Assessment of Genetic variability, Character Association of yield related traits and Genetic Divergence study in Rice (*Oryza sativa* L.)

Comment [CP1]: Reframe the title!! "Genetic variability, character association and genetic diversity for yield related traits in Rice (*Oryza sativa* L.)"

ABSTRACT

Comment [CP2]: Revise it as per comments file

The present study was carried out to assess the genetic diversity for various rice traits and their association with yield at Chandra Shekhar Azad University of Agriculture and Technology, Kanpur (Uttar Pradesh), India. 64 rice genotypes were evaluated on the basis of various morphological traits in a field experiment. Significant variation were observed among genotypes for all the traits studied. The results indicated that the highest genetic variability was observed in case of plant height, days to maturity, numbers of spikelet per panicle and biological yield per plant. The phenotypic coefficient of variation (PCV) was higher than the genotypic coefficient of variation (GCV) for all the traits studied. High GCV and PCV were observed for grain yield per plant (PCV=31.69%, GCV=31.23%). Broad sense heritability varied from 98.03% in case of days to maturity to 61.45% for harvest index. Significant positive correlation with grain yield was also noticed for harvest index (0.475**), test weight (0.503**), number of spikelet per panicle (0.827**) and biological yield per plant (0.963**). All the traits were also studied through path coefficient analysis and highest positive direct effect on grain yield per plant was recorded by biological yield per plant (0.9421) followed by harvest index (0.2673). The dendrogram of cluster analysis grouped 64 rice genotypes into seven clusters. Cluster II incorporated the highest number of genotypes. The maximum cluster mean for grain yield was observed in case of Cluster-II (25.62) followed by Cluster-V (24.76) showing high yield potential. Data from this study exhibited the presence of sufficient genetic diversity among the genotypes which can be employed in future rice breeding programmes.

Key Words: Rice; Oryza sativa; Genetic diversity; Correlation; Cluster

INTRODUCTION

Rice (*Oryza sativa* L.) is the most important cereal consumed by more than 3.5 billion people comprises about half of the world's population (Wing *et al.*, 2018). It contains a significant number of calories and a wide variety of essential vitamins, minerals, and other nutritional values (Mohidem*et al.*, 2022). The total production of rice recorded for 135.76 million metric tons in India, with a total area of 47.83 million hectare and the average of 4.26 metric tons per hectare after China (Foreign Agricultural Service/USDA Global Analysis 2023). A phenomenal increase in productivity per hectare over the years has contributed to higher overall production. The reasons attributed for this higher productivity is the green revolution, in which the short and HYVs (high yielding varieties), fertilizer application and irrigation practices were introduced (Surendran*et al.,* 2021).

As we know that currently India is facing the issue of nutritional deficiencies; so it's crucial to diversify our agricultural focus towards cultivating millets, pulses, and oilseeds alongside rice production. The aim is to enhance agricultural output without compromising rice production.Rapidly increasing demand due to increasing population has forced us to search for another quantum jump in rice productivity. In the present scenario the rice productivity has reached a plateau. In order to achieve the expected targets, we have to develop the varieties with higher yield potential by breaking the existing yield plateau through utilizing more diversified parents in breeding programmes. The success of any plant breeding programme largely depends on the existence of diversity among the genotypes (Allard, 1960). For this objective, the present experiment aims to assess the degree of genetic variability present in crop germplasm collections in order to identify superior lines which can further be used as donor parents in breeding programmes. D^2 analysis was employed to assess the degree of genetic diversity among genotypes, which is based on multivariate analysis developed by Mahalanobis (1936). This analysis provides a measurement of relative contribution of different components on diversity both at intra and intercluster level and genotypes drawn from widely divergent clusters are likely to produce heterotic combinations and wide variability in segregating generations (Singh *et al.*, 2019).

MATERIALS AND METHODS

The present investigation was carried out at Crop Research Station, Nawabganj, Kanpur (U.P.). The geographical coordinates of the site were 26°29' 35" North latitude and 80°16'25" East Longitudes and is located on an elevation of about 125.9 m above mean sea level in Gangetic plain. The experimental material for the investigation comprised 64 strains/varieties of rice (Oryza sativa L.).

Table 1..Description of the genotypes used in the study.

S.No.	Designation	S.No.	Designation
1	KNM 13568	33	RP 6745-MSAC 23-49
2	NLR 3819	34	CR 4385-RGA-6-2
3	NWGR 17075	35	UPR 4611-1-1-1-1-1
4	KGT-23-3	36	JNPT 581-64
5	CB 17504	37	AD 21184
6	Nath 20 -20	38	HKR 18-33
7	RP 6475-CGR 16-CGIL 54-CGK 2- I-2131-S	39	KPS 10642
8	OR 2577-5	40	IR 19LJ054
9	RP 6746- IR 17A2831	41	RP 6459-C2-sel12
10	CR 4428-1-1-2-1-3-1	42	CR 4388-RGA-245
11	CR 4077-1357-5-4-2-1-1	43	CSR AP10
12	KMP 252	44	PR 113, Lalat, MTU 1020, Karjat-7 (ZC)
13	NDRK 11-27	45	RP 6744-19180-1-1
14	RP 6721-LVS 24-CN 2103-21-11-2	46	HURS-23-2-IR 18A1565
15	CR 3506-1-2-3-2-1	47	NVSR 941
16	CR 4396-291-2-6	48	Surya 27
17	MTU 1392	49	HURS-23-17-IR-143534-114-1-1-387-31-38
18	Pusa 2086-36-11-12-1	50	BNP-401
19	ORJ 1348	51	R 2341-329-2-169-1
20	RP5683-101-30-2	52	BRR-2134
21	SKL-8-33-1570-107-320-242-127	53	BRR 0287-IR 143532-95-1-1-177-44-4
22	CR 4388-RGA-60-53-1	54	CR 4396-1-13-11
23	NDR TFR-10	55	RP 6529-RMS-64-5-7-9
24	Pusa 2087-40-19-4-1	56	TRC 2023-51/ IR 126999-B-32-2-1-3
25	OROI-11-IR 88243-17-1-1-3	57	RP 6529-52-5-7-9
26	BRR 0053-IR 96321-10999-347-B-1-2	58	PAU 6707-22-1-2-2 (RYT 3889)
27	BKR 510	59	YNPK-7258
28	RNR 38125	60	RNR 38966
29	WGL 1740	61	GNV 2188-1
30	ORR 1815	62	CR 4415-3-1-3-1-3-1
31	NDR 8806-TFR-3	63	Gontra Bidhan-3 (NC)
32	CSR-30 (LC)	64	CR 4343-15-2-1-1

The observations were recorded on days to 50% flowering, days to maturity, plant height, flag leaf length, flag leaf width, number of tillers per plant, number of panicle per plant, panicle length, number of spikelets per panicle, biological yield, harvest index, test weight, and grain yield per plant.The data was recorded on three randomly selected plants from each replication for all characters except days to 50% flowering and days to maturity. Plant height was measured in centimeters from the ground level to the top of the panicle (excluding awn) at the time of maturity. The total number of tillers and number of panicles in each of the three randomly selected plants were counted and averaged. Length of main panicle was recorded by measuring from the base of the panicle to the top most spikelet excluding awn in centimeters.The length of the flag leaf was measured in centimeters from the base to the tip of randomly selected flag leaves and flag leaf width was measured (cm) in the middle part of the leaf from one margin to another margin. Number of Spikelets per panicle was recorded by counting the total number of spikelets from the main panicle. Biological yield was recorded in gram separately and averaged for each replication before threshing. Grain yield (g) was recorded separately and averaged too. Harvest index is the ratio of economic yield to biological yield.

Harvest index (%) = Economic yield (Grain yield) / Biological yield (grain yield + straw) X100

The obtained data were analyzed using two-way analysis of variance (ANOVA). This analysis was aimed to get the information about genotypes and their interaction. The phenotypic and genotypic coefficient of variation, heritability in broad sense and genetic advance as percentage of mean were calculated by using the formula proposed by Burton and Devane in 1953. Simple correlation coefficients were computed at genotypic and phenotypic levels between pairs of characters adopting the following formula given by Johnson et al. (1955).Path analysis is worked out by using the estimates of simple correlation coefficients. For this, all possible correlations among the dependent and independent variables are worked out. To assess the genetic diversity among 64 genotypes along with three checks, D^2 analysis was performed and a dendrogram was constructed.

RESULTS AND DISCUSSIONS

Analysis of variance for grain yield and quality traits

The analysis of variance (ANOVA) revealed highly significant differences among all the traits, indicating a substantial amount of genetic variability among the genotypes. This variability supports the potential for selection in the desired direction.

Mean performance of genotypes for various traits

The general mean, range, standard error, and critical difference (CD) for 13 quantitative traits of rice studied during the *Kharif* season of 2023-24 provided crude information about the extent of genetic variability among the genotypes. Days to50% flowering exhibited range from 71.33 days (Pusa 2086-36-11-12-1) to 99.33 days (CR 4343-15-2-1-1) with a general mean of 86.87 days. For days to maturity, the recorded range was 112.00 days (Gontra Bidhan-3) to 140.33 days (Pusa 2087-40-19-4-1) with a general mean of 125.61 days. The mean value for plant height was recorded 115.13 days and the range was observed from 98.00 cm (GNV 2188-1) to 136.57 cm (RNR 38966). Panicle length exhibited the range from 16.60 (cm) in case of IR 19LJ054 to 32.23 (cm) in case of AD 21184 with a general mean of 24.14 (cm). Number of spikelet per panicle varied from 46.37 (Pusa2086-36-11-12-1) to 128.67 (OROI-11-IR 88243-17-1-1-3) with a general mean of 92.50. For the mean performance of genotypes, biological yield exhibited the range from 26.53 g (Pusa2086-36-11-12-1) to 80.37 g (BRR-2134) with a general mean of 56.44 g. The mean value for harvest index varied from 26.27% (GNV 2188-1) to 44.60% (IR 19LJ054). The general mean was recorded 35.26%. The data revealed that mean value for test weight ranged from 13.14 g (CR 4343-15-2-1-1) to 26.39 g (HKR 18-33) with a general mean of 19.05 g. Whereas, mean value for grain yield varied from 8.11 g (CR 4396-1-13-11) to 30.31 g (RP 6459-C2-sel12), while the general mean for this character was recorded 20.02 g.

The coefficient of variation (CV) for the studied traits exhibited range from 1.04 to 7.68. The variables contributing towards yield, such as number of tillers per plant, number of panicles per plant, number of spikelets per panicle and biological yield showed high coefficients of variation indicating the presence of adequate variability.

Phenotypic and genotypic coefficient of variation

Grain yield per plant (PCV=31.69%, GCV=31.23%), biological yield per plant (PCV=27.71%, GCV=27.33%), %), number of spikelets per panicle (PCV=26.52%, GCV=26.15%) and number of tillers per plant (PCV=21.66%, GCV=21.11%) exhibited the highest estimates of both phenotypic and genotypic coefficient of variation. The PCV and GCV estimates for these traits indicating adequate amount of diversity among genotypes. For all traits PCV exceeded GCV suggested that observed variation was also influenced by environmental factors rather than solely by genetic factors. The findings were in accordance to Sumanth *et al*., (2017), Zeleke *et al.*, (2021), Kumar *et al*., (2023), Demeke *et al*., (2023), Chaudhary *et al*.,

(2023) and Singh *et al.*, (2023).

Correlation and Path coefficient analysis

The grain yield per plant exhibited highly significant positive correlation with panicle length (0.205), number of spikelet per panicle (0.827), biological yield (0.963), harvest index (0.475) and test weight (0.503).Biological yield was recorded to have highly significant and positive correlation with panicle length (0.206) and number of spikelet per panicle (0.873).This research aids breeders in upcoming breeding initiatives by identifying beneficial traits that are positively correlated with yield. Similar findings were recorded by Kumar *et al.*, (2018), Singh *et al.*, (2018), Hossain*et al.*,(2020),Zeleke *et al.*,(2021),Renuprasath*et al.*,(2023), and Ali et al., (2024).

The genotypic path coefficient analysis was worked out by using simple correlation among 13 characters to estimate the direct and indirect effect of different characters on grain yield per plant.The highest positive direct effect on grain yield per plant was exhibited by biological yield (0.9421) followed by harvest index (0.2673), flag leaf width (0.0246) and number of panicle per plant (0.0156). Whereasnumber of spikelet per panicle *via* biological yield (0.8223) andtest weight *via* biological yield (0.4603) exhibited highest positive indirect effect on grain yield per plant. The residual effect observed was 0.00466 which indicates that some of the characters which might contribute to yield have not been included in the study.Similar findings were recorded by Naseer *et al.*, (2013), Kumar *et al.*, (2018) and Singh *et al.*, (2018), Thuy *et al.*, (2023), Kujur *et al.*, (2023).

Table 2: Simple correlations among different morphological traits of rice

Characters	DFF	DOM	PH	FLL	FLW	NTPP	NPPP	PL	NSPP	BY	HI	TW	GY
DFF	1	0.811**	-0.370**	-0.202**	0.041	-0.053	-0.018	-0.073	0.081	0.009	-0.319**	-0.013	-0.09
DOM			-0.206**	-0.012	0.092	-0.046	0.038	0.043	0.055	-0.045	-0.299**	-0.019	-0.129
PH				0.153	-0.027	0.232**	0.069	-0.025	-0.138	-0.088	0.115	-0.066	-0.044
FLL					0.194*	0.081	0.025	0.037	0.024	-0.088	0.028	-0.201*	-0.074
FLW						0.057	0.037	-0.04	0.157*	0.084	-0.116	0.008	0.065
NTPP							0.659**	0.220**	0.007	-0.023	-0.033	0.196*	-0.026
NPPP								0.324**	-0.062	-0.188*	-0.11	0.313**	-0.192*
PL									0.143	0.206**	0.064	0.409**	0.205**
NSPP										0.873**	0.183*	0.441**	0.827**
BY											0.231**	0.489**	0.963**
HI												0.224**	0.475**
TW													0.503**
GY													1

Characters	DFF	DOM	PH	FLL	FLW	NTPP	NPPP	PL	NSPP	BY	HI	TW	GY
DFF	-0.02	0.0068	0.0007	0.001	0.001	0.0003	-3E-04	0.0003	-0.0037	0.0087	-0.0853	0	-0.09
DOM	-0.016	0.0084	0.0004	0.0001	0.0023	0.0003	0.0006	-0.0002	-0.0025	-0.0429	-0.0798	0	-0.129
PH	0.0074	-0.002	-0.002	-0.0008	-0.0007	-0.0014	0.0011	0.0001	0.0063	-0.0827	0.0307	0	-0.044
FLL	0.004	-1E-04	-0.0003	-0.005	0.0048	-0.0005	0.0004	-0.0002	-0.0011	-0.0833	0.0075	0	-0.074
FLW	-8E-04	0.0008	0.0001	-0.001	0.0246	-0.0004	0.0006	0.0002	-0.0071	0.079	-0.0311	0	0.065
NTPP	0.0011	-4E-04	-0.0005	-0.0004	0.0014	-0.006	0.0103	-0.001	-0.0003	-0.0218	-0.0087	0	-0.026
NPPP	0.0004	0.0003	-0.0001	-0.0001	0.0009	-0.004	0.0156	-0.0015	0.0028	-0.177	-0.0295	0	-0.192*
PL	0.0014	0.0004	0.0001	-0.0002	-0.001	-0.0013	0.0051	-0.0047	-0.0065	0.1944	0.0172	0	0.205**
NSPP	-0.002	0.0005	0.0003	-0.0001	0.0039	0	-0.001	-0.0007	-0.0453	0.8223	0.0489	0	0.827**
BY	-2E-04	-4E-04	0.0002	0.0004	0.0021	0.0001	-0.003	-0.001	-0.0396	0.9421	0.0618	0	0.963**
HI	0.0063	-0.003	-0.0002	-0.0001	-0.0029	0.0002	-0.002	-0.0003	-0.0083	0.2177	0.2673	0	0.475**
TW	0.0003	-2E-04	0.0001	0.001	0.0002	-0.0012	0.0049	-0.0019	-0.02	0.4603	0.0598	-0.0001	0.503**

Table 3: Path coefficient analysis among different morphological traits of rice

Euclidean cluster analysis by Mahalnobis D^2 statistics

In the present investigation, the genetic divergence among 64 genotypes was studied by D^2 method given by Mahalnobis (1928) followed by clustering of genotypes into various non-overlapping clusters by Tocher's method. The pseudo F-test revealed that the most appropriate number of clusters for grouping64 genotypes was seven. Therefore, the 64 genotypes were grouped in to seven non-over lapping clusters.The highest number of genotypes appeared in the cluster-II, cluster-VIIand cluster-I containing 15, 12 and 11 entries respectively followed by cluster-IV with 10, cluster-VI with 7 and cluster-III with 5 entries. While cluster-V contained minimum number of 4 entries. The distribution of 64 lines in seven clusters is presented in Table 4

Table 4. Clustering pattern of 64 rice genotypes on the basis of non-hierarchical Euclidean cluster analysis

Clusters	No of genotypes	Genotypes
I	11	11 16 17 26 27 31 41 42 56 57 63
II	15	5 6 10 12 13 25 28 29 30 36 37 40 48 58 64
III	5	1 2 34 35 59
IV	10	14 22 23 24 32 33 52 53 54 61
V	4	7 38 39 49
VI	7	3 4 15 21 43 50 51
VII	12	8 9 18 19 20 44 45 46 47 55 60 62

Inter and intra-cluster distance

The estimates of inter and intra-cluster distance for 7 clusters are presented in the Table 5. The maximum intra-cluster distance was observed in case of Cluster-VII (2.942) followed by Cluster-III (2.798). The high intra-cluster distance in cluster VII indicated the presence of wide genetic diversity among the genotypes present in the same. The maximum inter-cluster distance was observed between the Cluster-II and III (4.727) followed by cluster-V and VII (4.436) and Cluster-II and IV (4.390). On the other hand, Cluster-I and II (2.903) exhibited minimum inter-cluster distance. Based on these findings, crosses between Cluster-II and III, V and VII, as well as II and IV is recommended to obtain robust heterotic recombinants and transgressive segregants in future breeding programmes. The inter-cluster distance between cluster I and II was found minimum, indicating a close relationship between genotypes and a low degree of diversity among them. To realize maximum variability and high heterotic effect, Mishra et al. (2003) and Chaturvedi and Maurya (2005) recommended that parents should be selected from two clusters having wider inter cluster distance.

Table 5. Estimates of average intra and inter-cluster distances for the seven clusters

Clusters	I	II	III	IV	V	VI	VII
I	**2.286**						
II	2.903	**2.572**					
III	3.887	4.727	**2.798**				
IV	4.132	4.39	3.527	**2.651**			
V	3.544	4.028	3.87	4.281	**2.113**		
VI	2.958	3.492	4.201	2.935	3.343	**2.54**	
VII	3.997	3.938	3.409	3.483	4.436	4.038	**2.942**

Cluster means for different characters

The cluster means for the 13 characters under study have been presented in Table 6. The findings indicated a wide range of mean values for all the characters. The highest cluster mean for days to 50% flowering was recorded for Cluster-IV (95.43 days) and lowest for Cluster-I (80.18 days). Days to maturity had a range of 133.86 days for Cluster-VI to 112.13 days for Cluster-III; plant height exerted the range varied from 125.09 cm for Cluster-VII to 100.19 cm for Cluster-III; maximum cluster mean for number of tillers per plant was observed in case of Cluster-II (9.41). Whereas, Cluster-VI (6.24) showed the lowest mean for number of tillers per plant. Number of panicles per plant had a range of 9.84 for Cluster-II to 6.60 for Cluster-V; panicle length varied from 27.11 cm for Cluster-V to 17.89 cm for Cluster-I; cluster mean for number of spikelets per panicle observed between 112.65 for Cluster-II to 60.23 for Cluster-III; biological yield per plant recorded as high as 70.34 g for Cluster-II to 40.90 g in case of Cluster-III; harvest index varied from Cluster-V (39.26) to Cluster-IV (32.55). Test weight varied as high as 22.98 g for Cluster-II and as low as 16.56 g for Cluster-IV. In case of grain yield per plant, the maximum cluster mean was observed in case of Cluster-II (25.62 g) and the lowest cluster mean for the same was exerted by the genotypes of Cluster-VII (12.83 g). Similar findings were obtained by earlier workers Sharma *et al.*, 2011; Senguttuvel*et al.*,2013; Jha *et al.*,2014; Maurya *et al.*,2017; Ahmed *et al.*,2018; Iqbal *et al.*,2018showing substantial amount of genetic divergence in the rice materials.

Table 6. Estimates of cluster means for 13 characters of Rice genotypes by D^2 analysis

Clusters		DFF	DOM	PH	FLL	FLW	NTPP	NPPP	PL	NSPP	BY	HI	TW	GY
I	Mean	80.18	119.24	114.95	38.41	1.47	6.85	8.04	27.11	109.96	64.42	37.19	19.22	23.93
	SE±	3.4	3.28	8.69	2.68	0.12	1.17	0.61	4.14	10.8	10.69	2.36	3.98	4.21
II	Mean	87.64	124.78	116.74	32.68	1.36	9.41	9.84	26.03	112.65	70.34	36.42	22.98	25.62
	SE±	6.96	6.64	9.72	4.22	0.17	0.99	0.83	4.11	11.02	7.35	2.71	2.43	3.44
III	Mean	82.27	112.13	100.19	32.81	1.29	7.33	7.74	23.15	60.23	40.9	35.59	17.4	14.48
	SE±	3.39	15.24	8.85	4.67	0.09	1.23	0.44	4.58	11.88	7.09	5.58	2.49	3.2
IV	Mean	95.43	133.53	104.41	33.79	1.48	6.8	8.06	19.68	82.7	48.09	32.55	16.56	15.75
	SE±	4.03	5.75	5.34	4.33	0.19	1.71	0.87	1.81	22.41	11.6	2.91	3.19	4.45
V	Mean	82.83	122.33	122.65	31.15	1.16	6.73	6.6	17.89	85.92	63.25	39.26	17.96	24.76
	SE±	6.22	6.1	5.55	1.46	0.07	1.22	1.03	1.28	24.65	8.2	3.7	3.01	3.47
VI	Mean	93.1	133.86	114.77	36.33	1.25	6.24	7.02	26.36	101.63	63.04	34.54	18.62	21.61
	SE±	3.56	5.61	8.89	4.27	0.11	0.89	1.75	3.78	16.16	12.37	3.12	2.85	3.72
VII	Mean	84.53	125.53	125.09	35.52	1.35	9	9.83	23.98	69.78	39.09	33.22	17.36	12.83
	SE±	7.19	7.39	6.63	5.26	0.17	0.78	0.99	4.89	17.32	9.97	4.03	4.14	3.08

Percentage contribution towards total divergence

The selection and choice of parents mainly depends upon contribution of characters towards divergence. The per cent contribution towards genetic divergence by all the 13 characters are presented in Table 7.The highest contribution towards genetic divergence was exhibited by harvest index (11.54%), followed by plant height (10.44 %), number of panicles per plant (9.25%), flag leaf length (8.17%), number of tillers per plant (7.57%), days to 50% flowering (7.35%), panicle length (7.24%) and grain yield (7.01%). Remaining characters contributed comparatively lower towards total divergence.

Table 7. Contribution of different characters towards genetic divergence among 64 genotypes of rice (Oryza sativa L.).

Characters	Contribution total divergence (%)
Days to flowering	7.35
Days to maturity	5.69
Plant height (cm)	10.44
Flag Leaf Length (cm)	8.17
Flag Leaf Width (cm)	6.51
No. of tillers /plant	7.57
No. of panicle/plant	9.25
Panicle length (cm)	7.24
No. of spikelet/ panicle	6.51
Biological yield (g/plant)	6.53
Harvest index (%)	11.54
Test weight (g)	6.18
Grain yield (g/plant)	7.01

Conclusion

Comment [CP3]: Reduce words /summarize

In the present study, the analysis of variance (ANOVA) revealed existence of highly significant variations among 64 genotypes of rice. Among these genotypes, RP 6459-C2-sel12 followed by KMP 252, RNR 38966, RNR 38125, CSR AP10, CB 17504 and CR 4388-RGA-245 regarded as best for grain yield per plant. These genotypes also exhibited consistently high mean performance for other traits related to yield; indicating their potential for being effective in terms of yield and other yield contributing characteristics. Genotypes Pusa 2086-36-11-12-1, IR 19LJ054, CR 4388-RGA-245 for earliest flowering, Gontra Bidhan-3, GNV 2188-1, Pusa 2086-36-11-12-1 for DM, GNV 2188-1, CSR AP10 for PH, HKR 18-33, Gontra Bidhan-3, WGL 1740 for NTPP, NVSR 941, RP 6746-IR 17A2831 for NPPP, AD 21184, NVSR 941, Gontra Bidhan-3 for PL, OROI-11-IR 88243-17-1-1-3, CSR AP10, BRR-2134 for NSPP, Pusa2086-36-11-12-1, HKR 18-33, CR 4388-RGA-245 for BY were found to be promising for respective characters. The lines showing superior performance for yield and other traits may be used as male parents in the hybridization programme for the characters to which they exhibited high mean performance. High estimates of GCV and PCV were observed for GY, BY and NSPP. Grain yield per plant, biological yield per plant and number of spikelets per panicle showed high values of heritability and genetic advance as well. The genotypes were grouped in 7 clusters. In case of intra and inter-cluster distance, the maximum intra-cluster distance was observed in case of Cluster-VII whileCluster-Vexerted the lowest intra-cluster distance. The maximum inter-cluster distance was observed between the Cluster-II and III whereas, minimum inter-cluster distance were found in case of Cluster-I and II. The highest percentage contribution towards genetic divergence was exhibited by harvest index followed by plant height, number of panicles per plant, panicle length and grain yield. The genetic variation found among rice genotypes provides a crucial basis for creating new varieties with enhanced characteristics. By leveraging this diversity in breeding programs, breeders can effectively utilize the genetic potential of various genotypes to develop superior rice varieties.

Compliance with ethical standards

Ethical issues: None.

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