Oryza Vol. 51 No.3, 2014 (204-207)

# Clustering among genotypes for zinc deficiency tolerance and yield traits under aerobic condition in rice

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## ABSTRACT

*Genetic improvement of rice genotypes for zinc deficiency tolerance and yield traits under aerobic condition is essential to exploit the water saving potential of aerobic condition. In the present study, sixty rice genotypes were raised under aerobic condition at Coimbatore, Tamil Nadu during dry season 2012-13 to identify the diverse genotypes. They were evaluated for eleven agronomic traits using $D^2$ to study the diversity pattern among the genotypes. Based on the analysis, the genotypes were grouped in to 7 clusters. Maximum numbers of genotypes (26) were grouped in cluster I. Cluster IV and VI consists of eight genotypes followed by cluster V and VII with seven genotypes. Clusters II and III were represented by two genotypes each. The maximum inter cluster distance was observed between cluster V and cluster VI (22.95) followed by between cluster III and cluster VI (20.56). Among the eleven traits studied, the traits* viz., *single plant yield, plant height, 100-grain weight, zinc score, plant harvest index, SPAD value and days to 50% flowering contributed 94.69% towards total divergence.*

***Key words:*** *aerobic rice, genetic diversity, zinc deficiency tolerance*

In Asia, 17 million ha of irrigated rice areas may experience "physical water scarcity'' and 22 million ha may have "economic water scarcity'' by 2025 (Tuong and Bouman, 2002). In India, 55 per cent of rice area does not have sufficient moisture during its growth phase due to inadequate or no rainfall and inadequate irrigation systems ultimately causing enormous loss in crop yield. In Tamil Nadu, rice is cultivated in an area of 20.16 Lakh ha with the production of 62.53 Lakh MT and productivity of 3102 kg $ha^{-1}$ (Season and crop report, Dept. of economics and Statistics, Tamil Nadu, 2011). Among the several production constraints, availability of irrigation water is a major factor as rice crop consumes about 70 per cent of the water available for agriculture (Vibhu Nayar and Ravichandran, 2012). Therefore, ways must be sought to reduce water requirement in rice and increase its productivity. Experimental results and evidences from China and Brazil show that among several technologies, aerobic rice proves to be a viable technology by reducing water losses through seepage, percolation, and evaporation which saves water up to 50%. However, under aerobic condition several essential nutrients, especially (Zn) becomes unavailable due to positive soil redox potential (Gao *et al.*, 2012). Therefore, Zn deficiency in addition to intermittent water limitation under aerobic condition results in yield reduction ranging between 15 and 40%. Hence, genetic improvement of rice cultivars for aerobic condition is essential to exploit the water saving potential of aerobic condition.

Hybridization is one of the major tools for the improvement of a crop that needs the analysis of genetic diversity for the selection of parents (Singh, 1983). Multivariate analysis with $D^2$ technique measures the amount of genetic diversity in a given population in respect of several characters and assesses relative contribution of different components to the total divergence. Keeping this in view, the present study was focussed to assess the genetic diversity among sixty rice genotypes under aerobic condition using Mahalanobis $D^2$ statistics.

## MATERIALS AND METHODS

Genetic material comprising of 60 lines upland and lowland cultures in rice were raised under aerobic condition at Paddy Breeding Station, TNAU, Coimbatore during dry season 2012-13. Each entry was direct sown in a plot size of 3.6 m x 0.8 m by adopting a spacing of 20 cmx20 cm. The entries were replicated twice in randomized block design. Single seedling per hill was maintained. The crop was irrigated everyday till establishment and thereafter, the crop was irrigated once in 4-5 days (when hairline crack occured). Genotypes were visually scored for tolerance/ susceptibility based on 1-9 scale for Zn deficiency (IRRI, 2002). At maturity, data on yield and yield components were recorded in five randomly tagged plants in each genotype per replication.

Data were recorded on 11 agronomic characters *viz*., vegetative vigour, Zn score, SPAD value, plant height at maturity, days to 50% flowering (days after sowing), panicle length, productive tillers(nos.), 100-grain weight, panicle harvest index, harvest index and single plant yield.

Panicle harvest index was calculated as the ratio of grain weight to the total weight of a single panicle and expressed as percentage

$$\text{Panicle harvest index} = \frac{\text{Grain weight of a panicle}}{\text{Total weight of a panicle}} \text{X100}$$

Data were analyzed by $D^2$ analyses using the GENRES software. The genotypes were grouped into clusters based on Mahalanobis's $D^2$ analysis (Mahalanobic 1936).

## RESULTS AND DISCUSSION

Analysis of variance showed significant differences for all the eleven characters studied among the genotypes. Based on $D^2$ value, sixty genotypes were grouped in to 7 clusters (Table 1).The distribution pattern indicates that the maximum number of genotypes (26) were grouped in cluster I. Cluster IV and VI consists of eight genotypes followed by cluster V and VII with seven genotypes. Clusters II and III were represented by two genotypes each. The overall composition of the clustering pattern showed that genotypes collected from the same geographic origin were distributed in different clusters. Similar findings of non-correspondence of geographic origin with genetic diversity were also reported by Nayak *et al.*, (2004). Genotypes exhibited Zn deficiency symptom six to eight weeks after sowing although the Zn content of the experimental field soil was above the critical limit (2.74 ppm). This is because under aerobic condition due to the changes in the physical and chemical properties of the soil, Zn becomes unavailable to the plants.

Inter cluster distance was higher than the intra cluster distance indicating wider genetic diversity among the genotypes (Table 2). The maximum inter cluster distance was observed between cluster V and cluster VI (22.95) followed by between cluster III and cluster VI (20.56), cluster VI and cluster VII (20.52) and cluster I and cluster VI (20.26) indicating wider genetic diversity among the genotypes between these groups (Banumathy *et al.,* 2010 and Subudhi *et al.*, 2009). The hybrids developed from the selected members of these clusters would produce highly variable population in the segregating generations. The magnitude of heterosis mainly depends on the genetic distance. Greater the genetic distance between the clusters indicate wider genetic diversity between the genotypes. So, the hybridization between the genotypes from the cluster V and VI will result in more number of useful transgressive segregants and the high level of expression of the heterotic vigour. The minimum inter cluster distance was found between cluster II and cluster III (8.06). Genotypes in these clusters are genetically very close and hence hybridization among the genotypes will not give fruitful results. The maximum intra cluster distance was observed in cluster VI (17.08) followed by cluster IV (15.54) and cluster VII (14.66). Hence, selection within these cluster may be exercised based on the highest areas for the desirable traits which would be made use of in improvement through inter varietal hybridization (Joshi *et al.*, 2008).

Cluster VI with eight genotypes (Table 3) exhibited highest mean values for panicle length (18.56), panicle harvest index (83.20), single plant yield (18.03) and lowest mean value for days to fifty percent flowering (75.13).Cluster II with two genotypes had lowest mean value for Zn score (3.00) and vegetative vigour (1.50). Cluster V had seven genotypes with SPAD value (34.49) and maximum number of productive tillers per plant (20.55). Cluster III with two genotypes had lowest mean value for 100-grain weight (1.66) and plant height at maturity (62.83) the cluster I with 26 genotypes had high plant harvest index (22.83).

**Table 1.** Clustering pattern of 60 genotypes

| Cluster | No. of genotypes | Genotypes |
|---|---|---|
| 1 | 26 | CB-08-702,CB-06-803,CB-08701, CB-07-701-252, CB-07-701-274,CB-07-701-256, CB-07-701-143, CB-07-701-279, IR84895-B-127-CRA-5-1-1, IR83381-B-B-18-3, IR83387-B-B-110-1, CB-09-512, CB-09-516, CB-07-701-12, CB-07-701-22, CB-07-701-23, CB-07-701-115, CB-07-701-126, CB-07-701-128, CB-07-701-129, CB-07-701-146, CB-07-701-148, CB-07-701-150, CB-07-701-151, CB-07-701-174, CB-07-701-199. |
| 2 | 2 | CB-07-701-230, Anna-4 |
| 3 | 2 | CB-00-15-23, CO51 |
| 4 | 8 | CB-07-701-218, CB-07-701-255, CB-07-701-262, CB-07-701-264, CB-07-701-265, CB-07-701-268, ARB-6, CB-08-709-2 |
| 5 | 7 | CB-07-701-278, CB-07-701-280, CB-07-701-283, CB-07-701-284, CB-07-701-181, CB-07-701-288, PSBRC-83 |
| 6 | 8 | CB-00-11-4, CB-00-11-7, CB-00-11-19, CB-00-11-21, CB-00-11-22, CB-00-11-23, CB-00-12-192, CB-06-803-2 |
| 7 | 7 | CB-00-15-10, CB-00-15-44, CB-00-755-2, CB-00-15-24, Apo, PSBRC-80, IR64 |

**Table 2.** Intra (diagonal) and inter cluster average $D^2$ in 60 rice genotypes

| Cluster | 1 | 2 | 3 | 4 | 5 | 6 | 7 |
|---|---|---|---|---|---|---|---|
| I | **13.37** | 10.55 | 14.08 | 17.40 | 13.79 | 20.26 | 13.97 |
| II | | **3.92** | 8.60 | 15.89 | 11.98 | 17.93 | 12.66 |
| III | | | **4.20** | 19.33 | 16.25 | 20.56 | 16.35 |
| IV | | | | **15.54** | 19.44 | 17.07 | 16.72 |
| V | | | | | **10.65** | 22.95 | 14.10 |
| VI | | | | | | **17.08** | 20.52 |
| VII | | | | | | | **14.66** |

Based on *per se* performance it was observed that, Zn deficiency tolerant genotypes under aerobic condition *viz.*, CB- 06- 803, IR84895-B-127-CRA-5-1-1,CB -00-11-21, CB-00-11-22 and CB-06-803-2 with Zn score of 1.00 were distributed in clusters I and VI. Early flowering genotypes *viz.,* CB-00-11-22, CB-00-11-4 and CB-00-11-21were grouped in cluster VI. With respect to productive traits, genotype CB-07-701-283 possessing maximum number of productive tillers per plant under aerobic condition is grouped in cluster V where as genotype CB-06 -803-2 with high panicle harvest index and single plant yield is grouped in cluster VI. With regard to harvest index, the genotype CB -09-512 recorded highest mean value and is grouped in cluster I. None of the clusters contained genotypes with all the desirable traits which could be directly selected and utilized thereby indicating that hybridization between the genotypes of different clusters is necessary for the development of desirable genotypes. Similar results were also reported by Monika *et al*. (2008); Banumathy *et al.* (2010) and Ramanjaneyulu *et al*. (2014). However, genotypes in cluster VI, cluster II and cluster III recorded desirable mean values for Zn score, panicle length, panicle harvest index, single plant yield, days to fifty percent flowering, 100-grain weight and plant stature. So, genotypes in cluster VI, II and III may be used as a parents in the breeding programme for the development of improved cultivars for aerobic condition.

**Table 3.** Cluster mean for different quantitative trait among 60 rice genotypes

| Vegetative vigour | Zinc score | SPAD value | Days to 50% flowering (days after sowing) | Plant height at maturity (cm) | Panicle length (cm) | Productive tillers(nos.) | 100-grain weight (g) | Panicle harvest index | Plant harvest index | Single plant yield (g) |
|---|---|---|---|---|---|---|---|---|---|---|
| 2.00 | 3.89 | 30.81 | 85.77 | 69.83 | 17.26 | 18.78 | 2.26 | 81.75 | 22.83 | 17.97 |
| 1.50 | 3.00 | 31.68 | 85.25 | 72.33 | 17.50 | 15.67 | 2.45 | 78.78 | 20.62 | 17.17 |
| 3.00 | 3.50 | 29.84 | 83.50 | 62.83 | 17.08 | 16.66 | 1.66 | 77.88 | 16.55 | 13.19 |
| 2.50 | 5.50 | 29.41 | 79.87 | 65.39 | 15.91 | 18.08 | 2.02 | 77.98 | 19.60 | 14.26 |
| 2.29 | 5.14 | 34.49 | 88.86 | 68.12 | 16.88 | 20.55 | 2.14 | 76.95 | 19.26 | 16.49 |
| 2.25 | 4.50 | 30.40 | 75.13 | 79.37 | 18.56 | 19.00 | 2.27 | 83.20 | 19.19 | 18.03 |
| 3.57 | 5.00 | 30.02 | 86.21 | 66.29 | 16.59 | 17.52 | 2.03 | 76.16 | 20.75 | 16.78 |

**Table 4.** Contribution of each character to total divergence

| Character | No. of first rank | % Contribution |
|---|---|---|
| Vegetative vigour | 0 | 0.00 |
| Zinc score | 222 | 12.54 |
| SPAD value | 141 | 7.97 |
| Days to 50% flowering (days after sowing) | 487 | 27.51 |
| Plant height at maturity (cm) | 107 | 6.05 |
| Panicle length (cm) | 41 | 2.32 |
| Productive tillers(nos.) | 10 | 0.57 |
| 100-grain weight (g) | 99 | 5.59 |
| Panicle harvest index | 43 | 2.43 |
| Plant harvest index | 159 | 8.98 |
| Single plant yield (g) | 461 | 26.05 |
| Total | 1770 | 100.00 |

The utility of $D^2$ statistics as a potent tool to quantify the extent of divergence in biological populations at genetic level is further enhanced by its applicability to estimate the relative contribution of the various plant characters to total genetic divergence. The contribution of various characters towards the expression of total genetic divergence indicated that days to 50% flowering (27.51%) and single plant yield (26.05%) contributed a maximum level than other parameters (Table 4). It was followed by characters like Zn score (12.54%), plant harvest index (8.98%), SPAD value (7.97%), plant height (6.05%), 100 grain weight (5.59%), panicle harvest index (2.43%), panicle length (2.32%), productive tillers (0.57%) had contributed to total genetic divergence. The present findings were in accordance with the findings of Subudhi *et al*. (2008). The traits *viz.*, single plant yield, plant height, 100-grain weight, Zn score, plant harvest index, SPAD value and days to 50% flowering contributed 94.69% towards total divergence. Hence these characters should be given importance during hybridization and selection in the segregating population.

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