Original Research Article

Divergence studies for ESV, yield and yield related parameters in rice (*Oryza sativa* L.)

ABSTRACT

The present study was carried out in the Kharif season of 2020-21 using a Randomized Complete Block Design (RCBD) with three replications. Forty-two different genotypes of rice were evaluated in this investigation. These genotypes were assessed based on 21 quantitative traits, which includes yield and yield related traits and early seedling vigour related traits.The Mahalanobis D2 statistic was used for characterizing the genotypes.Based on the D2 analysis, the 42 rice genotypes were grouped into seven clusters. Among these clusters, cluster I was the largest, consisting of 22 genotypes. Cluster III exhibited the highest intracluster distance (22.04), while the maximum inter-cluster distance was observed between clusters II and III (49.06), followed by clusters III and VII (45.84). These results highlight the significance of the genotypes present in these clusters for harnessing heterosis and exploiting the desirable traits associated with them.

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Key words: Genetic divergence, Early seedling vigour, Mahalanobis D^2, Rice

INTRODUCTION

Rice (*Oryza sativa* L.) is a crucial staple food for a significant portion of the global population, providing 23% of calories and accounting for approximately 20% of total grain production worldwide (Sharma et al., 2012). It serves as the primary source of income and livelihood for over 100 million households in Asia and Africa (FAO, 2004), earning the nickname "Grain of Life" (FAO, 1966). The global rice cultivation area spans around 167.06 million hectares, producing 782 million tonnes of rice (Food and Agricultural Organization, 2019).

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The global rice cultivation area was about 167.06 million hectares, which produced 782 million tons o
rice (Food and Agriculture Organization, 2019).

In Asia, rice is commonly grown through transplanting in puddled soils, with intermittent flooding, and is considered an upland crop (Singh et al., 2006; Kumar and Ladha, 2011). However, the traditional method of transplanting rice has drawbacks such as water and labor shortages, prompting the exploration of alternative approaches. Direct rice seeding has emerged as a viable option to address the challenges associated with traditional cultivation methods (Farooq et al., 2011; Kumar and Ladha, 2011; Nie et al., 2012). This method is increasingly practiced in many Asian countries, offering benefits such as reduced water and labor requirements, as well as overcoming time and soil-related conflicts, thereby promoting sustainable rice production (Kumar et al., 2008). To optimize crop establishment and productivity in direct-seeded rice (DSR), it is important to select varieties with high germination rates, rapid seedling emergence, and vigorous seedlings. These traits contribute to quick emergence from submerged fields, ensure an adequate crop stand, and suppress weed growth, thereby enhancing the success of direct seeding. Seedling vigor, which is closely linked to seedling development and germination, plays a crucial role in direct-seeded varieties (Diwan et al., 2013).

The genetic diversity among rice genotypes provides ample opportunities for crop improvement. Understanding the genetic diversity within and among closely related rice varieties is essential for effective utilization of genetic resources. It enables genotype monitoring and helps predict genetic gains. Furthermore, quantifying the genetic diversity within and between groups of genotypes is crucial, as crosses between parents with the greatest genetic divergence often exhibit the most favorable response to genetic improvement (Arunachalam, 1981). This approach allows for the attainment of higher heterosis and superior recombinants (Arunachalam, 1981). In light of these considerations, a study was conducted using MahalanobisD2 analysis on 42 rice genotypes to investigate the genetic divergence of twenty-one yield-related traits, yield attributing traits, and traits related to early seedling vigor.

Materials and methods

In Kharif 2020-21, a study was conducted at the wetland farm of S. V. Agricultural College in Tirupati, Andhra Pradesh. The study used a RCB design with three replications to evaluate forty-two different genotypes. Each entry was grown in three rows, each measuring three meters in length and spacing followed was 20 x 15cm between and within the rows. Standard agronomic practices and recommended fertilizer doses were followed for optimal crop growth. The observations on eight yield components, including plant height, panicle length, number of panicles per plant, 1000-grain weight, number of filled grains per panicle, number of grains per panicle, spikelet fertility, and grain yield per plant were recorded. We also recorded the number of days it took for the plants to reach 50% flowering. In addition, eleven components related to early seedling vigor were evaluated, such as germination percentage, germination rate, seedling fresh and dry weight, shoot length, root length, seedling height, root to shoot ratio, and two seedling vigor indices. To analyze the genetic divergence, we used the D2 statistics proposed by Mahalanobis in 1936.

Results and discussion

Significant differences were observed among the genotypes for all the traits according to the analysis of variance. To classify the 42 genotypes of rice, Tocher's method (Rao, 1952) was employed, resulting in seven clusters. The distribution of genotypes within the clusters appeared to be random. Cluster I was the largest, consisting of 22 genotypes, followed by cluster II with 12 genotypes and cluster III with 4 genotypes. Clusters IV, V, VI, and VII each had a single genotype, indicating a high level of heterogeneity among the genotypes. This finding is consistent with previous studies by Mishra et al. (2018), Devi et al. (2020), and Alamir et al. (2020). Table.1 and Fig..1 provide a representation of the distribution of genotypes across the seven clusters.

The average values of intra-cluster and inter-cluster D^2 and D distances were presented in Table 2, and the corresponding cluster diagram is shown in Fig. 2 Intra-cluster

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distances ranged from 0.00 to 22.04. Cluster III exhibited the highest intra-cluster distance (22.04), followed by cluster II (20.20) and cluster I (17.81). Clusters IV, V, VI, and VII had zero intra-cluster distances since they consisted of only one genotype. The maximum inter-cluster distance was observed between cluster II and III (49.06), followed by cluster III and VII (45.84) and cluster II and V (39.21). Conversely, the minimum inter-cluster distance was found between cluster V and VI (21.29), followed by cluster I and IV (23.54). These results align with previous findings by Devi et al. (2015), Chamundeswari (2016), and Bendi et al. (2018).

By employing Mahalanobis's method of clustering based on inter-cluster distances, it was determined that the pairs of clusters II vs III, III vs VIII, II vs V, V vs VII, III vs VI, IV vs VI, III vs V, and VI vs VIII exhibited increasing levels of genetic distances. The computation of intra and inter-cluster D^2 values from the divergence analysis indicated that the inter-cluster distances exceeded the intra-cluster distances, indicating the presence of significant genetic diversity among the accessions.

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Table.3 presents the results of cluster mean for 21 yield-related traits and early seedling vigor attributes in rice. Analysis of the data revealed significant differences between clusters for most of the studied characters. A closer look at the cluster means for different traits demonstrated considerable variations among the clusters (Table.3).

For the trait "days to 50 percent flowering," the cluster means ranged from 79.67 days (Cluster III) to 140.67 days (Cluster VII), with an average of 101.98 days. Plant height cluster means varied from 91.67 cm (Cluster III) to 158.40 cm (Cluster V), with a general mean of 124.10 cm. Clusters II, IV, VII, VI, and V recorded higher values than the general mean. The cluster means for panicle length ranged from 20.74 cm (Cluster IV) to 33.00 cm (Cluster V), with an overall mean of 26.17 cm. Cluster III had the highest number of panicles per plant (14.65), while Cluster IV had the lowest (8.53).

The 1000-grain weight cluster means ranged from 14.19 g (Cluster IV) to 35.70 g (Cluster VI). The number of filled grains per panicle varied from 107.53 (Cluster III) to 326.33 (Cluster II). The number of grains per panicle exhibited an overall mean value of 244.43, with cluster means ranging from 122.39 (Cluster III) to 373.67 (Cluster II). Spikelet fertility varied from 87.04 percent (Cluster II) to 93.39 percent (Cluster VI).

The first count of germination ranged from 83.33 percent (Cluster V) to 97.33 percent (Cluster VI), while the cluster means for the final count of germination were highest in Cluster IV (98.00%) and lowest in Cluster V (88.33%). Clusters IV, VII, and VI were superior in terms of germination rate, exceeding the general mean (97.00), with values distributed between 94.00 (Cluster V) and 99.00 (Cluster VI).

Cluster means for germination index ranged from 26.70 (Cluster VII) to 41.59 (Cluster IV). Seedling fresh weight cluster means ranged from 55.60 mg (Cluster IV) to 92.58 mg (Cluster V). Seedling dry weight had cluster means ranging from 5.86 mg (Cluster IV) to 11.90 mg (Cluster VI). Shoot length varied from 8.33 cm (Cluster VII) to 14.94 cm (Cluster V), with a general mean of 10.54 cm. Root length ranged from 11.13 cm (Cluster IV) to 22.69 cm (Cluster V). Seedling height exhibited an overall mean value of 28.42 cm, with cluster means ranging from 23.14 cm (Cluster II) to 37.63 cm

(Cluster V). Root to shoot ratio was highest in Cluster VI (2.55) and lowest in Cluster IV (1.21).

Cluster means for seedling vigor index-I ranged from 1989.24 (Cluster IV) to 3324.28 (Cluster V). Clusters V and VI were superior in seedling vigor index-II, surpassing the general mean (764.31), with values distributed between 565.89 (Cluster II) and 1165.81 (Cluster VI). The cluster means for grain yield per plant ranged from 18.07 g (Cluster III) to 41.92 g (Cluster VI), with a general mean of 28.45 g. Clusters II, VII, and VI had higher values than the general mean. Overall, there were considerable differences among the clusters for all the studied traits (Table.3).

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Among all the traits analyzed, the number of filled grains per panicle contributed the most (55.40%) to the overall diversity, ranking first in 477 instances. Root length (11.61%) ranked first 100 times, while days to 50 percent flowering (11.50%) ranked first 99 times. 1000-grain weight (8.83%) ranked first 76 times, and germination index (4.53%) ranked first 39 times. The first count of germination (1.74%) ranked first 15 times, followed by grain yield per plant (1.63%) ranking first 14 times, shoot length (1.51%) ranking first 13 times, total grains per panicle (1.28%) ranking first 11 times, and seedling vigor index-II (1.28%) ranking first 11 times. Seedling vigor index-I, panicle length, and the number of panicles per plant contributed 0.35%, 0.23%, and 0.12%, respectively, to the total genetic divergence in decreasing order. The remaining traits, including plant height, spikelet fertility, germination rate, seedling fresh weight, seedling dry weight, seedling height, and root to shoot ratio, had a minimal contribution to the total genetic divergence, suggesting a lack of diversity for these traits in the studied genetic material. This lack of diversity might be attributed to directional selection practices employed by breeders in developing these genotypes. The findings regarding the significant contribution of the number of filled grains per panicle to genetic diversity align with previous studies by Vennila et al. (2011), Bhati et al. (2015), Nagavath et al. (2017)(Table.4 and Fig.2).

Considering the performance of genotypes and the traits that contribute the most to divergence, it is important to consider the improvement of rice based on these factors. The number of filled grains per panicle being the most significant contributor to genetic diversity supports previous research findings.

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Table 1. Clustering composition of 42 rice genotypes based on Tocher's method.

Cluster number	**No. of genotypes**	**Genotypes**
I	22	130C, 425C3, 405C3, 273C2, 488C, 457C2, 81C, 76C2, ND13, 153C1, 46C2, ND44, MDP6, ND60, 28C1, ND42, NAGINA 22, MDP2, 476C3, MD4, MD5, NLR34449
II	12	419-1, 538-3, 150-3, 239-3, 419-3, 187-3, 150-3, 54-3, MTU1121, SM227, 221C3, NDP3
III	4	MDP3, MTU1010, MDP4, IR64
IV	1	BPT5204
V	1	SMB3
VI	1	MTU3626
VII	1	NLR33892

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Table.2. Average intra (diagonal) and inter-cluster distances (D^2 values) for seven clusters of rice genotypes.

Cluster	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI	Cluster VII
Cluster I	317.31 (17.81)	1114.36 (33.38)	692.75 (26.32)	553.61 (23.53)	663.35 (25.76)	645.61 (25.41)	1129.21 (33.60)
Cluster II		408.06 (20.20)	2406.55 (49.06)	976.17 (31.24)	1537.81 (39.21)	1292.00 (35.94)	680.82 (26.09)
Cluster III			485.63 (22.04)	960.94 (31.00)	1252.57 (35.39)	1400.46 (37.42)	2101.14 (45.84)
Cluster IV				0.00 (0.00)	1347.04 (36.70)	1268.62 (35.62)	870.53 (29.50)
Cluster V					0.00 (0.00)	453.10 (21.29)	1412.14 (37.58)
Cluster VI						0.00 (0.00)	1234.54 (35.14)
Cluster VII							0.00 (0.00)

Table 3. Cluster means for yield, yield attributes and early seedling vigour related traits in rice.

Character / Cluster	Days to 50 % flowering	Plant height (cm)	Panicle length (cm)	Number of panicles plant^{-1}	1000-grain weight (g)	Number of filled grains panicle^{-1}	Number of grains panicle^{-1}	Spikelet fertility (%)	First count of germination (%)	Final count of germination (%)	Rate of germination
Cluster I	88.45	105.78	24.67	13.21	22.24	196.29	223.27	87.69	87.95	91.32	96.00
Cluster II	109.06	124.11	26.42	11.69	17.85	326.33	373.67	87.04	84.72	89.14	95.00
Cluster III	79.67	91.67	22.36	14.65	20.19	107.53	122.39	88.10	88.83	91.75	97.00
Cluster IV	107.00	122.33	20.74	8.53	14.19	200.13	219.33	91.26	96.00	98.00	98.00
Cluster V	91.00	158.40	33.00	8.67	26.98	214.56	231.56	92.66	83.33	88.33	94.00
Cluster VI	98.00	139.13	27.00	13.67	35.70	235.11	251.78	93.39	97.33	98.00	99.00
Cluster VII	140.67	127.27	29.00	13.33	19.35	261.56	289.00	90.52	93.33	95.00	98.00
Mean	101.98	124.10	26.17	11.96	22.36	220.22	244.43	90.09	90.21	93.07	97.00

Character Cluster	Germination index	Seedling fresh weight (mg)	Seedling dry weight (mg)	Shoot length (cm)	Root length (cm)	Seedling height (cm)	Root to shoot ratio	Seedling vigour index-I	Seedling vigour index-II	Grain yield plant^{-1} (g)
Cluster I	33.56	66.90	7.73	10.11	16.69	26.80	1.70	2449.47	706.79	27.84
Cluster II	31.57	58.93	6.31	8.42	14.72	23.14	1.76	2073.04	565.89	30.24
Cluster III	34.37	65.80	6.99	9.61	18.41	28.01	1.97	2591.31	648.23	18.07
Cluster IV	41.59	55.60	5.86	9.17	11.13	20.30	1.21	1989.24	573.81	24.55
Cluster V	28.72	92.58	11.12	14.94	22.69	37.63	1.53	3324.28	982.40	25.73
Cluster VI	39.88	86.25	11.90	13.23	20.26	33.49	1.53	3282.23	1165.81	41.92
Cluster VII	26.70	62.71	7.44	8.33	21.22	29.56	2.55	2807.77	707.27	30.77
Mean	33.77	69.82	8.19	10.54	17.87	28.42	1.75	2645.33	764.31	28.45

Table.4. Per cent contribution of various characters towards genetic diversity in 42 genotypes of rice.

Sl. No.	Character	Times Ranked first	Contribution (%)
1.	Days to 50 % flowering	99	11.50
2.	Plant height	0	0.00
3.	Panicle length	2	0.23
4.	Number of panicles plant^{-1}	1	0.12
5.	1000-grain weight	76	8.83
6.	Number of filled grains panicle^{-1}	477	55.40
7.	Number of grains panicle^{-1}	11	1.28
8.	Spikelet fertility	0	0.00
9.	First count of germination	15	1.74
10.	Final count of germination	0	0.00
11.	Rate of germination	0	0.00
12.	Germination index	39	4.53
13.	Seedling fresh weight	0	0.00
14.	Seedling dry weight	0	0.00
15.	Shoot length	13	1.51
16.	Root length	100	11.61
17.	Seedling height	0	0.00
18.	Root to shoot ratio	0	0.00
19.	Seedling Vigour Index-I	11	1.28
20.	Seedling Vigour Index-II	3	0.35
21.	Grain yield plant^{-1}	14	1.63

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2:150(3)	9:BPT5204	16:MDP2	23:28C1	30:273C2	37:IR64
3: (1871)	10:NLR34449	17:MDP3	24:46C2	31:405C3	38:SM227
4:187(3)	11:NDP3	18:MDP4	25:76C2	32:425C3	39:NLR33892
5:239(3)	12:ND13	19:MDP6	26:81C	33:457C2	40:SMB3
6:419(1)	13:ND42	20:MD4	27:130C	34:476C3	41:MTU3626
7:419(3)	14:ND44	21:MD5	28:153C1	35:488C	42:MTU1121

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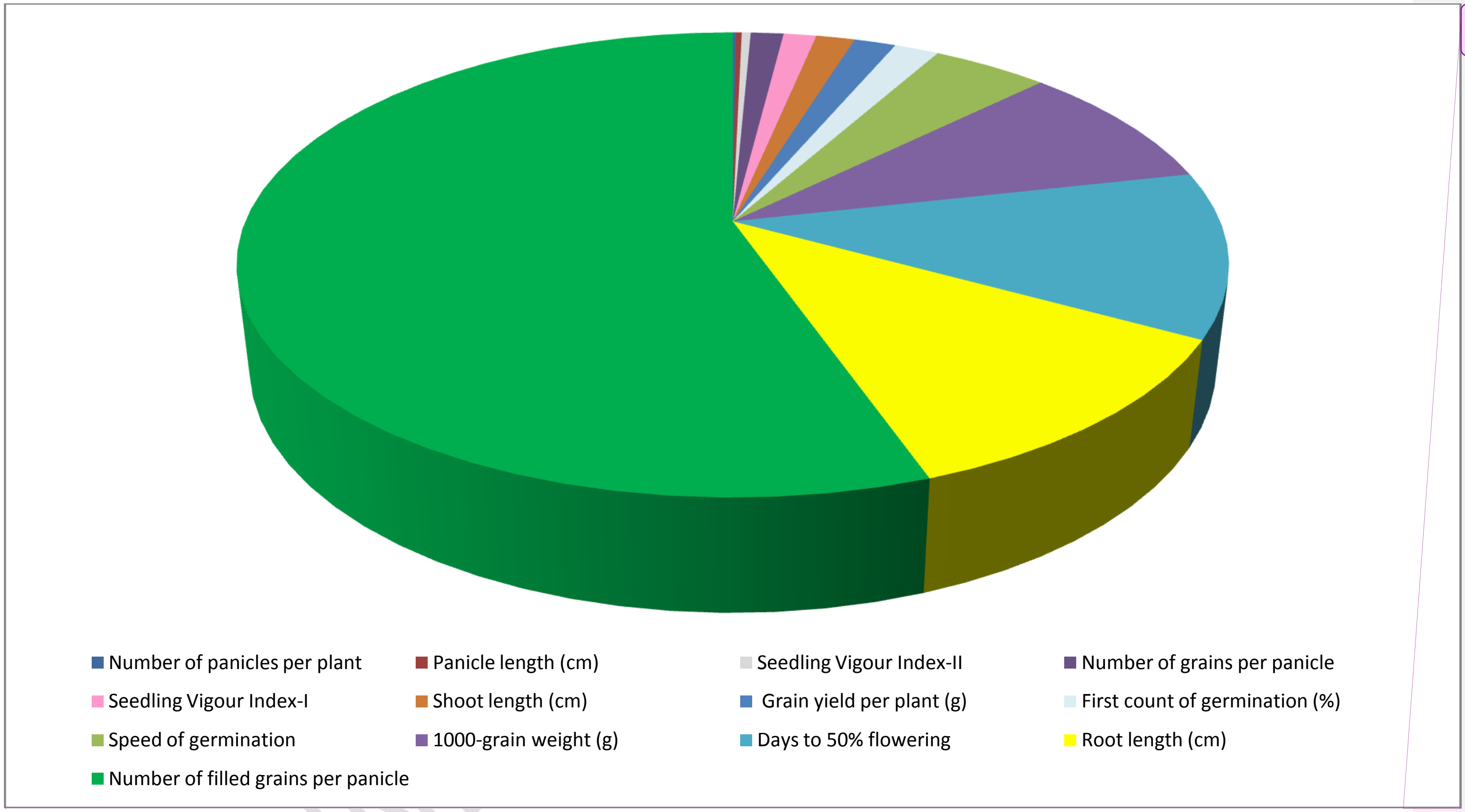

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Fig..2. Relative percentage contribution of 21 characters to total genetic diversity in 42 genotypes of rice.

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