

Morphological Traits as Selection Indices in Rice: A Statistical View

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Abstract The objectives of this study were to estimate variability and genetic parameters of sixty-eight rice genotypes for twelve agronomically important characters. Significant variations were observed for all characters. Considering genetic parameters, high genotypic and phenotypic coefficients of variations, high heritability (broad sense) and high genetic advance as percentage of mean were shown by eight characters viz. tillers per plant, days to 50% flowering, harvest index, spikelets per panicle, spikelets per plant, spikelet density, panicles per plant and grain yield. Thus these characters were under the influence of additive gene action and a satisfactory selection programme for agronomic improvement on the basis of these characters is possible.

Keywords Genotypic Coefficients of Variation, Phenotypic Coefficients of Variation, Heritability, Genetic Advance

1. Introduction

Genetic improvement mainly depends on the amount of genetic variability present in the population which is a ubiquitous property of all species in nature. The importance of genetic diversity in the selection of suitable genotypes for hybridization has been stressed by several scientists in different crops [1-3]. It results due to differences either in the genetic constitutions of the individuals of the population or due to the differences in the environment in which they grown. The genetic variability present in the germplasm of a crop and its estimation is pre-requisite for making any effective breeding programme. These genetic variations might be either heritable or non-heritable. The magnitude of variation due to heritable component is very important because, it would be a guide for selection of parents for crop improvement programmes of the population. Thus genetic variability for agronomic traits is the key component of breeding programs for broadening the gene pool of rice and

other crops. For any trait of interest, observed phenotypic differences among individuals may be due to differences in the genetic codes for that trait or may be the result of variation in environmental condition. A large number of agronomically significant characters are known to be affected by environmental factors. Selection based on the phenotype might not be fruitful in such traits. In breeding programmes, it is often difficult to manipulate such traits, since several inter-componential characters indirectly control these traits [4]. So the measurement of genetic variation and understanding of mode of inheritance of quantitative traits, therefore, are essential steps in any crop improvement programme. Heritability estimates provide authentic information about a particular genetic attribute which will be transmitted to the successive generations. A broad-sense heritability estimate provides information on the relative magnitude of genetic and environmental variation in the population [5-7] and help breeders to determine the possible extent for improvement through selection. Again the heritable portion of the total variation might not be always due to additive gene action. Thus estimates of heritability alone give no clear indication of the associating genetic progress that would result from selecting the best plants. It is also essential to find out the relative magnitude of additive and non additive genetic variances with regard to the characters of concern. The heritability along with phenotypic variance and the selection intensity, however, promise the estimation of genetic advance or response to selection which is more useful in the selection of promising lines [8-10].

Therefore considering all these facts and recognizing the importance of genetic diversity in plant breeding experiments, the present research work has been taken up.

2. Materials and Methods

The details of the materials used and techniques adopted during the course of investigation are described below.

2.1. Experimental Site and Climate

The present investigation was conducted during the seasons 2009-2010, 2010-2011 and 2011-2012 at a paddy growing field of Dhemaji district, Assam (North Latitude 27 15' to 28 00' and East Longitude 94 05' to 95 30'). The soil of the experimental field was alluvial sandy loamy with pH 5.5. The average humidity during 2009 has been recorded as 81.2%, average temperature as 24.4°C with maximum 30°C and minimum 17.7°C and total rainy days was 128. The average humidity during 2010 has been recorded as 86.2%, average temperature as 23.6°C with maximum 29.1°C and minimum 17.5°C and total rainy days was 143. The average humidity during 2011 has been recorded as 81.7%, average temperature as 23.9°C with maximum 29.7°C and minimum 17.7°C and total rainy days was 94. The average humidity during 2012 has been recorded as 81.1%, average temperature as 23.4°C with maximum 28.8°C and minimum 17.3°C and total rainy days was 128. (Source: Meteorological station 423090 (VELR) and E and D Office, Dhemaji).

2.2. Experimental Materials and Layout Plan

The experimental material of the study comprised of 68 rice genotypes collected from different pockets of the state. The experiment was laid in Randomized Block Design replicated thrice. 45 days old seedlings were transplanted into the experimental site with 20 X 15 cm spacing. Row to row and hill (plant) to hill distance was 20 cm and 15 cm respectively.

2.3. Observations Recorded

The data were recorded for five randomly selected plants from each replication leaving the first two border rows from all the four sides, in order to avoid the sampling error. The observations were recorded as per the following procedure. Mean of readings from five plants were taken replication wise and the mean data was used for statistical analysis for the characters.

Plant height was measured in centimeter from the ground level to the top of the panicle (excluding awn) at the time of maturity. Number of tillers/plant was counted as per plant basis. Days to 50% flowering was determined by counting number of days from date of sowing to the 50 per cent flowering of the plants in the plot initiated [11].

For determining Harvest index, dry weight of both straw and grains of the sampled plants were weighed separately after harvest. By straw, the above ground portions of the plant devoid of grains was meant. According to formula given by Yoshida [11], harvest index was computed as the fraction of grain yield to the total biomass including straw and grain yields, as

$$HI = [(grain\ yield) / (grain\ yield + straw\ yield)] \times 100$$

For length of panicle the average panicle length of five plants on the main Culm from the base of the panicle to the top of the last spikelet excluding awns was recorded in

centimeter. A sample of 100 well developed fresh whole seeds was collected and weighed in grams and computed to 1000 grains weight. Total number of spikelet on main panicle was counted and recorded at the time of maturity. Percentage of viable seeds was estimated by counting the number of well filled grains of five randomly selected panicles for each genotype and expressed in percentage. Spikelet density was calculated according to Chang *et al.*, [12] by dividing total number of spikelet by length of panicle for five randomly selected replicates for each genotypes and expressed in number/cm. Spikelet per plant was determined by counting the number of both well filled and aborted spikelet of five randomly selected replicates. The total numbers of panicles per plant was recorded in five replications for each genotypes. Grain yield/plant was computed according to Datta, [13] with slight modification as

$$GY/P = [(Number\ of\ panicles / plant) \times (number\ of\ spikelet / plant) \times (\% \text{ of Viable seeds}) \times (1000\ seeds\ wt.) \times 10^{-5}]$$

2.4. Statistical Analysis

The mean data recorded on the above observations were subjected to following biometrical analyses:

2.4.1. Standard Error

The standard error of the mean difference (SEM±) was calculated according to the expression suggested by Snedecor and Cochran [14].

2.4.2. Critical Difference

The significance or otherwise the differences between individual means were ascertained by the comparison with appropriate critical difference as described by Panse and Sukhatme [15].

$$C.D. = SEM \times t \ 0.05$$

Where,

t = tabulated value at error degree of freedom at 5 percent level of significance

SEM = standard error of the mean difference

Significant 'F-value' indicates that there is significant difference among the treatments. But to compare any two particular treatments, it is tested against C.D. value.

2.4.3 Analysis of Variance

The analysis of variance was worked out to test the differences among genotypes by F-test. It was carried out according to the procedure of Randomized Block Design for each character as per methodology advocated by Panse and Sukhatme [15]. ANOVA helps in partitioning the total variance into three components viz. replication, treatment and error.

2.4.4. Test of Significance

If the variance ratio (or) F-calculated value for treatment was greater than the f-table value at 5% and 1% level of

significance, the variance between treatments was considered to be significant. If the F-calculated value is less than F-tabulated value, the difference between treatments was considered to be non-significant [16].

2.4.5. Components of Variance

Components of variances were calculated according to the formula given by Lush [17] and Chaudhary and Prasad [18].

2.4.6. Coefficient of Variation (C.V)

It is the measure of variability evolved. Coefficient of variation is the ratio of standard deviation of a sample to its mean and expressed in percentage.

$$CV (\%) = \frac{\text{Standard Deviation}}{\text{Mean}}$$

In the present investigation three types of coefficient of variations were estimated viz., phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV) and error/environmental coefficient of variation (ECV). The formulae used to calculate PCV, GCV and ECV were given by Burton and Devane [19].

Phenotypic coefficient of variation (PCV):

$$PCV\% = \frac{\sigma^2_p}{\bar{X}} \times 100$$

Where,

σ^2_p = Phenotypic standard deviation

\bar{X} = Mean

Genotypic coefficient of variation (GCV):

$$GCV\% = \frac{\sigma^2_g}{\bar{X}} \times 100$$

Where,

σ^2_g = Genotypic standard deviation

\bar{X} = Mean

Environmental of error coefficient of variation (ECV):

$$ECV\% = \frac{\sigma^2_e}{\bar{X}} \times 100$$

Where,

σ^2_e = Error standard deviation

\bar{X} = Mean

GCV and PCV values were categorized as low, moderate and high values as indicated by Sivasubramanian and Menon [20].

2.4.7. Heritability in Broad Sense (h²)

Heritability in broad sense is the ratio of genotypic variance to the total variance. It is that portion of total variability or phenotypic variability which is heritable due to the genotype. Broad sense heritability was estimated as the ratio of genotypic variance to the phenotypic variance and was expressed in percentage [21].

$$h^2 = \frac{\sigma^2_g}{\sigma^2_p} \times 100$$

Where,

σ^2_g = genotypic variance

σ^2_e = phenotypic variance

The heritability percentage was categorized as low, moderate and high as suggested by Robinson *et al.*, [22].

2.4.8. Expected Genetic Advance

Genetic advance is the improvement in mean genotypic value of selected plants over the parental population. The extent of genetic advance as expected from selecting five per cent of the superior progeny was calculated by using the following formula given by Johnson *et al.* [8].

$$GA = K. \sigma_p. h^2$$

Where,

K = Constant selection differential at 5% level intensity (= 2.06)

σ_p = Phenotypic standard deviation

h^2 = Heritability in broad sense

2.4.9. Genetic Advance as Percent of Mean (GAM)

The formula of Genetic advance as percent of mean was as follow:

$$GAM = \frac{GA}{\bar{X}} \times 100$$

Where,

GA = genetic advance

\bar{X} = Grand mean

Genetic advance as per cent of mean was categorized as low, moderate and high by following Johnson *et al.* [8].

3. Results and Discussion

3.1. Height

Plant height is an important trait contributing yield. Prasad *et al.*, [23] also reported that plant height has significant correlation with grain yield. The trait varied significantly (Table I and Table II) among the studied entries which are in agreement with the results of Mohammad *et al.*, [24]. Plant height in rice is generally considered to be controlled by both qualitative and quantitative genes [25]. Ashrafuzzaman *et al.*, [26] also considered that plant height is mostly governed by genetic makeup of the genotypes, but the environmental factors also influence it. The phenotypic variance for this character was higher than corresponding genotypic variance. The phenotypic coefficient of variation (PCV) was also higher than genotypic coefficient of variation (GCV) (Table 3). It is interesting to note that the differences between GCV and PCV values were minimum implying least influence of

environment. Similar result was also found by Okelola *et al.*, [27] and Prajapati *et al.*, [28] for this trait. The character showed high phenotypic and genotypic coefficient of variation, high heritability, high genetic advance and high genetic advance as percentage of mean. This indicates that this character is governed by additive genes and phenotypic selection is adequate to bring about desirable improvement of this character. Pal and Sabesan [29]; Lal and Chauhan [30] and Prajapati *et al.* [28], also found high GCV and PCV, high

heritability and high genetic advance as percentage of mean. These results were also in agreement with the observations of Ahmadikhah [31]. On the other hand Okelola *et al.* [27], Ahmed *et al.*, [32] and Ullah *et al.*, [33] reported moderate GCV and PCV, high heritability and high genetic advance as percentage of mean for this trait and Chakraborty and Chakraborty [34] revealed moderate GCV and PCV, high heritability and moderate genetic advance as percentage of mean for this trait

Table 1. Analysis of variance of 12 yield and yield attributing traits

SOURCE	DF	MEAN SQUARES											
		Height	Tiller/plant	Days to flowering	Harvest index	Length panicle	1000 seeds weight	Spikelet /panicle	%grain filling	Spikelet density	Spikelet/plant	Panicle/plant	Grain yield
REPLICATION	4	11.37	0.64	18.25	42.30	4.78	0.63	219.96	26.00	1.17*	169548.9	2.46	29740.51
GENOTYPE	67	3592.90**	88.23**	7819.46**	615.80*	67.44**	122.93*	32313.93**	182.20*	37.91**	7402099.62**	84.88**	1415233.22**
ERROR	268	31.751185	2.08	10.01	18.97	1.96	0.98	136.18	14.10	0.34	71597.42	1.34	17571.42

** indicates significance at 1% level of significant

Table 2. Mean performance of 68 genotypes for 12 yield and yield attributing traits

SL No.	Genotypes Name	Traits											
		HEIGHT	TILLER/PLANT	DAYS TO FLOWERING	HARVEST INDEX	LENGTH PANICLE	1000 SEEDS WEIGHT	SPIKELET /PANICLE	%GRAIN FILLING	SPIKELET DENSITY	SPIKELET /PLANT	PANICLE/PLANT	GRAIN YIELD
1	Basdhan	99.60	19.40	98.80	32.49	22.14	15.93	135.40	90.82	6.11	2418.00	17.60	638.89
2	Ijong	78.80	21.80	100.40	55.42	24.12	15.49	192.80	90.32	7.99	3848.80	20.00	1077.98
3	Mala	93.40	20.40	106.80	57.77	25.60	21.59	175.40	94.13	6.85	3440.00	19.60	1375.01
4	Ronjit	83.60	29.60	107.80	56.81	21.80	15.61	99.60	95.06	4.58	2866.80	28.80	1251.06
5	Adoliabao	108.60	8.80	122.40	8.06	25.94	23.91	116.40	84.53	4.49	813.20	7.00	116.89
6	Ahumsali	130.80	15.20	146.20	59.09	33.50	28.87	356.60	89.51	10.64	4993.00	14.00	1819.94
7	Beoilahi	121.40	10.20	149.00	31.72	29.60	23.76	238.80	82.61	8.07	2053.60	8.60	347.38
8	Bogijul	142.40	9.20	140.40	34.40	31.55	18.43	339.80	93.21	10.79	2642.20	7.80	356.76
9	Bogisali	141.80	9.60	146.40	47.02	34.54	29.36	407.60	90.27	11.81	3261.00	8.00	697.05
10	Bora	133.40	17.60	123.00	44.51	29.25	25.00	209.40	86.74	7.23	3438.40	16.40	1221.69
11	Bordhan	155.00	10.80	136.00	40.46	25.55	27.20	184.80	90.78	7.37	1661.20	9.00	367.67
12	Borjahingia	135.40	10.40	128.80	27.02	24.10	21.77	159.60	81.67	6.63	1215.00	7.60	168.24
13	Chutibora	109.00	7.60	135.20	20.25	29.00	24.38	180.80	92.86	6.23	1734.20	9.60	378.95
14	Gorokhiasali	119.60	10.60	143.60	28.97	22.85	21.45	140.60	93.82	6.16	992.20	7.00	141.70
15	Gorundapakhi	114.40	11.20	125.80	25.62	28.52	25.25	186.40	84.71	6.53	1641.20	8.80	308.90
16	Gejepsali	125.80	12.40	131.60	53.18	23.28	25.15	112.80	89.77	4.98	1061.20	9.40	225.41
1	Gumibora	108.80	10.20	126.00	28.65	22.42	26.14	395.80	93.74	17.67	4361.00	11.00	1181.66
18	Guwahatiabora	106.80	10.80	119.20	33.01	20.96	23.65	127.40	85.35	6.10	1124.60	8.80	199.92
19	Harmoni	121.20	9.00	117.00	29.60	27.15	21.72	246.00	68.32	9.06	2459.20	10.00	368.40
20	Jahingia	137.60	11.60	123.80	41.50	28.80	27.58	207.40	88.29	7.20	1580.40	7.60	300.09
21	Joldubi	127.80	10.40	132.60	36.94	24.00	36.39	164.80	89.58	6.88	1815.20	11.00	655.33
22	Joha	130.20	11.60	126.40	35.46	27.87	28.95	334.00	91.02	11.99	2804.60	8.40	622.48

23	Johabora	112.00	9.80	120.40	41.62	29.00	23.55	212.60	87.38	7.35	2081.80	9.80	421.81
24	Kolajoha	102.40	14.60	134.20	27.11	20.54	25.22	212.80	91.75	10.36	1871.00	8.80	381.18
25	Kolapakhi	138.20	16.40	139.40	32.63	23.57	15.43	202.80	88.06	8.60	2713.80	13.40	494.89
26	Konjoha	149.40	11.00	115.80	50.34	27.05	26.03	196.40	87.58	7.35	2904.00	14.80	982.10
27	Katibora	123.00	11.60	126.00	31.37	29.80	10.45	447.80	91.49	15.03	4477.00	10.00	429.33
28	Khoiron	133.40	11.40	135.00	52.20	18.62	22.24	213.40	88.97	11.54	2089.80	9.80	408.95
29	Laudubi	138.20	9.40	139.80	39.02	20.36	22.44	366.40	92.56	18.01	3591.60	9.80	736.30
30	Malbhug	117.20	15.60	121.00	55.63	28.16	29.31	222.00	90.25	7.88	1739.40	7.80	366.49
31	Manuharsali	135.20	11.40	114.40	53.57	27.60	27.12	356.00	85.25	12.93	4769.20	13.40	1479.38
32	Memlahi	136.00	11.60	124.40	58.30	33.60	24.54	335.00	92.26	9.97	3681.00	11.00	919.84
33	Monlohi	149.20	9.80	130.20	24.20	26.05	25.88	210.40	79.25	8.08	1557.20	7.40	238.87
34	Moubora	121.80	10.00	115.00	18.26	32.24	35.86	333.40	97.36	10.34	3267.20	9.80	1119.94
35	Nolsitiki	140.20	12.80	138.20	24.52	21.77	28.44	130.00	92.40	5.98	981.60	7.60	198.38
36	Nania	107.20	13.00	137.80	39.66	32.85	22.15	194.40	72.99	5.92	2299.00	11.80	449.42
37	Nekera	117.80	12.00	128.60	41.76	32.10	21.17	285.80	94.93	8.91	3257.00	11.40	748.60
38	Niakadam	128.20	11.40	145.40	36.01	32.67	22.11	408.00	96.43	12.49	3426.00	8.40	615.54
39	Pakhoribora	134.00	11.00	136.20	28.02	28.52	40.86	186.80	90.41	6.55	1826.80	9.80	661.82
40	Rongabora	104.40	14.40	125.40	33.69	28.26	25.15	192.60	81.41	6.94	2038.40	10.60	442.40
41	Rongajoha	133.40	11.40	134.60	31.91	28.12	24.02	190.60	70.05	6.81	2260.20	11.80	480.12
42	Sokuwa	118.00	11.80	118.20	42.00	23.62	21.22	227.40	90.48	9.69	2227.40	9.80	419.54
43	Solpuna	134.00	10.20	120.80	33.42	29.00	28.80	232.80	93.36	8.09	2046.00	8.80	484.66
44	Sorujahingia	149.60	11.60	134.40	34.89	28.42	21.55	206.60	89.68	7.24	1627.00	7.80	250.83
45	Sowagmoni	148.40	14.20	143.20	51.18	24.90	20.01	219.40	83.43	8.83	2197.60	10.00	367.99
46	Sunmoni	110.40	12.00	115.80	34.50	25.80	26.64	214.80	91.31	8.38	2703.80	12.60	826.39
47	Tilbora	136.20	11.60	136.20	42.18	27.40	26.22	235.40	83.93	8.59	2592.20	11.00	629.71
48	Titaphuliabora	153.00	11.60	144.60	41.24	26.92	26.20	246.80	83.90	9.17	2416.20	9.80	523.77
49	Torawali	117.00	12.20	134.00	29.66	24.90	30.35	282.00	93.02	11.34	2706.00	9.60	732.54
50	Vasmoti	129.60	14.60	112.60	25.25	25.80	22.76	142.40	86.60	5.52	1481.80	10.40	307.42
51	Amanabao	200.00	20.80	212.40	42.04	26.67	14.81	145.00	85.23	5.44	1859.80	12.80	302.08
52	Bhuiabao	198.40	14.80	198.40	16.64	27.65	23.52	367.80	94.06	13.31	6766.80	18.40	2757.82
53	Dolbao	217.80	13.60	220.40	28.45	28.30	21.02	265.60	85.46	9.39	2865.20	10.80	557.05
54	Happybao	196.00	14.60	207.00	31.84	33.67	24.12	232.80	91.67	6.92	2562.80	11.00	625.39
55	Kokuwabao	171.80	28.80	226.20	38.20	26.75	24.38	252.40	87.79	9.45	3989.20	15.80	1350.31
56	Maguribao	187.40	14.60	210.40	38.21	32.30	22.78	222.60	76.75	6.90	5530.40	25.00	2414.10
57	Miabao	166.60	15.20	219.00	33.73	33.06	24.54	304.60	88.63	9.22	3590.80	11.80	934.43
58	Negheribao	168.20	17.80	209.00	29.96	33.74	25.27	326.40	81.64	9.68	4116.60	12.60	1070.98
59	Panidhan	153.00	16.20	215.00	22.99	29.80	21.69	306.00	88.00	10.27	4536.60	14.80	1308.41
60	Panikakuwa	159.20	18.40	222.40	34.61	28.80	22.51	249.00	89.32	8.65	3436.20	13.80	956.62
61	Bejilahi	133.40	11.00	68.20	34.50	28.42	24.03	313.20	94.59	11.01	5251.20	16.80	2004.10
62	Betguti	120.00	8.60	74.60	18.44	29.12	25.68	242.00	89.29	8.33	2086.60	8.60	415.42
63	Borguni	120.40	9.80	65.60	23.76	25.30	19.04	157.40	80.89	6.22	1168.00	7.40	133.56
64	Kola-aahu	109.20	9.20	69.40	30.69	24.67	21.70	209.00	86.55	8.48	1672.00	8.00	259.00

65	Kopouguni	128.60	12.40	76.00	24.09	25.35	18.44	140.40	78.40	5.54	1377.60	9.80	200.48
66	Maiguni	103.20	11.00	80.00	30.40	25.37	18.30	280.60	87.16	11.05	2525.20	9.00	362.33
67	Ronga-ahu	117.00	9.20	73.20	27.63	27.67	23.96	206.00	74.81	7.44	1728.20	8.40	261.02
68	Rongadoria	130.80	11.00	66.60	41.24	27.85	17.40	293.40	90.06	10.54	2872.80	9.80	442.21
	Mean	132.70	13.00	134.16	35.73	27.28	23.77	237.22	87.71	8.69	2661.60	11.30	680.81
	C.V.	4.25	11.09	2.36	12.19	5.13	4.17	4.92	4.28	6.76	10.05	10.20	19.47
	Minimum	78.8	7.6	65.6	8.06	18.62	10.45	99.6	68.32	4.49	813.2	7	116.89
	Maximum	217.8	29.6	226.2	59.09	34.54	40.86	447.8	97.36	18.01	6766.8	28.8	2757.82
	S.E.	2.52	0.64	1.42	1.95	0.63	0.44	5.22	1.68	0.26	119.66	0.52	59.28
	C.D. 5%	7.02	1.80	3.94	5.42	1.74	1.23	14.53	4.68	0.73	333.19	1.44	165.06
	C.D. 1%	9.25	2.37	5.19	7.15	2.30	1.63	19.15	6.16	0.96	439.03	1.89	217.50

Table 3. Genetic parameters of the traits.

	Traits	GCV	PCV	h ²	Genetic advance	Genetic advance as % of mean
1	HEIGHT	20.11	20.55	0.96	53.79	40.53
2	TILLER/PLANT	31.94	33.81	0.89	8.08	62.15
3	DAYS TO 50% FLOWERING	29.46	29.55	0.99	81.15	60.49
4	HARVEST INDEX	30.58	32.92	0.86	20.91	58.51
5	LENGTH OF PANICLE	13.27	14.23	0.87	6.95	25.5
6	1000 SEEDS WEIGHT	20.78	21.19	0.96	9.97	41.96
7	SPIKELET/PANICLE	33.82	34.17	0.98	163.54	68.94
8	% OF GRAIN FILLING	6.61	7.88	0.7	10.03	11.43
9	SPIKELET DENSITY	31.53	32.25	0.96	5.52	63.51
10	SPIKELET/PLANT	45.49	46.59	0.95	2435.54	91.51
11	PANICLE/PLANT	36.21	37.63	0.93	8.1	71.78
12	GRAIN YIELD	77.66	80.06	0.94	1056.44	155.17

3.2. Tillers per Plant

Tiller trait in rice is a major determinant for panicle production [35, 36] and as a result, it affects total yield [37]. The genotypes, which produced higher number of effective tillers per plant showed higher grain yield in rice [38, 39].

The trait tillers per plant showed high GCV-PCV, high heritability and high genetic advance as percentage of mean (Table III) indicating the effect of additive gene on this trait. Thus, this trait may be used directly as selection index in plant improvement program. The PCV was higher than corresponding GCV in this trait also. This implies that this trait was also under the influence of environment. Sinha, *et al.*, [40] and Padmaja *et al.*, [41] also found similar results. Singh *et al.*, [42] found moderate coefficients of variation for this trait. Anbanandan *et al.*, [43] and Prajapati *et al.*, [28] reported high heritability and high genetic advance as percentage of mean for this trait. Ahmad *et al.*, [32] reported moderate GCV-PCV, high heritability and high genetic advance and Bisne *et al.*, [44] reported moderate heritability for this trait. High genetic advance for tillers per plant was also recorded by Kuldeep *et al.*, [45] and Karthikeyan *et al.*, [46].

3.3. Days to 50% Flowering

High phenotypic and genotypic variances were exhibited by days to 50% flowering (Table III) and these results were in agreement with the observations of Sawant *et al.* [47]; Padmaja *et al.*, [41] and Prajapati *et al.*, [28]. Genotypic and phenotypic coefficients of variation were high and PCV was higher than corresponding GCV for this trait but is noteworthy that the differences between GCV and PCV values were minimum implying least influence of environment. This result is in accordance with the finding of Shahidullah *et al.*, [48]. The broad sense heritability, genetic advance and genetic advance as percentage of mean were also high indicating the governance of additive genes for this character. This implies that phenotypic selection on the basis of this character will be adequate to bring about desirable improvement. Moderate GCV-PCV, high heritability and moderate genetic advance for days to 50% flowering were found by Ahmed *et al.*, [32] and Prajapati *et al.*, [28] and moderate GCV-PCV, high heritability and high genetic advance were reported by Vange [49]. Bisne *et al.*, [44] also reported moderate genetic advance for this trait.

3.4. Harvest Index

Harvest index is a vital character having physiological importance. It reflects translocation on alternatively dry matter partitioning of a given genotype to the economic parts. This trait showed high GCV and PCV indicating prominent variation among the genotypes for the trait. PCV was higher than their corresponding GCV which implies that the variation is not only due to genotypes but also due to the influence of environment. Estimates of heritability, genetic advance and genetic advance as percentage of mean for the

trait were also high. This feature suggested that the environmental influence on the phenotypic expression of this character was not apparent and the phenotypic expression of this trait was true representation of the genetic makeup. Therefore selection based on this character would be effective. These results coincide with the findings of Karim *et al.*, [50] and Bisne *et al.*, [44]. Prajapati *et al.*, [28] also found high GCV and PCV, heritability and genetic advance for the trait harvest index. Whereas Habib *et al.*, [51] and Ahmed *et al.*, [32] reported moderate genotypic and phenotypic coefficients of variation, high heritability and high genetic advance as percentage of mean for this trait.

3.5. Length of Panicle

Panicle length showed moderate genotypic and phenotypic coefficients of variation, high heritability, low genetic advance and high genetic advance as percentage of mean (Table III) which was in accordance with the findings of Vange *et al.*, [49]. This indicates that although the variation is not so apparent still there is an opportunity to improve this trait through selection. The difference between genotypic and phenotypic coefficients of variation was negligible indicating little influence of environment. Prajapati *et al.*, [28] also observed moderate GCV and PCV, high heritability and moderate genetic advance as percentage of mean for this trait. Ahmadikhah [31] also observed high heritability for this trait. On the other hand, Habib *et al.*, [51] reported low GCV and PCV and high heritability, Bisne *et al.*, [44] observed high heritability and moderate genetic advance, Shahidullah *et al.*, [48] low GCV and PCV, Chakraborty and Chakraborty [34] reported low heritability and low genetic advance as percentage of mean and Singh *et al.*, [52] reported low GCV PCV and low genetic advance as percentage of mean for this trait.

3.6. 100- Seeds Weight

The genotypic and phenotypic coefficients of variation were high for 1000 seeds weight and the difference was very close indicating apparent variation with negligible environmental influence and possibility of yield improvement through selection of this trait. This trait also exhibited high heritability and high genetic advance as percentage of mean (Table III). This feature suggested that the character 1000 seeds weight was mainly controlled by additive genes and thus phenotypic selection based on this trait might be rewarding. Akanda *et al.*, [53] Choudhury and Das [54], Karim *et al.*, [50] and Ullah *et al.*, [33] have also been reported similar results. Habib *et al.*, [51] reported moderate GCV and PCV, high heritability and high genetic advance as percentage of mean for this trait. Bisne, *et al.*, [44] reported high genotypic and phenotypic coefficients of variability, Anbanandan *et al.*, [43] observed high heritability and high genetic advance and Kumar *et al.*, [55] revealed high heritability for this trait. On the other hand Lal and Chauhan [30] reported moderate GCV and PCV and high

genetic advance as percentage of mean.

3.7. Spikelet per Panicle

Spikelet per panicle is an important character contributing to grain yield. According to Kusutani *et al.*, [38] and Dutta *et al.*, [39] genotypes which produced higher number of grains per panicle showed higher grain yield in rice. Coefficients of variability observed at both phenotypic and genotypic level were high for the character spikelet per plant indicating apparent variation among the genotypes for this trait. The phenotypic coefficient of variation was higher than corresponding genotypic coefficient of variation. However a close proximities between GCV and PCV, gave evidence that the variability existing in each genotypes was mainly due to their genetic makeup. Estimates of heritability and genetic advance as percentage of mean were also high for this trait. Thus it can be interpreted that this trait was controlled by additive gene action and hence can be improved through simple selection methods. Similar results were also observed by Vange [49] Prajapati *et al.*[28], Ullah *et al.*, [33] and Singh *et al.*,[52]. Lal and Chauhan [30] reported high GCV and PCV and high genetic advance and Mustafa and Elsheikh, [56] observed high genotypic and phenotypic coefficient of variation for the trait spikelets per panicle.

3.8. Percentage of Viable Seeds

The trait percentage of viable seeds showed low GCV-PCV, high heritability, moderate genetic advance and moderate genetic advance as percentage of mean (Table III) in the present study. It revealed that non-additive gene action was involved for expression of this character. The high heritability was exhibited due to the influence of favourable environment rather than genotype and selection for such trait might not be rewarding. Hence this trait may not be useful as a criterion for selection for increased grain yield. Karim *et al.*, [50] reported high GCV and PCV, moderate heritability and high genetic advance as percentage of mean for this trait.

3.9. Spikelet Density

This trait showed high GCV PCV, high heritability and high genetic advance as percentage of mean (Table III) indicating the suitability of the trait as selection index in plant improvement program. Although phenotypic coefficient of variation was higher than corresponding genotypic coefficient of variation implying the influence of environment on the expression of the trait, the difference of GCV and PCV was negligible. It revealed that the genotypic variation contribute maximum to phenotypic variation and the environmental deviation had minor contribution for the trait. Ali *et al.*, [57] observed Moderate variability, high heritability and high genetic advance as percentage of mean and Ahmed *et al.*, [32] reported low GCV and PCV, moderate heritability and low genetic advance as percentage

of mean for spikelet density.

3.10. Spikelet per Plant

Genotypic and phenotypic coefficients of variations were high (Table III) indicating pronounced variation for the character. The phenotypic coefficient of variation was higher than genotypic coefficient of variation but the difference was negligible. This feature suggested that the environmental influence was not considerable and the variation of genotypes regarding this trait was mainly due to genetic makeup. The heritability and genetic advance as percentage of mean were also high. This suggested the feasibility of genetic improvement of this trait under low selection pressure. Lal and Chauhan [30] reported moderate genotypic and phenotypic coefficient of variation for this trait.

3.11. Panicles per Plant

Panicles per plant registered high genotypic and phenotypic coefficients of variability (Table III) and this result was in agreement with the earlier observations of Karim *et al.*, [50] and Singh *et al.*, [52]. This indicated the presence of substantial amount of genetic variability for the trait in the study material and there is scope for selection. The PCV was slightly higher than GCV which implies less influence of environment on the trait. As genetic variability remains unaffected by environmental conditions, this type of variability was more useful for genetic improvisation through selection or hybridization. This character also showed high heritability and high genetic advance as percentage of mean, and this is in compliance with the findings of Prajapati *et al.*, [28]. Thus it can be interpreted that the trait panicles per plant might be controlled by additive gene action, which could be improved through simple selection methods. Karim *et al.*, [50] and Lal and Chauhan [30] also reported high genetic advance as percentage of mean. On the other hand, Habib *et al.*, [51] reported moderate GCV and PCV, moderate heritability and moderate genetic advance as percentage of mean and Ullah *et al.*, [33] observed moderate genotypic and phenotypic coefficients of variation, high heritability and moderate genetic advance as percentage of mean for this trait.

3.12. Grain Yield

Highest phenotypic and genotypic co-efficient of variability was exhibited by grain yield among studied traits indicating prominently high variations of the genotypes (Table III). These findings are in accordance with earlier reports of Habib *et al.*, [51]. Anbanandan *et al.*, [43], Vange [49] and Ahmadikhah *et al.*, [31]. The PCV was quite higher than corresponding GCV for this trait. Presence of wide gap between PCV and GCV indicated the predominant role of environment in the expression of the trait which is in consonance with the results obtained by earlier workers [31, 49 and 50].

The estimates of heritability and genetic advance as percentage of means were also high for this trait suggesting preponderance of additive gene action in expression of this character. The presence of additive genetic variance offers immense opportunity for exploitation of heterosis. These results were in accordance with the findings of Das *et al.*, [58], Kumar *et al.*, [55], Habib *et al.*, [51], Anbanandan *et al.*, [43], Bisne *et al.*, [44] and Ullah *et al.*, [33]. Vange, [49] reported high genotypic and phenotypic coefficients of variation, moderate heritability and high genetic advance as percentage of mean, while Mustafa and Elsheikh [56] and Prajapati *et al.*, [28] observed high GCV and PCV, high heritability and moderate genetic advance.

The order of genetic variability for different yield attributing characters was as follows, grain yield > spikelets per plant > panicles per plant > spikelets per panicle > tillers per plant > harvest index > spikelet density > days to 50% flowering > 1000 seeds weight > height > length of panicle > percentage of viable seeds.

4. Conclusions

Estimated heritability value alone is less reliable as these values are prone to alter with change in the environment and experimental material (Swarup and Changale [59]). Hence, the use of heritability values coupled with genetic advance would be more reliable than heritability alone. In the present investigation, along with high genetic variability, high heritability coupled with high genetic advance as percentage of mean were observed for traits viz. tillers per plant, days to 50% flowering, harvest index, spikelets per panicle, spikelet density, spikelet per plant, panicles per plant and grain yield. Thus these traits are most probably controlled by additive gene action and hence these traits can be fixed by selection. Based on the above results, it is suggested that the characters with high genotypic variability would be responsive to selection in the positive direction.

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