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

Abstract:

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

Keywords:

Analysis of variance, Coefficient of variation, Genetic variability, Genetic advance, Heritability

Introduction:

Rice (*Oryza Sativa* L.) belongs to family Gramineae (Poaceae), is a dipoid species 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 developing world as well as majority of The Asian countries. It is the major source of the calories for more than half of the global population. In India, it stretches from 8^0 N latitude to 34^0 N latitude. Rice is also grown even in areas below the sea level, as in the Kuttanand region of Kerala. It is also grown well at altitudes above 1980 meter, as in parts of Jammu & Kashmir. Total production of rice during 2020-21 is estimated at 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 & Farmers Welfare 2021)**. Scented rice were known since the ancient times, and were considered the best among the specially 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 rice crop is the main concerned of rice breeders, so plant breeders throughout the world have been utilizing the available genetic resources to change the existing varieties and evolving 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 flavour, 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. Quantitative analysis of variability for economically significant features among available genotypes is critical not only for the choice of appropriate varieties, but also for use in improvement breeding programmes. The evaluation of the relationship between yield and its attributing features provides a foundation for selecting 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 variety in the material has also been emphasised in crop development programmes. The more different the parents, the greater the likelihood of a wider range of variability.

Materials and Method:

The experiment of present investigation was conducted to evaluate the 85 rice germplasm lines along with four checks (namely Sarjoo-52, NDR-97, NDR-6093 and Kalanamak) in Augmented Block Design at Crop Research Station Masodha, of A.N.D.U.A. & T., Kumarganj, Ayodhya. These genotypes exhibited wide spectrum of variation for various agronomical and morphological characters. The experimental field was divided in to 5 blocks and 21 plots in each block (17 test genotypes along with 4 checks) was accommodated in each block. Each plot was consisted three rows of 3 m length with spacing of 10 cm within the plant to plant and 20 cm between the rows. The recommended cultural practices will be followed to raise a well normal crop. To avoid the border effect experimental plots were surrounded on all side 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 was recorded on land basis while the other data will be recorded on plant basis that is Plant height(cm), No. of productive tillers per plant, Panicle length (cm), flag leaf area (cm^2), No. 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 characters revealed that sufficient variation present among the genotypes. Existence of sufficient variability in a crop is an inevitable fulfillment for an effective crop improvement. In this study revealed from significant estimates of mean squares for different characters. The result of the analysis of variance for augmented design in respect of all the 13 characters are presented in Table .1 the variation due to blocks was significant or highly significant for all the characters under study except non –significant means squares observed 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 (%) for which mean squares were non-significant.The analysis of variance for different characters in augmented design was done following 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
No. of Productive Tillers/plant	1.61**	2.31**	0.13
Panicle length (cm)	91.71**	38.15**	0.93
Flag leaf area (cm2)	405.17**	44.55**	0.69
Days to maturity	141.40**	397.53*	14.76
No. 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% & 1% probability levels of significance, respectively.

2. Mean performance

The mean performances for different characters of 89 ice genotypes are given in table no 2. Data recorded that there is a wider range of variability revealed for the traits plant height (88.31-167.22) followed by No. of fertile spikelet per panicle (80.96-125.45), biological yield per plant (30.12-70.12), spikelet fetility (83.18-110.17), days to 50 % flowering (84-103),panicle length(17.43-48.39) and harvest index (30.04-57.55). The followed finding showed that these traits should use as selection prospects to improve the performance through 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 broad sense	G.A.	G.A. in % of mean at 5 %
	Min.	Max.		GCV (%)	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
No. 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
No. 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:

In the table.2 given all the findings of genotypic coefficient of variation and phenotypic coefficient of variation of all the 13 characters. It is accepted that the value of phenotypic coefficient of variation was also higher than genotypic coefficient of variation for all the characters. The higher estimates (>20%) exhibited by No. 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, No. of fertile spikelet 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. The 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 mean (Ga) for different characters are given in Table 2. The estimates of heritability in broad sense (h2bs) 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 No. of productive tillers per plant (96.15%), Grain yield per plant (90.42%), Harvest index (89.48%), Biological yield per plant (88.38%), No. 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%) were observed for and 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 in 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 per cent of mean (>20%) were recorded by No. of productive tillers per plant (75.47%) and Harvest index (20.53%). The moderate estimate for genetic advance (10-20%) in per cent of mean was shown by L:B ratio (18.90%), No. of fertile spikelet 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

5. Genetic divergence analysis:

I	9	Ujrous, 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

The Non-hierarchical Euclidian cluster analysis was employed to study the genetic diversity existing among 85 rice germplasm collections and four checks on the basis of 13 quantitative characters. The pseudo F-test revealed that eight cluster arrangement 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 is presented in table 3.

The highest no of genotypes were present in cluster III which contained 23 entries, followed by cluster IV and cluster VII with 14 and 11entries, respectively. Cluster I II and V contained 9 genotypes only while cluster VI contained 10 genotypes and cluster VIII contained only 4 genotypes.

Table 3. Clustering pattern of 89 rice genotype on the basis of Non- hierarchical Euclidian cluster analysis of thirteen characters

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 by between cluster VII and II (4.603) and also between cluster II and I (4.443) and also between cluster III and II (4.272) . The minimum inter cluster distance was observed between V and III cluster (2.808) followed by cluster IV and III (2.544).its all about inter and intra cluster distances.

The intra-cluster group means for 13 characters (Table 5.) revealed marked differences between the clusters in respect of cluster means for different characters. For days to 50 % flowering the cluster mean ranged from 96.76 days cluster (I) to 104.15days cluster (II), For plant height , the cluster mean ranged from (117.25cm) cluster (VI) to cluster (VIII) **(**185.68 cm), For the no. of productive tillers per plant , cluster mean ranged from cluster (II) (9.35) to cluster (IV) (11.20), For the panicle length , cluster mean ranged from 26.45cm cluster (III) to 33.46cm cluster (II), For the flag leaf area, cluster mean ranged from 26.56cm^2 for cluster (II) to 58.95cm^2 for cluster (VIII), For the Days to maturity , cluster mean ranged from 118.01 days for cluster (I) to 130.33 days for cluster (II), For the No. of fertile spikelet per panicle, cluster mean ranged from 110.06 for cluster (V) to 136.69 for cluster (VI), For the spikelet fertility %, cluster mean ranged from 83.22 for cluster (II) to 91.16 for cluster (VII), For the Biological yield per plant , cluster mean ranged from 32.84 for cluster (VII) to 48.17 for cluster (III), For the Harvest index , cluster mean ranged from 24.20 for cluster (III) to 60.03 for cluster (VII), For the 1000-grain weight, cluster mean ranged from 20.73 for cluster (I) to 24.70 for cluster (V), For the L:B ratio, cluster mean ranged from 2.34 for cluster (V) to 2.99 for cluster (II). Maximum mean for the L:B ratio was recorded for cluster 2.99(II), For the grain yield per plant, cluster mean ranged from 11.49 for cluster (IV) to 19.72 for cluster (VIII). 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 present investigation shows 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.

Characters		Days to 50% flowering	Plant height (cm)	No.of Productive Tillers /plant	Panicle length (cm)	Flag leaf area(cm2)	Days to maturity	No.of fertile spikelets / panicle	Spikelets fertility (%)	Biological yield /plant (g)	Harvest Index(%)	1000-grain weight(g)	L:B ratio	R with Grain yield/plant(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	185.6	10.7	26.4	58.95	128.50	121.96	89.64	40.52	48.27	22.90	2.48	19.72*

			8**	8	7	**								*

***, ** 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 (22.68gm) recorded best performance for grain yield per plant 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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