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Genetic variability, heritability and correlation coefficient analysis in rice (*Oryza sativa* L.) germplasm

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Abstract

The present investigation entitled "Assessment of genetic variability and qualitative traits of Rice (*Oryza sativa* L.) germplasm for yield and yield attributing characters" was undertaken to evaluate 72 germplasm accessions along with three local checks in rice for yield and yield attributing characters in rice with row to row and plant to plant spacing 20×15 cm. The experiment was carried out to study the morphological characters, to access the genetic variability and to estimate the correlation coefficient among yield and its contributing traits in rice germplasm. The experiment was carried out at experimental area of rice in instructional farm, College of Agriculture, Rewa (M.P.) during kharif-2018. The experiment was laid out in Randomized Block Design with three replications.

The analysis of variance revealed that highly significant variations were recorded among all the germplasm accessions for all the traits under study. It indicated that adequate amount of genetic variability were present in all studied characters. High estimates of phenotypic coefficient of variations (PCV%), genotypic coefficient of variations (GCV%) and high heritability coupled with high genetic advance as percentage of mean was recorded for number of tillers per plant, number of productive tillers per plant, number of grains per panicle, biological yield per plant and grain yield per plant. These characters showed additive gene action in their expression.

The grain yield per plant had significant positive correlation with biological yield per plant followed by harvest index, panicle length, number of tillers per plant, number of productive tillers per plant, seed index and number of grains per panicle. The grain yield also showed negative correlation with plant height, days to 50 percent flowering and days to maturity.

Keywords: Rice, variability, heritability, genetic advance and correlation

Introduction

Rice (*Oryza sativa* L.) is an important member of family Poaceae (2n = 24), *Oryza* genus has 2 cultivated and 22 wild species. Three eco-geographic races of rice i.e. Indica, Japonica and Jawanica are widely cultivated in Asian country. Rice is primary food, usually consumed in less developed or developing country. It is predicted that up to 2025, the world's population may exceed beyond 8 billion which will require about 765 mt of rice which is expected 70 percent more than today's consumption. Hence, increase in rice productivity is the urgent need to feed over increasing world's population, which can be achieved through the application of hybrid varieties in commercial cultivation along with proper utilization of land, water, chemicals and other inputs. The crop improvement is the best solution of yield enhancement in rice.

The area, production and productivity of rice in India is 43.39 m ha, 108.32 mt and 2404 kg/ha, respectively. Similarly, in Madhya Pradesh it is also grown in an area of 1.93 m ha with a production of 2.74 mt and the productivity of 1768 kg/ha. (Anonymous 2016) [3].

The genetic variability refers to presence of the differences among the different germplasm lines present in the population. Selection is effective when there is significant amount of genetic variability among the individuals of different germplasm lines. The presence of genetic variability along with high genetic advance for the characters which is significant positive correlated with grain yield per plant is basic requirements to formulate selection criteria for transgressive breeding programme in rice.

Material and Methods

The experiment was conducted in kharif-2018 at experimental area of rice in Instructional

Farm, College of Agriculture, Rewa (M.P.) to investigate the seventy-two germplasm accessions with three local checks in Randomized Block Design. The experimental field divided into nine blocks and three replications each block consisted twenty-four germplasm accessions and one check, respectively. Each genotype was grown in a plot which size 0.6x1.0 m and row to row spacing 20 cm and plant to plant spacing 15 cm, respectively. Checks are randomized within in the blocks twenty-four days old seedlings transplanted in the experimental field manually. Recommended dose of fertilizer 120N:60P:40K kg/ha was applied. The entire dose of K₂O and P₂O₅ was applied with half dose of N as basal dose at the time of field preparation and remaining dose of N was split in two splits at twenty-five days interval in the crop field.

Ten randomly plants were a selection of from each genotype in each replication and observations were noted on these plants for the characters like, Plant height (cm), number of tillers per plant, number of productive tillers per plant, panicle length (cm), number of grains per panicle, 100 seed weight (g), biological yield per plant (g), harvest index (%) and grain yield per plant (g), while days to 50% flowering and days to maturity were recorded on plot basis.

Experiment material

The material consisted of seventy-two germplasm accessions collected from various areas of Rewa (M.P.) with three local checks that is LC-767, LG-964 and MTU-1010. The material used for investigation is given table 1.

Table 1: Source of germplasm

S. No.	Entry number	Name of Germplasm
1	6	Badki Luchai
2	10	Badal phool
3	11	Baghmechha
4	12	Bagari
5	15	Banko
6	24	Bela
7	25	Berjali
8	26	Bhata phool
9	27	Bhejari
10	33	Biranj
11	38	Chinmauri
12	50	Dhaniyadhan
13	52	Dilbaxa
14	55	Dubraj
15	56	Doodhi
16	58	Geeta
17	61	Hardgudi
18	63	Jeeraphool
19	64	Jeerasar
20	72	Kanga
21	93	Karanphool
22	104	Karmodhan
23	106	Kerakhambh
24	111	Khansari
25	114	Kumbran
26	115	Kuthalidhan
27	120	Lamera
28	135	Lohadhi
29	141	Malati
30	142	Masooriya
31	143	Nadawal
32	154	Rajgauhi
33	155	Ramkajari
34	162	Safari
35	167	SAiri
36	172	Samasar
37	177	Samda
38	181	Sauthi
39	182	Sonkharchi
40	187	Surja
41	191	Hauhi
42	199	Bhalshankar
43	200	Pilkormera
44	201	Shyamjeera
45	203	Galari
46	204	Bilailuchai
47	205	Badshahbhog
48	208	Hardigathi
49	209	Shervani
50	210	Badshahprasan

51	211	Nevari
52	212	Kotava
53	215	Durgaprasad
54	217	Assamchidi
55	218	Koshamkhand
56	219	Senkursar
57	220	Keraphool
58	221	Bhaloodubraj
59	228	Kadamphool
60	229	Turailuchai
61	230	Phoolmechha
62	231	Hansraj
63	238	Ajan
64	243	Kannauji
65	244	Kerakhambh
66	250	Kansari
67	257	Karagi
68	261	Kosamsar
69	267	Kalajeera
70	290	Karahani
71	291	Katanga
72	292	Kudurlai
73	LC-767	
74	LC-964	
75	MTU-1010	

Statistical analysis

Different genetic parameters like, genotypic and phenotypic variance, GCV and PCV, heritability, genetic advance, genetic advance as percent of mean were estimated by using following formula:

Analysis of variance

The analysis of variance for twelve studied characters were estimated as per the model proposed by Panse and Sukhatme (1961) [11].

The genotypic and phenotypic variance was calculated as per the formulae (Burton and Devane 1952).

Genotypic variance (σ^2g) =

$$\frac{(\text{Mean sum of squares due to treatments} - \text{Mean sum of squares due to error})}{\text{Number of replications}}$$

Phenotypic variance (σ^2p) = (σ^2g) + (σ^2e)

Where, (σ^2e) = Error variance

Genotypic and phenotypic coefficients of variance

The genotypic and phenotypic coefficient of variance was calculated by the formulae given by Burton (1952).

$$\text{Genotypic coefficient of variation (GCV \%)} = \frac{\text{Genotypic standard deviation}}{\text{Mean}} \times 100$$

$$\text{Phenotypic coefficient of variation (PCV \%)} = \frac{\text{Phenotypic standard deviation}}{\text{Mean}} \times 100$$

Categorization of the range of variation was affected as proposed by Siva Subramanian and Madhavamenon (1973) as low (<10%), moderate (10-20%) and high (>20%).

Heritability (Broad sense) h^2

Heritability in broad sense h^2 (h^2) was calculated by the formula given by Lush (1940) [9].

$$\text{Broad sense Heritability} = \frac{\sigma^2g}{\sigma^2p} \times 100$$

Where, σ^2g = Genotypic variance and σ^2p = Phenotypic variance.

As proposed by Johnson *et al.* (1955), heritability was categorized as: low (<30%), moderate (30 - 60%) and high (>60%).

Genetic advance

The genetic advance was calculated by the following formula given by Johnson *et al.* (1955).

$$GA = k \sigma_p H$$

Where, GA = Genetic advance, k = Selection differential at 5% selection intensity.

σ_p = Phenotypic standard deviation and H = Heritability

Genetic advance as percent of mean (GA as percent mean)

Genetic advance as percent of mean was calculated as per the formula

$$\text{GA as percentage of mean} = \frac{\text{Genetic advance}}{\text{General mean}} \times 100$$

The degree of genetic advance as percent of mean was classified as suggested by Johnson *et al.* (1955) as low (<10%), moderate (10-20%) and high (>20%).

Correlation coefficient analysis

Genotypic and phenotypic correlation coefficients were calculated using the method given by Johnson *et al.* (1955).

The significance of correlation coefficients was tested by comparing the genotypic and phenotypic correlation coefficients with table value [Fisher and Yates (1967)] at (n-2) degrees of freedom at 5% and 1% level where, 'n' denotes the number of treatments used in the calculations.

Result and Discussion

Analysis of variance

The analysis of variance revealed that highly significant variations were recorded among all the germplasm accessions for all the traits under study. It indicated that adequate amount

of genetic variability were present in all studied characters. Similar findings were also reported by Sameera *et al.* (2013)^[15] and Sarawgi *et al.* (2013)^[17]. The analysis of variance for yield and yield attributing traits are presented in Table 2.

Table 2: Analysis of variance for yield and yield attributing characters of rice germplasm accessions

Source of variation	Mean sum of squares											
	D.F.	DTF	DTM	PH	PL	NTPP	NPTPP	NGPP	S.I.	BYPP	HI	GYPP
Replication	2	4.80	1.24	0.64	0.51	3.28	3.58	237.9	0.00	20.18	0.12	0.94
Treatment	74	88.94 **	95.71 **	332.18 **	15.03 **	12.60 **	11.09 **	1818.92 **	0.36 **	204.93 **	93.70 **	51.05 **
Error	148	9.17	3.18	2.09	0.22	1.09	1.13	61.95	0.006	11.45	0.59	1.11

**Significant at 1% level of probability.

Mean performance

The mean performance of seventy-two rice germplasm accessions along with three local checks for yield and yield attributing characters is presented in Table 3. The studied genotypes had large range of variation for all the characters. The maximum grain yield per plant was observed 28.50 g by MTU-1010 followed by LC-964, while minimum grain yield per plant was recorded by Malati (3.16 g) with an overall mean value of 8.42 g. The higher grain per plant in this germplasm accession was attributed due to increase in number of tillers per plant, number of productive tillers per plant, panicle length, number of grain per panicle, seed index and harvest index. Similar kinds of results were also reported by Tariku *et al.* (2013)^[20] and Rolando *et al.* (2016)^[14].

Estimation of parameters of genetic variability: The

parameters of genetic variability like mean, range, GCV (%), PCV (%), h²bs (%), GA as percentage of mean for all the characters under study were recorded and are given in table 4. High estimates of phenotypic coefficient of variations (PCV%) and genotypic coefficient of variations (GCV%) were recorded for number of tillers per plant, number of productive tillers per plant, number of grains per panicle, biological yield per plant and grain yield per plant. These characters showed additive gene action in their expression. Similar results were also reported by Rashid *et al.* (2017)^[13] and Patel *et al.* (2014)^[12] for number of grain per panicle. Prakash *et al.* (2018), Abebe *et al.* (2017)^[1], Gour *et al.* (2017)^[6], Veludandi *et al.* (2017)^[23] and Patel *et al.* (2014)^[12] for biological yield per plant, Singh *et al.* (2018)^[18] for number of productive tillers per plant and Kishore *et al.* (2015)^[8] for number of tillers per plant.

Table 3: Mean performance of different characters

S. No.	Genotype	DTF	DTM	PH	PL	TPP	PTPP	NGPP	100-GW	BYPP	HI	GYPP
1	Badaki Luchai	98.00	130.00	126.400	22.100	7.433	7.100	83.200	1.367	21.367	25.933	4.933
2	Badal phool	94.667	125.333	116.133	22.833	9.700	9.067	82.533	2.400	33.867	29.800	10.300
3	Baghmechha	94.833	126.667	103.900	22.500	8.200	7.900	84.100	2.167	32.500	26.267	9.233
4	Bagari	86.667	118.667	109.467	21.567	11.967	11.300	73.867	2.433	29.400	32.667	10.267
5	Banko	94.333	127.000	87.900	21.533	10.200	9.400	62.333	2.400	22.000	39.300	9.067
6	Bela	85.000	118.667	96.867	22.800	9.767	9.333	59.533	2.467	24.367	28.333	7.400
7	Berjali	78.667	111.000	90.100	22.567	13.967	12.467	53.367	2.633	31.833	34.933	11.600
8	Bhata phool	87.333	120.667	94.700	21.067	7.833	7.200	65.767	2.467	24.000	26.900	6.967
9	Bhejari	89.333	120.667	110.267	21.867	9.300	8.367	31.467	2.467	28.200	31.300	8.433
10	Biranj	96.000	128.667	88.200	19.233	8.833	7.767	83.333	2.233	15.600	30.767	5.167
11	Chinmauri	87.167	117.333	92.333	21.233	10.400	8.800	73.800	2.300	25.267	30.100	6.767
12	Dhaniyadhan	98.000	130.000	112.300	20.167	6.800	6.067	70.467	2.200	21.567	27.567	5.600
13	Dilbaxa	91.667	123.667	105.700	20.867	6.387	5.867	99.800	2.200	23.600	26.100	5.567
14	Dubraj	92.667	124.000	101.933	20.767	10.567	9.867	90.567	2.300	20.967	31.900	6.700
15	Doodhi	85.333	117.333	113.100	23.167	7.833	6.967	71.033	2.400	25.200	33.267	8.700
16	Geeta	88.000	118.667	121.067	24.733	6.967	6.500	76.333	2.567	23.967	24.233	6.200
17	Hardgudi	93.333	125.000	119.467	24.133	7.167	6.633	60.200	1.867	25.600	30.867	7.400
18	Jeeraphool	77.333	109.667	105.633	19.900	13.733	12.633	58.200	2.367	26.400	29.133	7.400
19	Jeerasar	91.000	124.000	116.067	22.367	8.567	7.567	77.033	2.433	19.600	31.323	5.933
20	Kanga	88.667	122.333	128.300	22.900	15.700	14.533	76.800	2.333	40.600	31.907	13.067
21	Karanphool	80.667	109.333	84.600	20.867	11.800	10.200	58.933	3.267	29.567	31.117	8.867
22	Karmodhan	89.333	123.333	101.967	21.200	8.100	7.100	77.367	2.367	23.067	32.203	7.633
23	Kerakhambh	85.667	118.667	104.300	21.450	8.467	7.600	80.533	1.900	19.600	29.833	6.467
24	Khansari	86.667	118.333	120.000	23.933	7.600	6.467	80.900	2.300	29.967	30.667	8.967
25	Kumhran	89.667	118.000	111.540	20.300	7.800	6.867	97.467	2.467	25.967	22.970	6.567
26	Kuthalidhan	82.667	115.333	111.033	21.600	11.500	9.700	71.333	2.467	26.100	23.557	6.933
27	Lamera	84.000	111.000	105.167	23.667	7.467	6.633	92.100	1.983	29.633	31.367	9.500
28	Lohandhi	84.000	116.000	105.233	20.937	8.000	6.767	94.000	1.500	17.667	30.100	4.700
29	Malati	88.000	119.333	118.000	21.967	5.467	4.733	75.500	2.433	12.400	25.733	3.167
30	Mansooriya	94.333	123.000	113.967	18.033	8.200	7.367	46.500	2.333	26.107	22.033	5.767
31	Nadawal	86.667	116.667	104.200	22.267	10.200	8.967	42.967	2.267	23.500	34.800	8.000
32	Rajgauhi	99.000	126.667	119.433	21.700	7.333	6.400	67.100	2.133	27.600	25.000	6.733
33	Ramkajari	92.667	123.333	116.733	25.067	8.233	6.733	93.367	2.600	26.267	25.633	6.400

34	Safari	94.667	123.667	106.900	22.967	10.433	9.500	74.967	2.200	35.067	26.333	9.667
35	Sairi	87.267	118.667	98.967	24.967	11.933	10.233	57.500	2.167	28.900	35.367	12.133
36	Samasar	82.333	114.333	102.300	24.400	10.167	9.633	81.400	1.567	29.400	35.467	9.633
37	Samda	83.000	112.667	102.400	22.067	9.167	7.183	63.667	2.700	27.333	37.967	9.500
38	Saunthi	91.333	123.333	122.867	31.633	9.300	8.067	74.467	2.650	25.500	31.333	8.333
39	Sonkharchi	92.967	122.667	107.567	22.267	6.800	5.633	64.533	2.667	23.967	22.367	5.900
40	Surja	92.000	124.667	112.067	22.300	9.633	8.300	81.367	2.567	24.833	29.333	7.667
41	Hauhi	91.167	120.600	125.167	22.067	8.167	6.967	39.267	2.533	21.567	25.733	6.133
42	Bhalshankar	80.833	112.333	80.400	20.300	11.600	10.133	51.367	2.167	31.933	37.133	10.400
43	Pilkormeva	96.900	127.000	110.733	19.967	7.800	6.633	60.767	2.067	23.733	18.133	4.300
44	Shyamjeer	91.000	121.000	111.167	18.300	9.067	7.500	75.667	2.100	26.067	33.300	9.167
45	Galari	96.333	123.667	110.667	22.733	9.733	8.500	81.700	1.400	21.733	22.100	4.767
46	Bilailuchai	93.000	124.667	114.033	23.667	8.433	7.367	162.033	2.000	19.267	22.367	4.833
47	Badshahbhog	84.333	116.333	105.467	22.000	11.300	9.400	36.333	2.200	25.567	39.233	9.200
48	Hardigathi	92.000	121.667	109.067	25.300	7.833	6.367	65.567	2.200	27.167	25.033	6.200
49	Shervani	96.333	126.333	107.967	21.067	7.733	6.333	73.400	2.600	26.567	33.767	8.833
50	Badshahparsan	82.000	112.667	112.733	23.333	9.667	8.633	67.000	1.833	31.167	29.400	9.800
51	Nevari	83.667	114.000	106.273	25.533	10.600	8.833	63.133	2.233	23.833	37.300	9.167
52	Kotava	77.667	108.000	108.600	21.967	9.267	7.633	108.133	2.300	22.667	28.600	6.900
53	Durgaprasad	90.000	120.667	119.433	23.467	8.633	6.867	65.267	2.400	27.467	20.333	5.300
54	Assamchidi	80.667	112.667	109.167	22.500	9.200	7.133	50.733	2.600	21.533	29.233	6.533
55	Kosamkhand	83.667	115.333	105.733	22.333	11.733	9.667	80.267	2.433	26.400	33.867	9.133
56	Senkursar	93.667	124.000	123.733	22.700	9.400	7.367	128.767	1.600	24.733	18.700	5.000
57	Keraphool	81.667	112.333	86.967	21.500	10.567	8.700	58.600	2.967	22.567	32.300	7.167
58	Bhaloodubraj	95.000	124.333	119.400	25.167	7.800	6.233	110.400	1.500	21.100	26.100	5.667
59	Kadamphool	91.333	123.333	88.900	18.733	7.233	6.467	55.400	1.733	21.733	26.600	6.600
60	Turailuchai	87.000	118.667	87.733	19.867	7.233	5.800	133.667	2.267	26.100	36.933	9.767
61	Phoolmechha	90.667	119.667	91.500	19.700	8.050	6.433	89.367	1.567	15.400	29.067	4.567
62	hansraj	94.667	128.667	104.000	22.167	8.067	6.667	54.300	1.833	24.800	28.833	7.100
63	Ajan	85.000	115.667	111.100	22.767	10.167	8.783	49.433	2.167	25.500	35.500	8.333
64	Kannauji	92.333	121.000	114.067	24.467	7.867	6.807	67.200	2.367	26.633	26.133	6.800
65	Kerakhambh	98.000	128.333	99.833	20.533	7.900	6.500	75.367	2.433	27.673	36.067	9.500
66	Kansari	81.333	107.000	104.200	21.167	13.083	11.167	36.367	2.467	31.133	37.033	10.533
67	Karagi	99.000	131.667	104.567	19.833	9.533	7.700	58.400	2.367	26.433	27.800	7.567
68	Kosamsar	92.667	125.333	103.900	21.000	7.667	6.233	93.500	2.200	26.833	33.167	8.433
69	Kalajeera	87.667	121.000	95.833	21.033	13.567	12.267	95.400	2.667	44.933	31.000	13.600
70	Karahani	94.000	125.667	113.667	22.700	6.833	6.000	64.567	2.267	26.600	28.767	7.767
71	Katanga	82.167	113.333	109.767	24.367	6.767	5.667	71.467	2.333	33.600	26.300	9.367
72	Kudurlai	92.667	124.333	115.667	20.367	7.400	6.233	68.700	2.533	25.167	31.110	7.800
73	MTU-1010	87.667	119.000	89.067	21.900	7.633	6.433	159.267	2.400	55.933	51.267	28.500
74	LC-767	95.000	127.000	106.300	28.867	7.167	6.367	132.967	2.533	47.667	38.367	19.833
75	LC-964	91.333	122.000	103.333	28.200	13.567	11.967	75.067	2.467	69.400	40.233	27.800
	Overall mean	89.297	120.368	106.923	22.313	9.162	7.962	75.580	2.270	27.053	30.168	8.421
	C.V.	6.668	5.757	7.920	8.702	11.414	13.400	10.414	12.204	12.510	14.953	12.505
	S.E.	4.862	5.658	6.914	1.585	0.854	0.871	6.427	0.226	2.763	3.683	0.860
	C.D. %	8.225	9.571	11.697	2.682	1.444	1.474	1.445	0.383	4.674	6.231	1.454
	Range Lowest	77.333	107.000	80.400	18.033	5.467	4.733	31.467	1.367	12.400	18.133	3.1667
	Range Highest	99.000	131.670	128.300	31.633	15.700	14.533	162.03	3.267	69.400	51.267	28.500

Table 4: Estimation of variability, heritability and genetic advance for yield and yield attributing traits of rice germplasm

Characters	Range		Mean	GCV%	PCV%	h ² (bs)%	GA as % mean
	Min	Max					
DTF	77.333	99.000	89.297	4.848	8.244	34.578	5.872
DTM	107.000	131.670	120.368	3.375	6.673	25.578	3.516
PH	80.400	128.300	106.923	8.820	11.854	55.358	13.518
PL	18.033	31.633	22.313	8.673	12.286	49.830	12.611
TPP	5.467	15.700	9.162	21.375	24.233	77.804	38.839
PTPP	4.733	14.533	7.962	22.885	26.520	74.468	40.682
NGPP	31.467	162.03	75.580	32.019	33.670	90.434	62.726
100-GW	1.367	3.267	2.270	13.643	18.304	55.551	20.947
BYPP	12.400	69.400	27.053	29.686	32.214	84.920	56.354
HI	18.133	51.267	30.168	16.393	22.189	54.583	24.949
GYPP	3.1667	28.500	8.421	48.449	50.037	93.754	96.638

High heritability coupled with high genetic advance as percentage of mean were recorded for number of tillers per plant, number of productive tillers per plant, number of grains

per panicle, biological yield per plant and grain yield per plant. These characters showed additive gene action in their expression. Heritability refers the contribution of genetic

variability to the phenotypic variability for traits under consideration and it is good indicator of the transmission of traits from parents to their progeny. The heritability estimate can be utilized for the forecasting of the genetic gain, which implies the genetic improvement that would result from the selection of best genotype. High heritability estimates were recorded for all studied characters; it indicated that all the characters inherited from generation to generation. Similar findings were also reported by Gour *et al.* (2017) ^[6] for biological yield per plant, Bandi *et al.* (2018) ^[4], Abebe *et al.* (2017) ^[1] and Tejaswini *et al.* (2016) ^[21] for grain yield per plant, Akter *et al.* (2018) ^[2], Singh *et al.* (2018) ^[18], Rashid *et al.* (2018) and Tuwar *et al.* (2013) ^[22] for number of grains per panicle, Bandi *et al.* (2018) ^[4], Gour *et al.* (2017) ^[6] and Sameera *et al.* (2016) ^[16] for number of tillers per plant, while Singh *et al.* (2018) ^[18], Sameera *et al.* (2016) ^[16] for number of productive tillers per plant.

Correlation analysis

The correlation coefficient was partitioned into phenotypic and genotypic correlation coefficient. Genotypic correlation coefficients provide a measure of genetic association between characters and were generally used in selection of one character as a means of improving another. The magnitude of genotypic correlation was higher than phenotypic correlation. The grain yield per plant had significant positive correlation with biological yield per plant followed by harvest index, panicle length, number of tillers per plant, number of productive tillers per plant, seed index and number of grains per panicle. It indicated that improvement in these characters ultimately increased the grain yield, it means these characters may be included in selection criteria for rice improvement programme. However similar findings were also reported by Gour *et al.* (2017) ^[6] for number of tillers per plant, number of productive tillers per plant, biological yield per plant and harvest index, Panigrahi *et al.* (2018) ^[10] for number of tillers per plant, number of productive tillers per plant and number of grains per panicle, Singh *et al.* (2018) ^[18] for number of tillers per plant, number of productive tillers per plant, panicle length, number of grains per panicle, seed index, biological yield per plant and harvest index.

Conclusion

Analysis of variance exhibited that variance due to the correlation analysis was significant for all the traits, this suggested that adequate variability is available in germplasm accessions used for present investigation. Analysis of data exhibited highly significant differences among germplasm accessions for all the characters.

High estimates of phenotypic coefficient of variations (PCV%), genotypic coefficient of variations (GCV%) and high heritability coupled with high genetic advance as percentage of mean was recorded for were recorded for number of tillers per plant, number of productive tillers per plant, number of grains per panicle, biological yield per plant and grain yield per plant. These characters showed additive gene action in their expression.

The grain yield per plant had significant positive correlation with biological yield per plant followed by harvest index, panicle length, number of tillers per plant, number of productive tillers per plant, seed index and number of grains per panicle. The grain yield also showed negative correlation with plant height, days to 50 percent flowering and days to maturity. It indicated that improvement in these characters

simultaneously increased the grain yield in rice. It showed that these characters may be included in selection criteria to enhance the grain yield in rice.

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