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Genetic diversity analysis of mutant Kalanamak rice genotypes for yield and yield attributing traits under submergence condition

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Abstract

The investigation was carried out at Student Instructional Farm of A.N.D. University of Agriculture and Technology, Kumarganj, Ayodhya (U.P) India during the Kharif season 2019-20 and 2020-21. D2 analysis was studied for yield and its component characters in fifty mutant Kalanamak rice lines with one untreated control. The objective was to study the effect of submergence stress on yield and yield attributes performance of mutant lines. All the fifty genotypes were evaluated for twelve yield and yield attributing characters using Mahalanobis D2 statistics. Divergence analysis grouped these genotypes into seven clusters. Cluster adjusted II and VI maximum number of mutant lines (11) followed by cluster I (8), cluster VII (7) while cluster IV and V had cluster (5), cluster III had minimum number of mutant lines (3). Maximum intra cluster distance was observed in cluster VII (2.893) followed by cluster III (1.634) and cluster VI indicated that the genotypes grouped under these clusters were more diverse. Hence intercrossing of these clusters is suggested to obtain high yielding submergence tolerant rice varieties.

Keywords: Kalanamak, mutant, attributing, submergence, condition

Introduction

Rice is a nutritional staple food which provides instant energy as its most important component is carbohydrate. The two major rice varieties grown worldwide today are *Oryza sativa indica* and *Oryza sativa japonica*. Rice plant is a member of Poaceae family. Total production of rice during 2021-22 is estimated at record 127.93 million tonnes. It is higher by 11.49 million tonnes than the last five years' average production of 116.44 million tonnes. (Press information Bureau, government of India, 16 Feb 2022).

In the present investigation was undertaken to study of divergence using Mahalanobis D2 statistics and different clustering procedures, based on yield and yield attributing characters assessing the different components to total divergence. Genetic divergence among the genotypes plays an important role in the selection of parents having wider variability for different yield and yield attributing character.

Materials and Methods

The material for the present investigation consisted of 50 rice genotypes along with one untreated, collected from Student Instructional Farm Acharya Narendra Deva University of Agriculture and technology, Kumarganj, Ayodhya. The experiment was modified augmented design. After 50 days of sowing well developed and healthy seedlings were transplanted with inter and intra row distance of 20 x 15cm. Observations were recorded on five randomly selected plants in each replication for traits days to 50% flowering, plant height (cm), tillers per plant, panicle length (cm), spikelet/plant, Filled grains, sterility (%), test weight (gm), Total shoot elongation (cm), Relative shoot elongation, Tolerance score, yield/plant (gm). Genetic divergence was estimated by using D² statistics of Mahalanobis (1936) [4] and grouping of the genotypes in different clusters was done by using Tocher's method (Rao, 1952) [6].

Results and Discussion

Fifty Kalanamak mutant lines were grouped into seven different clusters using clustering technique. D² does not change with number of characters.

Clustering pattern

The 50 mutant lines with one control taken for genetic divergence analysis differed significantly with regard to the twelve different morph-physiological characters studied and

displayed marked divergence. Cluster adjusted II and VI maximum number of mutant lines (11) followed by cluster I (8), cluster VII (7) while cluster IV and V had cluster (5), cluster III had minimum number of mutant lines (3).

Table 1: Clustering pattern of 50 mutant lines with one checks of rice on the basis of D2 statistics under submerged condition

| Cluster No. | No. of mutants within cluster | Mutant lines in cluster |
|-------------|-------------------------------|--|
| I | 8 | ML21,ML25,ML27,ML28,ML29,ML33,ML42,ML43 |
| II | 11 | ML14,ML22,ML26,ML31,ML32,ML36,ML37,ML38,ML39,ML40,ML45 |
| III | 4 | ML10,ML11,ML12,ML13 |
| IV | 5 | ML7,ML8,ML19,ML20,ML44 |
| V | 5 | ML15,ML16,ML17,ML18,ML34 |
| VI | 11 | ML1,ML2,ML3,ML4,ML5,ML6,ML9,ML20,ML24ML,ML35,ML46 |
| VII | 7 | ML23,ML41,ML47,ML48,ML49,ML50, Control |

Cluster means for different characters

Cluster mean values with respect to eleven morpho-physiological characters of 50 mutant lines were presented in Table 2. Wide range of mean values among the clusters were recorded for different traits. The cluster VII showed highest mean values for plant height (165.19). Cluster IV showed highest mean value for days to 50% flowering (130.60), total shoot elongation (29.09), relative shoot elongation (31.49).

The cluster showed highest mean value for days of 50% flowering (130.60). Cluster V showed highest mean value for filled grain (154.73), grain yield/plant (23.51), test weight (18.00), spikelet/panicle (18.73), tolerance score (8.65). Cluster III showed highest mean value for panicle length per plant (24.89), sterility % (18.08). Cluster VI showed highest mean showed highest mean value for number of tiller per plant (9.42).

Table 2: Cluster mean values of seven clusters for different quantitative characters of mutant lines of rice under submerged condition

| Clusters | Day of 50% flowering(days) | Plant height(cm) | No of tillers per plant | Panicle length per plant(cm) | Spikelet per Panicle (s/p) | Filled grains | Test weight (gm) | Sterility (%) | Total shoot elongation (cm) | Relative shoot elongation | Tolerance score | Grain yield /plant |
|----------|----------------------------|------------------|-------------------------|------------------------------|----------------------------|---------------|------------------|---------------|-----------------------------|---------------------------|-----------------|--------------------|
| I | 119.83 | 137.81 | 7.96 | 20.05 | 8.83 | 98.04 | 8.04 | 14.88 | 12.09 | 13.08 | 6.49 | 8.37 |
| II | 120.42 | 117.68 | 5.61 | 24.37 | 7.82 | 98.94 | 8.79 | 13.91 | 12.57 | 13.63 | 6.82 | 12.08 |
| III | 100.25 | 152.90 | 4.33 | 24.89 | 6.75 | 96.25 | 8.42 | 18.08 | 25.21 | 26.79 | 4.98 | 10.30 |
| IV | 130.60 | 137.77 | 6.00 | 22.71 | 12.73 | 131.27 | 14.33 | 15.67 | 16.81 | 17.69 | 7.00 | 12.80 |
| V | 111.53 | 119.03 | 9.00 | 24.11 | 18.73 | 154.73 | 18.00 | 8.33 | 20.93 | 22.22 | 8.65 | 23.51 |
| VI | 121.21 | 122.79 | 9.42 | 22.78 | 10.42 | 124.61 | 14.12 | 13.30 | 20.18 | 21.01 | 5.72 | 14.67 |
| VII | 110.05 | 165.19 | 8.40 | 24.39 | 11.86 | 141.29 | 17.00 | 9.62 | 29.09 | 31.49 | 7.01 | 22.22 |

Inter and Intra-Cluster Distances

Average distances within and between clusters among seven clusters of mutant rice lines Table 3 examination revealed that the typical intra-cluster distance ranged from 1.634 to 2.893. Cluster VII had the most intra cluster distance (2.893),

followed by cluster I (2.147), and cluster III had the smallest intra cluster distance (1.634). Cluster V and cluster III had the greatest intercluster distance (6.828), which was followed by cluster V and cluster I (6.066), cluster VII and cluster I (5.886), and cluster V and cluster II (5.489).

Table 3: Average intra & inter-cluster distances among seven cluster of mutant lines of rice under submerged condition

| Clusters | Clusters I | Clusters II | Clusters III | Clusters IV | Clusters V | Clusters VI | Clusters VII |
|----------|------------|-------------|--------------|-------------|------------|-------------|--------------|
| I | 2.147 | | | | | | |
| II | 2.376 | 2.006 | | | | | |
| III | 4.328 | 4.037 | 1.634 | | | | |
| IV | 2.985 | 2.822 | 4.428 | 1.657 | | | |
| V | 6.066 | 5.489 | 6.828 | 4.309 | 2.155 | | |
| VI | 3.112 | 2.942 | 4.15 | 2.248 | 4.034 | 2.033 | |
| VII | 5.886 | 5.65 | 4.983 | 4.38 | 3.693 | 3.826 | 2.893 |

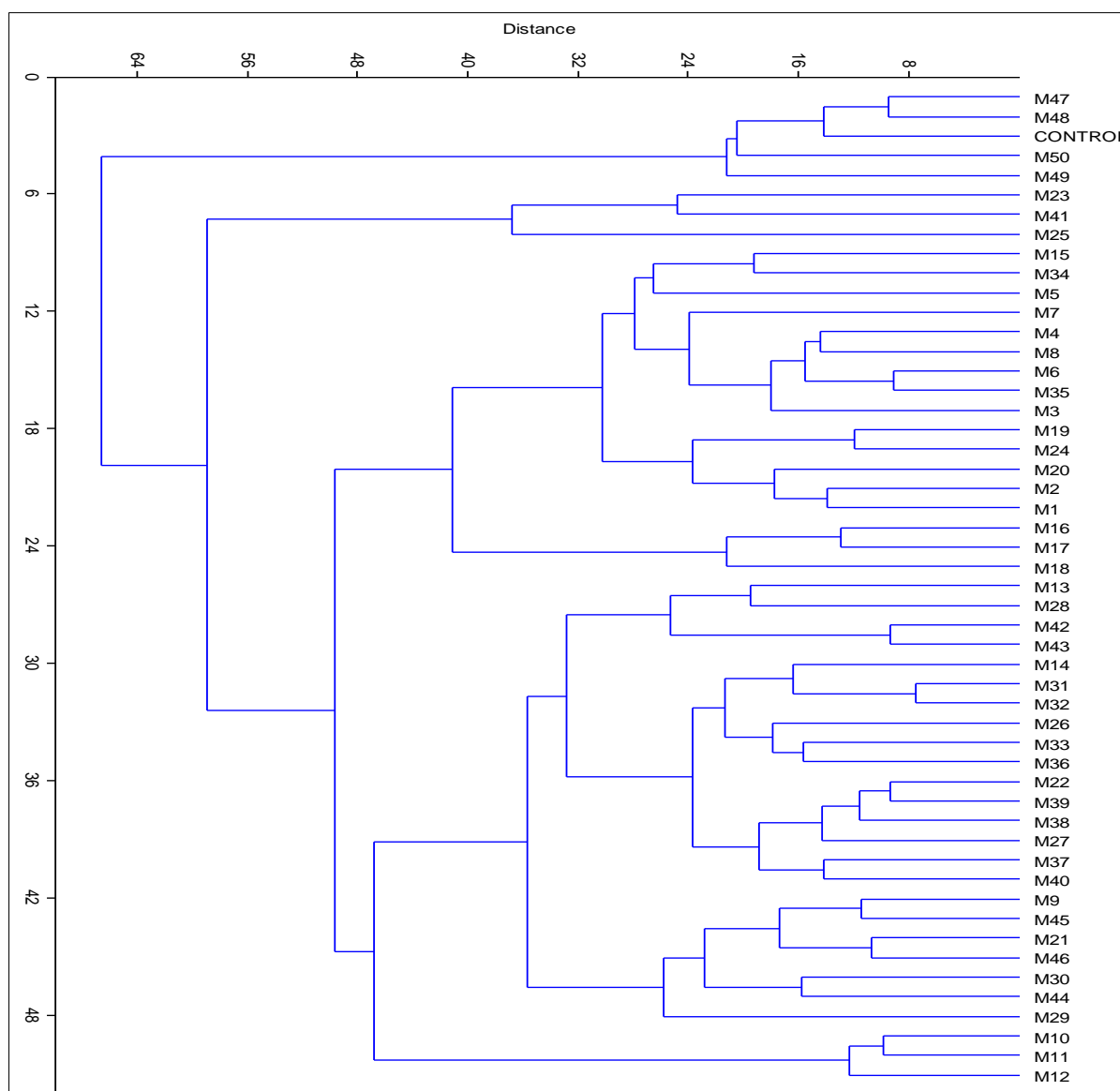


Fig 1: Dendrogram of 50 genotype along with control based on inter and intra cluster distance

Conclusion

The genetic divergence evaluated by Mahalanobis D^2 -statistic grouped 50 genotypes with one control into seven clusters. Maximum genetic divergence was observed between cluster VII and III. On the basis of cluster mean values, cluster VII was superior for plant height and cluster V for grain yield. From the D^2 analysis of genetic diversity, based upon high yielding genotypes and large inter-cluster distances, it is advisable to attempt crossing of the genotypes from clusters III and V and cluster V and I, which may lead to broad spectrum of favorable genetic variability for yield improvement in rice.

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