceae*. The genus *Oryza* is distributed throughout the trop-

Table 1. Analysis of variance for 19 characters in 38 genotypes of basmati rice. *, ** significance at 5 % and 1 % level respectively.

Sl. No.	Character	Mean sum of squares		
		Replications (df:2)	Treatments (df:39)	Error (df:78)
1	Days to 50 % flowering (days)	14.408	177.377**	7.896
2	Days to maturity (days)	17.908	242.094**	12.250
3	Plant height (cm)	61.11	742.27**	12.98
4	No. of tillers per plant (no.)	6.891	34.481**	2.454
5	No. of panicles per plant (no.)	16.2110	7.9035**	0.6243
6	Panicle length (cm)	6.5959	13.2815 **	2.8911
7	No. of spikelets per plant (no.)	789.4	4107.3**	87.8
8	No. of filled grains per plant (no.)	2718.1	3442.5**	63.3
9	No. of un filled grains per plant (no.)	352.26	449.89**	12.14
10	1000 - grain weight (g)	192.279	14.602**	4.382
11	Spikelet fertility	580.65	149.72**	16.81
12	Harvest index (%)	0.92	444.63**	6.29
13	Grain yield per plant (g)	10.125	70.845**	1.555
14	Relative water content (RWC) (%)	172.030	122.831**	2.927
15	Specific leaf area (cm ² g ⁻¹)	234.37	2084.54**	5.61
16	Relative membrane injury (%)	87.557	42.368*	1.127
17	SPAD chlorophyll meter reading (SCMR value)	134.013	121.883**	1.289
18	Canopy temperature	9.6430	8.4777*	4.7868
19	Total chlorophyll content (mg/g)	0.073	46.463**	1.137

ics and subtropics of the world. The genus contains both diploid ($2n = 24$) as well as tetraploid ($2n = 48$) species (Dunna and Roy 2013). It is a staple cereal consumed by more than half of the world's population cultivated in wide agro-ecological conditions including rain-fed conditions. Rice is being provided 27% of the world nutritional energy and 20% of overall nutritional protein for human (Kennedy *et al.* 2015). In the evolution of rice and its genetic differentiation into distinct varietal group, consumer quality preferences have played a significant role besides agro ecological factors. One such varietal group comprising the aromatic pulao biryani rice of the Indian subcontinent known as “Basmati” is the highly priced rice in domestic as well as international markets. Basmati is very popular and is cultivated solely in the foothills of the Himalayas, the Uttar Pradesh and Haryana regions of India and the Punjab province of Pakistan and India. Basmati rice is a very well-known type of rice in the world due to the unique characteristics like long grain, aroma, and intermediate amylose content (Boers *et al.* 2015). Among all abiotic stresses, drought remains at the top in limiting rice production and thus causing major threat to food security (Zhang 2018). Drought stress is one of the major factors that leads to decreased rice production (Swamy and Kumar 2013) and it can expand to above

50% of the global arable land by 2050 (Singhal *et al.* 2016) due to loss of ground water, global climate change leading to decreased water sheds.

Drought stress was noted in approximately 42 M ha of rice producing area (Yang *et al.* 2019). Water availability and drought are becoming major constraints for rice cultivation because of greatly fluctuated and generally reduced rainfall in the majority of rice growing areas worldwide resulting from the global climate change (Singh *et al.* 2021). The development of promising cultivars is primarily governed by the magnitude of existing genetic variability for the desired characters. Variability studies on a crop are pre-requisite for starting any crop improvement program. Rice is more sensitive to drought stress than other cereals and large genotypic variation in DT exists within the cultivated rice gene pool and its wild relatives. There is a need to improve the productivity in order to keep pace with increasing demand of country. To initiate such breeding program aiming for varietal improvement, the knowledge of genetic variability existing among different genotypes is a prerequisite. Estimation of genetic variability in conjunction with the estimates of heritability and genetic advance indicates the possible improvement achieved through selection. The degree of success depends

Table 2. Mean performance of rice genotypes for 13 yield and yield attributing traits.

Genotypes	DFF	DM	PH	NTP	NPP	PL	NSP	NFP	NUFP	TGW	GYPP	SF	HI
PB-1121	101.67	141.00	115.43	14.20	8.10	27.86	119.01	86.55	32.74	25.73	20.02	72.78	43.67
PB-1509	85.00	119.67	96.35	15.40	7.33	25.48	100.96	79.99	24.08	23.53	19.16	79.35	44.57
PB-1609	85.33	119.33	108.86	8.00	5.20	26.43	217.98	199.31	19.49	26.32	14.33	91.43	32.01
PB 1612	82.33	122.67	97.57	11.80	7.70	25.16	168.11	129.24	40.16	18.15	29.96	76.88	66.51
PB-1637	86.00	128.00	91.53	12.20	5.90	25.45	163.88	138.17	27.64	24.57	17.66	84.31	37.64
PB-1692	81.67	119.33	91.37	12.60	7.00	25.66	158.03	127.42	31.40	16.51	23.44	80.63	59.03
PB-1718	86.67	136.33	104.55	18.00	9.50	27.25	151.01	122.65	33.53	22.36	25.32	81.24	51.13
PB-1728	96.00	140.00	87.89	11.20	11.43	29.05	158.75	125.37	35.02	24.04	27.36	78.99	62.96
PB-1	102.00	135.67	111.95	27.20	7.10	28.70	185.30	149.45	35.55	23.18	18.94	80.74	47.66
PB-6	102.00	143.67	94.28	23.20	10.80	26.31	140.81	114.75	35.20	20.40	20.67	82.23	53.04
IPB-1	103.00	147.67	137.67	11.40	6.67	26.15	229.49	173.93	53.25	24.26	22.40	75.80	49.69
Bas-mati-370	84.67	137.67	131.01	18.35	9.60	27.17	235.24	194.97	41.74	22.61	14.46	82.89	38.38
Bas-mati-386	101.00	127.67	141.91	12.20	6.70	27.72	134.48	113.68	22.81	22.73	11.46	84.57	38.66
Bas-mati-564	92.00	134.33	111.08	22.00	8.80	33.73	190.28	153.12	38.42	18.98	12.66	80.18	26.44
Pant bas-mati-1	89.67	136.33	112.50	13.20	6.00	26.95	190.96	158.98	45.86	21.38	15.77	83.54	42.23
Pant bas-mati-2	89.67	126.33	110.68	10.00	8.60	27.68	206.57	162.81	38.82	22.95	12.66	78.88	27.35
Pant sugandh													
dhan-15	91.00	142.33	104.74	11.00	8.20	25.62	212.67	195.41	18.37	24.41	25.18	91.89	58.26
Punjab bas-mati-2	93.33	132.67	103.00	16.20	11.70	27.07	112.27	98.80	14.77	20.88	16.32	88.00	29.90
Punjab bas-mati-3	89.33	136.00	117.73	8.90	7.23	25.87	161.17	141.44	23.13	21.77	23.21	87.82	57.52
Punjab bas-mati-4	92.33	129.67	98.68	11.00	8.10	24.86	143.77	137.82	17.35	23.32	17.14	97.17	32.65
Punjab bas-mati -5	93.67	132.67	110.34	13.80	7.90	27.17	139.22	127.64	14.33	22.21	20.92	91.70	44.38
PS-3	96.33	131.33	98.84	9.00	6.20	27.72	221.23	182.22	42.12	21.15	20.69	82.38	52.30
PS-5	84.00	122.67	105.62	9.00	9.83	29.23	134.48	113.89	23.76	22.88	12.95	84.76	27.09
Hariyana													
Bas-1	110.00	136.67	106.01	8.80	6.80	25.61	207.15	173.99	43.64	21.79	18.44	84.04	32.29
Hariyana bas-2	97.67	132.00	112.63	17.20	8.90	29.05	171.41	137.03	34.91	16.48	26.85	79.94	64.12
Palim bas-mati	96.33	143.33	87.13	15.00	10.30	23.48	165.04	120.95	46.61	19.54	21.51	73.32	45.25
Sanwal bas-mati	91.67	137.67	106.44	15.00	9.97	25.86	184.57	111.11	74.58	22.26	21.51	60.20	46.28
Ranbir bas-mati	92.67	131.00	137.02	12.60	10.90	26.03	198.18	171.31	38.26	24.73	17.39	86.43	42.26
Vallabh bas-21	85.67	127.33	102.96	16.40	7.40	28.89	162.85	146.06	20.67	21.17	11.85	89.82	25.50
Vallabh bas-22	87.33	139.67	97.92	14.60	9.70	26.70	156.83	111.70	47.04	19.81	14.00	71.24	30.66
Vallabh bas-23	88.33	130.00	105.08	12.88	8.00	25.48	117.85	94.54	27.70	19.53	17.51	80.32	37.37
Vallabh bas-24	82.00	130.00	120.42	16.80	8.00	28.04	180.12	138.65	33.74	20.62	19.09	76.68	39.97
Vallabh													
Nagina-1	77.67	109.00	100.63	12.80	8.70	26.06	141.97	100.68	39.65	23.00	21.65	70.94	51.63
CSR 30	106.33	140.00	113.72	14.60	8.70	24.89	142.76	114.81	34.73	24.20	11.79	80.32	20.66

Table 2. Continued.

Genotypes	DFF	DM	PH	NTP	NPP	PL	NSP	NFP	NUFP	TGW	GYPP	SF	HI
Kasturi	97.67	128.67	116.63	9.20	6.40	29.44	174.81	160.80	16.41	22.04	19.37	92.01	43.41
Malviya	94.00	130.33	102.83	9.40	8.80	25.28	205.84	171.75	40.12	20.52	23.05	83.44	48.58
Taravadi	91.33	133.33	158.69	14.20	10.50	22.67	250.27	199.44	45.79	23.41	25.61	79.63	61.77
Type-3	97.33	123.00	131.24	19.30	8.98	26.66	171.39	139.23	33.85	22.34	17.88	81.21	32.45
Mean	92.12	131.26	109.23	14.49	8.37	26.61	172.39	141.81	33.24	22.01	19.26	82.20	42.71
CV (%)	3.05	2.67	3.30	10.89	9.44	6.39	5.44	5.61	10.48	9.51	6.48	4.99	5.87
SE (m)	1.62	2.02	2.08	0.90	0.46	0.98	5.41	4.59	2.01	1.21	0.72	2.37	1.45
CD 5%	4.57	5.69	5.86	2.55	1.28	2.76	15.23	12.93	5.66	3.40	2.03	6.66	4.08
CD 1%	6.06	7.55	7.77	3.38	1.70	3.67	20.20	17.15	7.51	4.51	2.69	8.84	5.41

FF: Days to 50% flowering

DM: Days to maturity

PH : Plant height(cm)

NTP: Number of tillers per plant

NPP: Number of panicles per plant

PL: Panicle length (cm)

NSP: Number of spikelets per panicle

NFP: Number of filled grains per panicle

NUFP: Number of unfilled grains per panicle

TGW:1000 grain weight(g)

GYPP : Grain yield per plant (g)

SF: Spikelet fertility (%)

HI: Harvest index (%)

Table 2. Continued. Mean performance of rice genotypes for six physiological traits.

Genotypes	RWC	SPAD	SLA	RMI	TCC	CT
PB-1121	77.94	47.85	189.63	22.38	8.07	34.10
PB-1509	94.68	38.02	124.54	12.13	17.26	32.83
PB-1609	94.71	35.89	189.69	16.85	8.04	34.00
PB 1612	94.29	37.90	149.89	19.31	20.56	33.90
PB-1637	93.15	35.03	181.49	10.54	6.10	36.13
PB-1692	84.13	30.14	133.65	15.02	9.07	35.77
PB-1718	93.68	37.64	127.89	18.44	8.07	36.03
PB-1728	97.52	43.47	193.73	15.23	7.28	33.57
PB-1	93.82	51.81	150.77	12.99	11.91	36.27
PB-6	86.64	42.68	172.47	18.52	5.44	34.13
IPB-1	91.95	39.80	136.82	21.66	12.51	34.43
Basmati-370	92.10	38.21	128.00	23.47	5.78	36.13
Basmati-386	79.23	35.01	129.11	10.89	15.51	32.87
Basmati-564	87.09	33.71	186.47	15.44	6.03	35.47
Pant basmati-1	84.31	43.11	150.96	18.19	19.96	37.57
Pant basmati-2	86.05	36.56	151.58	19.52	6.83	35.27
Pant sugandh dhan-15	80.87	29.54	135.24	11.39	12.62	33.43
Punjab basmati-2	77.10	34.06	183.38	24.07	14.66	35.47
Punjab basmati-3	96.50	29.46	146.89	20.58	8.72	33.20
Punjab basmati-4	85.30	48.52	193.01	25.22	10.96	33.00
Punjab basmati -5	93.59	39.49	155.10	21.20	7.44	34.90
PS-3	88.69	33.91	153.15	17.25	9.05	32.30
PS-5	87.94	43.83	112.38	22.56	10.83	37.57
Hariyana bas-1	78.23	33.76	165.49	12.70	9.28	36.87
Hariyana bas-2	93.15	37.63	141.17	15.66	9.93	34.50
Palim basmati	92.31	34.39	143.12	17.06	4.54	33.30
Sanwal basmati	93.63	44.59	111.65	17.73	5.37	33.77
Ranbir basmati	95.59	45.41	144.39	12.92	9.70	31.40
Vallabh bas-21	94.01	37.11	190.98	20.36	5.49	32.23
Vallabh bas-22	90.28	47.30	120.75	16.82	10.85	33.63
Vallabh bas-23	81.77	53.92	137.53	15.66	8.03	38.33
Vallabh bas-24	72.93	42.72	123.79	18.06	5.76	31.70
Vallabh Nagina-1	96.61	32.86	192.80	20.44	9.94	33.23
CSR-30	95.15	49.07	183.32	15.11	7.88	33.30

Table 2. Continued.

Genotypes	RWC	SPAD	SLA	RMI	TCC	CT
Kasturi	97.05	49.34	122.69	16.19	7.06	35.53
Malviya	93.75	31.70	134.57	13.87	5.60	32.77
Taravadi	94.08	36.53	132.51	16.96	7.82	32.87
Type 3	85.77	31.98	136.04	17.90	5.23	33.17
Mean	89.44	39.24	153.16	17.55	9.24	34.39
CV (%)	1.91	2.89	1.55	6.05	11.54	6.36
SE (m)	0.99	0.66	1.37	0.61	0.62	1.26
CD5%	2.78	1.85	3.85	1.73	1.73	3.56
CD1%	3.69	2.45	5.11	2.29	2.30	4.72

RWC : Relative water content (%)

SPAD : SPAD Chlorophyll meter reading

SLA : Specific leaf area (cm²g⁻¹)

RMI : Relative membrane injury (%)

TCC : Total chlorophyll content (mg/g)

CT : Canopy temperature (°C)

on the magnitude of heritability which measures the relative amount of the heritable portion of total variation and aids in selection. Similarly, genetic advance (GA) under selection gives an idea about how much of the genetic gain was obtained due to selection. Hence, the estimates of genetic variability, heritability and genetic advance will be of immense value in selection and breeding for high yielding hybrids coupled with quality.

MATERIALS AND METHODS

Thirty eight genotypes were evaluated in a Randomized Block Design (RBD) with three replications, which have been induced with drought stress before onset of reproductive stage, during *kharif* 2021 in the plot of 2 row of 4 meter length at Crop Research Center and Technology Park of Sardar Vallabhbhai Patel University, Meerut. Spacing between the row to row 30 cm and plant to plant distance was maintained 20 cm by proper thinning. All recommended package of practices has been followed to retain a good crop. Five competitive plants were randomly selected for each genotype from each replication (stress treated plots) for recording the observations on days to 50% flowering, days to maturity, plant height (cm), tiller number, number of panicles per plant, length of panicle (cm), number of spikelets/panicle, number of filled grains per panicle, number of unfilled grains per panicle, 1000 grain weight (g), grain yield (g), spikelet fertility (%), harvest index (%) and specific physiological traits for water limited

condition were also recorded on relative water content (%), SPAD chlorophyll meter reading (SCMR), total chlorophyll content (mg/g), specific leaf area (cm²/g), relative membrane injury (%) and canopy temperature (°C). The characters viz., days to 50% flowering and days to maturity were recorded on per plot basis. Means were computed and data were analyzed for variances by Panse and Sukhatme (1967) and coefficient of variation as suggested by Burton (1952) and heritability (broad sense) as the ratio of genotypic to phenotypic variance. The procedure of Johnson *et al.* (1955) was followed for calculating the expected genetic advance and genetic advance as per cent of mean. All the statistical analysis was conducted by IBM SPSS 22 statistical package (IBM Cooperation 2019).

RESULTS AND DISCUSSION

In the present study the analysis of variance revealed highly significant differences for all the 19 characters studied among the genotypes, indicating a good deal of variation among 38 genotypes of basmati rice (Table 1). Maximum range of variation was observed for number of spikelets/panicle followed by number of filled grains per panicle, specific leaf area, plant height, number of unfilled grains per panicle and harvest Index.

Based on *per se* performance of genotypes for the studied traits, the below recommendations were

Table 3. Mean, range, coefficient of variation, heritability (broad sense) and genetic advance as per cent of mean for yield and its attributes and physiological traits of basmati rice.

Sl. No.	Character	Mean	Range		Variance		Coefficient of variation		Heritability (broad sense) (%)	Genetic advance (GA)	Genetic advance as per cent of mean (%)
			Min	Max	Geno-typic	Pheno-typic	Geno-typic	Pheno-typic			
1	Days to 50% flowering	92.12	77.67	110.00	56.49	64.39	8.16	8.71	87.74	14.50	15.74
2	Days to maturity	131.26	104.67	147.67	76.61	88.86	6.67	7.18	86.21	16.74	12.76
3	Plant height (cm)	109.23	87.13	158.69	243.10	256.08	14.27	14.65	94.93	31.29	28.65
4	Number of tillers per plant	14.49	9.73	25.59	10.68	13.13	22.55	25.01	81.31	6.07	41.89
5	Number of panicles per plant	8.37	5.20	11.70	2.43	3.05	18.62	20.88	79.54	2.86	34.21
6	Panicle length (cm)	26.61	21.08	33.73	3.46	6.35	6.99	9.47	54.5	2.83	10.63
7	Number of spikelets per panicle	172.39	100.96	250.27	1339.84	1427.65	21.23	21.92	93.85	73.05	42.37
8	Number of filled grains per panicle	141.81	79.99	221.25	1126.41	1189.72	23.67	24.32	94.68	67.27	47.44
9	Number of unfilled grains per panicle	33.24	14.33	74.58	145.92	158.06	36.34	37.82	92.32	23.91	71.93
10	1000 grain weight (g)	22.01	16.48	26.32	3.41	7.79	8.38	12.68	43.74	2.51	11.42
11	Grain yield per plant (g)	19.26	11.46	29.96	24.10	24.65	24.96	25.78	93.69	9.58	49.76
12	Spikelet fertility (%)	82.20	60.20	97.17	44.30	61.11	8.10	9.51	72.49	11.67	14.20
13	Harvest index (%)	42.71	20.66	66.51	146.11	152.41	28.30	28.90	95.87	24.38	57.09
14	Relative water content (%)	89.44	72.93	97.52	39.97	42.90	7.07	7.32	93.18	12.57	14.05
15	SPAD chlorophyll meter reading	39.24	29.46	53.92	40.20	41.49	16.16	16.42	96.89	12.86	32.76
16	Specific leaf area (cm ² g ⁻¹)	153.16	111.65	198.23	692.98	698.59	17.19	17.26	99.2	54.01	35.26
17	Relative membrane injury (%)	17.55	10.54	25.22	13.75	14.87	21.12	21.97	92.43	7.34	41.83
18	Total chlorophyll content (mg/g)	9.24	4.50	20.56	15.11	16.25	42.08	43.63	93.00	7.72	83.59
19	Canopy temperature (°C)	34.39	31.40	38.33	1.23	6.02	3.23	7.13	20.45	1.03	3.00

made. Mean performance for 38 genotypes was provided in Table 2. The genotypes Pusa Basmati 1612, Pusa Basmati 1728, Pusa Basmati 1718, Pusa Basmati 1692 and Palim basmati were found to have higher grain yield coupled with lesser plant height and hence, could be exploited for developing dwarf cultivars with high yield. For the remaining traits, the genotypes, Pusa basmati-1, Pusa basmati-6 and Basmati-564 for

number of tillers plant⁻¹, Punjab basmati-2 followed by Ranbir basmati and Pusa basmati-6, for number of panicles plant⁻¹, Basmati-564 followed by Kasturi and Pusa Sugandh-5 for panicle length, Pusa basmati-1609 followed by Pusa basmati-1121 and Pusa basmati-1637 for 1000 grain weight, Taravadi, Pusa basmati-1609 and Pant sugandh dhan-15 for number of filled grains per panicle, Punjab basmati-4, Kas-

turi and Pant sugandh dhan-15 for spikelet fertility, had exhibited higher mean performance and hence, on a overall study of desirable yield related traits the genotypes, Pusa basmati-6, Basmati-564, Pusa basmati-1609, Pant sugandh dhan-15 and Kasturi could be further exploited for development of agronomically superior cultivars of basmati rice as they have shown higher *per se* performance for the desired yield contributing traits.

Considering the drought related physiological traits, the genotypes, Vallabh basmati-23, Kasturi, and CSR-30 registered the maximum mean value for SCMR and Sanwal basmati, Pusa sugandh-5 and Vallabh basmati-22 shown minimum mean values for specific leaf area, Pusa basmati-1637, Basmati-386, and Pant sugandh dhan-15 for RMI, Ranbir basmati, Vallabh basmati-24 and Vallabh basmati-21 for CT. Similarly the genotypes, Vallabh basmati-24, Kasturi, and Vallabh Nagina-1 registered the maximum mean values for RWC and Pusa basmati 1612, Pant basmati-1, and Pusa basmati-1509 for TCC. From this study it is inferred that the genotypes Vallabh basmati 24, Kasturi, and Vallabh Nagina-1 could be considered as the best for exploiting the higher yields in drought environment in further breeding programs. The two lines viz., Pusa basmati -1728 possessing high harvest index coupled with higher yield, Vallabh basmati-24 possessing maximum SCMR and minimum SLA, higher RWC and thus could be utilized for the improvement of grain yield along with drought avoidance capabilities in further breeding programs. The higher chlorophyll content compared to other genotypes thus proved efficient in current photosynthesis and higher grain filling percentage in turn it facilitates for identification of relatively drought tolerant genotypes.

The results of variability, heritability and genetic advance as percentage of mean are presented in Table 3. In the present study, the genotypic coefficients of variation for all the characters studied were lesser than the phenotypic coefficients of variation indicating the modifying effect of the environment in association with the characters at genotypic level. The difference between magnitude of genotypic and phenotypic coefficient of variation showed low dif-

ference for all the characters studied indicating good correspondence between genotypic and phenotypic expression of traits with low level of environmental factors operating on the traits. The highest estimate of coefficient of variation was registered for total chlorophyll content (GCV = 42.08% ; PCV = 43.63%) followed by number of unfilled grains per panicle (GCV = 36.34% ; PCV = 37.82%), harvest index (GCV = 28.30%; PCV = 28.90%), grain yield per plant (GCV = 24.96%; PCV = 25.78%), number of filled grains per panicle (GCV = 23.67%; PCV = 24.32%), number of tillers per plant (GCV = 22.55%; PCV = 25.01%), relative membrane injury (GCV = 21.12%; PCV = 21.97%) and number of spikelets per panicle (GCV = 21.23% ; PCV = 21.92%), which indicated the existence of immense inherent variability that remained unaltered by environmental conditions among the genotypes, which in turn more useful for exploitation in hybridization and/or selection. High variance in yield per plant was observed by Aditya and Bhartiya (2013) and Tripathi *et al.* (2018).

Moderate estimates of coefficients of variation were observed for number of panicles per plant (GCV = 18.62% ; PCV = 20.88%) followed by specific leaf area (GCV = 17.19% ; PCV = 17.26%), SPAD chlorophyll meter reading (GCV = 16.16% ; PCV = 16.42%) and plant height (GCV = 14.27% ; PCV = 14.65%). This indicated the existence of sufficient variability for attempting selections to improve these traits in the genotypes studied. On contrary, low estimates of coefficients of variation were recorded for days to 50% flowering (GCV = 8.16% ; PCV = 8.71%) followed by spikelet fertility (GCV = 8.10% ; PCV = 9.51%), relative water content (GCV = 7.07% ; PCV = 7.32%), panicle length (GCV = 6.99% ; PCV = 9.47%), days to maturity (GCV = 6.67%; PCV = 7.18%) and canopy temperature (GCV = 3.23% ; PCV = 7.13%) indicating narrow range of variability for these traits there by restricting the scope for selection. Low estimates of genotypic coefficient of variation and moderate estimates of phenotypic coefficient of variation were reported for 1000 grain weight (GCV = 8.38%; PCV = 12.68%). Tripathi *et al.* (2018), Singh and Verma (2018), Paikomba *et al.* (2014) and Aditya and Bhartiya (2013); all observed low coefficients of variance for 1000 grain weight.

High estimate of heritability was recorded for specific leaf area (99.2%), SPAD chlorophyll meter reading (96.89%), harvest index (95.87%), plant height (94.93%), number of filled grains per panicle (94.68%), number of spikelets per panicle (93.85%), grain yield per plant (93.69%), relative water content (93.18%), total chlorophyll content (93.00%), relative membrane injury (92.43%), number of unfilled grains per panicle (92.32%), days to 50% flowering (87.74%), days to maturity (86.21%), number of tillers plant⁻¹ (81.31%), number of panicles per plant (79.54%) and spikelet fertility (72.49%), in the decreasing order of their magnitude. High heritability for the quantitative characters indicated the presence of additive genes and suggested the scope of genetic improvement of these characters through simple selection. Moderate heritability was registered for panicle length (54.5%) and 1000 grain weight (43.74%). Low heritability was registered for canopy temperature (20.45%). Islam *et al.* (2015) stated high genetic advance and heritability for the number of grains per plant and also for the grain yield per plant. Tuhina-Khatun *et al.* (2015) reported high heritability in the NFG and GY/plant (g) among the 22 traits under upland condition. Swamy and Kumar (2013) reported that the medium to high heritability for GY under both RS and NS trials. In addition, Sedeek *et al.* (2009) and Sohrabi *et al.* (2012) reported a high heritability for DTF under RS condition.

The estimate of genetic advance was highest for number of spikelets/panicle (73.05), number of filled grains per panicle (67.27), specific leaf area (54.01), plant height (31.29), harvest index (24.38) and number of unfilled grains per panicle (23.91), whereas moderate genetic advance was recorded in days to maturity (16.74), days to 50% flowering (14.50), SPAD chlorophyll meter reading (12.86), relative water content (12.57) and spikelet fertility (11.67) indicating that these characters were governed by additive genes and selection will be rewarding for improvement of these traits. The remaining traits viz., grain yield per plant (9.58), total chlorophyll content (7.72), relative membrane injury (7.34), number of tillers per plant (6.07), number of panicles per plant (2.86), length of panicle (2.83), 1000 grain weight (2.51) and canopy temperature (1.03) registered low genetic advance in their decreasing order

and indicated that most of the traits were controlled by polygenes of non-additive nature.

The maximum genetic advance as percent of mean was registered for total chlorophyll content (83.59%), number of unfilled grains per panicle (71.93%), harvest index (57.09%), grain yield per plant (49.76%), number of filled grains per panicle (47.44%), number of spikelets/panicle (42.37%), number of tillers per plant (41.89%), relative membrane injury (41.83%), specific leaf area (35.26%), number of panicles per plant (34.21%), SPAD chlorophyll meter reading (32.76%) and plant height (28.65%) in the decreasing order. On contrary, moderate values of genetic advance as percent of mean were observed for days to 50% flowering (15.74%), spikelet fertility (14.20%), relative water content (14.05%), days to maturity (12.76%), 1000 grain weight (11.42%) and length of panicle (10.63%). While, low estimates of genetic advance as percent of mean were recorded for canopy temperature (3.00%).

Heritability is the heritable portion of phenotypic variance. It is a good index of transmission of characters from parents to their offspring. The estimates of heritability help the plant breeder in selection of elite genotypes from divergent population. But heritability itself does not provide any indication towards the amount of genetic progress that would result in selecting best individual rather it depends upon the amount of genetic advance. Hence, high heritability coupled with high genetic advance as percent of mean could be considered for selection of elite genotypes. In the present investigation, high heritability coupled with high genetic advance as percent of mean were recorded for plant height, number of tillers per plant, number of panicles per plant, number of spikelets/panicle, number of filled grains per panicle, number of unfilled grains per panicle, grain yield per plant, harvest index, SPAD chlorophyll meter reading, total chlorophyll content, specific leaf area and relative membrane injury which indicated the predominance of additive gene effects in controlling these traits suggesting the early and simple selection could be exercised due to fixable additive gene effects. High heritability coupled with moderate genetic advance was registered for days to 50% flowering, days to maturity, spikelet fertility and relative water

content indicating that the character is governed by additive genes and may express consistently in succeeding generations, leading to greater efficiency of breeding program. These results were supported by Adhikari *et al.* (2018). Moderate heritability coupled with moderate genetic advance as percent of mean was observed for length of panicle and 1000 grain weight indicating that both additive and non-additive gene actions had a role in inheritance and phenotypic selection would be effective. In contrast, low heritability coupled with low genetic advance as percent of mean was accounted for canopy temperature.

By and large, in the present study, higher GCV, high heritability and high genetic advance as percent of mean were observed for plant height, number of tillers per plant, number of panicles per plant, number of spikelets/panicle, number of filled grains per panicle, number of unfilled grains per panicle, grain yield per plant, harvest index, SPAD chlorophyll meter reading, total chlorophyll content, specific leaf area and relative membrane injury revealed that simple directional selection would be effective for improving these traits with connotation that genetic variation was mainly due to the presence of additive gene effects. Conversely, low GCV, moderate heritability and moderate genetic advance as percent of mean were registered for length of panicle and 1000 grain weight indicating that these traits were more likely to be governed by the non-additive gene action. In this case, simple selection alone may not be effective and needs recurrent selection procedures with intensive intermatings.

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