Multivariate Analysis in Rice (*Oryza sativa* L.) Mutant Families from Anna (R) 4 Cultivar

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**ABSTRACT**

**Background:** The drought is one of the major limiting factors in rice production especially in rainfed environment. The rice production loss in rainfed has ranged from 17 to 40 percent during severe drought seasons. The rice cultivar Anna (R) 4 is having best adaptive characteristics to suits direct seeded rice under rainfed cultivation. But it has less market preference due its undesirable grain characters at consumer level. Hence, induced mutagenesis approach resorted to correct the undesirable traits and improve this variety to suits present needs. The mutant lines are having desirable changes and shows more similarity with Anna (R) 4 were identified by multivariate analyses.

**Methods:** The present investigation was carried out during *rabi* 2018-19 to access the genetic relatedness of the 32 mutant families derived from Anna (R) 4 rice cultivar through electron beam, gamma rays and recurrent EMS mutagenesis. Data on twelve morphological traits were analysed for genetic divergence, principal component analysis and UPGMA clustering.

**Result:** The mutant families were grouped in eight clusters with maximum and minimum diversity (D²) values of 457.21 and 10.90 respectively. The principal component analysis revealed that 75.32 per cent of total variability was explained by first five PCs and traits contributed to the divergence among the mutant families was discussed. The cluster tree obtained from UPGMA clustering based on the dissimilarity among the mutants was narrated.

**Key words:** Clustering, Genetic divergence, Mutant lines, PCA, Rice.

**INTRODUCTION**

Rice is one of the most versatile and the staple food crop of tropics and subtropics and it feeds around 3.5 billion people across the world (Muthayya *et al.*, 2014). The cultivated species of *Oryza* having diploid (2n=24) chromosome with AA genome. Rice occupies an area of 162.97 million hectares with the production of 495.03 million metric tonnes (USDA, 2019). Traditionally Asian countries have a highest share, accounting 90 percent of the world's rice production and consumption. In India rice production is nearly half of the world production with contribution of 210 million metric tonnes in 2017 with the productivity of 2130 kg/ha.

The rice cultivar Anna (R) 4 is best adoptive characteristics to suits direct seeded rice under rainfed cultivation. But it has less market preference due long slender grain characters. Hence, induced mutagenesis approach through electron beam and gamma rays resorted to correct the undesirable traits and improve this variety to suits present needs. The mutant lines are having desirable changes and shows more similarity with Anna (R) 4 were identified by multivariate analyses.

**MATERIALS AND METHODS**

The experimental material comprised of 32 best performed mutant lines (ML) selected based on earliness, grain shape and yield characteristics from Anna (R) 4 rice mutants in M₃ generation (Table 1). Among them, 11 mutants from gamma irradiation, 18 mutants from electron beam irradiation, 3 mutants from irradiation and EMS recurrent treatment. The

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Field experiment in M₄ generation was carried out during *rabi* 2018-19 at Agricultural College and Research Institute, Tamil Nadu Agricultural University, Madurai. Seedling of 25 days old were transplanted into the main field as plant row progenies in two replications. Each replication consisted of two rows of two-meter length accommodating 15 plants per each row and the recommended package of practices were performed to maintain a good plant stand. From each mutant family based on desirable traits 10 plants were tagged and grouped under a section of a cluster. The cluster tree obtained from UPGMA clustering based on the dissimilarity among the mutants was narrated.
The mean values over two replications were used for statistical analysis to measure the genetic divergence using Mahalanobis $D^2$ followed by principal component analysis using STAR nebula 2.0.1 (2013). UPGMA cluster analysis was performed using DARwin 6.0.21. The morphological data were converted to text (tab delimited) format and DARwin workbook and saved as var format. The dissimilarity was calculated for single data using dissimilarity index continuous - usual Euclidean standardized and with bootstrap (1000) options.

$$d_{ij} = \sqrt{\sum_{k} (X_{ik} - X_{jk})^2}$$

Where,

$d_{ij}$ - dissimilarity between units $i$ and $j$; $X_{.}$ - overall mean; $X_{ik}$ - values of variable $k$ for units $i$ and $j$; $k$ - number of variables

After calculating dissimilarities among the mutants, the tree was constructed using hierarchical clustering (UPGMA).

**RESULTS AND DISCUSSION**

**Genetic divergence analysis**

The genetic divergence among the 32 mutant lines (ML) showed that maximum diversity ($D^2$) values of 457.21 between ML-3 and ML-15 followed by 455.48 between ML-5 and ML-15. The least divergence (10.90) observed between ML-26 and ML-27. It inferred that mutant families were distanced from each other. However mutant lines of ML-9 (25.91) and ML-29 (43.24) were more closely related whereas mutant lines of ML-26, ML-27 families were distanced from each other. However mutant lines of ML-23, ML-32 in cluster II recorded the lowest mean values for days to flowering inferring that cluster II comprises of early lines as compared to Anna (R) 4 cultivar. The relative contribution of 12 quantitative traits (Table 2) revealed that grain length (53.41%), followed by panicle weight (17.05%), grain yield per plant (9.65%), grains per panicle (5.49%) and days to flowering (5.49%) contributed maximum for the divergence among the mutant families. These findings were in line with Chandramohan et al. (2016) and Ranjith et al. (2018). Though selection was carried out for desirable traits, most of the mutant lines were different from Anna (R) 4 rice for these above traits. Most of selected mutants were five to seven days earlier than Anna (R) 4 suggesting less contribution from days to flowering (1.89%) to the divergence in $M_s$ generation. This conclusion that these mutant lines offer scope to isolate the short duration, high yielding and medium slender genotypes in further generations.

Based on the genetic divergence of 32 mutant lines, eight clusters were formed (Table 3). The maximum number of 14 mutant lines assembled in cluster I whereas, cluster VIII comprises of 7 mutant lines. And the remaining six clusters (II, III, IV, V, VI, VII) comprises of two lines each.

**Average inter and intra cluster $D^2$ values**

The estimated average intra and inter cluster $D^2$ values as per the procedure given by Toucher’s and were presented in Table 4. Among the different clusters, inter cluster $D^2$ values were higher for cluster V and VII (144.80) followed by cluster III and VI (137.37), cluster III and VII (123.68) and the lowest for cluster III and V (22.59) which indicated the divergence among the mutant families dealt under these clusters. The highest intra cluster $D^2$ value was noticed as 124.55 in cluster VIII whereas, cluster II (10.33) recorded the lowest $D^2$ values.

The eight cluster mean values of 32 mutants from Anna (R) 4 rice were presented in Table 5. Among the clusters, mutant families of ML-23, ML-32 in cluster II recorded the lowest mean values for days to flowering inferring that cluster II comprises of early lines as compared to Anna (R) 4 cultivar. Higher grain yield per plant (29g) and lesser grain length (5.8 mm) in cluster III indicates that ML-26, ML-27 families

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Table 1: Details of 32 mutant lines raised in $M_s$ generation.

| Mutant lines | Pedigree | Mutant from | Mutant lines | Pedigree | Mutant from |
|--------------|----------|-------------|--------------|----------|-------------|
| ML-1         | M3-GT1-124-3 | 100 Gy GR  | ML-17        | M3-ET1-79-29 | 100 Gy EB |
| ML-2         | M3-GT1-145-7 | 100 Gy GR  | ML-18        | M3-ET1-91-21 | 100 Gy EB |
| ML-3         | M3-GT1-145-15 | 100 Gy GR | ML-19        | M3-ET1-91-23 | 100 Gy EB |
| ML-4         | M3-GT1-146-3 | 100 Gy GR  | ML-20        | M3-ET2-51-13 | 150 Gy EB |
| ML-5         | M3-GT1-146-4 | 100 Gy GR  | ML-21        | M3-ET2-62-1  | 150 Gy EB |
| ML-6         | M3-GT2-124-22 | 100 Gy GR | ML-22        | M3-ET2-62-3  | 150 Gy EB |
| ML-7         | M3-GT2-129-15 | 100 Gy GR | ML-23        | M3-ET2-62-4  | 150 Gy EB |
| ML-8         | M3-GT2-12-15  | 150 Gy GR  | ML-24        | M3-ET2-69-16 | 150 Gy EB |
| ML-9         | M3-GT2-73-16  | 150 Gy GR  | ML-25        | M3-ET2-75-8  | 150 Gy EB |
| ML-10        | M3-GT2-73-17  | 150 Gy GR  | ML-26        | M3-ET2-118-16| 150 Gy EB |
| ML-11        | M3-GT1-145-15 | 100 Gy GR | ML-27        | M3-ET2-118-18| 150 Gy EB |
| ML-12        | M3-ET1-37-6   | 100 Gy EB  | ML-28        | M3-ET2-118-19| 150 Gy EB |
| ML-13        | M3-ET1-45-1   | 100 Gy EB  | ML-29        | M3-ET2-118-20| 150 Gy EB |
| ML-14        | M3-ET1-61-16  | 100 Gy EB  | ML-30        | M3-RGT2-10-3 | 150 Gy GR+30 mM EMS |
| ML-15        | M3-ET1-64-3   | 100 Gy EB  | ML-31        | M3-RGT2-19-8 | 150 Gy GR+30 mM EMS |
| ML-16        | M3-ET1-61-17  | 100 Gy EB  | ML-32        | M3-RET1-18-15| 100 Gy EB +30 mM EMS |

GT - Gamma rays; EB - Electron beam; EMS - Ethyl Methyl Sulphonate.
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Table 2: Relative contribution of 12 quantitative traits to divergence in M3 lines of Anna (R) 4 rice cultivar.

| Traits                     | No. of first rank | % Contribution |
|----------------------------|-------------------|----------------|
| Days to flowering          | 29                | 5.49           |
| Plant height (cm)          | 14                | 2.65           |
| Productive tillers per plant (nos.) | 1    | 0.19           |
| Flag leaf length (cm)      | 2                 | 0.38           |
| Flag leaf width (cm)       | 0                 | 0.00           |
| Panicle length (cm)        | 5                 | 0.95           |
| Panicle weight (g)         | 90                | 17.05          |
| Grains per panicle (nos.)  | 29                | 5.49           |
| Grain weight (g)           | 16                | 3.03           |
| Grain yield per plant (g)  | 51                | 9.65           |
| Grain width (mm)           | 9                 | 1.70           |
| Grain length (mm)          | 282               | 53.41          |

Table 4: Inter and intra cluster D^2 values and distance (in parenthesis) in M3 generation of Anna (R) 4 rice cultivar.

| Cluster | I          | II         | III        | IV         | V          | VI         | VII        | VIII       |
|---------|------------|------------|------------|------------|------------|------------|------------|------------|
| I       | 66.29(8.14)| 43.43(6.59)| 63.27(7.95)| 52.12(7.22)| 71.25(8.44)| 85.16(9.23)| 118.12(10.87)| 108.16(10.40)|
| II      | 10.33(3.22)| 50.51(7.02)| 40.99(6.94)| 72.06(8.49)| 63.03(7.94)| 101.52(10.08)| 108.19(10.40)|
| III     | 19.89(4.46)| 45.43(6.74)| 48.21(6.94)| 137.37(11.72)| 123.68(11.12)|
| IV      |            |            |            |            |            |            |            |            |
| V       |            |            |            |            |            |            |            |            |
| VI      |            |            |            |            |            |            |            |            |
| VII     |            |            |            |            |            |            |            |            |
| VIII    |            |            |            |            |            |            |            |            |

Table 3: Toucher’s cluster from D^2 values of 32 mutant lines of Anna (R) 4 rice cultivar.

| Cluster number | Number of mutant lines | Name of the mutant lines |
|----------------|------------------------|--------------------------|
| I              | 14                     | ML-1, ML-2, ML-3, ML-4, ML-5, ML-6, ML-7, ML-8, ML-9, ML-10, ML-11, ML-12, ML-13, ML-14 |
| II             | 2                      | ML-23, ML-32             |
| III            | 2                      | ML-26, ML-27             |
| IV             | 2                      | ML-21, ML-22             |
| V              | 2                      | ML-25, ML-28             |
| VI             | 2                      | ML-30, ML-31             |
| VII            | 2                      | ML-18, ML-19             |
| VIII           | 7                      | ML-23, ML-16, ML-17, ML-20, ML-24, ML-29, Anna (R) 4 |

Table 5: Cluster mean values for 12 quantitative traits in M3 generation of Anna (R) 4 rice cultivar.

| Cluster | Days to flowering (cm) | Plant height (cm) | Productive tillers per plant (nos.) | Flag leaf length (cm) | Panicle length (cm) | Panicle weight (g) | Grains per panicle (nos.) | Grain weight (g) | Grain yield per plant (g) | Grain length (mm) |
|---------|------------------------|------------------|-------------------------------------|-----------------------|---------------------|---------------------|-------------------------|-----------------|--------------------------|-----------------|
| I       | 84.07                  | 81.13            | 14.18                               | 23.49                 | 1.38                | 23.06               | 3.97                    | 175.54          | 2.16                     | 20.27           |
| II      | 82.00                  | 80.65            | 16.50                               | 24.95                 | 1.28                | 22.08               | 4.20                    | 180.50          | 2.10                     | 25.10           |
| III     | 84.00                  | 77.33            | 16.25                               | 23.38                 | 1.50                | 21.58               | 3.85                    | 179.75          | 2.25                     | 29.00           |
| IV      | 86.25                  | 75.23            | 15.50                               | 20.68                 | 1.40                | 21.63               | 3.80                    | 183.21          | 2.25                     | 20.23           |
| V       | 86.75                  | 77.13            | 14.75                               | 23.38                 | 1.48                | 21.53               | 4.23                    | 182.16          | 2.35                     | 21.35           |
| VI      | 84.75                  | 78.25            | 15.00                               | 23.80                 | 1.25                | 25.90               | 4.40                    | 199.05          | 2.20                     | 13.90           |
| VII     | 83.50                  | 74.75            | 18.00                               | 23.63                 | 1.40                | 21.50               | 2.60                    | 167.75          | 2.01                     | 24.15           |
| VIII    | 87.71                  | 79.03            | 15.14                               | 23.90                 | 1.33                | 22.78               | 3.64                    | 166.74          | 2.29                     | 22.57           |

Principal component analysis

Already 32 mutant lines were grouped into eight different clusters based on divergence among the lines using D^2 analysis. Hence, principal component analysis was carried out to find out the largest contributing traits which cause divergence of mutant families. Findings of PCA (Table 6)

Table 6: Cluster mean values for 12 quantitative traits in M3 generation of Anna (R) 4 rice cultivar.

| Cluster | Days to flowering (cm) | Plant height (cm) | Productive tillers per plant (nos.) | Flag leaf length (cm) | Panicle length (cm) | Panicle weight (g) | Grains per panicle (nos.) | Grain weight (g) | Grain yield per plant (g) | Grain length (mm) |
|---------|------------------------|------------------|-------------------------------------|-----------------------|---------------------|---------------------|-------------------------|-----------------|--------------------------|-----------------|
| I       | 84.07                  | 81.13            | 14.18                               | 23.49                 | 1.38                | 23.06               | 3.97                    | 175.54          | 2.16                     | 20.27           |
| II      | 82.00                  | 80.65            | 16.50                               | 24.95                 | 1.28                | 22.08               | 4.20                    | 180.50          | 2.10                     | 25.10           |
| III     | 84.00                  | 77.33            | 16.25                               | 23.38                 | 1.50                | 21.58               | 3.85                    | 179.75          | 2.25                     | 29.00           |
| IV      | 86.25                  | 75.23            | 15.50                               | 20.68                 | 1.40                | 21.63               | 3.80                    | 183.21          | 2.25                     | 20.23           |
| V       | 86.75                  | 77.13            | 14.75                               | 23.38                 | 1.48                | 21.53               | 4.23                    | 182.16          | 2.35                     | 21.35           |
| VI      | 84.75                  | 78.25            | 15.00                               | 23.80                 | 1.25                | 25.90               | 4.40                    | 199.05          | 2.20                     | 13.90           |
| VII     | 83.50                  | 74.75            | 18.00                               | 23.63                 | 1.40                | 21.50               | 2.60                    | 167.75          | 2.01                     | 24.15           |
| VIII    | 87.71                  | 79.03            | 15.14                               | 23.90                 | 1.33                | 22.78               | 3.64                    | 166.74          | 2.29                     | 22.57           |
showed that first five PCs (Fig 1) recorded eigen values greater than one and contributed to 75.32 per cent of variability among the 32 mutant families in M₃ generation. In the previous studies Riaz et al. (2018), Tejaswini et al. (2018) found that first five PCs were explained the maximum variance of the total set.

The PC 1 explained 23.87 per cent of total variation which was elucidated by all the quantitative traits with positive eigen vector whereas, panicle weight, panicle length and plant height were higher contributing traits to the total variation. However, grain length, plant height, panicle length and panicle weight were the traits for 16.96 per cent variation in the PC 2. Similarly, Riaz et al. (2018) and Girma et al. (2018) reported positive contribution of growth and yield contributing traits in PC 1 and PC 2. In PC 1 Vs PC 2 biplot explained 40.83% of total variation in this biplot mutant lines trapped under first quarter (Fig 2) were exhibiting better performance than Anna (R) 4 control for panicle length, panicle weight, plant height and grain length positively contributed to the variation with high eigen vector.

In third principal component flag leaf length, days to flowering and panicle length exhibited higher contribution to the variation of 16.06%. Nachimuthu et al. (2014) also reported earliness and yield contributing traits in PC 3. In PC 4 and PC 5 grains per panicle accounted for maximum variation.

**UPGMA Cluster analysis**

Cluster analysis in mutant population is useful for homogenous grouping of the mutant lines based on similarity or dissimilarity existing among the lines. Here, Euclidean distance based UPGMA cluster analysis facilitates the grouping of mutant lines based on the dissimilarity values. Findings revealed that maximum dissimilarity of 9.41 was existed between ML-3 and ML-15, however minimum 2.07 was observed among the mutant lines of M-12 and M-22. It confirmed that in M₃ generation almost all those mutant lines were similar to each other due to stringent selection pressure exercised in the previous generation for earliness, grain shape and yield characteristics.

**Table 6: Eigen vector of various quantitative traits, eigen value, standard deviation and proportion of five principal components of M₃ generation of Anna (R) 4 rice mutants.**

| Traits                      | PC1   | PC2  | PC3   | PC4  | PC5  |
|-----------------------------|-------|------|-------|------|------|
| Days to flowering           | 0.022 | -0.208 | 0.362 | -0.656 | 0.201 |
| Plant height (cm)           | 0.335 | 0.410 | 0.149 | -0.044 | -0.369 |
| Productive tillers per plant (nos.) | 0.080 | -0.363 | 0.183 | -0.215 | -0.025 |
| Flag leaf length (cm)       | 0.324 | -0.094 | 0.427 | 0.108 | 0.121 |
| Flag leaf width (cm)        | 0.438 | -0.179 | -0.163 | 0.178 | -0.134 |
| Panicle length (cm)         | 0.418 | 0.323 | 0.252 | -0.072 | 0.200 |
| Panicle weight (g)          | 0.442 | 0.037 | -0.060 | 0.163 | 0.150 |
| Grains per panicle (nos.)   | 0.246 | -0.312 | -0.079 | 0.346 | 0.430 |
| Grain weight (g)            | 0.260 | -0.005 | -0.363 | -0.510 | 0.195 |
| Grain yield per plant (g)   | 0.257 | -0.303 | -0.058 | -0.122 | -0.702 |
| Grain width (mm)            | 0.134 | -0.129 | -0.597 | -0.163 | 0.086 |
| Grain length (mm)           | 0.047 | 0.552 | -0.198 | -0.162 | 0.063 |
| Eigen Values                | 2.865 | 2.035 | 1.927 | 1.212 | 1.000 |
| Standard deviation          | 1.69  | 1.43  | 1.39  | 1.10  | 1.00  |
| Proportion of variance (%)  | 23.87 | 16.96 | 16.96 | 10.10 | 8.33  |
| Cumulative proportion (%)   | 23.87 | 40.84 | 56.89 | 67.00 | 75.33 |

**Fig 1:** Scree plot of PCA from 32 mutants from Anna (R) 4 rice in M₃ generation.
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Table 7: Clustering of mutant lines in M₃ based on UPGMA.

| Cluster no. | Mutant lines | Minimum dissimilarity value as compared to control | Maximum dissimilarity value as compared to control |
|-------------|--------------|--------------------------------------------------|--------------------------------------------------|
| I           | ML-1, ML-2, ML-4, ML-5, ML-7, ML-8, ML-11, ML-24, ML-25, ML-30, Anna (R) 4 | 2.88 (ML-30) | 4.63 (ML-1) |
| II a        | ML-10, ML-29 | 4.51 (ML-10) | 4.85 (ML-29) |
| II b        | ML-12, ML-21, ML-22, ML-23 | 4.88 (ML-22) | 5.69 (ML-21) |
| III         | ML-26, ML-27, ML-28 | 4.92 (ML-28) | 6.06 (ML-27) |
| IV          | ML-13, ML-31 | 4.29 (ML-31) | 5.72 (ML-13) |
| V a         | ML-9, ML-20 | 3.65 (ML-9) | 4.16 (ML-20) |
| V b         | ML-6, ML-14, ML-16, ML-17, ML-18, ML-19, ML-32 | 4.94 (ML-32) | 6.49 (ML-19) |
| VI          | ML-3, ML-15 | 5.09 (ML-3) | 8.61 (ML-15) |

A total of six main clusters consisting of 32 mutant lines along with Anna (R) 4 were formed based on the dissimilarity values (Table 7, Fig 3). Since the objective is to isolate the mutants similar to Anna (R) 4 for all other characters except for grain characters, the dissimilarity between mutant lines and Anna (R) 4 cultivar was taken into consideration to characterise each cluster and identify the best cluster having desirable mutant lines. Vengadessan et al. (2016) reported that hierarchical clustering of 45 rice cultivars resulted in two major clusters; all the improved lines grouped together in first major cluster whereas, control alone fell under second cluster.

Cluster I was closely related to Anna (R) 4 for most of the quantitative traits except for panicle weight (4.17 g), grains per panicle (181.67) and grain length (6.3 mm). Mutant lines such as ML-1, ML-2, ML-4, ML-5, ML-7, ML-8, ML-11, ML-24, ML-25, ML-30 were medium slender (6.2 to 6.4 mm) in nature. Among lines ML-30 recorded minimum (2.88) and ML-1 recorded maximum (4.63) dissimilarity with control.

Six mutant lines were grouped together in the cluster II with the maximum and minimum dissimilarity values of 4.51 (ML-10) and 5.69 (ML-21) respectively. Mutant lines in this cluster mainly differed from Anna (R) 4 for plant height (76.85 cm), panicle length (21.06 cm) and grain length (6.1 mm). Based on dissimilarity values and grain length, cluster II was subdivided into IIa and IIb. ML-10 and ML-29 families in cluster IIa had reduced grain length and minimum dissimilarity values than the mutant lines in cluster II b.

The mutant lines of ML-26, ML-27, ML-28 were grouped together in cluster III and these lines were medium in grain length (less than 5.9 mm) and high yielding than Anna (R) 4 with maximum dissimilarity values of 6.06. Therefore, these lines can be advanced to further generations to develop improved mutant lines.

Cluster IV differed from control for dissimilarity of 5.72, but the mutant lines ML-13, ML-31 were long slender (6.6 mm) and low yielding (16.15g) in nature. So, these lines had less economic significance due to their tendency to break during milling.

Cluster V was subdivided into two sub clusters namely Va and Vb based on grain length and dissimilarity. Cluster Vb (ML-9, ML-20) was slightly differed from Anna (R) 4 for all the quantitative as well as grain characteristics (long slender). Mutant lines ML-6, ML-14, ML-16, ML-17, ML-18, ML-19 and ML-32 in Vb were medium slender but poor yielding. Best performing lines among the Vb were selected and forwarded to M₄ based on segregation among the lines and yield advancement may be achieved by selecting high yielding progenies of the particular line.
Mutant lines namely ML-3 and ML-15 extremely differed from Anna (R) 4 for earliness and grain shape. ML-3 was medium slender (6.3 mm) earlier maturity by seven days with the dissimilarity of 5.09. Mutant ML-15 was short slender (5.0 mm) and late flowering (11 days) compared to Anna (R) 4 with the highest dissimilarity of 8.61. Therefore, these two lines were separately grouped together in Cluster VI. Cluster analysis of 32 mutant lines concluded that mutant lines in cluster I, II a, IV, V b and VI were different from Anna (R) 4 for earliness, grain shape and yield characteristics.

CONCLUSION
The multivariate analysis in the mutant population concludes that most of the mutant families were similar to Anna (R) 4 due to stringent selection pressure excised in M$_2$ generation for earliness, reduced grain length and yield characteristics. The maximum dissimilarity observed among mutant lines in M$_3$ generation was 9.41 as per cluster analysis. Genetic divergence analysis revealed that grain length, panicle weight, grain yield per plant, grains per panicle and days to flowering were contributed more to the divergence among the mutant families. First five PCs contributed 75.32 per cent of variability and traits viz., yield attributing traits, days to flowering, plant height and grain length were recorded high eigen vector values and cause divergence among the mutant families. As per UPGMA clustering the mutant families in cluster I, II a, IV, V b and VI were holding desirable traits with minimum dissimilarity values, therefore these salient mutant lines to be forwarded for further yield advancement and stabilization.

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REFERENCES
Chandramohan, V., Srinivas, B., Thippeswamy, S. and D. Padmaja. (2016). Diversity and variability analysis for yield parameters in rice (Oryza sativa L.) genotypes. Indian Journal of Agricultural Research. 50(6):609-613.
Girma, B.T., Kitil, M.A., Banje, D.G., Biru, H.M. and Serbessa, T.B. (2018). Genetic variability study of yield and yield related traits in rice (Oryza sativa L.) genotypes. Advances in Crop Science and Technology. 6(4):381.
Muthayya, S., Sugimoto, J.D., Montgomery, S. and Maberly, G.F. (2014). An overview of global rice production, supply, trade and consumption. Annals of the New York Academy of Sciences. 1324 (1):7-14.
Nachimuthu, V.V., Robin, S., Sudhakar, D., Raveendran, M., Rajeswari, S. and Manonmani, S. (2014). Evaluation of rice genetic diversity and variability in a population panel by principal component analysis. Indian Journal of Science and Technology. 7(19): 1555-1562.
Ranjith, P., Sahu, S., Dash, S., Bastia, D.N. and Pradhan, B.D. (2018). Genetic diversity studies in rice (Oryza sativa L.). Journal of Pharmacognosy and Phytotechnology. 7(2):2529-2531.
Riaz, A., Bibi, T., Raza, T., Sabar, M. and Akhter, M. (2018). Evaluation of rice (Oryza sativa L.) advance uniform lines using multivariate analysis. African Journal of Plant Science. 12(11): 284-289.
Tejaswini, K.L.Y., Manukonda, S., Kumar, R., Rao, P.V.R., Lal Ahamed, M. and Raju, S.K. (2018). Application of principal component analysis for rice F$_5$ families characterization and evaluation. Emergent Life Sciences Research. 4(1):72-84.
USDA. (2019). World Agricultural Production. edited by World Agricultural Outlook Board. Washington: U.S. Department of Agriculture, Foreign Agricultural Service / Office of Global Analysis.
Vengadessan, V., R. S and S. N. (2016). Morpho-molecular diversity analysis of traditional and improved cultivars in rice. International Journal of Multidisciplinary Education and Research. 1(4):59-65.