

International Journal of Advanced Biochemistry Research



ISSN Print: 2617-4693
ISSN Online: 2617-4707
NAAS Rating (2026): 5.29
IJABR 2026; SP-10(4): 1109-1113
www.biochemjournal.com
Received: 08-01-2026
Accepted: 13-02-2026

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Genetic variability and multivariate analysis of seedling traits in rice under direct-seeded conditions

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DOI: <https://www.doi.org/10.33545/26174693.2026.v10.i4Sn.8266>

Abstract

The present investigation was undertaken during the *rabi* season at the South Farm of Karunya Institute of Technology and Sciences, Coimbatore, to examine genetic variability and early seedling vigour traits in 108 rice genotypes under direct-seeded conditions. The trial was conducted using a randomized block design with three replications, and ten seedling-related traits were evaluated. The analysis of variance indicated highly significant differences among genotypes for all characters, reflecting substantial variability within the experimental material. Correlation studies revealed that seedling vigour indices had strong positive associations with seedling length, shoot length, and dry weight, highlighting their importance in early establishment. Principal component analysis showed that the first four components explained a major proportion (81.18%) of the total variation. Cluster analysis grouped the genotypes into six distinct clusters, indicating wide genetic diversity. The findings emphasize the importance of seedling vigour traits in selection strategies for improving rice performance under direct-seeded and water-limited production systems.

Keywords: Dry direct-seeded rice, genetic variability, seedling vigour, correlation analysis, principal component analysis, cluster analysis

Introduction

Rice (*Oryza sativa* L.) is a major staple crop that supports food security for a large portion of the global population, particularly in Asia. However, conventional puddled transplanting methods are becoming increasingly unsustainable due to water scarcity, labour shortages, and climate variability. In this context, dry direct-seeded rice (DDSR) has emerged as an efficient alternative production system ^[1], reported that DDSR reduces water use and labour requirements while enabling faster crop establishment. However, its success is largely dependent on efficient seedling establishment, which is often constrained by poor germination and weak early growth under field conditions.

Early seedling vigour is a key trait influencing crop establishment and productivity under DDSR systems, as it promotes rapid germination, early growth, and weed competitiveness. Important seedling traits such as germination percentage, root length, shoot length, and seedling biomass are complex and governed by multiple genetic factors. Studies by ^[2] and ^[3] have reported significant variability and high heritability for these traits, indicating the predominance of additive gene action and the potential for effective selection. Such genetic variability plays a crucial role in identifying superior genotypes for breeding programmes.

Genetic variability is the foundation for crop improvement, as it enables the selection of desirable genotypes with improved performance ^[4] and ^[5] observed substantial variation and genetic advance in early growth traits under direct-seeded conditions. In addition, multivariate statistical techniques such as principal component analysis (PCA) and cluster analysis are useful in understanding the relationships among traits and classifying genotypes based on genetic divergence ^[6] emphasized the effectiveness of these approaches in identifying key traits contributing to variability. However, limited information is available on the genetic variability and interrelationship of seedling traits under direct-seeded conditions. Therefore, the present study was undertaken to assess genetic variability and to analyze seedling traits using multivariate approaches in rice.

Materials and Methods

The present investigation was carried out during the *rabi* season at the South Farm, Karunya Institute of Technology and Sciences, Coimbatore, Tamil Nadu, to assess genetic variability and seedling traits in rice (*Oryza sativa* L.) under direct-seeded conditions. The experimental material consisted of 108 rice genotypes, and the experiment was laid out in a Randomized Block Design (RBD) with three replications to minimize environmental variation. Each genotype was sown under direct-seeded conditions, and observations were recorded on ten randomly selected plants in each replication.

Germination percentage was calculated based on the number of seeds germinated out of the total seeds sown, following standard procedures [7]. Days to first emergence and days to full emergence were recorded as the number of days taken for initial and complete seedling emergence under field conditions. Root and shoot lengths were measured in centimetres at the seedling stage, and seedling length was computed as the sum of root and shoot lengths. The root-to-shoot ratio was calculated by dividing root length by shoot length. Seedling dry weight was recorded after oven drying the sampled seedlings at 70 °C until constant weight. Seedling Vigour Index-I (SVI-I) was calculated as germination percentage multiplied by seedling length, and Seedling Vigour Index-II (SVI-II) was calculated as germination percentage multiplied by seedling dry weight, following [8].

The recorded data were subjected to statistical analysis to determine the significance of variation among genotypes. Analysis of variance (ANOVA) was performed following the method of [9] appropriate for RBD, and the significance of differences among treatments was tested using the F-test at 5% and 1% levels. Genotypic correlation coefficients among seedling traits were estimated according to [10] to assess the degree of association between traits. Principal Component Analysis (PCA) was performed to identify the major traits contributing to total variability and to reduce data dimensionality, considering components with

eigenvalues greater than one as significant [11]. Cluster analysis was carried out using Ward's method based on Euclidean distance, and a dendrogram was constructed to classify genotypes into distinct groups and to assess genetic divergence [12].

Results and Discussion

The analysis of variance revealed highly significant differences among genotypes for all the studied seedling traits under direct-seeded rice conditions, indicating the presence of substantial genetic variability. As presented in (Table 1), the mean sum of squares due to genotypes was highly significant ($p < 0.01$) for germination percentage, emergence traits, root and shoot parameters, and seedling vigour indices. This suggests that the evaluated genotypes possess a wide range of variability that can be effectively exploited in breeding programs. Similar findings were reported by [13], who emphasized that significant genotypic variation under DDSR conditions is essential for selecting superior early vigour traits. The low error variance observed for most traits further confirms the reliability of the experimental results.

Correlation analysis (Table 2) provided insights into the association among seedling traits. Germination percentage showed a strong positive correlation with Seedling Vigour Index-I (0.451***) and a moderate association with SVI-II (0.222*), indicating its importance in determining seedling establishment. Seedling length exhibited a highly significant positive correlation with shoot length (0.925***) and root length (0.517***), suggesting that overall seedling growth is largely influenced by both root and shoot development. Additionally, seedling dry weight showed strong positive correlations with SVI-II (0.948***), highlighting its contribution to seedling vigour. Negative associations of root: shoot ratio with several traits indicate a trade-off between biomass allocation patterns. These results are in agreement with findings of [14], who reported strong interrelationships among seedling vigour traits under direct-seeded conditions.

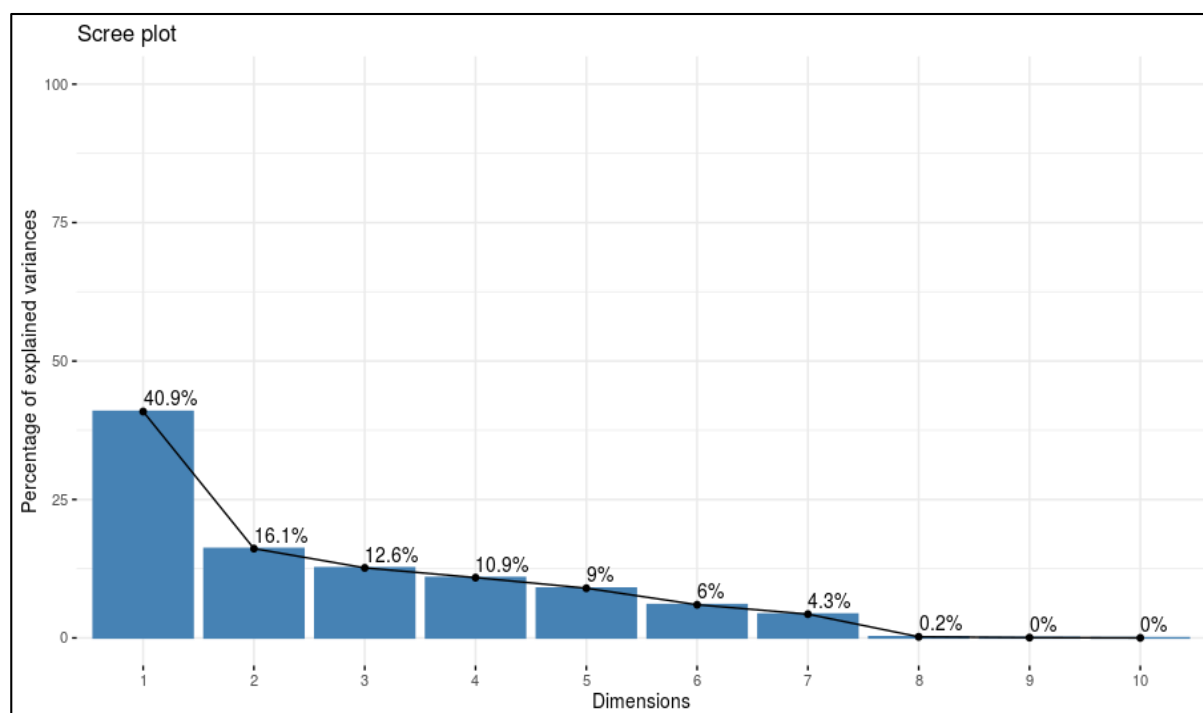


Fig 1: Scree plot under DDSR.

Principal component analysis (Table 3) revealed that the first four principal components accounted for 81.18% of the total variation, indicating that these components sufficiently explain the variability present in the dataset. PC1 alone contributed 40.62% of total variation, followed by PC2 (17.06%), PC3 (12.56%), and PC4 (10.93%). The scree plot illustrated in Figure 1 clearly shows a sharp decline after PC1, confirming that the majority of variation is captured in the first few components. Similar patterns were observed by [15], who suggested that traits contributing to early vigour are often concentrated in the first principal components under stress-prone environments.

The contribution of individual traits to principal components (Table 4) indicated that seedling length (20.81%), SVI-I (20.15%), shoot length (19.9%), and SVI-II (16.25%) were the major contributors to PC1, highlighting their importance in determining overall variability. PC2 was mainly influenced by days to first emergence (38.13%) and days to full emergence (37.94%), indicating the role of emergence traits in differentiating genotypes. Root length (34.97%) contributed significantly to PC3, while root: shoot ratio (22.75%) had a major influence on PC4. These findings suggest that both growth and emergence traits play a crucial role in genotype differentiation, as also reported by [1].

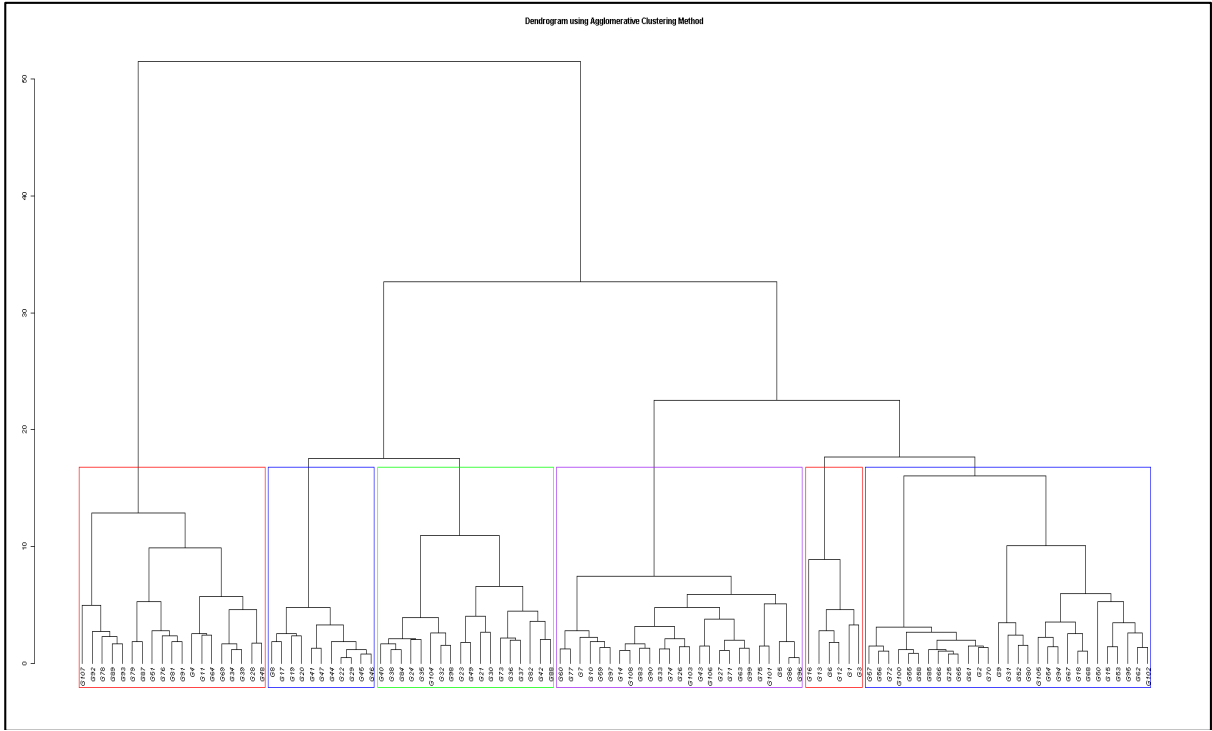


Fig 2: Cluster analysis of all one hundred and eight genotypes of Mahalanobis D¹² under DDSR.

Cluster analysis grouped the 108 genotypes into six distinct clusters (Table 5), indicating the presence of considerable genetic divergence among the studied materials. Cluster II contained the highest number of genotypes [29], followed by Cluster IV [25] and Cluster III [19], while Cluster I had the least (6 genotypes). The dendrogram presented in (Figure 2) clearly illustrates the genetic relationships among genotypes and the formation of distinct clusters. The wide distribution of genotypes across clusters suggests the existence of diverse genetic backgrounds, which can be effectively utilized for hybridization programs. Genotypes belonging to distant clusters are expected to produce higher heterosis and

desirable recombinants. These results are consistent with the findings of [16], who reported that clustering based on seedling traits is effective in identifying genetically diverse parents under DDSR systems. Overall, the study demonstrated that seedling vigour traits such as seedling length, shoot length, and vigour indices are key determinants of variability and selection under direct-seeded conditions. The integration of ANOVA, correlation, PCA, and cluster analysis provided a comprehensive understanding of trait relationships and genetic diversity, which is crucial for improving rice adaptation to water-saving cultivation systems.

Table 2: Correlation analysis for seedling traits under DDSR conditions.

Traits	GP	DFE	DFFE	RL	SL	SL	RSR	SDW	SVI - I	SVI - II
Germination Percentage	1									
Days to first emergence	0.07	1								
Days to full emergence	0.133	0.53***	1							
Root Length	-0.158	-0.047	0.018	1						
Shoot Length	0.009	0.047	0.213*	0.154	1					
Seedling Length	-0.052	0.023	0.191*	0.517***	0.925***	1				
Root: Shoot Ratio	-0.111	-0.073	-0.129	-0.049	-0.207*	-0.198*	1			
Seedling Dry Weight	-0.029	-0.007	0.058	0.131	0.644***	0.608***	-0.066	1		
Seedling Vigour Index - I	0.451***	0.064	0.227*	0.39***	0.823***	0.862***	-0.211*	0.526***	1	
Seedling Vigour Index - II	0.222*	0.028	0.067	0.094	0.617***	0.571***	-0.071	0.948***	0.625***	1

***Significant at 0.01% level, **Significant at 1% level, *Significant at 5% level

Table 3: Eigenvalues, Percentage of variance and Cumulative variance of principal component analysis under DDSR.

Principal Components	Eigen value	Percentage of variance (%)	Cumulative variance
PC1	4.06	40.62	40.62
PC2	1.71	17.06	57.68
PC3	1.26	12.56	70.24
PC4	1.09	10.93	81.18
PC5	0.90	8.98	90.16
PC6	0.60	5.97	96.12
PC7	0.37	3.69	99.81
PC8	0.01	0.14	99.96
PC9	0.005	0.04	100.00
PC10	0.00	0.00	100.00

Table 4: Per cent contribution of variables on the first four PCs.

Variables	PC1	PC2	PC3	PC4
Germination Percentage	0.73	10.76	32.63	24.12
Days to first emergence	0.21	38.13	3.20	10.88
Days to full emergence	1.58	37.94	4.37	3.33
Root Length	3.30	3.35	34.97	8.44
Shoot Length	19.90	0.06	0.21	0.28
Seedling Length	20.81	0.83	7.13	0.42
Root: Shoot Ratio	1.43	4.26	0.56	22.75
Seedling Dry Weight	15.58	3.13	4.34	14.48
Seedling Vigour Index - I	20.15	0.60	0.21	8.76
Seedling Vigour Index - II	16.25	0.89	12.32	6.49

Table 5: Distribution of six clusters under DDSR.

Clusters	Number of genotypes	Member of clusters
Cluster I	6	G1, G3, G6, G12, G13, G16
Cluster II	29	G2, G9, G15, G18, G25, G31, G50, G52, G53, G54, G55, G56, G57, G58, G61, G62, G65, G66, G67, G68, G70, G72, G80, G85, G94, G95, G100, G102, G105
Cluster III	19	G4, G11, G28, G34, G39, G48, G51, G64, G69, G76, G78, G79, G81, G87, G89, G91, G92, G93, G107
Cluster IV	25	G5, G7, G10, G14, G26, G27, G33, G43, G59, G60, G63, G71, G74, G75, G77, G83, G86, G90, G96, G97, G99, G101, G103, G106, G108
Cluster V	11	G8, G17, G19, G20, G22, G29, G41, G44, G45, G46, G47
Cluster VI	18	G21, G23, G24, G30, G32, G35, G36, G37, G38, G40, G42, G49, G73, G82, G84, G88, G98, G104

Conclusion

The results of the study confirmed the existence of considerable genetic variability among rice genotypes for seedling traits under direct-seeded conditions. Traits such as seedling length, shoot length, and vigour indices were identified as important contributors to overall variability and showed strong positive associations, making them effective criteria for selection. The principal component analysis revealed that most of the variability could be explained by a limited number of components, indicating the efficiency of multivariate approaches. Cluster analysis further demonstrated significant genetic divergence among genotypes, suggesting the possibility of selecting diverse parents for hybridization to achieve superior recombinants. Overall, the study highlights the usefulness of integrating statistical tools such as ANOVA, correlation, PCA, and cluster analysis in identifying promising genotypes for breeding programs aimed at improving rice adaptability under direct-seeded conditions.

Acknowledgements

The authors sincerely acknowledge the farmers and agricultural research stations across Tamil Nadu, Kerala, Telangana, and Andhra Pradesh for providing the germplasm materials used in this study.

Competing Interest

The authors confirm that there are no conflicts of interest related to this research work.

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