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Genetic Diversity of Ayeyarmin Mutant Rice Population Revealed by Quantitative Traits

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ABSTRACT

One of the most important aspects of selecting genotypes with desirable characteristics for a successful breeding program is knowledge of the nature and magnitude of genetic variability. The goal of this study was to estimate the level of genetic divergence among mutant rice genotypes. During the 2020 dry season, a field experiment was carried out using 550 mutant lines with parent Ayeyarmin. The experiment was carried out using a simple CRD design. Six divergent groups were discovered by cluster analysis. Cluster I had the highest cluster mean for grain yield per plant, and the majority of the plants in these clusters resembled the parent Ayeyarmin. Cluster V, which had the fewest mutant lines (9), exhibited dwarf stature, short growth duration, fewer effective tillers per hill, and moderate yielding varieties. Cluster VI, which contained 11 mutant lines, had the most effective tillers per hill and the longest panicle length, both of which were appropriate for yield improvement. Cluster V had the greatest intra-cluster distance (5.77). Cluster V and IV had the greatest inter-cluster distance, followed by Cluster III and V, Cluster II and V, Cluster I and V, and the smallest between Cluster I and IV. Hybridization of Cluster I with V, Cluster V and VI could result in genotypes with desirable characteristics such as dwarf stature, short growth duration, and high yielding rice. The first three eigenvalues were found to have 62% variation using principal component analysis (PCA). Because of the high genetic variability in this mutant rice population, selection could be used to obtain desirable genotypes.

1. Introduction

Rice is one of the most important food crops, providing a primary source of nutrition to more than one-third of the world's population **(Singh & Singh, 2008)**. To meet the food needs of an expanding population, high yielding varieties must be developed. It is the world's second most-produced cereal after wheat and is a staple food source for more than half of the world's population **(Luz et al., 2016)**. Asia grows and consumes the majority of the world's rice **(Chakravarthi & Naravaneni, 2006)**. However, in order to meet the food demands of the country's growing population and achieve food security, heterosis breeding and other innovative breeding approaches must be used **(Padmavathi, 2012)**.

The availability of genetic variation and the selection of parents for hybridization are critical to the success of plant breeding research. The amount of genetic variability present in the population is primarily responsible for the development of new high yielding and high quality rice varieties that outperform existing varieties. Diverse parents should be involved in the development of varieties **(Banumathy et al., 2010)**. The basic factor to consider when making selection is genotype variability for yield and yield component traits **(Haydar et al., 2007)**.

Induced mutations allow for the induction of desired changes in a variety of attributes, which can be exploited directly or through recombination breeding **(Akbar and Manzoor, 2003; Khin, 2006)**. The concept of creating artificial mutations and using them to breed cultivars was first proposed in 1901 with the induction of mutations for factors that govern quantitative character heredity as a promising tool for releasing new genotypes **(Gomaa et al., 1995)**. Induced mutations have been widely used for genetic enhancement of various crops **(Oladosu et al., 2014)**. Ethylmethane sulfonate (EMS) is a chemical mutagen that causes a high density of random irreversible point mutations to be distributed uniformly throughout the genome **(Kim et al., 2004)**. Induced mutation has been used to improve both quantitative and qualitative characteristics **(Fardous et al., 2013)**. Mutants have enabled the identification of critical elements for developing high yield potential varieties with desirable characteristics such as semi-dwarfism, early maturity, a higher number of panicles per plant, and increased fertility. The availability of adequate genetic variability is the basic requirement for direct improvement of any agronomic trait.

As a result, genetic divergence research is critical for selecting parents in a hybridization program. Genetic diversity information in terms of nature and degree of divergence for grain yield, yield components, and quality characters would assist plant breeders in selecting the right type of parents for hybridization programs and designing effective breeding strategies. It is critical for breeders to understand genetic divergence, which divides a sample of subjects into different groups based on a set of different variables, so that similar subjects are placed in the same group **(Fellahi et al., 2013)**. It also groups genotypes into clusters, so the degree of association between members of the same cluster may be strong while it is weak between members of different clusters.

Ayeyarmin is a popular indica rice variety among Myanmar consumers. However, due to its long duration and susceptibility to logging, it has many production limitations. Through induced mutation, it is necessary to develop short growth duration and short stature for lodging resistance, as well as high yield. It is critical to obtain the desired amount of genetic variability to select genotypes with target traits. As a result, the goal of this experiment was to examine the genetic diversity of mutant lines derived from Ayeyarmin mutant rice lines using cluster and PCA analysis.

2. Materials and Methods

The experiment was conducted at the field of the Department of Plant Breeding, Physiology and Ecology, Yezin Agricultural University during dry season 2020. The 505 lines were selected from M2 generation and their parent Ayeyarmin was used for this experiment with simple CRD design. The seeds were sown in seed beds and 21 day-old seedlings were transplanted into the field. Each rice lines were involved 12 plants per row, 2.5 m long and with a spacing of 20 cm between plants and 25 cm between rows. Recommended fertilizers were applied as necessary. The data were collected on days to 50% flowering, plant height, effective tillers per hill, panicle length, spikelets per panicle, filled grain percent, thousand seed weight and yield per plant. Cluster analysis was performed using Ward's method and principal component analysis was analyzed to assess the genetic diversity of 505 mutant lines using STAR statistical analysis software version 2.0.1 (International Rice Research Institute, IRRI 2013).

3. Results and Discussions

3.1 Cluster analysis

Using Ward's method and morphological traits, 505 mutant rice lines were divided into six clusters (Table 1; Figure 1). The genotype distribution pattern revealed that 192 mutant lines were grouped into Cluster II, 171 lines in Cluster I, 77 lines in Cluster IV, 45 lines in Cluster III, and 11 lines in Cluster VI. In Cluster V, a minimum of nine mutant lines were included. Table 2 displays the cluster mean values for yield and yield component characters. The results of cluster means revealed that the highest mean value of plant height (151.95 cm) was occured in Cluster III and the lowest value (133.23 cm) was found in Cluster V. In Cluster II, the highest value of day to 50% flowering (128.92 days) and the lowest value (111.78 days) were found in Cluster V. The value of effective tillers per hill (13.76) in Cluster VI was higher than the other Clusters. Among the Clusters, the highest value of panicle length (38.37 cm) was found in Cluster VI and the lowest value (23.06 cm) were occurred in Cluster II. The highest value of spikelets per panicle (171.62) was found in Cluster IV. In Cluster V, the highest values of filled gain percent (64.97 %) and thousand seed weight (25.19 g) were obtained. Among the Clusters, the highest mean value of yield per plant (24.01 g) was showed in Cluster I and also the lowest value (10.84 g) was showed in Cluster III. Majority of the lines in the Cluster I were silmilar with parent Ayeyarmin. Therefore, the lines from Cluster I have the potential to produce higher yield traits than the other clusters. This indicated that the lines within this Cluster I could be used for increasing yield but they had long duration. Therefore, the genotypes of Cluster I can be used in hybridization program to produce higher yielding genotypes. The lines from Cluster V were characterized as early flowering with the lowest plant height, the highest number of filled grain percent and thousand grain weight. Among the clusters showing the lowest number of genotypes.

Table 1. Distribution of 505 Ayeyarmin mutant rice lines in different clusters of M3 generation.

Cluster	No. of Mutant Lines	Mutant Line Numbers in M3 Generation
I	171	1, 3, 4,5, 6, 7, 9, 12, 13, 14, 17, 18, 20, 22, 24, 26, 27, 28, 29, 31, 34, 35, 36, 40, 54, 55, 57, 58, 60, 63, 67, 69, 70, 71, 72, 79, 80, 99, 112, 122, 123, 127, 128, 135, 136, 142, 145, 149, 150, 153, 154, 164, 172, 174, 180, 182, 189, 193, 215, 218, 219, 223, 233, 257, 259, 260, 262, 264, 265, 267, 268, 269, 271, 274, 276, 284, 285, 294, 296, 297, 299, 302, 304, 307, 308, 313, 315, 321, 322, 323, 324, 325, 326, 329, 330, 331, 336, 338, 343, 345, 347, 349, 350, 354, 375, 379, 380, 382, 383, 384, 388, 390, 393, 395, 398, 399, 403, 407, 408, 409, 412, 413, 416, 417, 419, 421, 425, 426, 427, 431, 432, 433, 435, 441, 442, 443, 446, 447, 450, 451, 452, 453, 454, 458, 461, 464, 467, 468, 469, 470, 471, 472, 473, 474, 475, 476, 478, 479, 480, 483, 484, 489, 492, 493, 494, 495, 498, 500, 501, 503, AYM

II	192	2, 10, 15, 19, 21, 33, 37, 39, 42, 44, 45, 46, 47, 48, 52, 53, 61, 64, 65, 68, 77, 78, 90, 105, 110, 124, 129, 131, 132, 134, 137, 138, 139, 141, 143, 144, 146, 148, 151, 152, 155, 156, 157, 158, 159, 160, 161, 163, 165, 166, 167, 169, 170, 173, 175, 178, 181, 183, 186, 188, 190, 191, 195, 197, 202, 203, 206, 207, 209, 210, 212, 214, 216, 221, 222, 224, 227, 228, 229, 231, 239, 249, 253, 254, 255, 256, 258, 261, 263, 266, 270, 272, 273, 275, 277, 278, 279, 280, 281, 282, 283, 286, 288, 289, 290, 291, 292, 295, 298, 300, 301, 303, 305, 306, 309, 310, 311, 312, 314, 316, 317, 318, 319, 320, 327, 328, 332, 333, 334, 337, 340, 341, 342, 344, 346, 357, 358, 360, 361, 363, 364, 369, 370, 373, 377, 381, 385, 386, 387, 389, 392, 394, 396, 397, 400, 402, 404, 405, 406, 410, 411, 414, 415, 418, 420, 422, 423, 424, 428, 430, 434, 436, 437, 438, 439, 440, 445, 448, 456, 459, 462, 463, 465, 481, 482, 485, 487, 490, 496, 497, 499, 502
III	45	8, 25, 38, 41, 51, 66, 73, 81, 87, 89, 91, 93, 94, 96, 98, 101, 104, 106, 107, 108, 109, 111, 113, 114, 115, 116, 117, 121, 125, 126, 230, 235, 236, 238, 240, 241, 242, 244, 247, 248, 251, 252, 362, 368, 372
IV	77	11, 16, 23, 30, 32, 43, 49, 50, 59, 62, 74, 75, 82, 83, 84, 85, 86, 88, 92, 95, 97, 100, 102, 103, 118, 119, 120, 130, 140, 147,162, 168, 171, 176, 177, 179, 187, 192, 194, 196, 198, 199, 200, 201, 205, 208, 211, 213, 217, 220, 225, 226, 232, 234, 237, 243, 245, 246, 250, 335, 353, 355, 356, 359, 365, 366, 367, 371, 374, 376, 378, 444, 455, 466, 477, 488, 491
V	9	56, 76, 339, 351, 391, 401, 429, 457, 486
VI	11	133, 184, 185, 204, 293, 348, 352, 449, 460, 504, 505

3.2 Dendogram using Ward's Clustering Method

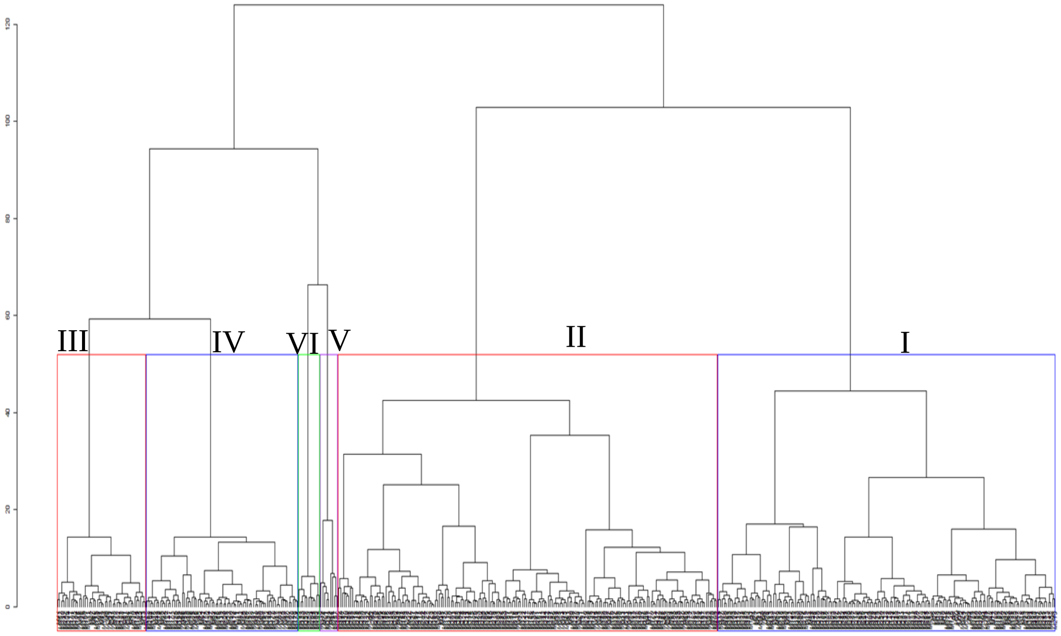

Figure 1. Cluster analysis of 505 mutant rice lines based on phenotypic characters.

Cluster V included varieties with desirable characteristics such as dwarf stature, short growth duration, fewer effective tillers per hill, and moderate yield. As a result, Cluster V genotypes can be used as one parent in a crossing program with Cluster I genotypes to produce semi-dwarf stature, short growth duration, the highest number of filled grain percent, and high yielding genotypes. Furthermore, it was clear that the selection would be effective for early heading date and semi-dwarf plant while taking these superior traits into account for crop improvement.

Table 3 displays intra- and inter-cluster distances. Cluster V had the greatest intra-cluster distance (5.77) followed by Cluster II (3.004), indicating a high genetic diversity among the genotypes in these clusters. Cluster IV (2.157) had the shortest intra-cluster distance, followed by Cluster III (2.265), indicating that the genotypes within the clusters were homogeneous. Intra-cluster distances were more or less low in all clusters, indicating that genotypes within the same cluster were closely related.

The inter-cluster distances ranged from 10.472 to 2.975. Clusters V and VI had the greatest inter-cluster distance (10.472), followed by Cluster III and V (9.137), indicating a high degree of diversity between these clusters. It is clear that Cluster V produced the greatest inter-cluster distances with other clusters in the majority of cases, implying a wide diversity of genotypes within Cluster V with mutant lines from other clusters. As a result, genotypes from these clusters could be used as parents in a hybridization program to produce transgressive segregants. Similar findings have been reported by **(Bansal et al., 1999); (Mokate et al., 1998); (Kumari & Rangasamy, 1997)** and others **(Singh et al., 1996)**.

Table 2. Mean values of each cluster and contribution of different characters for 505 Ayeyarmin mutant rice lines in M3 Generation.

Variables	**Cluster I**	**Cluster II**	**Cluster III**	**Cluster IV**	**Cluster V**	**Cluster VI**
PltHt	142.94	140.70	151.95	147.71	133.23	141.66
DTF	128.01	128.92	126.78	126.45	111.78	127.45
EffT	13.55	13.20	12.64	12.64	9.82	13.76
PLen	23.99	23.06	23.72	24.33	24.17	38.37
SPP	152.65	122.40	145.48	171.62	131.49	126.70
FGP	64.74	57.40	32.79	50.43	64.97	58.80
TSWt	18.04	18.02	18.00	18.35	25.19	17.93
YPP	24.01	16.39	10.84	19.94	19.72	18.36

PltHt = Plant Height (cm), DTF = Days to 50% Flowering (days), EffT = Effective Tillers Per Hill (number), PLen = Panicle Length (cm), SPP = Spiklets Per Panicle (number), FGP = Filled Grain Percent (%), TSWt = Thousand Seed Weight (g), YPP = Yield Per Plant (g)

Table 3. Average intra-cluster (bold) and inter cluster distances for different quantitative characters in mutant rice lines.

Cluster	I	II	III	IV	V	VI
I	**2.646**	3.378	4.435	2.975	8.827	6.459
II		**3.004**	3.796	3.425	8.972	6.764
III			**2.265**	3.215	9.137	6.929
IV				**2.157**	8.477	6.384
V					**5.770**	10.472
VI						**2.665**

3.3 Principal Component Analysis (PCA)

Principal component analysis (PCA) is a method for identifying character contribution in variation among different genotypes that may be a useful selection tool for rice improvement **(Salem, Saleh, Aldahak and Elabd, 2021)**. Table 4 displays eigenvalues, percentages of total variation, and principal components. The first three PCAs (PC1, PC2, and PC3) were approved to show variation in the studied characteristics because their eigenvalues exceeded 1.0 (1.913, 1.693, and 1.342, respectively). The three major components accounted for 62% of total variability (Table 4). According to the findings, the first principal component (PC1) accounted for a maximum of 23.9% of the total variation among genotypes. The second and third major constituents (PC2 and PC3) contributed 21.2% and 16.8%, respectively.

The PC1 variables that were important were panicle length (0.222), filled grain percent (0.523), and grain yield per plant (0.662), indicating that both vegetative and reproductive characteristics contributed to this component (Table 4). The second most important factor was thousand seed weight (0.451), which is weighted by yield contributing traits. Plant height (0.493), days to 50% flowering (0.323), effective tillers per hill (0.174), and spikelets per panicle (0.550) are all related to PC3; both phenological and vegetative characteristics contributed positively and negatively to the component, where **Sanni et al., (2012)** and **Sinha & Mishra, (2013)** was found similar results.

Table 4. Principal components (PCs) for morphological traits of 505 mutant rice line genotypes.

Variables	PC1	PC2	PC3
Eigen values	1.913	1.693	1.342
Percentage of total variation	0.239	0.212	0.168
Cumulative variance %	0.239	0.451	0.619
Plant height (cm)	-0.186	0.322	0.493
Days to 50% flowering (days)	-0.171	-0.499	0.323
Effective tillers per hill (no.)	-0.009	-0.447	0.174
Panicle length (cm)	0.222	0.132	0.221
Spikelets per panicle (no.)	0.343	0.310	0.550
Filled grain percent (%)	0.523	-0.329	-0.270
1000 seed weight (g)	0.240	0.451	-0.387
Yield per plant (g)	0.662	-0.153	0.219

4. Conclusions

The mutant lines were divided into six clusters, with Cluster I containing 171 lines (including parent Ayeyarmin) and Cluster V containing only 9 mutant lines. Some of the mutant lines showed phenotypic divergence from the parent Ayeyarmin and were grouped in different clusters and subgroups, indicating that the mutant lines were genetically distant from each other. Cluster V outperformed the other clusters in terms of traits such as early heading date and semi-dwarf plant types. This revealed that there is a high genetic variability and that selection for superior traits would be effective. In Clusters V and VI, the inter-cluster distances were greater than the intra-cluster distances, indicating that there was more divergence among the genotypes of distant group. As a result, the parents for the hybridization program should be chosen based on the magnitude of genetic distance, the contribution of different characters to total divergence, and the magnitude of cluster means for different character performance with the highest heterosis. It could be suggested that the study be repeated to confirm the mutant traits in this population.

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6. Authors Note

The authors declare that there is no conflict of interest regarding the publication of this article. Authors confirmed that the paper was free of plagiarism.

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