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Genetic variability analysis for grain yield and its attributing traits among the aromatic rice (*Oryza sativa* L.) genotypes of Chhattisgarh region

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Abstract

The variability analysis showed the presence of highly significant variations for all the listed genotypes tested under the research experiment. Phenotypic coefficient of variation for all the traits under investigation was found higher than their corresponding genotypic coefficient of variation, indicating masking effect of environment in the expression of traits. High heritability was reported in plant height (cm), days to 50% flowering, 1000 seed weight (g), total number of spikelets per panicle, number of filled spikelets per panicle, grain yield per plant (g), effective tillers per plant, harvest index (%), and spikelet fertility%. High degree of the genetic advance as a percent of mean observed for the characters 1000 seed weight (g), total number of spikelets per panicle, number of filled spikelets per panicle, effective tillers per plant, grain yield per plant (g), biological yield per plant (g), Plant height (cm) and harvest index (%). High heritability coupled with the high genetic advance as a percent of mean was reported for the traits 1000 seed weight (g), total number of spikelets per panicle, number of filled spikelets per panicle, grain yield per plant (g), effective tillers per plant and plant height (cm) indicating that the expression of such characters controlled by the additive gene action and thus simple selection will be effective for the improvement of this character.

Keywords: Genetic variability, phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), heritability, genetic advance

Introduction

Rice (*Oryza sativa* L.), a widely cultivated cleistogamous cereal crop with chromosome number, 2n = 24, belongs to the genus *Oryza*, the family Graminaceae (Syed and Khaliq, 2008). Rice is one of the most significant food grain crops in the world, more than 2.7 billion people used as basic diet. India holds the largest area around 45 million hectares, producing 178.3 million tonnes at a productivity of 3962 kg per hectare, an increase of 2.71 percent over 2019 in terms of area and 0.37 percent in terms of production (Anonymous, 2020) [2]. Rice is primary staple food of Chhattisgarh, and there are many different varieties of rice being grown there. The state of Chhattisgarh, known as the "Rice bowl of India". The maximum area is covered with paddy during *kharif* and contributes a substantial part to the national paddy output. The state is fully reliant on the monsoon with a yearly rainfall of 1200-1600 mm. In Chhattisgarh, rice is cultivated in an area of 3.79 million hectares with a production of 91.03 lakh tonnes and productivity of 2400 kg per hectare (Anonymous, 2021) [3]. Chhattisgarh is rich and well known for diversity of rice hence, protects the immense genetic diversity of rice in the three climatic zones of the state. The current shift in market demand has increased the potential of rice breeding for aromatic purposes as customer preferences are shifting toward the pleasant fragrances of rice in addition to its good eating qualities. In addition to its superior cooking and milling qualities, aromatic rice commands a high price in the market. The present investigation was undertaken to gather some useful information on genetic variability of different elite rice genotypes crossed under line × tester mating design.

Enhancing yield is one of the primary concerns in genetic crop improvement programme to meet the demands of the constantly growing population. Another significant aspect in rice breeding is improvement in quality traits. The selection of genotypes with all desirable quality and yield-contributing traits constitutes the most significant factor in any crop breeding programme. Any successful hybridization programme for varietal enhancement mainly depends on the choice of parents with significant genetic variability and the selection of the desired trait combination to increase grain yield and improve grain quality.

Additionally, understanding heritability is crucial for selection-based improvement since, it indicates whether a trait will be passed on to successive generations.

Materials and Methods

The present experiment was conducted during growing season *Kharif* 2020-21, at the Research cum Instructional Farm, IGKV, Raipur (C.G.). The material comprises of five non-aromatic rice varieties *viz.*, PKV HMT, RFS-2019- 3, Zinco Rice MS, HMT Sona and Improved Samba Mahsuri as female parents and five indigenous aromatic rice varieties *viz.*, Pusa1121, Badshahbhog Sel.-1, Trombay Chhattisgarh Dubraj Mutant (TCDM-1), Chhattisgarh Devbhog and R2281-308-1-185-1 as male parent or tester and they were crossed in line × tester fashion to generate a total of twenty-five F_1 hybrid combinations during *kharif* 2020. The above crosses were attempted in such a way that each line was pollinated by all pollen parents. All the crosses along with their parents were grown in a randomized block design with two replications. The five competitive plants from each replication were tagged and observations were recorded from these tagged plants at various phases of the crop plant's growth. The observations were recorded for 11 grain yield characters and 14 quality characters.

Fisher’s technique (1967) [10] was used to calculate the variance analysis, the genotypic coefficient of variance (GCV) and phenotypic coefficient of variance (PCV) were determined by method given by Burton's (1952) [5], Broad sense heritability was determined by using the Hanson *et al.*, (1956) [11] formula. The formula, provided by Johnson *et al.*, (1955) [12] was used to determine the genetic advance from the heritability estimates. Statistical analysis is done with the RBD analyzer and Windostat software.

Table 1: List of genotypes used under study

S. No.	Genotypes
	Female Parents
1.	PKV HMT
2.	RFS-2019-3
3.	Zinco Rice MS
4.	HMT Sona
5.	Improved Samba Mahsuri
	Male Parents
1.	Pusa 1121
2.	Badshahbhog Sel.-1
3.	Trombay Chhattisgarh Dubraj Mutant (TCDM-1)
4.	Chhattisgarh Devbhog
5.	R2281-308-1-185-1
	Crosses
1.	PKV HMT/ Pusa 1121
2.	PKV HMT/ Badshahbhog Sel.-1
3.	PKV HMT/ Trombay Chhattisgarh Dubraj Mutant (TCDM-1)
4.	PKV HMT/ Chhattisgarh Devbhog
5.	PKV HMT/ R2281-308-1-185-1
6.	RFS-2019-3/ Pusa 1121
7.	RFS-2019-3/ Badshahbhog Sel.-1
8.	RFS-2019-3/ Trombay Chhattisgarh Dubraj Mutant (TCDM-1)
9.	RFS-2019-3/ Chhattisgarh Devbhog
10.	RFS-2019-3/ R2281-308-1-185-1
11.	Zinco Rice MS/ Pusa 1121
12.	Zinco Rice MS/ Badshahbhog Sel.-1
13.	Zinco Rice MS/ Trombay Chhattisgarh Dubraj Mutant (TCDM-1)
14.	Zinco Rice MS/ Chhattisgarh Devbhog
15.	Zinco Rice MS/ R2281-308-1-185-1
16.	HMT Sona/ Pusa 1121
17.	HMT Sona/ Badshahbhog Sel.-1
18.	HMT Sona/ Trombay Chhattisgarh Dubraj Mutant (TCDM-1)
19.	HMT Sona/ Chhattisgarh Devbhog
20.	HMT Sona/ R2281-308-1-185-1
21.	Improved Samba Mahsuri/ Pusa 1121
22.	Improved Samba Mahsuri/ Badshahbhog Sel.-1
23.	Improved Samba Mahsuri/ Trombay Chhattisgarh Dubraj Mutant (TCDM-1)
24.	Improved Samba Mahsuri/ Chhattisgarh Devbhog
25.	Improved Samba Mahsuri/ R2281-308-1-185-1

Table 2: Plan of parent crossing for Line × Tester mating design in rice genotypes during *kharif* 2020-21

Female parent	Male parents				
	Pusa 1121	**Badshahbhog Sel.-1**	**Trombay Chhattisgarh Dubraj Mutant (TCDM-1)**	**Chhattisgarh Devbhog**	**R2281-308-1-185-1**
PKV HMT	×	×	×	×	×
RFS-2019-3	×	×	×	×	×
Zinco Rice MS	×	×	×	×	×
HMT Sona	×	×	×	×	×
Improved Samba Mahsuri	×	×	×	×	×

Results and Discussion

Genetic variability parameter

The analysis of variance revealed the existence of significant differences among the genotypes for the different characters under study. So, the selection would be effective to develop the varieties with desired traits of crop plants. The coefficient of variation study implies that the values of the phenotypic coefficient of variation were found higher than that of genotypic coefficient of variation indicating the influence of the environment. Similar findings were reported earlier by Akshay *et al.*, (2022) [1] and Sudeepthi *et al.*, (2020) [20]. The results of analysis of variance are presented in Table 3. The results of mean, variability, heritability and genetic advance of each trait in the current study are presented in Table 4.

The mean value for days to 50% flowering was 96 and it ranged from 85 to 105 days, the genotype HMT Sona/ Badshahbhog Sel.-1 required highest value for days to 50% flowering while genotype HMT Sona / Trombay Chhattisgarh Dubraj Mutant (TCDM-1) required the lowest period for days to 50% flowering. The mean for plant height (cm) was 116.9 and it ranged from 95.6 to 179.2 cm, the maximum plant height observed for genotype Improved Samba Mahsuri/ Badshahbhog Sel.-1 and minimum for HMT Sona/ Pusa 1121. Panicle length (cm) had a mean of 24.2 and it ranged from 19.6 to 29.9 cm. The mean for total number of spikelets per panicle was 182.7 and it ranged from 113.2 to 390.5. The mean for number of filled spikelets per panicle was 156.9 and it ranged from 81.2 to 316.8. The mean value for spikelets fertility (%) was 85.8 and it ranged from 72.0 to 94.1%. The mean value for grain yield per plant (g) was 16.6 and it ranged from 9.0 to 29.4 g the maximum grain yield per plant recorded for genotype PKV HMT and minimum for Zinco Rice MS/ Pusa 1121. The mean value for biological yield per plant (g) was 66.1 and it ranged from 40.3 to 100.4 g. The mean value for 1000 seed weight (g) was 18.1 and it ranged from 12.0 to 32.0 g. The mean value for harvest Index (%) was 25.4 and it ranged from 18.6 to 39.3%.

The value of phenotypic coefficient of variation was ranged from 4.9 percent for days to 50% flowering to 28.1 percent for 1000 seed weight (g). Higher estimates of PCV recorded for 1000 seed weight (g) (28.1%), total number of spikelets per panicle (26.9%), number of filled spikelets per panicle (26.5%) and effective tillers per plant (26.3%). Moderate estimates of PCV were recorded for grain yield per plant (g) (22.6%), biological yield per plant (g) (22.5%), plant height (cm) (18.8%) and harvest index (%) (16.6%). Lower estimates of the phenotypic coefficient of variation were reported by panicle length (10.5%), spikelets fertility% (6.5%) and days to 50% flowering (4.9%). The findings are in accordance with the report of Mishu *et al.*, (2016) [15]

The values of genotypic coefficient of variation ranged from 4.8 percent for days to 50% flowering to 27.1 percent for 1000 seed weight (g). Higher estimates of GCV were recorded in 1000 seed weight (g) (27.1%) followed by total number of spikelets per panicle (25.9%), number of filled spikelets per panicle (25.5%) and effective tillers per plant (24.8%). Characters showed moderate values of genotypic coefficient of variation were grain yield per plant (g) (21.6%), biological yield per plant (g) (20.5%), plant height (cm) (18.4%) and harvest index (15.5%). Lower estimates of the genotypic coefficient of variation were exhibited by panicle length (7.8%), spikelets fertility% (5.7%) and days to 50% flowering (4.8%). The graph indicating the GCV and PCV for grain yield and its attributing traits were presented in the Figure 1. The slight difference between GCV and PCV was also reported by Seyoum *et al.*, (2012) [18], Kole *et al.*, (2008) [14].

The ranges of PCV and GCV were found to be in close agreement for days to 50% flowering, plant height (cm), effective tillers per plant, total number of spikelets per panicle, number of filled spikelets per panicle, spikelet fertility percentage, grain yield per plant, 1000 seed weight and harvest index indicating less influence of environment on these traits. Higher estimates of genotypic coefficient of variation and phenotypic coefficient of variation were recorded in 1000 seed weight (g) followed by total number of spikelets per panicle, number of filled spikelets per panicle and effective tillers per plant indicating presence of sufficient variability in the hybrids and thereby suggesting that selection of these traits will be useful for genetic improvement. Similar findings were reported by Bhargavi *et al*., (2021) [4], Dhidhi *et al*., (2021) [8], Emi *et al*., (2021) [9] and Devi *et al*., (2017) [7]

Estimates of heritability and genetic advance as a percent of mean

The reliability of the phenotypic value depends on the estimates of heritability for a particular character. Therefore, high heritability helps in the effective selection for a particular character. In the present investigation all the characters under study except the panicle length showed higher estimates of broad-sense heritability *i.e*., (> 60% as suggested by Johnson *et al*., 1955). The heritability for all the 11 traits ranged from 54.7% for panicle length to 95.6% for plant height. The heritability was reported high in most of the traits such as, plant height (cm) (95.6%), days to 50% flowering (93.7%), 1000 seed weight (g) (93.5%), total number of spikelets per panicle (93.4%), number of filled spikelets per panicle (93.1%), grain yield per plant (g) (91.5%), effective tillers per plant (88.8%), harvest index (%) (87.9%), biological yield per plant (g) (82.8%) and spikelet fertility% (78.7%). Moderate range of heritability was observed for panicle length (54.7%).

High degree of the genetic advance as a percent of mean observed for the given characters like 1000 seed weight (69.3%), total number of spikelets per panicle (66.3%), number of filled spikelets per panicle (65.1%), effective tillers per plant (61.7%), grain yield per plant (54.7%), biological yield per plant (g) (49.2%), plant height (47.5%) and harvest index (38.5%). Characters exhibiting moderate ranges for genetic advance as a percent of mean were panicle length (15.2%) spikelets fertility% (13.5%) and days to 50% flowering (12.3%). The graph indicating estimates of heritability and genetic advance as% of mean for grain yield and its contributing traits is presented in Figure 2, confirmed the findings of Karim *et al*., (2007) [13] for 1000 - grain weight (g), number of filled grain per panicle and grain yield per hill (g).

High heritability coupled with the high genetic advance as a percent of mean was reported for the traits like 1000 seed weight, total number of spikelets per panicle, number of filled spikelets per panicle, grain yield per plant (g), effective tillers per plant and plant height (cm) indicating that the expression of such characters controlled by the additive gene action and thus simple selection will be effective for the improvement of these characters. Similar results were recorded by Chavan *et al*., (2022) [6], Sharma *et al*., (2020) [19] and Devi *et al*., (2017) [7] for effective tillers, plant height (cm), flag leaf length, filled grains per panicle, test weight (g) and yield per plant (g).

High heritability coupled with the moderate genetic advance as a percent of mean was observed for the characters like spikelet fertility% and days to 50% flowering suggesting that control of expressions by both additive and non-additive gene action suggesting that the selection cannot be practiced for improving these traits thus heterosis breeding could be successful.

Table 3: Analysis of variance for grain yield and its contributing traits in rice genotypes during *kharif* 2020-21

S. No.	Characters	Mean sum of squares		
		Replication D.F = 1	Treatment D.F = 34	Error D.F = 34
1.	Days to 50% flowering	2.80	45.13**	1.47
2.	Plant height (cm)	4.24	949.21**	21.24
3.	Panicle length (cm)	6.61	10.12**	2.95
4.	Effective tillers per plant	2.60	12.42**	0.73
5.	Total no. of spikelets per panicle	499.72	4674.62**	159.71
6.	Number of filled spikelets per panicle	459.78	3340.42**	118.58
7.	Spikelets fertility (%)	0.03	55.82**	6.60
8.	Grain yield per plant (g)	0.54	27.13**	1.21
9.	Biological yield per plant (g)	5.72	406.03**	38.10
10.	1000 seed weight (g)	0.80	50.33**	1.69
11.	Harvest Index (%)	3.96	33.43**	2.16

** Significant at 1% level

Table 4: Genetic variability parameters for grain yield and its contributing traits in rice genotypes

S. No.	Characters	Mean	Range		GCV (%)	PCV (%)	H^2 (bs)	Genetic advance as % of mean
			Min	Max				
1.	Days to 50% flowering	96	85	105	4.8	4.9	93.7	12.3
2.	Plant height (cm)	116.9	95.6	179.2	18.4	18.8	95.6	47.5
3.	Panicle length (cm)	24.2	19.6	29.9	7.8	10.5	54.7	15.2
4.	Effective tillers per plant	9.7	5.3	13.9	24.8	26.3	88.8	61.7
5.	Total number of spikelets per panicle	182.7	113.2	390.5	25.9	26.9	93.4	66.3
6.	Number of filled spikelets per panicle	156.9	81.2	316.8	25.5	26.5	93.1	65.1
7.	Spikelets fertility (%)	85.8	72.0	94.1	5.7	6.5	78.7	13.5
8.	Grain yield per plant (g)	16.6	9.0	29.4	21.6	22.6	91.5	54.7
9.	Biological yield per plant (g)	66.1	40.3	100.4	20.5	22.5	82.8	49.2
10.	1000 seed weight (g)	18.1	12.0	32.0	27.1	28.1	93.5	69.3
11.	Harvest Index (%)	25.4	18.6	39.3	15.5	16.6	87.9	38.5

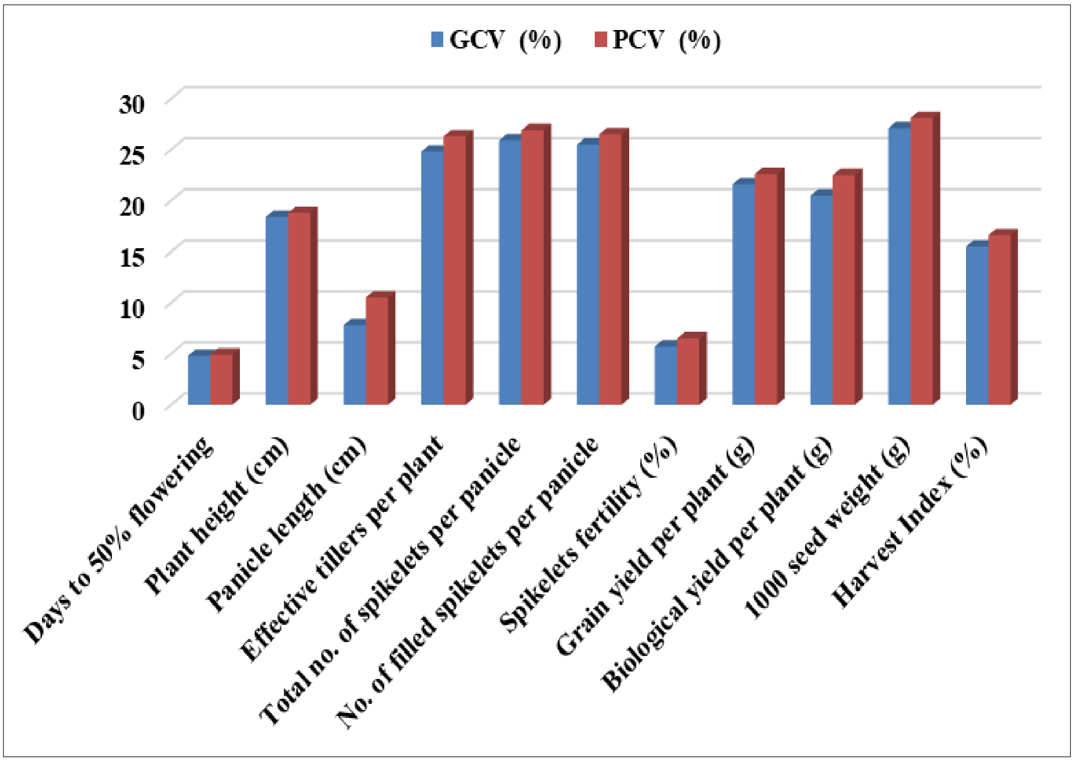

Fig 1: Estimation of PCV and GCV for grain yield and its contributing traits in rice genotypes

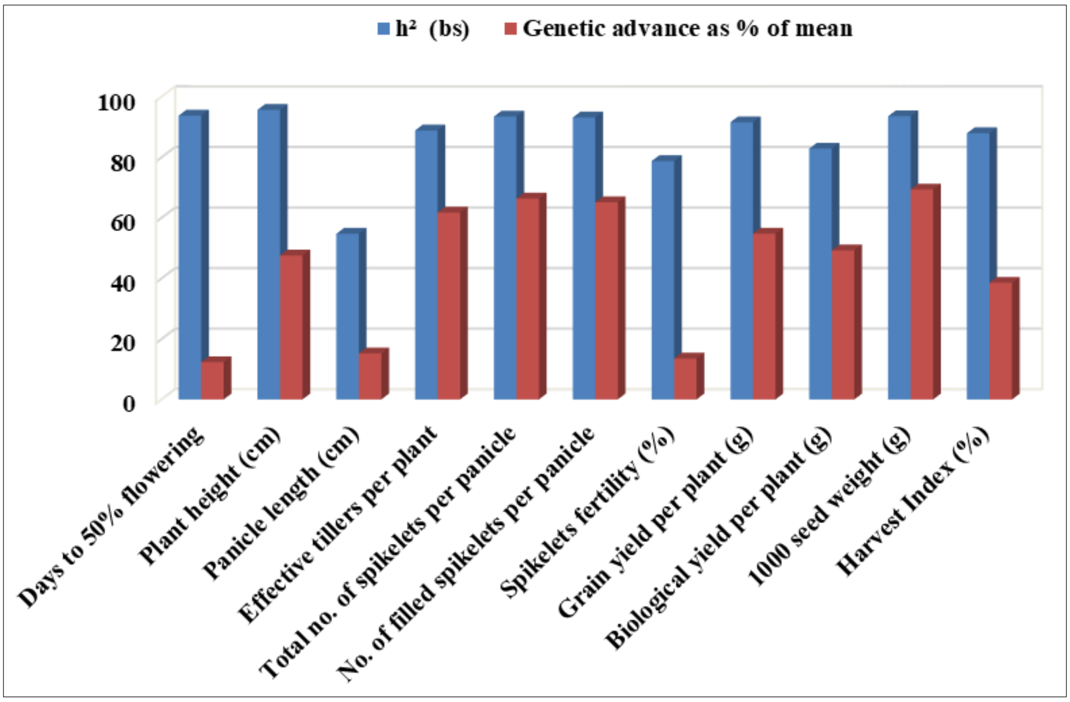

Fig 2: Estimation of Heritability and Genetic advance as% of mean for grain yield and its contributing traits in rice genotypes

Conclusions

The present study indicated that there is adequate genetic variability present in the material studied. The estimates of phenotypic coefficient of variation were higher than that of genotypic coefficient of variation for all the characters under study indicating the effect of environment. Higher estimates of PCV, GCV, broad sense heritability and genetic advance as a percent of mean were reported for effective tillers per plant, total number of spikelets per panicle, number of filled spikelets per panicle, grain yield per plant (g), biological yield (g) and 1000 seed weight (g), indicating presence of sufficient variability in the genotypes and thereby suggesting that selection of these traits will be rewarding for crop improvement.

References

1. Akshay M, Chandra SB, Devi KR, Hari Y. Genetic variability studies for yield and its attributes, quality and nutritional traits in rice (*Oryza sativa* L.). The Pharma Innovation Journal. 2022;11(5):167-172.
2. Anonymous. Food and Agriculture Organization of the United Nations. FAOSTAT statistical database: FAO;

c2020.

3. Anonymous. Annual progress report 2021. Directorate of Agriculture, Govt of Chhattisgarh; c2021.
4. Bhargavi M, Shanthi P, Reddy VLN, Reddy DM, Reddy BR. Estimates of genetic variability, heritability and genetic advance for grain yield and other yield attributing traits in rice (*Oryza sativa* L.). The Pharma Innovation Journal. 2021;10(5):507-511.
5. Burton GW. Quantitative inheritance in grasses. Proc. 6th International Grassland Congress. 1952;1:127-83.
6. Chavan BR, Dalvi VV, Kunkerkar RL, Mane AV, Gokhale NB. Studies on genetic variability for yield and yield contributing traits in aromatic rice (*Oryza sativa* L.). The Pharma Innovation Journal. 2022;11(2):1732-1735.
7. Devi KR, Chandra SB, Lingaiah N, Hari Y, Venkanna V. Analysis of variability, correlation and path coefficient studies for yield and quality traits in rice (*Oryza sativa* L.). Agriculture Science Digest. 2017;37(1):1-9.
8. Dhidhi S, Gauraha D, Sarawgi AK, Sao A. Genetic variability studies for yield and yield components in rice (*Oryza sativa* L.). The Pharma Innovation Journal. 2021;10(10):1057-1059.
9. Emi FR, Khatun H, Yasmine F, Hasan AK, Hossain MA. Morphological variability and genetic diversity of Aman rice germplasm of Bangladesh cultivated in Mymensingh region. Plant Science Today. 2021;8(4):972-985.
10. Fisher RA, Yates E. Statistical Tables for Biological, Agricultural and Medical Research. 6th edition. Oliver and Boyd Ltd. Edinburgh. London; c1967. p. 53-56.
11. Hanson WD, Robinson HF, Comstock RE. Biometrical studies of yield in segregating population Korean Lespandeza. Agronomy Journal. 1956;48(6):268-272.
12. Johnson HW, Robinson HF, Comstock RE. Estimates of genetic and environmental variability in soybean. Agronomy Journal. 1955;47(7):314-318.
13. Karim D, Sarkar U, Siddique MNA, Miah MAK, Hasnat MZ. Variability and Genetic Parameter Analysis in Aromatic Rice. International Journal of Sustainable Crop Production. 2007;2(5):15-1.
14. Kole PC, Chakrabarthy NR, Bhat JS. Analysis of variability, correlation, path coefficients in induced mutants of aromatic non-basmati rice. Tropical Agricultural Research and Extension. 2008;113:60-64.
15. Mishu MFK, Rahman MW, Azad MAK, Biswas BK, Talukder MAI, Kayess MO, *et al*. Study on Genetic Variability and Character Association of Aromatic Rice (*Oryza sativa* L.) Cultivars. International Journal of Plant & Soil Science. 2016;9(1):1-8.
16. Mustafa MA, Elsheikh MAY. Variability, correlation and path coefficient analysis for yield and yield components in rice. African Crop Science Journal. 2016;15:183-189.
17. Sao A. Studies on combining ability and heterosis in F_1 rice hybrids using cytoplasmic male sterile lines. M.Sc. (Ag.) Thesis, IGKV, Raipur, C.G; c2002.
18. Seyoum M, Sentayehu A, Kassahum B. Genetic variability, heritability, correlation coefficient and path analysis for yield and yield related traits in upland rice. Journal of Plant Sciences. 2012;7(1):13- 20.
19. Sharma DJ, Parihar R, Pandey D, Ahmad A, Sarawagi AK, Sharma D. Genetic evaluation of aromatic short grain rice genotypes (*Oryza sativa* L.). Journal of Pharmacognosy and Phytochemistry; c2020. p. 68-72.
20. Sudeepthi K, Srinivas T, Ravikumar BNVSR, Jyothula DPB, Umar SKN. Genetic divergence studies for yield and yield component traits in rice (*Oryza sativa* L.). Multilogic in science. 2020;9(2020b):415-418.
21. Syed E, Khaliq I. Quantitative inheritance of some physiological traits for spring wheat under two different population densities. Pakistan Journal of Botany. 2008;40(2):581-587.