

**EXPLORING GENETIC DISTANCE AND VARIABILITY IN MULTI-PARENT ADVANCE  
GENERATION INTER CROSS (MAGIC) POPULATIONS DERIVED RESTORERS FOR  
TRAIT IMPROVEMENT IN HYBRID RICE.**

**Suman Kumar Jha; Hoshiyar Singh; Monika S; Karthikeya S. G.**

**Abstract**

The present study aimed to investigate genetic diversity among fifty-two rice genotypes (comprising 44 restorers and 8 founder lines) derived from a multi-parent advanced generation intercross (MAGIC) using cluster analysis of eight morphological and quantitative traits. The hybrids developed by using 1 CMS line and fifty-two restorer lines were evaluated at two locations, Hyderabad and Lucknow, employing a Randomized Complete Block Design (RCBD) with two replications across two consecutive Kharif seasons in 2022 and 2023. Wilk's Lambda criterion ( $\lambda \sim 0$  and  $V = 1024.855$  with 408 degrees of freedom) indicated highly significant differences among the genotypes for the pooled effect of all traits. The genotypes were categorized into ten clusters, with Cluster I containing the largest number of genotypes. Cluster II exhibited the maximum intra-cluster distance, while the greatest inter-cluster distance was observed between Clusters VII and III. Grain yield per hectare emerged as the primary trait contributing to divergence within this rice population. Based on these results, it is recommended to select parents from both within and between clusters for initiating the crossing program.

**Introduction**

Rice (*Oryza sativa* L.), which includes the two major ecotypes *indica* and *japonica*, is a staple crop that plays a crucial role in global food security. *Indica* rice, in particular, dominates world production, primarily cultivated in Asia, which accounts for nearly 90% of global rice output (Thuy et al., 2022, Pathak et al., 2024). India ranks first in the world for rice cultivation area (44.8 million hectares) and second in production (130 million tonnes) (source: <https://pib.gov.in> 2023). This cereal grain is a fundamental dietary staple, providing approximately two-thirds of the caloric intake for over two billion people in the humid and sub-humid regions of Asia. Additionally, it contributes to one-third of the calorie consumption for nearly one billion people across Africa and Latin America.

As we enter the new millennium, we reflect on the remarkable strides in rice production achieved during the 1960s to 1980s due to Green Revolution technologies. However, in recent decades, the growth in productivity has slowed, presenting a significant challenge to meet future productivity targets. This challenge is compounded by a declining and deteriorating resource base, including land, water, labour, and other essential inputs, all while needing to protect the environment. To ensure food security, rice breeders face several concerns, including declining genetic gains, a narrow genetic base in modern rice varieties, pressures from biotic and abiotic stresses, and the growing demand for higher quantities and better quality rice (Nakano et al., 2019; Shanmugam et al., 2023; Prakash et al., 2024).

Among the genetic strategies available to increase yield potential, hybrid rice stands out as the most viable and easily adoptable technology, as evidenced by its success in many countries. To satisfy the food demands of a growing population and ensure food security, the current production levels must be increased by 2 million tonnes annually. This can be achieved through heterosis breeding and other innovative breeding methods. Genetic divergence is a valuable tool for selecting parents in hybridization programs, as it helps identify genetically diverse parents that can produce desirable combinations in the segregating generations (Keerthana et al., 2024; ).

The primary limitation in crop improvement and a significant obstacle in breeding efforts is the narrow genetic foundation. Understanding genetic diversity is crucial for hybrid breeding and population improvement programs, as it facilitates the analysis of genetic variability, the characterization of germplasm, and the categorization into different heterotic groups. Genetic diversity is essential in plant breeding, both for exploiting heterosis and generating productive recombinants. Selecting appropriate parents is especially critical in breeding programs. Therefore, assessing genetic diversity in germplasm is vital for choosing diverse genotypes for hybridization programs.

In hybrid rice programs, most restorer lines have been developed through single crosses between two parents. To enhance genetic variation in breeding populations, breeders have also experimented with multiple crosses, such as three-way crosses involving three parents or double crosses involving four parents (Bandillo et al., 2013). The creation of indica/indica MAGIC populations, the extraction of diverse lines from these random mating populations, and the use of these lines for developing new hybrid combinations appear to effectively exploit high levels of heterosis in rice hybrids. Identifying improved restorer lines from MAGIC-derived populations seems to be a viable strategy for maximizing genetic diversity and heterosis in hybrid breeding programs (Stadlmeier et al., 2018).

Mahalanobis D2 statistics is a crucial tool for assessing genetic divergence among genotypes. By clustering genotypes, it facilitates the selection of suitable parents for hybridization programs. In response to these considerations, the present study was designed to evaluate genetic diversity of 52 rice hybrids within a Multi-Parent Advanced Generation Intercrosses (MAGIC) population using Mahalanobis D2 statistics. The goal was to develop improved restorer lines with extensive genetic diversity to enhance the production of highly heterotic rice hybrids.

## **Material and Methods**

### ***Experimental site, design and genetic materials used***

The present investigation was conducted during Kharif 2022 and Kharif 2023 at SeedWorks International Pvt. Ltd. research farms in Lucknow (26°51'N, 80°57'E, 123 m) and Hyderabad (17°37'N, 78°28'E, 505 m) using a Randomized Complete Block Design (RCBD) with two replications. The primary objective was to group 78 genotypes of rice (*Oryza sativa* L.) into distinct classes of restorers based on their fertility percentage in test cross hybrids during the first season, followed by the evaluation of the best restorers and their hybrids in the second season. The experiment was conducted in two sets across two consecutive seasons. The first set of experiments consisted of 78 test cross hybrids in Season 1 and 52 test cross hybrids in Season 2, developed using a single tester CMS line and restorer lines created through the Multi-parent Advanced Generation Inter Cross (MAGIC) population approach, utilizing eight founder restorer lines (Table 1). The second set of experiments included 70 parental restorer lines and 8 founder restorer lines in Season 1, and 44 parental restorer lines and 8 founder restorer lines in Season 2. These parental lines were involved in the test cross hybrids. The founder restorer lines used in this study were developed at SeedWorks International Pvt. Ltd. Hyderabad, India, using the pedigree method of selection in bi-parental crosses. The first set focused on identifying restorers and maintainers, while the second set involved the evaluation of MAGIC-based rice hybrids and their parents in Kharif 2022 at Lucknow. Simultaneously, seventy-eight parental lines were evaluated at the Hyderabad location during Kharif 2022. The hybrids and restorer parents identified in Kharif 2022 were re-evaluated in Kharif 2023 at Lucknow, along with the founder lines, while the restorers and founder lines were evaluated at Hyderabad.

### ***Phenotypic characterization***

The parents of the hybrids were evaluated during Kharif 2022 and Kharif 2023 for various traits, including days to 50% flowering (DFF), plant height (PLHT), number of tillers per plant (TLN), number of panicles per plant (PNN), panicle length (PNL), 1000-grain weight (TSWT), grain yield per plot (GRNYLD), and grain yield per hectare (GRNYLD\_AC). Twenty-one-day-old seedlings were transplanted, with one seedling per hill and a spacing of 20 cm x 15 cm (row to row and plant to plant). Each entry was planted in four rows, each 1.8 meters in length (12 hills per row). The crop was fertilized with 120 kg N, 60 kg P<sub>2</sub>O<sub>5</sub>, and 60 kg K<sub>2</sub>O per hectare. Half of the nitrogen and the entire quantities of P<sub>2</sub>O<sub>5</sub> and K<sub>2</sub>O were applied as a basal dose. The remaining nitrogen was applied in two equal split doses: one at the maximum tillering stage and the other at the active flowering stage. Standard agronomic practices and plant protection methods were implemented as needed according to the schedule. To identify restorers and maintainers, five random plants from each entry of test crosses were selected to measure spikelet fertility percentage. From each selected plant, the main panicle from the middle row, excluding border rows and border plants, was randomly chosen for the evaluation of panicle traits and fertility percentage in hybrids and checks. These same plants were also measured for plant height, number of tillers per plant, number of panicles per plant, main shoot panicle length, panicle weight, and 1000-grain weight.

Mahalanobis generalized distance D<sup>2</sup> (1936) was employed to assess the genetic variation among populations based on various traits. To group the populations into clusters, Tocher's method (Rao, 1952) was used. Ward's method was employed to construct tree diagrams using Euclidian distances, and clustering was performed accordingly.

## **Statistical analysis**

### ***Computation of D<sup>2</sup> value***

The data collected on different characters were analyzed through Mahalanobis's generalized distance D<sup>2</sup> given by Mahalanobis (1936). The generalized distances between any two populations are defined as

$$\Delta^2 = (\lambda_{ij}) d_i \times d_j$$

Where,

$\lambda_{ij}$  = Reciprocal matrix to the common dispersion matrix.

$d_i$  = Difference between the mean values of the two populations for the i<sup>th</sup> Character.

$d_j$  = difference between the mean values of the two populations for j<sup>th</sup> character.

The quantity is estimated by the D<sup>2</sup> statistic as

$$D^2 = (S_{ij}) d_i d_j$$

Where, S<sub>ij</sub> = sample estimate of ij<sup>th</sup> character.

## **Result and Discussion**

The analysis of variance showed significant difference among genotypes for all the eight characters. Wilks Lambda criterion (( $\lambda \sim 0$  and V= 1024.855 with 408 df) revealed highly significant differences among the genotypes for the pooled effect of all the characters. To study the diversity among the

genotypes, cluster analysis was carried out using Ward's method (Fig. 1). The 52 MAGIC lines were grouped into ten clusters of which cluster I was the largest grouping with 17 genotypes followed by cluster II with 14 genotypes, cluster VI with 5 genotypes, cluster III and V with 4 genotypes, clusters IV have 3 genotypes, cluster VII has 2 genotypes and clusters VIII, IX and X were solitary clusters (Table 2), hence no intra-cluster distances ( $D^2$  values). The formation of distinct solitary cluster may be because geographic barriers preventing gene flow or intensive natural and human selection for diverse and adaptable gene complexes must be responsible for this genetic diversity (Arunachalam and Ram, 1967). Comparable findings were observed regarding the study by Aarthi et al., 2021 Sar et al., 2022.

Average intra and inter-cluster  $D^2$  values estimated and presented in Table 3. Intra-cluster  $D^2$  values ranged from 37.25 (cluster III) to 150.49 (cluster II). Cluster II showed maximum intra cluster  $D^2$  value (150.49). Whereas, highest inter cluster divergence was observed between cluster VII and cluster III (2450.47), followed by cluster II vs. III (671.63) and cluster I vs. II (491.37) followed by cluster IX and III (2230.14), cluster VII and II (2194.95), cluster IX and II (1974.85). The large inter-cluster distance indicates a significant diversity among the genotypes, while the small inter-cluster distance suggests a close relationship (Shanmugam et al., 2023). The distance within clusters shows the diversity among genotypes that are grouped together. Genotypes in the same cluster are generally similar based on the overall traits measured (Sharma et al., 2021). Figure 3 displays the nearest and most distant clusters for each of the ten clusters. A greater inter-cluster distance compared to intra-cluster distance indicates that there is homogeneity and limited genetic variability within a cluster (Singh and Gupta, 1979). Additionally, a large inter-cluster distance suggests a broad range of variability in segregating populations, which can be exploited for selection (Singh et al., 1981). The greatest diversity for all studied traits was observed between SW5462R and SW24333R (Cluster VII) and SW23674R, SW24321R, SW24295R, and SW24299R (Cluster III). Therefore, hybridization between these genotypes is expected to maximize heterosis. It is generally believed that greater genetic divergence between parental genotypes leads to higher heterosis in crosses (Falconer, 1964). Consequently, it is advisable to attempt crosses between genotypes from distant clusters to obtain highly heterotic crosses, which are likely to produce a wide range of segregants for selection. Similar studies have been conducted by Amegan et al., (2020), Sudeepthi et al., (2020), Sujata et al., (2021), Sharma et al., (2021), Jebkani et al., (2023), and Pathak et al., (2024).

Cluster means indicate average performance of all genotypes present in a particular cluster. The cluster mean values for eight characters are presented in Table 4. Days to 50% flowering had a range of 109 days for cluster VII to 121 days for cluster X, productive tillers per plant had a range of 8.5 for cluster VIII to 11.5 for cluster X, plant height had a range of 118.33 cm for cluster III to 134.5 cm for cluster IV, panicle length had a range of 4.11 cm for cluster X to 6.6 cm for cluster V, grains per panicle had ranged from 22.5 for cluster VIII to 24.88 for cluster X, test weight had range of 23 for cluster I to 26.25 for cluster VII, and grain yield per acre 1310 for cluster V to 3760 for cluster III. The above results indicated a wide range of mean values between the clusters. Cluster I had maximum panicle length value and moderate for days to 50% flowering, number of tillers per plant, number of panicle per plant, panicle length, panicle weight, plant height, grain yield per hectare and 1000 grain weight. Cluster II, III, VIII, IX, X are indicated moderate value for all traits studied. Cluster IV showed minimum value for plant height, while all traits found moderate value. Cluster V has noted maximum value for number of tillers per plant and number of panicles per plant and found moderate value for remaining traits. Cluster VI observed maximum value for panicle weight conversely, low for number of tillers per plant and number of panicles per plant and panicle length and moderate for remaining traits. The lowest mean value for different traits was also significant. Cluster VII exhibited the lowest

for day to 50% flowering and highest for grain yield per plot, highlighting its superior contribution to genetic diversity. The genotypes SW5462R and SW24333R from this cluster demonstrated exceptional agronomic traits, making them prime candidates for direct selection in breeding programs to enhance crop variability. This result were in conformity with the Muthuramu *et al.*, 2017 Amegan *et al.*, (2020), Sudeepthi *et al.*, (2020), Sujata *et al.*, (2021), Sharma *et al.*, (2021) and Shanmugam *et al.*, (2023).

D<sup>2</sup> analysis showed that grain yield per acre (46.83%) had the highest contribution to total genetic divergence, followed by panicle weight (15.08%), plant height (10.71%), number of panicles per plant (9.88%), number of tillers per plant (7.09%), panicle length (6.33%), and 1000-grain weight (3.85%). These traits were the key factors contributing to divergence in the rice population studied. Similar observations were made by Muthuramu *et al.*, (2017) Sujata *et al.*, (2021) and Shanmugam *et al.*, (2023). On the other hand, days to 50% flowering had a minimal impact on genetic divergence. These findings differ from those of Sar *et al.* (2022), who identified test weight and days to 50% flowering as major contributors to genetic divergence. Understanding the traits that contribute most to genetic divergence is essential for selecting genetically diverse parents in breeding programs.

## **Conclusion**

Considering the complementary traits among parents, genotypic divergence, and cluster means, an inter-cluster hybridization program between SW5462R, SW24333R, SW23674R, SW24321R, SW24295R, and SW24299R (Cluster VII x Cluster III), is recommended for achieving higher yield and early maturity. These crosses are expected to generate significant heterosis in the F1 generation and provide a diverse range of recombinants in the segregating generations, from which promising segregates can be identified. This study also found that the 44 restorer lines exhibited greater genetic divergence compared to the 8 founder lines, particularly in terms of grain yield and other yield associated traits. This greater divergence among restorer lines suggests a higher potential for producing hybrid offspring with improved performance. The broader genetic variability among the restorer lines provides a more diverse genetic pool, which is crucial for the selection of superior hybrids and the development of new rice varieties.

## **References**

- Aarathi, M., Subramanian, A., Jeyaprakash, P. and Rajanbabu, V., 2021. Multivariate analysis of wild rice MAGIC population under sodic soil condition. *Electronic Journal of Plant Breeding*, 12(3), pp.748-756.
- Amegan, E., Efiuse, A., Akoroda, M., Shittu, A. and Tonegnikes, F. 2020. Genetic diversity of Korean rice (*Oryza sativa* L.) germplasm for yield and yield related traits for adoption in rice farming system in Nigeria. *Genomics*, 8(1):19- 28.
- Keerthana, S., Kumar, P.S., Doggalli, G., Patil, V.S., Elango, S., Deepak, C.A., Lamani, A. and Gireesha, D., diversity analysis in improved and traditional genotypes of rice (*Oryza sativa* L.). *Plant Archives* Vol. 24, No. 1, 2024 pp. 1596-1600.
- Mahalanobis, P.C. 1936. On the generalized distance in statistics. National Institute of Science of India.
- Muthuramu, S. and Sakthivel, S. 2017. Genetic diversity analysis for yield traits in upland rice (*Oryza sativa* L.). *Journal of Rice Research*, 10(1):40-43.

Nakano, H., Takai, T. and Kondo, M., 2019. Identification of quantitative trait loci for panicle structure and grain filling using a cross between indica-and japonica-type high-yielding rice cultivars. *Plant Production Science*, 22(4), pp.443-455.

Pathak, V., Prasuna, C., Umakanth, B., Surekha, K., Subbarao, L. And Padmavathi, G., Genetic variability, association and diversity analysis of yield and its component traits in rice (*Oryza sativa*) germplasm. *The Indian Journal of Agricultural Sciences*, 94(7), pp.786-790.

Prakash, S., Reddy, S.S., Chaudhary, S., Vimal, S.C. and Kumar, A., 2024. Multivariate analysis in rice (*Oryza sativa* L.) germplasms for yield attributing traits. *Plant Science Today*, 11(1), pp.64-75.

Rao CR (1952). *Advanced Statistical Methods in Biometrical Research*. John Wiley and Sons. New York.

Sar, P. and Kole, P.C., 2022. Genotypic diversity in rice (*Oryza sativa* L.) based on morphological characters. *Environment and Ecology* 40 (2C): 1005—1009

Shanmugam, A., Suresh, R., Ramanathan, A., Anandhi, P. and Sassikumar, D., 2023. Unravelling genetic diversity of South Indian rice landraces based on yield and its components. *Electronic Journal of Plant Breeding*, 14(1), pp.160-169.

Sharma, M., Abdullah, G.M., Salgotra, R.K., Hangloo, S., Singh, A.K., Sharma, V. and Singh, A., 2021. Genetic diversity analysis in rice (*Oryza sativa* L.) germplasm of Jammu region of Jammu and Kashmir. *Indian Journal of Genetics and Plant Breeding*, 81(04), pp.529-537.

Singh, S. and Gupta, P. K. 1979. Genetic divergence in pearl millet. *Indian Journal of Genetics & Plant Breeding*, 39: 210-215.

Singh, Y. P., Kumar, A. and Chauhan, B. P. S. 1981. Genetic divergence in pearl millet. *Indian Journal of Genetics and Plant Breeding*, 41(2): 186-190.

Stadlmeier, M., Hartl, L. and Mohler, V., 2018. Usefulness of a multiparent advanced generation intercross population with a greatly reduced mating design for genetic studies in winter wheat. *Frontiers in plant science*, 9, p.1825.

Sudeepthi, K., Srinivas, T., Kumar, B.N.V.S.R.R., Jyothula, D.P.B. and Umar, S.N. 2020. Genetic divergence studies for anaerobic germination traits in rice (*Oryza sativa* L.). *Current Journal of Applied Science and Technology*, 39(1):71-78.

Sujata, S.A., Kumar, B.D., Gangaprasad, S. and Halingali, B.I. 2021. Assessment of Morphological, genetical and diversity studies in landraces of rice (*Oryza sativa* L.). *Indian Journal of Agricultural Research*, 1:5.

Thúy, L.T., Vu, T.N., Pham, V.T., Nguyen, A.D. and Nguyen, T.K., 2022. Variability, correlation and path analysis for several quantitative traits derived multi-parent advanced generation inter-cross (Magic) F2 population of rice (*Oryza sativa* L.). *International Journal of Scientific Research and Management*, 10(11), pp.356-363.

**Table 1. List of genetic materials (44 Indica MAGIC parental lines and 8 Founder Indica parental lines)**

S.No.	Lines	Detail	Sources
1	SW001R	Founder line	SeedWorks (I) Pvt. Ltd. Hyderabad
2	SW002R	Founder line	SeedWorks (I) Pvt. Ltd. Hyderabad
3	SW003R	Founder line	SeedWorks (I) Pvt. Ltd. Hyderabad
4	SW004R	Founder line	SeedWorks (I) Pvt. Ltd. Hyderabad
5	SW005R	Founder line	SeedWorks (I) Pvt. Ltd. Hyderabad
6	SW006R	Founder line	SeedWorks (I) Pvt. Ltd. Hyderabad
7	SW007R	Founder line	SeedWorks (I) Pvt. Ltd. Hyderabad
8	SW008R	Founder line	SeedWorks (I) Pvt. Ltd. Hyderabad
9	SW23671R	MAGIC line	SeedWorks (I) Pvt. Ltd. Hyderabad
10	SW23673R	MAGIC line	SeedWorks (I) Pvt. Ltd. Hyderabad
11	SW23674R	MAGIC line	SeedWorks (I) Pvt. Ltd. Hyderabad
12	SW23675R	MAGIC line	SeedWorks (I) Pvt. Ltd. Hyderabad
13	SW23755R	MAGIC line	SeedWorks (I) Pvt. Ltd. Hyderabad
14	SW23756R	MAGIC line	SeedWorks (I) Pvt. Ltd. Hyderabad
15	SW24292R	MAGIC line	SeedWorks (I) Pvt. Ltd. Hyderabad
16	SW24293R	MAGIC line	SeedWorks (I) Pvt. Ltd. Hyderabad
17	SW24294R	MAGIC line	SeedWorks (I) Pvt. Ltd. Hyderabad
18	SW24295R	MAGIC line	SeedWorks (I) Pvt. Ltd. Hyderabad
19	SW24296R	MAGIC line	SeedWorks (I) Pvt. Ltd. Hyderabad

20	SW24297R	MAGIC line	SeedWorks (I) Pvt. Ltd. Hyderabad
21	SW24298R	MAGIC line	SeedWorks (I) Pvt. Ltd. Hyderabad
22	SW24299R	MAGIC line	SeedWorks (I) Pvt. Ltd. Hyderabad
23	SW24301R	MAGIC line	SeedWorks (I) Pvt. Ltd. Hyderabad
24	SW24302R	MAGIC line	SeedWorks (I) Pvt. Ltd. Hyderabad
25	SW24306R	MAGIC line	SeedWorks (I) Pvt. Ltd. Hyderabad
26	SW24307R	MAGIC line	SeedWorks (I) Pvt. Ltd. Hyderabad
27	SW24312R	MAGIC line	SeedWorks (I) Pvt. Ltd. Hyderabad
28	SW24318R	MAGIC line	SeedWorks (I) Pvt. Ltd. Hyderabad
29	SW24321R	MAGIC line	SeedWorks (I) Pvt. Ltd. Hyderabad
30	SW24322R	MAGIC line	SeedWorks (I) Pvt. Ltd. Hyderabad
31	SW24324R	MAGIC line	SeedWorks (I) Pvt. Ltd. Hyderabad
32	SW24325R	MAGIC line	SeedWorks (I) Pvt. Ltd. Hyderabad
33	SW24326R	MAGIC line	SeedWorks (I) Pvt. Ltd. Hyderabad
34	SW24327R	MAGIC line	SeedWorks (I) Pvt. Ltd. Hyderabad
35	SW24333R	MAGIC line	SeedWorks (I) Pvt. Ltd. Hyderabad
36	SW23670R	MAGIC line	SeedWorks (I) Pvt. Ltd. Hyderabad
37	SW23672R	MAGIC line	SeedWorks (I) Pvt. Ltd. Hyderabad
38	SW24308R	MAGIC line	SeedWorks (I) Pvt. Ltd. Hyderabad
39	SW24313R	MAGIC line	SeedWorks (I) Pvt. Ltd. Hyderabad
40	SW24315R	MAGIC line	SeedWorks (I) Pvt. Ltd. Hyderabad
41	SW24316R	MAGIC line	SeedWorks (I) Pvt. Ltd. Hyderabad
42	SW24317R	MAGIC line	SeedWorks (I) Pvt. Ltd. Hyderabad
43	SW24319R	MAGIC line	SeedWorks (I) Pvt. Ltd. Hyderabad
44	SW24320R	MAGIC line	SeedWorks (I) Pvt. Ltd. Hyderabad
45	SW24334R	MAGIC line	SeedWorks (I) Pvt. Ltd. Hyderabad
46	SW5462R	MAGIC line	SeedWorks (I) Pvt. Ltd. Hyderabad
47	SW5464R	MAGIC line	SeedWorks (I) Pvt. Ltd. Hyderabad
48	SW3210R	MAGIC line	SeedWorks (I) Pvt. Ltd. Hyderabad
49	SW3358R	MAGIC line	SeedWorks (I) Pvt. Ltd. Hyderabad
50	SW3372R	MAGIC line	SeedWorks (I) Pvt. Ltd. Hyderabad
51	SW3404R	MAGIC line	SeedWorks (I) Pvt. Ltd. Hyderabad
52	SW3374R	MAGIC line	SeedWorks (I) Pvt. Ltd. Hyderabad

**Table 2. Distribution of Rice genotypes in different clusters**

Cluster	No. of genotypes	Genotypes
I	17	SW24312R, SW24334R, SW24294R, SW24297R, SW24301R, SW3358R, SW001R, SW008R, SW24322R, SW24322R, SW24306R, SW24292R, SW005R, SW3372R, SW3404R, SW24293R, SW24319R



II	14	SW23673R, SW002R, SW24302R, SW24318R, SW24296R, SW003R, SW23671R, SW24298R, SW24298R, SW23672R, SW23756R, SW24327R, SW23675R
III	4	SW23674R, SW24321R, SW24295R, SW24299R
IV	3	SW24307R, SW24307R, SW24316R
V	4	SW3372R, SW004R, SW3374R, SW24324R
VI	5	SW5464R, SW24317R, SW24313R, SW006R, SW007R
VII	2	SW5462R, SW24333R
VIII	1	SW3210R
IX	1	SW3210R
X	1	SW24326R

**Table 3. Average intra and inter-cluster distances ( $D^2$  values) for ten clusters of 52 rice genotypes**

Cluster	I	II	III	IV	V	VI	VII	VIII	IX	X
I	126.73	515.86	761.22	219.13	995.03	400.98	1696.87	1217.29	1476.72	679.73
II		150.49	278.49	317.10	1492.08	891.29	2194.95	1715.27	1974.85	1176.63
III			37.25	557.86	1746.37	1142.72	2450.47	1970.17	2230.14	1430.22
IV				46.86	1190.42	588.85	1894.01	1413.71	1673.63	873.78
V					105.17	613.11	709.23	234.40	489.41	321.56
VI						119.11	1312.84	833.49	1092.65	299.73
VII							83.03	481.90	224.02	1020.92
VIII								0.00	260.04	540.25
IX									0.00	800.15
X										0.00

**Table 4. Cluster means for eight yield and yield attributes among 52 rice genotypes**

Cluster	DFE	TILL	PAN	PANL	PANWT	PLHT	GRNYLD_AC	TSWT
<b>I</b>	116.12	10.97	10.44	24.88	5.62	124.24	2065.88	25.82
<b>II</b>	116.50	10.43	9.86	24.61	4.11	121.82	1567.86	25.25
<b>III</b>	113.63	8.50	7.88	23.50	4.25	125.88	1310.00	25.25
<b>IV</b>	116.83	10.50	9.50	22.50	5.17	118.33	1866.67	25.50
<b>V</b>	119.50	15.13	12.13	23.88	5.63	124.25	3055.00	25.13
<b>VI</b>	115.60	9.60	9.70	23.00	6.60	125.60	2450.00	25.60
<b>VII</b>	109.50	11.75	11.25	23.75	5.50	125.25	3760.00	26.25
<b>VIII</b>	111.50	15.00	12.00	24.50	5.50	134.50	3280.00	24.00
<b>IX</b>	110.00	13.50	11.50	24.00	6.50	131.50	3540.00	23.00
<b>X</b>	121.00	11,5	11.00	24.50	5.00	121.50	2740.00	23.00
<b>%Contribution</b>	0.23%	7.09%	9.88%	6.33%	15.08%	10.71%	46.83%	3.85%

DFE= Days to 50% flowering, PLHT= Plant height, TLN = Number of tillers per plant, PAN= Number of panicles per plant, PNL= Panicle length, PANWT- Panicle weight, TSWT = 1000 grain weight, GRNYLD\_AC = Grain yield per hectare

Fig. 1.

