

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 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 were 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 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. Non-hierarchical Euclidean analysis grouped the eighty nine germplasm into eight clusters and this study showed existence of wide genetic diversity within *Oryza sativa* germplasm. 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 11 entries, 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). The genotypes present in the diverse clusters may serve as parental material for hybridization programme which will lead to isolation of desirable sergents for developing high yielding rice varieties under irrigated condition.

Keywords: Rice, Analysis of variance, Coefficient of variation, Genetic variability, Genetic advance, Heritability.

Introduction:

Rice (*Oryza sativa* L.) belongs to family Gramineae (Poaceae), 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 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. 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 concern 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. 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 variety in the material has also been emphasized 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 89 rice germplasm including four checks (namely Sarjoo-52, NDR-97, NDR-6093 and Kalanamak) in Augmented Block Design at 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. In each block (17 test genotypes along with 4 checks) was accommodated. 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 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 were recorded on plant basis that is 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 characters revealed that sufficient variation present among the genotypes. 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 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 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% & 1% probability levels of significance, respectively.

2. Mean performance

Wider range of variability revealed for the traits plant height (88.31-167.22) followed by number of fertile spikelet 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 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 |
| 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 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 phenotypic coefficient of variation was also higher than genotypic coefficient of variation for all the characters. The higher estimates (>20%) exhibited by 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 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 presented in Table 2. The estimates of heritability in 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 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%) were observed for plant height (72.92%), while the low estimates of broad sense heritability (<50%) were showed 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 number 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 showed by L:B ratio (18.90%), number 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 | Ujrour, 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 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.

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 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.

| Characters | | Days to 50% flowering | Plant height (cm) | Number of Productive Tillers /plant | Panicle length (cm) | Flag leaf area(cm ²) | Days to maturity | Number 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 | 185.68** | 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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