

Germplasm evaluation, genetic variability, heritability, genetic advance, and character analysis in scented and non-scented rice (*Oryza sativa* L.) under irrigated conditions.

Abstract:

Eighty-nine germplasm of rice (*Oryza sativa* L.) along with four checks were evaluated in a well-prepared field to assess the genetic variability, heritability, and genetic advance for different characters under irrigated conditions in Augmented Block Design. In this study, the analysis of variance revealed highly significant or significant for all the 13 characters except non-significant for 1000-grain weight. High and moderate broad sense heritability was recorded for all the characters except 1000-grain weight, days to maturity, days to 50 % flowering, and spikelet fertility which showed low heritability. Genetic advance in percent of mean recorded high and moderate for all the characters except 1000-grain weight, days to 50 % flowering, number of fertile spikelet per panicle, and spikelet fertility which had the low genetic advance. The phenotypic and genotypic coefficient of variation was recorded higher for flag leaf area and moderate for harvest index, days to maturity, and L/B ratio. Non-hierarchical Euclidean analysis grouped the eighty-nine germplasm into eight clusters and this study showed the existence of wide genetic diversity within *Oryza sativa* germplasm. Among the eight clusters, the **highest number of genotypes** were present in cluster III which contained 23 entries, followed by cluster IV and cluster VII with 14 and 11 entries, respectively. While least no genotypes were present in cluster VIII contained only 4 genotypes. The highest intra-cluster distance was observed in cluster II (3.664) while the lowest was in cluster V (2.327). In the case of inter-cluster distance, the highest value was observed between cluster VIII and cluster II (5.698) while the lowest value was observed between V and III clusters (2.808). The genotypes present in the diverse clusters may serve as parental material for the hybridization program which will lead to the isolation of desirable sergents for developing high-yielding rice varieties under irrigated conditions.

Keywords: *Oryza sativa* L., Coefficient of variation, Genetic variability, Genetic advance, Heritability.

Introduction:

Rice (*Oryza sativa* L.) belongs to the family Gramineae (Poaceae) and is a diploid species having chromosome number $2n = 24$ ($n=12$) and basic chromosome number $x=5$ (due to meiotic irregularity in chromosome number 2). It is one of the most important staple food for the developing world as well as the majority of Asian countries. It is the major source of calories for more than half of the global population. The total production of rice during 2020-21 is estimated at a record 121.46 million tonnes. It is higher by 9.01 million tonnes than the last five years'

average production of 112.44 million tonnes. (**Ministry of Agriculture and Farmers Welfare 2021**). Scented rice was known since ancient times, and was considered the best among the special rice. Throughout the world, they have been the choicest food of kings, royalty, the elite of society, as well as the common man. Increased grain yield of the rice crop is the main concern of rice breeders, so plant breeders throughout the world have been utilizing the available genetic resources to change the existing varieties and evolve new crop varieties to meet the ever-changing requirements of the societies. *Basmati* rice is a tiny yet unique sub-group of rice that is prized for its superior quality. For decades, basmati rice has been farmed in the traditional lands of the Indian subcontinent's northwestern areas. The climate in this region is suitable for the cultivation of transparent grain with a strong, pleasant scent. *Basmati* rice, which has a particular aroma and flavor, is widely consumed in India, Pakistan, and the Middle East, as well as in Europe. The price of basmati rice exported in these areas is more than double that of non-*Basmati* rice. The evaluation of the relationship between yield and its components provides a foundation for selecting suitable characters to increase economic traits. The path analysis method divides the correlation or connection into components of direct and indirect effects, revealing the relative importance of the component features that influence yield. The value of genetic variation in the material has also been emphasized in crop development programs. The more different the parents, the greater the likelihood of a wider range of variability.

Materials and Method:

The experiment of the present investigation was conducted to evaluate the 89 rice germplasm including four checks (namely Sarjoo-52, NDR-97, NDR-6093, and Kalanamak) in Augmented Block Design at the Crop Research Station of Acharya Narendra Deva University of Agriculture and Technology, Narendra Nagar, Ayodhya (UP). The experimental field was divided into 5 blocks and 21 plots. Each block (17 test genotypes along with 4 checks) was accommodated. Each plot consisted of three rows of 3 m in length with a spacing of 10 cm within the plant to plant and 20 cm between the rows. The recommended cultural practices are followed to raise a well normal crop. To avoid the border effect experimental plots were surrounded on all sides by non-experimental rows. The observation was recorded on 5 randomly selected plants from each plot except days to 50% flowering and days to maturity were recorded on a land basis while the other data were recorded on a plant basis as plant height(cm), number of productive tillers per plant, panicle length (cm), flag leaf area (cm²), number of fertile spikelet per panicle, spikelet fertility (%), biological yield per plant (g), harvest index (%), 1000-grain weight (g), L: B ratio and grain yield per plant (g).

Result and Discussion:

1. Analysis of variance

In the present investigation analysis of variance for yield and its contributing characteristics revealed that sufficient variation was present among the genotypes. The result of

the analysis of variance for augmented design in respect of all the 13 characters is presented in Table .1. The variation due to blocks was significant or highly significant for all the characters under study except non –significant for 1000- grain weight. The differences among the check varieties were also found to be significant or highly significant for all the characters under study except spikelet fertility (%) which showed non-significant. The analysis of variance for different characters in augmented design was done by the method given by Federer (1956).

Table.1: Analysis of variance of augmented design for 13 characters in rice under irrigated condition

Characters	Source of variation		
	Blocks	Checks	Error
	d. f.(4)	d. f.(3)	Error(12)
Days to 50% flowering	84.03**	173.43**	10.25
Plant height (cm)	778.97**	3482.09**	19.83
Number of Productive Tillers/plant	1.61**	2.31**	0.13
Panicle length (cm)	91.71**	38.15**	0.93
Flag leaf area (cm ²)	405.17**	44.55**	0.69
Days to maturity	141.40**	397.53*	14.76
Number of fertile spikelet/panicle	227.31**	445.65**	9.72
Spikelet fertility (%)	24.20**	15.61	7.45
Biological yield /plant (g)	251.66**	319.26**	1.62
Harvest Index (%)	1996.58**	159.13**	2.10
1000-grain weight (g)	1.52	43.09**	1.05
L:B ratio	0.27**	0.66**	0.01
Grain yield/plant (g)	143.38**	93.52**	0.26

*, ** Significant at 5% and 1% probability levels of significance, respectively.

2. Mean performance

A wider range of variability was revealed for the traits of plant height (88.31-167.22) followed by a number of fertile spikelets per panicle (80.96-125.45), biological yield per plant (30.12-70.12), spikelet fertility (83.18-110.17), days to 50 % flowering (84-103), panicle length(17.43-48.39) and harvest index (30.04-57.55). The results showed that these traits should be used as selection prospects to improve performance through a breeding procedure like selection and hybridization.

Table.2 Coefficient of variation, Heritability, Genetic advance and mean performance of 13 characters in rice germplasm

Characters	Range		Grand mean	Coefficient of variation		Heritability in a broad sense	G.A.	G.A. in % of mean at 5 %
	Min.	Max.		Genotypic coefficient of variation (GCV) (%)	Phenotypic coefficient of variation (PCV) (%)			
Days to 50% flowering	84.00	103.00	97.07	1.34	3.56	14.20	1.01	1.04
Days to maturity	120.00	135.00	127.08	8.13	8.85	84.33	19.54	15.38
Plant height (cm)	88.31	167.22	124.31	0.48	0.57	72.92	1.06	0.85
Panicle length (cm)	17.43	48.39	27.68	6.56	7.43	77.92	3.30	11.93
Number of Productive Tillers/plant	7.51	17.72	11.11	37.36	38.10	96.15	8.38	75.47
Flag leaf area(cm ²)	12.07	37.88	23.98	9.73	18.74	26.97	2.50	10.41
Number of fertile spikelet/panicle	80.96	125.45	96.20	8.64	9.22	87.65	16.02	16.65
Spikelet fertility (%)	83.18	110.17	92.77	0.84	3.06	7.61	0.45	0.48
Biological yield /plant(g)	30.12	70.12	49.29	7.13	7.58	88.38	6.80	13.80
Harvest Index (%)	30.04	57.55	40.09	10.54	11.14	89.48	8.23	20.53
1000-grain weight(g)	18.15	29.45	24.78	3.43	5.37	40.77	1.12	4.51
L:B ratio	1.41	3.64	2.27	9.89	10.66	86.08	0.43	18.90
Grain yield/plant(g)	10.15	25.96	19.76	7.86	8.26	90.42	3.04	15.39

3. Coefficient of variation:

The results of the genotypic coefficient of variation and phenotypic coefficient of variation of all the 13 characters are presented in table 2. It is accepted that the value of the phenotypic coefficient of variation was also higher than the genotypic coefficient of variation for all the characters. The higher estimates (>20%) are exhibited by the Number of productive tillers per plant (37.36%) for GCV and (38.10%) for PCV. The character which exhibited moderate estimates (10-20%) of GCV and PCV were only for Harvest index (10.54%) for GCV and (11.14%) for PCV and flag leaf area for PCV (18.74%) also L: B ratio for PCV (10.66%) exhibited moderate estimates. The remaining characters *viz.*, Days to 50% flowering, Plant height, days to maturity, Panicle length, Number of fertile spikelets per panicle, Spikelet fertility, Biological yield per plant, 1000-grain weight, and Grain yield per plant showed low estimates(<10%) of GCV and PCV while flag leaf area and L:b ratio showed low estimates only for GCV. Similar results were observed for the above thirteen characters are broadly in agreement with earlier reports in rice. These findings were also reported by Chaudhary et al. 2004; Babar et al. 2009; Jayasudha and Sharma, 2010; Karthikeyan et al. 2010; Akhtar et al. 2011; Garg et al. 2011; Pandey, 2012; Basavaraja et al. 2013; Warkad et al. 2013)

4. Heritability and genetic advance in percent of mean:

The estimate of broad sense heritability (h^2_b) and genetic advance in percent of the mean (Ga) for different characters are presented in Table 2. The estimates of heritability in a broad sense have been classified by Robinson (1949) into three categories viz., high (>75%), medium (50-75%), and low (<50%). High estimates of broad sense heritability (>75%) were recorded for the number of productive tillers per plant (96.15%), grain yield per plant (90.42%), harvest index (89.48%), biological yield per plant (88.38%), number of fertile spikelet per panicle (87.65%), l:b ratio (86.08%) and days to maturity (84.33%) and panicle length(77.92%) . The moderate estimate of heritability (50-75%) was observed for plant height (72.92%), while the low estimates of broad sense heritability (<50%) were shown by 1000-grain weight (40.77%) , flag leaf area (26.97%), days to 50 % flowering (14.20%) and spikelet fertility (7.61%). The high estimates of heritability and genetic advance observed for the above characters are closed in agreement with the earlier reports on rice. These findings were also reported by Panwar et al. 2007; Pradhan et al. (2007), Rashid et al. (2008), Babar et al. 2009; Saleem et al. (2010), Kiani and Nematzadeh, 2012, The high estimates of genetic advance in percent of the mean (>20%) were recorded by the number of productive tillers per plant (75.47%) and harvest index (20.53%). The moderate estimate for genetic advance (10-20%) in percent of mean was shown by L: B ratio (18.90%), number of fertile spikelets per panicle (16.65%), grain yield per plant (15.39%), plant height (15.38%), biological yield per plant (13.80%), panicle length(11.93%) and flag leaf area (10.41%), while the low estimates of genetic advance (<10%) for 1000-grain weight (4.51%), days to 50% flowering (1.04%), plant height (0.85%) and spikelet fertility (0.48%).

Clusters	No of genotypes	Genotypes
I	9	Ujrou, Bashawa, PR-6, N-10-B, TN-1, KSR, UPR 2825-30-1-2, NVSR-604, NDR-97
II	9	Lindhinia-1, Dilaora local, Loungchoor, Local-chl-fzd, Bans, Sirdagarh, Palhari, NC-492, T-1242(1)
III	23	Harikesh, KR-103-96, GMP-12, CR-209, W-418, W-496, IGKV DH 42 Mutant, R 1656-2151-1-412-1, Dubraj, R-2369-475-2-252-1, Ketekijoha, NVSR 603, NDR-8400-3, OR 2594-13, Jeeraphool Mutant-5, IGKV-DH-66, NVSR-438, OR-2594-5, NDR-2020-2-1, RNR 28409, RNR-28401, Shobhini
IV	14	Geetu-2, Indrajon, Sahdalia, Katari bhog, Bilaspur, Vijets, NC-495, CR-118, BRR-2177, NDR-2020-1, Badshahbhog, BRR 2180, Vishnubhog Mutant-80, Kalanamak
V	9	Bee, Padheri, Mangal, KMP-41, KSR-4111, T-116, Kalanamak Mutant, Sarjoo-52, NDR-6093
VI	10	Mangole, Darahi, Turahwa, Yuvraj, NC-491, Nanital(Saryu), Kalakand, K-14, CH-1039, T-65
VII	11	Rajmunia, Benibhog, Harikrishna, Bakani, Farmahwa, Orissa-2, Nandi-C, Kerahani local -B1, Chingaurd-1, Tarochani, H-118

VIII	4	Singal, Kolamden, Mahechandour,Sarye
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Table 3. Clustering pattern of 89 rice genotype on the basis of Non- hierarchical Euclidian cluster analysis of thirteen characters

5. Genetic divergence analysis:

The pseudo F-test revealed that eight cluster arrangements was most appropriate for grouping the 89 genotypes. Therefore, the 89 genotypes were accepted to be grouped in to Eight non-over lapping clusters. The distribution of 89 rice germplasm in eight clusters are presented in table 3. The highest number of genotypes were present in cluster III which contained 23 entries, followed by cluster IV and cluster VII with 14 and 11 entries, respectively. Cluster I II and V contained 9 genotypes only while cluster VI contained 10 genotypes and cluster VIII contained only 4 genotypes.

The estimates of intra and inter cluster distances are presented in Table 4. The highest intra-cluster distance was observed in cluster II (3.664), followed by cluster VIII (2.917) and cluster VII (2.863). The lowest intra cluster distance was recorded for cluster V (2.327) followed by cluster VI (2.428) and cluster III (2.539). The maximum inter cluster distance was found between cluster VIII and cluster II (5.698). Cluster VIII also showed very high inter cluster distance from clusters I (5.173), VI (4.728) V (4.543), IV (4.397), III (4.279) and cluster VII (3.825). High order inter cluster distances were also recorded between cluster VII and II (4.603) followed by cluster II and I (4.443). The minimum inter cluster distance was observed between V and III cluster (2.808) followed by cluster IV and III (2.544).

The intra-cluster distance for 13 characters presented in Table 5 which revealed marked differences between the clusters for different characters. For days to 50 % flowering the cluster mean ranged from 96.76 days to 104.15 days, for plant height from 117.25cm to 185.68 cm, For the number of productive tillers per plant from 9.35 to 11.20, For the panicle length from

26.45cm to 33.46 cm, for the flag leaf area from 26.56cm² to 58.95cm², for the Days to maturity from 118.01 days to 130.33 days, for the number of fertile spikelet per panicle from 110.06 to 136.69, for the spikelet fertility % from 83.22 to 91.16, for the Biological yield per plant from 32.84 to 48.17, for the harvest index from 24.20 to 60.03, for the 1000-grain weight cluster mean ranged from 20.73 to 24.70, for the L:B ratio cluster mean ranged from 2.34 to 2.99. Similar study was also conducted by different rice breeders (Rukmini Devi et al., 2017). Based on cluster mean values, it is always advisable to go for genotypes belonging to different clusters but having more than one desirable trait (Rukmini Devi et al., 2020). The investigation showed that selection of genotypes having higher cluster mean could be used for the improvement of characters in rice breeding programme under irrigated condition.

Table. 4 Estimates of average intra and inter cluster distances for 8 clusters in rice germplasm

Clusters	I	II	III	IV	V	VI	VII	VIII
I	2.741							
II	4.443	3.664						
III	3.109	4.272	2.539					
IV	3.384	3.196	2.544	2.614				
V	3.461	3.697	2.808	3.273	2.327			
VI	3.430	3.552	3.224	2.868	2.936	2.428		
VII	3.424	4.603	4.028	3.835	3.050	3.315	2.863	
VIII	5.173	5.698	4.279	4.397	4.543	4.728	3.825	2.917

Bold figure indicates Intra cluster distance

Table. 5 Cluster means for different characters in rice germplasm.

Chara	Days to 50%	Plant height	Number of Produ	Panicle lengt	Flag leaf area(c	Days to maturit	Number of fertile	Spikelets fertility	Biological yield	Harvest Index(1000-grain weight(L:B ratio	R with Grain yield/pl
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clusters		flowering	(cm)	productive Tillers /plant	height (cm)	area (m ²)	yield	spikelets / panicle	(%)	/plant (g)	(%)	(g)		yield (g)
I	Mean	96.76*	118.06*	9.37	26.48	36.51	118.01*	124.12	90.32	37.92	35.32	20.73*	2.90	13.19
II	Mean	104.15**	130.28	9.35*	33.46**	26.56*	130.33**	132.09	83.22*	37.84	41.17	23.82	2.99**	15.05
III	Mean	99.86	139.22	10.36	26.45*	41.35	122.74	121.29	89.35	48.17**	24.20*	23.85	2.39	11.53
IV	Mean	103.64	139.15	11.20**	26.60	35.50	129.05	120.26	88.58	35.51	33.06	23.15	2.74	11.49*
V	Mean	96.86	124.18	10.79	29.18	34.13	122.58	110.06*	86.75	43.09	41.26	24.70*	2.34*	17.72
VI	Mean	102.87	117.25	11.16	27.50	31.63	127.30	136.69**	89.71	45.00	42.23	22.12	2.39	18.42
VII	Mean	97.62	136.34	10.39	26.70	40.48	119.91	132.19	91.16**	32.84*	60.03*	24.03	2.60	19.41
VIII	Mean	99.03	185.68**	10.78	26.47	58.95**	128.50	121.96	89.64	40.52	48.27	22.90	2.48	19.72*

*, ** indicates lowest and highest mean, respectively.

Conclusion:

For an effective crop improvement existence of sufficient variability in any crop population is an unalterable requirement. However, The results concluded that genotype Sarye recorded best performance for grain yield per plant (22.68gm) followed by CH-1039, Singal, Mahechandour and Tarochani. Characters like Number of productive tillers per plant, grain yield per plant and harvest index show high heritability coupled with high genetic advance as percent of mean therefore should be given top priority during selection. Further, cluster III and cluster IV constituted 23 and 14 genotypes, respectively were most diverse to each other. These clusters are suggested to provide a broad spectrum of variability in segregating generations and the genotypes present in them may be used as parents for future hybridization programme to develop desirable types.

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