RESEARCH ARTICLE Indian Journal of Agricultural Research, Volume 60 Issue 11: 1675-1683 (November 2026)

Trait Contributions to Yield in Rice Genotypes: Insights from PCA and Cluster Analysis with Emphasis on Pollen Fertility

R. Mahendran[1], B. Hariharan[1], K. Satheeskumar[2], R. Nagajothi[3], J. Vanitha[1]

10.18805/IJARe.A-6562

ABSTRACT

Background: Rice (*Oryza sativa* L.) productivity is increasingly constrained by climate variability, biotic stresses and limited natural resources, necessitating the effective utilisation of genetically diverse germplasm. Traditional rice landraces possess valuable adaptive, stress-tolerant and yield-related traits; however, their potential remains largely underutilized in breeding programmes.

Methods: The present investigation was conducted during the zaid season of 2025 under field conditions using 130 rice (*Oryza sativa* L.) landraces evaluated in an augmented experimental design. A total of 21 agronomic, physiological and reproductive traits were assessed. Genetic divergence and trait relationships were analysed using principal component analysis (PCA) and hierarchical cluster analysis to identify the major traits contributing to phenotypic variability and yield performance.

Result: Eight principal components with eigenvalues greater than one explained a substantial proportion of the total phenotypic variation. The first two components contributed most of the variability and were primarily associated with plant vigour, reproductive efficiency, biomass accumulation and yield-related traits. Plant height (X_3), flag leaf length (X_4), internode length (X_7), grains per panicle (X_9), 1000-seed weight (X_{10}) and pollen fertility (X_{19}) were the major contributors to genotype differentiation. Cluster analysis grouped the 130 genotypes into four distinct clusters. Groups I, II and IV exhibited high pollen fertility and superior yield performance, whereas Group III showed lower pollen fertility and poor yield traits. PCA biplot analysis further revealed a close association of high-yielding genotypes with pollen fertility, biomass traits and physiological efficiency. Pollen fertility emerged as a key trait influencing genetic divergence and yield performance. The genetically diverse and superior-performing genotypes identified in this study represent valuable resources for rice improvement programmes aimed at enhancing productivity and adaptability.

Key words: Genetic diversity, Pollen fertility, Principal component analysis (PCA), Rice landraces, Yield traits.

INTRODUCTION

Rice (*Oryza sativa* L.) is a crucial food crop for over half of the world's population, especially in Asia, where it carries significant cultural and historical importance. Despite advancements in breeding and crop management, rice productivity faces challenges from climate variability, erratic monsoons, pests, diseases, soil degradation and water scarcity. This situation underscores the need for resilient genetic resources, such as traditional Indian rice landraces-Karuppu Kavuni, Mappillai Samba, Poongar, Kattuyanam and Seeraga Samba which offer unique traits like drought tolerance, pest resistance and improved nutritional quality (Shoba *et al.,* 2021).

The potential of these landraces is often underutilized in breeding programs due to a lack of systematic characterization. Understanding genetic variability and traits associated with yield and adaptability is essential for effective utilization. Modern breeding strategies focus on integrating morphological, physiological and agronomic traits to enhance productivity and stress resilience (Ramesh *et al.,* 2023). Among these, reproductive traits, particularly pollen fertility, are crucial for successful fertilization and yield stability (Reddy *et al.,* 2021). Identifying genotypes with high pollen fertility is vital for improving hybrid seed production and yield reliability. Principal component analysis (PCA) is a valuable tool for assessing genetic diversity and trait relationships in crop germplasm, aiding in the selection of superior parental lines (Naik *et al.,* 2021). This study aimed to analyse genetic divergence among 130 rice genotypes based on agronomic, physiological and reproductive traits, with a focus on pollen fertility, to identify elite genotypes for yield improvement and climate-resilient breeding programs.

[1]Department of Genetics and Plant Breeding, SRM College of Agricultural Sciences, SRM Institute of Science and Technology, Chengalpattu-603 201, Tamil Nadu, India.

[2]Department of Basic Sciences, SRM College of Agricultural Sciences, SRM Institute of Science and Technology, Chengalpattu-603 201, Tamil Nadu, India.

[3]Section of Biochemistry and Crop Physiology, SRM College of Agricultural Sciences, SRM Institute of Science and Technology, Chengalpattu-603 201, Tamil Nadu, India.

Corresponding Author: B. Hariharan, Department of Genetics and Plant Breeding, SRM College of Agricultural Sciences, SRM Institute of Science and Technology, Chengalpattu-603 201, Tamil Nadu, India. Email: hb0296@srmist.edu.in

How to cite this article: Mahendran, R., Hariharan, B. Satheeskumar, K., Nagajothi, R. and Vanitha, J. (2026). Trait Contributions to Yield in Rice Genotypes: Insights from PCA and Cluster Analysis with Emphasis on Pollen Fertility. *Indian Journal of Agricultural Research.* **60(11):** 1675-1683. doi: 10.18805/IJARe.A-6562.

Submitted: 20-04-2026 **Accepted:** 16-06-2026 **Online:** 17-07-2026

MATERIALS AND METHODS

Field layout and replication structure

The experiment used an augmented design with two replications, evaluating 130 rice landraces and three standard check varieties. Planted in an augmented layout to reduce environmental variation, each genotype was spaced 60 × 30 cm.

Environmental conditions (season, location and soil type)

The study took place in the zaid season of 2025 at SRM College of Agricultural Sciences, experimental farm, located at 12.37977°N latitude and 79.732154°E longitude. The region has a tropical climate with warm temperatures and the soil is sandy clay loam, offering good drainage and moderate fertility.

Origin of the landraces

The 130 rice landraces studied were collected from various rice-growing regions, showcasing diverse traditional germplasm adapted to different agro-climatic conditions and exhibiting significant variability in morphological, physiological and yield-related traits.

Criteria for landrace selection

The rice landraces were chosen for their genetic diversity, adaptability to different agro-climatic conditions, unique agro-morphological traits and potential benefits for breeding programs aimed at yield improvement, stress tolerance and grain quality.

Traits studied and data recording

Observations were recorded on five randomly selected plants from each genotype for 21 agronomic, physiological and reproductive traits. Data were collected at appropriate growth and reproductive stages following standard evaluation procedures. The traits studied were: number of days to 50% flowering (X_1), number of days to maturity (X_2), plant height at maturity (X_3), flag leaf length (X_4), leaf width (X_5), panicle length (X_6), internode length (X_7), number of productive tillers per plant (X_8), number of grains per panicle (X_9), 1000-seed weight (X_{10}), fresh root length (X_{11}), fresh root weight (X_{12}), fresh shoot weight (X_{13}), dry root weight (X_{14}), dry shoot weight (X_{15}), SPAD reading value (X_{16}), total chlorophyll content (X_{17}), leaf area coverage (X_{18}), pollen fertility (X_{19}), flag leaf number (X_{20}) and single plant yield (X_{21}). All physiological traits, including SPAD chlorophyll content, DMSO chlorophyll content, leaf area index (LAI) and photosynthetic vigour, were measured at the tillering stage of crop growth. All observations were recorded on a per-plant basis and mean values were used for subsequent statistical analyses.

Pollen fertility assessment

Pollen viability was assessed using the iodine-potassium iodide (I_2-KI) staining method. In this test, pollen viability and starch content were determined based on staining intensity. The staining solution was prepared by dissolving 1 g potassium iodide and 0.5 g iodine in distilled water and making the final volume up to 100 ml. One or two drops of the stain were placed on a microscopic slide containing pollen grains and mixed thoroughly. After covering with a cover slip, observations were recorded after 5-10 min under a microscope. Darkly stained pollen grains were considered viable, whereas lightly stained or unstained pollen grains were considered non-viable. The percentage of pollen viability was calculated using the standard formula.

Statistical analysis

Mean values of 21 traits were calculated for all 130 rice genotypes and standardized before multivariate analysis to minimize scale differences. Genetic diversity was assessed using principal component analysis (PCA) and components with eigen values >1 were retained according to the Kaiser criterion. Eigen values, percentage variance, cumulative variance and trait loadings were examined to identify major sources of genetic variation. Scree plots and PCA biplots were used to visualize component contributions and genotype-trait relationships.

Hierarchical cluster analysis was performed using Euclidean distance and Ward's method to group genotypes based on trait similarity. Cluster formation and within- and between-group distances were used to assess genetic divergence. All analyses were conducted in RStudio. Cluster validity was assessed using the cophenetic correlation coefficient, which compared Euclidean and cophenetic distance matrices. Silhouette analysis was also performed to evaluate cluster consistency and separation among genotypes.

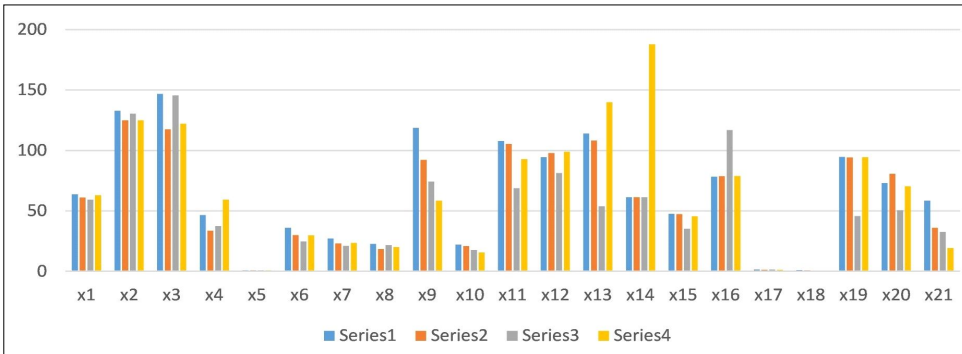
RESULTS AND DISCUSSION

Principal component analysis (PCA) of 21 traits in 130 rice (*Oryza sativa* L.) landraces identified eight principal components with eigenvalues >1, explaining 71.10% of total phenotypic variation, indicating substantial genetic diversity (Table 1). PC1 explained 16.16% of the variation and was mainly associated with plant height at maturity (X_3), flag leaf length (X_4), panicle length (X_6), internode length (X_7), number of productive tillers (X_8), fresh root weight (X_{12}), fresh shoot weight (X_{13}), pollen fertility (X_{19}) and single plant yield (X_{21}). These results suggest that plant architecture, biomass accumulation and reproductive efficiency are major determinants of yield variability, consistent with Anderson (1972); Rahangdale *et al.* (2021); Chandraker *et al.* (2024) and Khatun *et al.* (2023); Aisya *et al.* (2026).

PC2 accounted for 13.21% of the variation and was largely influenced by biomass-related traits, plant height (X_3) and pollen fertility (X_{19}), indicating the importance of biomass production and physiological efficiency. PC3 explained 10.34% of the variation and was associated with days to 50% flowering (X_1), days to maturity (X_2), grains per panicle (X_9), 1000-seed weight (X_{10}), leaf area coverage (X_{18}) and single plant yield (X_{21}), highlighting the role of source-sink relationships in productivity.

Similar observations were reported by Gunasekaran *et al.* (2017); Choudhary *et al.* (2022); Kumar *et al.* (2026) and Kim *et al.* (2024) (Fig 1). The remaining PCs contributed smaller proportions, confirming that yield, biomass and reproductive traits were the major contributors to genetic divergence.

UPGMA cluster analysis based on Euclidean distance grouped the 130 landraces into four clusters (Table 2; Fig 2), confirming substantial diversity, as also reported by Singh *et al.* (2020); Sahu *et al.* (2021); Swarup *et al.* (2021) and Sinha *et al.* (2023) and Islam *et al.* (2020); Kumar *et al.* (2026). Cluster I exhibited superior performance for yield-related traits, including plant height (X_3), panicle length (X_6), productive tillers (X_8), grains per panicle (X_9), single plant yield (X_{21}) and pollen fertility (X_{19}), indicating high yield potential. Cluster II showed moderate but stable



X_1: Number of days to 50% flowering, X_2: Number of days to maturity, X_3: Plant height at maturity, X_4: Flag leaf length, X_5: Leaf width, X_6: Panicle length, X_7: Internode length, X_8: Number of productive tillers per plant, X_9: Number of grains per panicle, X_{10}: 1000-seed weight, X_{11}: Fresh root length, X_{12}: Fresh root weight, X_{13}: Fresh shoot weight, X_{14}: Dry root weight, X_{15}: Dry shoot weight, X_{16}: SPAD reading value, X_{17}: Total chlorophyll content, X_{18}: Leaf area coverage, X_{19}: Pollen fertility, X_{20}: Flag leaf number and X_{21}: single plant yield.

Fig 1: Assessment of group means for yield and associated traits in 130 rice genotypes.

Table 1: PCA loading table.

Component	Dim 1	Dim 2	Dim 3	Dim 4	Dim 5	Dim 6	Dim 7	Dim 8
Eigen value	3.39	2.77	2.17	1.71	1.43	1.29	1.11	1.06
Variance (%)	16.16	13.21	10.34	8.12	6.81	6.13	5.29	5.04
Cumulative (%)	16.16	29.37	39.71	47.83	60.76	60.76	66.06	71.10
X_1	0.25	0.03	0.66	0.64	-0.14	0.02	-0.01	0.00
X_2	0.22	-0.06	0.70	0.62	-0.06	-0.02	-0.05	-0.02
X_3	0.47	-0.62	-0.21	0.15	0.16	-0.05	0.12	-0.03
X_4	0.52	-0.49	-0.18	0.21	0.16	-0.12	0.23	0.03
X_5	0.12	-0.27	0.09	-0.01	0.57	-0.46	0.34	-0.06
X_6	0.68	-0.34	-0.33	0.10	-0.42	-0.04	-0.04	-0.03
X_7	0.67	-0.38	-0.24	0.00	-0.46	-0.06	-0.16	0.03
X_8	0.46	-0.34	-0.05	-0.22	0.30	0.14	-0.33	-0.23
X_9	0.26	-0.04	0.58	-0.43	0.18	-0.30	-0.22	0.20
X_{10}	0.28	0.01	0.31	-0.23	-0.18	0.54	0.25	0.20
X_{11}	0.42	0.32	-0.06	-0.08	0.11	-0.16	0.12	-0.44
X_{12}	0.35	0.53	-0.18	0.20	0.12	-0.03	0.03	0.01
X_{13}	0.54	0.59	-0.17	0.13	0.23	0.00	-0.08	0.22
X_{14}	-0.03	0.01	-0.17	0.27	0.19	-0.18	-0.15	0.56
X_{15}	0.52	0.71	-0.08	0.03	0.17	0.00	0.06	0.03
X_{16}	-0.14	-0.21	0.08	0.26	0.41	0.49	-0.02	-0.40
X_{17}	0.13	-0.13	-0.02	-0.10	0.06	0.29	0.69	0.30
X_{18}	0.30	0.24	0.28	-0.24	-0.17	0.04	0.18	-0.19
X_{19}	0.49	0.50	-0.20	0.03	0.04	0.21	-0.08	-0.08
X_{20}	0.09	0.22	0.29	-0.20	-0.35	-0.44	0.29	-0.21
X_{21}	0.54	-0.23	0.50	-0.48	0.19	0.16	-0.21	0.16

Table 2: Cluster mean trait table.

Groups	DFF	DM	PH (cm)	flL (cm)	LW (cm)	PL (cm)	IL (cm)	NPT plant^{-1}	NGP	TGW (g)	RL (cm)	FRW (g)	FSW (g)	DRW (g)	DWS (g)	SPAD	DMSO	LAI %	PV	NFL (cm)	SPY (g)
1	63.70	132.90	146.70	46.50	1.00	36.10	27.20	22.70	118.70	22.10	107.70	94.50	114.00	61.30	47.50	78.20	1.50	1.10	94.70	73.00	58.50
2	61.20	125.00	117.40	33.60	0.90	30.00	23.20	18.50	92.20	21.00	105.30	97.80	108.10	61.30	47.40	78.60	1.40	1.00	94.20	80.80	36.10
3	59.20	130.40	145.60	37.50	1.00	24.70	21.20	21.70	74.30	17.70	68.70	81.30	53.90	61.30	35.30	116.80	1.50	0.80	45.70	50.70	32.70
4	63.00	125.00	122.10	59.20	0.90	29.80	23.60	20.00	58.50	15.60	92.87	99.00	140.00	187.90	45.50	78.90	1.30	0.80	94.50	70.50	19.30

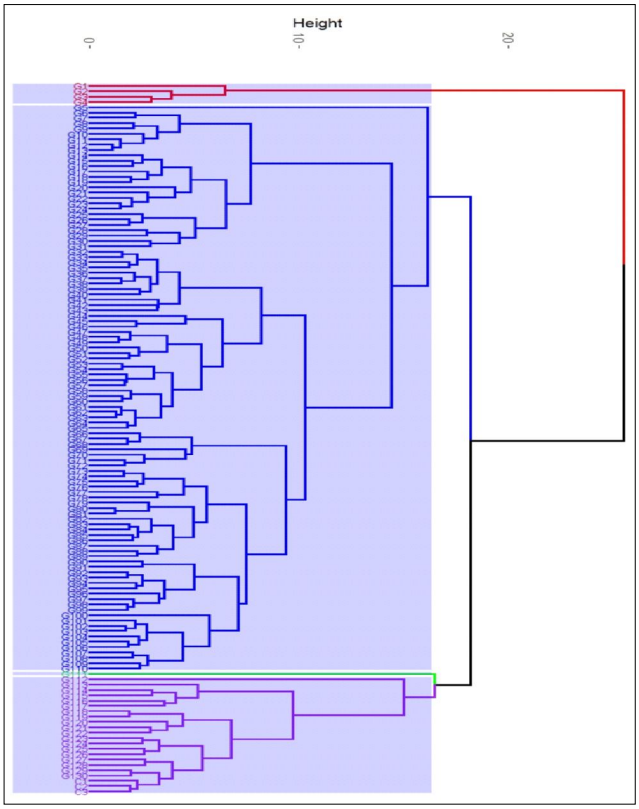


Fig 2: Cluster dendrogram.

performance, whereas Cluster III recorded lower yield traits and pollen fertility, reflecting poor reproductive efficiency. Cluster IV exhibited greater biomass accumulation through fresh and dry shoot weight (X_{13} and X_{15}), although this was not accompanied by higher grain yield. Similar relationships were reported by Sheela *et al.* (2020); Lakshmi *et al.* (2022); Kumar *et al.* (2021); Thakur and Sarma (2023) and Krishna *et al.* (2022).

Inter-cluster distance analysis revealed maximum divergence between Cluster III and Cluster IV, followed by Cluster I and Cluster IV, suggesting greater scope for genetic recombination through hybridization. Minimum divergence occurred between Cluster I and Cluster II, indicating close genetic similarity, in agreement with Singh *et al.* (2020) and Sinha *et al.* (2023).

The PCA biplot clearly separated high- and low-performing genotypes based on trait associations (Fig 3). Traits such as pollen fertility (X_{19}), fresh root weight (X_{12}), fresh shoot weight (X_{13}), panicle length (X_6), internode length (X_7), productive tillers (X_8) and single plant yield (X_{21}) showed longer vectors, indicating greater contributions to variability. Similar interpretations were reported by Christina *et al.* (2021), Khaire *et al.* (2022) and Choudhary *et al.* (2022). Trait contribution analysis identified single plant yield (X_{21}), productive tillers (X_8), flag leaf length (X_4) and leaf width (X_5) as major contributors to genetic divergence and useful selection criteria for yield improvement, whereas days to flowering (X_1) and maturity (X_2) contributed less to

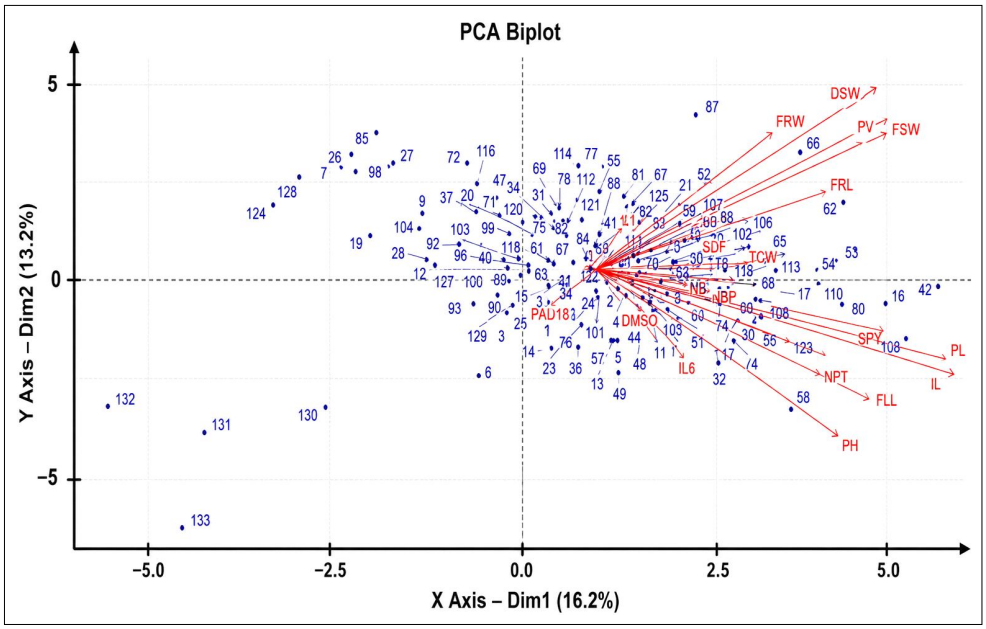


Fig 3: PCA biplot.

divergence (Table 3), as also reported by Manoj *et al.* (2022), Satyanarayana *et al.* (2023) and Madhukumar *et al.* (2023); Balachandran *et al.* (2026).

Pollen fertility (X_{19}) showed a strong positive association with yield-related traits and significantly influenced PCA clustering patterns, highlighting its importance in grain setting and reproductive success. It serves as an important indirect selection criterion for improving rice grain yield, as reported by Reddy *et al.* (2021) and Kim *et al.* (2024). The scree plot showed a gradual decline in variance contribution across principal components, with PC1, PC2 and PC3 accounting for 16.2%, 13.2% and 10.3% of total variation, respectively, while PC4-PC6 contributed smaller proportions (Fig 4). Similar patterns were reported by Pokhrel *et al.* (2020); Chandraker *et al.* (2024) and Khatun *et al.* (2023).

Cluster I exhibited superior yield traits, productive tillers (X_8), panicle length (X_6) and high pollen fertility (X_{19}), indicating high yield potential. Cluster IV showed greater biomass accumulation through higher fresh and dry shoot weight (X_{13} and X_{15}), suggesting stronger vegetative vigor and adaptability. Cluster III had lower pollen fertility and poor yield performance, indicating reduced reproductive efficiency. Similar relationships between physiological traits, reproductive efficiency and adaptability were reported by Lakshmi *et al.* (2022); Kim *et al.* (2024) and Krishna *et al.* (2022).

The study identified genetically diverse landraces and key yield-related traits useful for rice breeding. Hybridization between Cluster III × Cluster IV and Cluster I × Cluster IV may effectively exploit heterosis, as suggested by Singh *et al.* (2020); Sahu *et al.* (2021) and Sinha *et al.* (2023). Productive tillers (X_8), panicle length (X_6), grains per panicle (X_9), single plant yield (X_{21}) and pollen fertility (X_{19}) were identified as important selection traits, while flag leaf length (X_4), leaf width (X_5) and biomass-related traits (X_{12} -X_{15}) may also contribute to improvement.

Table 3: Relative contribution of individual traits towards divergence among rice genotypes.

Characters	Contribution	Characters	Contribution
X_{21}	5.77	X_{16}	4.7
X_3	5.53	X_{11}	4.66
X_{10}	5.28	X_{17}	4.43
X_{18}	5.24	X_5	4.41
X_4	5.10	X_7	4.32
X_9	5.07	X_{13}	4.25
X_6	5.05	X_2	4.2
X_{20}	5.01	X_{15}	4.2
X_5	4.96	X_1	4.16
X_{12}	4.93	X_{14}	3.96
X_8	4.79	X_{19}	3.77

Cluster mean analysis revealed substantial variation among clusters. Cluster I recorded higher values for plant height, panicle length, productive tillers, grains per panicle, pollen fertility and single plant yield, making it a valuable high-yielding parental source. Cluster IV exhibited greater biomass accumulation, whereas Cluster III showed lower pollen fertility and grain yield but greater genetic divergence.

Maximum inter-cluster divergence was observed between Cluster III and Cluster IV and between Cluster I and Cluster IV (Table 4), suggesting good potential for heterosis breeding. Cluster I × Cluster IV crosses may combine superior yield with high biomass, while Cluster III × Cluster IV crosses may generate diverse segregants.

Similar findings were reported by Singh *et al.* (2020), Sahu *et al.* (2021) and Swarup *et al.* (2021). Traits such as productive tillers (X_8), panicle length (X_6), grains per panicle (X_9), pollen fertility (X_{19}) and single plant yield (X_{21}) can serve as effective selection criteria, while biomass-related traits may contribute to adaptation and stress resilience (Fig 5).

Multiple linear regression analysis revealed a strong association between the studied traits and grain yield (R = 0.955), with the model explaining 91.1% of total variation (R^2 = 0.911). The adjusted R^2 value (0.896) and low standard error (8.25) confirmed model reliability (Table 5), consistent with findings of Gunasekaran *et al.* (2017) and Sudeepthi *et al.* (2017).

Regression analysis identified number of productive tillers per plant (NPT), number of grains per panicle (NGP) and thousand-grain weight (TGW) as the most influential

Table 4: Assessment of Within-group distance and between-group distance divergence among four groups in 130 rice genotypes.

Groups	Group I	Group II	Group III	Group IV
Group I	5.90			
Group II	2.64	5.21		
Group III	7.43	7.15	7.90	
Group IV	12.18	12.07	13.69	1.85

Table 5: Regression model summary.

Regression model summary				
Model	R	R Square	Adjusted R Square	Std. error of the estimate
1	.955[a]	.911	.896	8.245544208517712

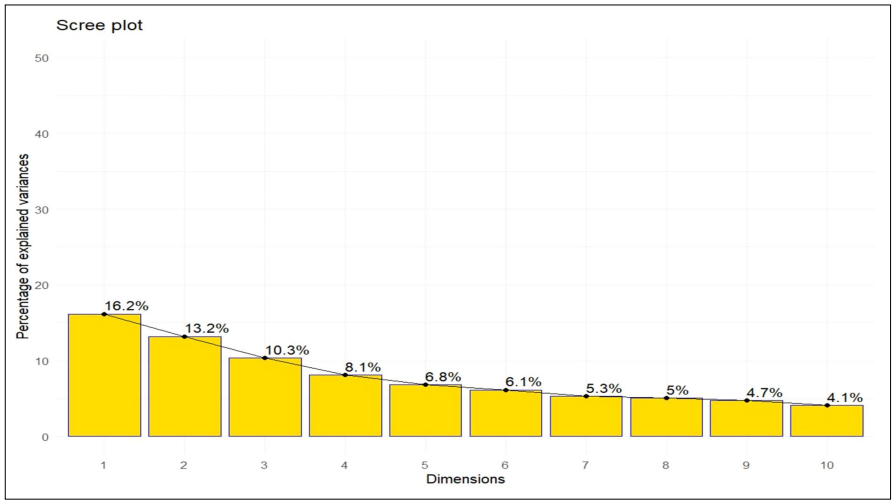


Fig 4: PCA Scree plot.

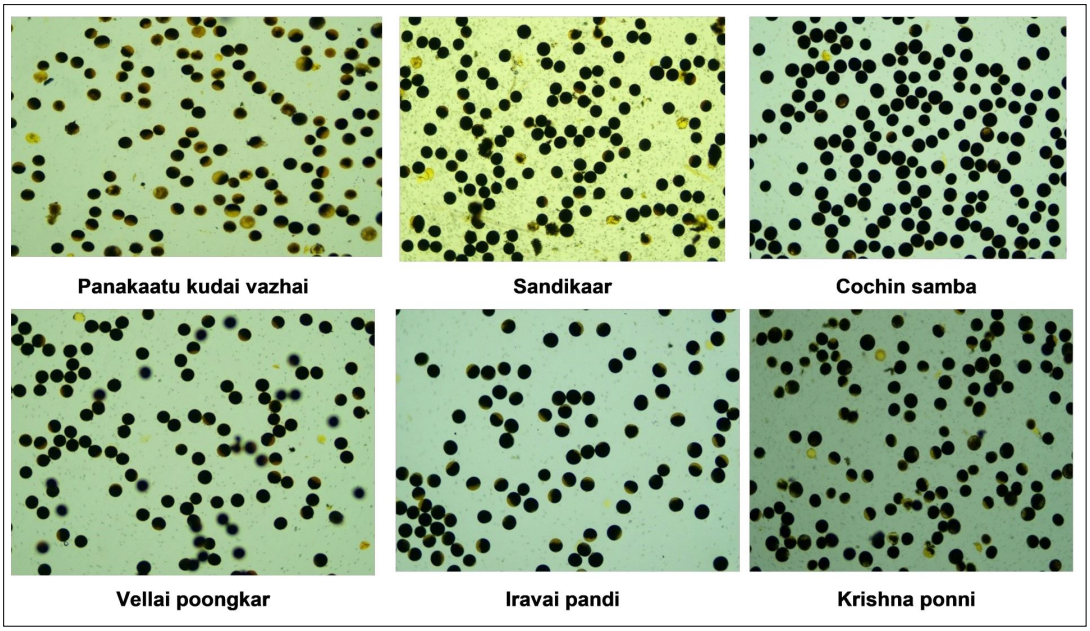


Fig 5: Pollen fertility of different rice germplasm lines.

Table 6: Regression coefficients.

Regression coefficients						
Model		Unstandardized coefficients		Standardized coefficients	t	Sig.
		B	Std. Error	Beta		
1	(Constant)	-76.267	16.434		-4.641	.000
	DFF	.133	.187	.050	.712	.478
	DM	-.050	.105	-.034	-.477	.634
	PH	.071	.043	.069	1.657	.100
	FLL	-.003	.082	-.001	-.034	.973
	LW	-6.128	4.748	-.043	-1.291	.199
	PL	.077	.222	.023	.347	.729
	IL	-.253	.342	-.049	-.739	.461
	NPT	2.093	.132	.511	15.913	.000
	NGP	.427	.022	.630	19.228	.000
	TGW	2.294	.147	.472	15.591	.000
	FRL	-.117	.063	-.061	-1.867	.065
	FRW	-.003	.101	-.001	-.033	.974
	FSW	.083	.064	.067	1.293	.199
	DRW	.020	.071	.008	.278	.782
	DSW	-.225	.346	-.036	-.650	.517
	SPAD	-.012	.060	-.006	-.200	.842
	DMSO	.502	3.387	.004	.148	.882
	LAI	-4.911	4.719	-.033	-1.041	.300
	PV	-.015	.051	-.011	-.291	.771
	NFL	.060	.055	.037	1.081	.282

traits affecting grain yield. These traits showed highly significant positive effects (P<0.001); agreeing with Pandya and Sarial (2015); Singh *et al.* (2020) and Singh *et al.* (2023). NGP had the highest standardized coefficient (β = 0.630), followed by NPT (β = 0.511) and TGW (β = 0.472) (Table 6) indicating that grain number per panicle was the strongest determinant of yield. Similar observations were reported by Jan *et al.* (2017); Adhikari *et al.* (2018). In contrast, the remaining agronomic, physiological and growth traits did not show significant direct regression effects on grain yield, although some may contribute indirectly, supporting earlier reports by Gunasekaran *et al.* (2017) and Pandya and Sarial (2015).

CONCLUSION

The present study revealed substantial genetic diversity among 130 rice genotypes based on PCA and cluster analysis of agronomic, physiological and reproductive traits. Yield-related, plant architectural and physiological traits were the major contributors to phenotypic variability. Pollen fertility emerged as a key reproductive trait influencing genetic divergence and yield performance. Genotypes with high pollen fertility exhibited superior yield-related traits, whereas reduced pollen fertility was associated with poor grain formation and lower productivity. The clear separation of genotypes based on pollen fertility (X_{19}) highlights its value as a reliable selection criterion in rice breeding programmes.

The wide between-group distances among clusters indicated the presence of genetically diverse parental lines suitable for hybridization and heterosis breeding. The identified high-performing and divergent genotypes constitute valuable genetic resources for rice improvement. These findings emphasize the conservation and utilization of diverse germplasm and the inclusion of reproductive traits, particularly pollen fertility, in breeding programmes for sustainable rice production. The regression model showed high predictive ability, with productive tillers per plant, grains per panicle and thousand-grain weight identified as the most influential traits affecting the dependent variable. These traits can serve as reliable selection criteria for improving selection efficiency and yield potential.

Description of the 130 rice genotypes included in the present study

The experimental material consisted of 130 rice (*Oryza sativa* L.) genotypes and three check varieties. The genotypes included G1 (Kattu samba), G2 (Thanga samba), G3 (Sempalai), G4 (Ottu kitchili), G5 (Panakaatu kudai vazhai), G6 (Sandikaar), G7 (Pisini), G8 (Burma kavuni), G9 (Thavalai kanna matta), G10 (Ona matten), G11 (Paal kudai vazhai), G12 (Poongar), G13 (Mappilai samba), G14 (Kadai kazuthaan), G15 (Cochin samba), G16 (Samba mosanam), G17 (Neelan samba), G18 (Varappu kudainchan), G19 (Jil jeera), G20 (Pachai perumal), G21 (Sona mansoori), G22 (Thirunelveli kichili), G23 (Vaasansi

seeraga samba), G24 (Kullakkar), G25 (Karundan samba), G26 (Karupu varma kavuni), G27 (Sengini), G28 (Iluppaipoo samba), G29 (Jil jil vaigunda), G30 (Thenkai poo samba), G31 (Selam sanna), G32 (Kandasala), G33 (Swarna masoori), G34 (ADT 39), G35 (Orissa vasanai seeraga samba), G36 (Kichili samba), G37 (Kulla kar), G38 (Kandasali), G39 (Kumsala), G40 (Navara), G41 (Kumpalai), G42 (Chengalpattu sirumani), G43 (Chithirai kar), G44 (Ottadai), G45 (Vellai kuruvikar), G46 (Adukku nel), G47 (Vellai poongkar), G48 (Arubatham kuruvai), G49 (Kuththarisi), G50 (Raja mudi), G51 (Kuruvai kalanjiyam), G52 (Karunjeeraga samba), G53 (Payan kundathan), G54 (Vaikunda), G55 (Kaivara samba), G56 (Sivappu kuruvikar), G57 (Kottara samba), G58 (Konakkuruvai), G59 (Mullan kaima), G60 (Sivappu sirumani), G61 (Rasakadam), G62 (Katta samba), G63 (Thulasi vasana seeraga samba), G64 (Melaku seeraga samba), G65 (Swarna masuri), G66 (Sorna kuruvai), G67 (Selam samba), G68 (Vellai milaku samba), G69 (Puzhuthi kar), G70 (Kotha malli samba), G71 (TKM13), G72 (Karun kuruvai), G73 (Mathimuni), G74 (Arcot kichili), G75 (Muttakkar), G76 (Poli nel), G77 (Pillai milagu samba), G78 (Iravai pandi), G79 (Raja manna), G80 (Norungan), G81 (Arikiravi), G82 (Kannaki nel), G83 (Kattu yanam), G84 (Chettinad karuppu kavuni), G85 (Sempini panni), G86 (Saagar), G87 (Kaala satta), G88 (Sempalai TKM), G89 (Aathur kichili), G90 (Poda peru nel), G91 (Thuya malli), G92 (Kattu ponni), G93 (Kanthasaari), G94 (Poonvan samba), G95 (Kalamanaku), G96 (Krishna ponni), G97 (Kollikar), G98 (Mysormalli), G99 (Chinnar), G100 (Kalabhat), G101 (Puzhuthi samba), G102 (Semputhi samba), G103 (Aanai komban), G104 (Kuruvai), G105 (Kallundai samba), G106 (Ottaiyan), G107 (Paiyur 1), G108 (Mani samba), G109 (Velan nel), G110 (Karuni Nel), G111 (MTU-1156), G112 (GEB-24), G113 (Karukaruvai samba), G114 (Seerga samba), G115 (Vadan samba), G116 (Thengai poo samba), G117 (Shivan samba), G118 (Kattu vaniban), G119 (Mozhikarruppu samba), G120 (Nattu basmati), G121 (Kudai vazhai), G122 (BPT 5204), G123 (Mutrina sannam), G124 (Kallu valai), G125 (NLR3354), G126 (Guna parva), G127 (Sinigar), G128 (Sabari), G129 (Jaya) and G130 (TPS-5). The check varieties used were Check-1 (CO-51), Check-2 (ADT-43) and Check-3 (CO-55).

ACKNOWLEDGEMENT

The authors gratefully acknowledge the facilities and support provided by SRM College of Agricultural Sciences, SRM Institute of Science and Technology, Baburayanpettai, Chengalpattu, Tamil Nadu, India, for conducting this research.

Disclaimer

The views expressed in this manuscript are those of the authors and do not necessarily reflect those of their affiliated institutions.

Conflict of interest

The authors declare that there are no conflicts of interest.

REFERENCES

Adhikari, B.N., Joshi, B.P., Shrestha, J. and Bhatta, N.R. (2018). Genetic variability, heritability, genetic advance and correlation among yield and yield components of rice (*Oryza sativa* L.). *Journal of Agriculture and Natural Resources*. **1(1):** 149-160.

Aisya, A.W., Ambarwati, E., Supriyanta, Alam, T., Kirana, R.P., Arsana, I.G.K.D., Aristya, V.E., Purba, A.E. and Taryono. (2026). Estimation of the genetic parameters associated with high-yielding and early harvesting in rice. *Indian Journal of Agricultural Research.* **60(3):** 331-338. doi: 10.18805/IJARe.AF-993.

Anderson, T.W. (1972). An Introduction to Multivariate Statistical Analysis. Wiley, New York.

Balachandran Arya, Lovely, B. and Visveswaran, S. (2026). Uniqueness of traditional rice cultivars of Kerala revealed by diversity analysis. *Indian Journal of Agricultural Research*. **60(3):** 346-352. doi: 10.18805/IJARe.A-6422.

Chandraker, P., Verulkar, S.B., Chandel, G. and Sharma, D. (2024). Multivariate analyses for identifying promising rice genotypes for yield and adaptability. *Journal of Crop Improvement*. **38(2):** 175-192.

Choudhary, M., Singh, A.K., Kumari, P. and Jaiswal, J.P. (2022). Genetic diversity and trait association analysis in rice using multivariate approaches. *Physiology and Molecular Biology of Plants*. **28(6):** 1259-1270.

Christina, A.J., Ramesh, M., Kumar, S. and Prakash, M. (2021). Multivariate analysis for genetic diversity in rice (*Oryza sativa* L.) under stress environments. *Electronic Journal of Plant Breeding*. **12:** 1046-1055.

Islam, S.S., Anothai, J., Nualsri, C. and Soonsuwon, W. (2020). Genetic variability and cluster analysis for phenological traits of Thai indigenous upland rice (*Oryza sativa* L.). *Indian Journal of Agricultural Research.* **54(2):** 211-216. doi: 10.18805/IJARe.A-461.

Gunasekaran, K., Sivakami, R., Sabariappan, R., Ponnaiah, G., Nachimuthu, V.V. and Pandian, B.A. (2017). Assessment of genetic variability, correlation and path coefficient analysis for morphological and quality traits in rice (*Oryza sativa* L.). *Agricultural Science Digest*. **37(4):** 251-256. doi: 10.18805/ag.D-4643.

Jan, N., Lal, E.P., Kashyap, S.C. *et al.* (2017). Genetic variability, character association and path analysis in rice genotypes. *Vegetos*. **30:** 87-93.

Khaire, A., Raut, V.M. and Kothekar, V.S. (2022). Genetic diversity analysis of rice genotypes using multivariate approaches. *Indian Journal of Genetics and Plant Breeding*. **82:** 123-130.

Khatun, F., Akter, A. and Rasul, M.G. (2023). Genetic variability and multivariate analysis in rice (*Oryza sativa* L.). *Bangladesh Journal of Agricultural Research*. **48(1):** 15-28.

Kim, J.H., Park, S. and Lee, G. (2024). Genome enabled selection and diversity assessment in rice breeding populations. *Plant Breeding.* **143(1):** 55-68.

Krishna, L., Naik, R. and Reddy, V.R. (2022). Multivariate analysis for identifying elite rice genotypes under field conditions. *International Journal of Agriculture Sciences*. **14:** 121-127.

Kumar, S., Jayasudha, S., Rajani and Singh, S.K. (2026). Genetic variability, heritability and genetic advance for yield and quality traits in rice (*Oryza sativa* L.). *Indian Journal of Agricultural Research*. **60(2):** 183-190. doi: 10.18805/IJARe.A-6402.

Kumar, A., Singh, R. and Patel, S. (2021). Integration of earliness and yield traits for improving crop productivity: Advances in breeding strategies. *Journal of Crop Improvement*. **35(4):** 512-528.

Lakshmi, B.V., Rao, V.S. and Satyanarayana, P.V. (2022). Genetic diversity and trait association studies in rice germplasm. *Oryza*. **59:** 98-107.

Madhukumar, K., Satyanarayana, P.V., Udayababu, P., Sreenivas, G. and Manojkumar, D. (2023). Principal component analysis for yield in green gram genotypes [*Vigna radiata* (L.) Wilczek] under rice fallow pulses conditions. *Frontiers in Crop Improvement*. **11(Special Issue-III):** 1966-1970.

Manoj, K.D., Srinivas, T., Rao, L.S., Suneetha, Y., Sundaram, R.M. and Kumari, V.P. (2022). Genetic variability and trait association analysis in F3 population of YH3 × AKDRMS 21-54 cross. *The Andhra Agricultural Journal.* **69(1):** 46-57.

Naik, R., Reddy, V.R. and Krishna, L. (2021). Principal component analysis in rice for yield and related traits. *Electronic Journal of Plant Breeding.* **12:** 780-786.

Pandya, T. and Sarial, A.K. (2015). Character association and direct and indirect effects on grain yield in rice. *The Indian Journal of Agricultural Sciences.* **85:** 221-226.

Pokhrel, A., Poudel, A. and Ghimire, S. (2020). Genetic diversity analysis of rice landraces using multivariate techniques. *Journal of Agriculture and Natural Resources.* **3:** 154-165.

Rahangdale, S.S., Singh, Y. and Singh, S.K. (2021). Multivariate analysis for genetic diversity in rice (*Oryza sativa* L.). *Journal of Plant Breeding and Crop Science.* **13:** 1-9.

Ramesh, M., Gunasekaran, M. and Prakash, M. (2021). Genetic divergence and trait prioritization in rice germplasm using PCA and D^2 analysis. *Journal of Crop Improvement*. **35:** 453-468.

Ramesh, M., Haritha, B. and Gunasekaran, M. (2023). Integrating physiological traits in rice breeding for climate resilience. *Functional Plant Biology.* **50:** 215-228.

Reddy, V.R., Naik, R. and Krishna, L. (2021). Influence of pollen fertility on yield stability in rice under stress environments. *Rice Science*. **28:** 451-459.

Sahu, P.K., Singh, S., Verma, O.P. and Kesh, H. (2021). Genetic divergence studies in rice using multivariate analysis. *International Journal of Genetics.* **13:** 121-128.

Satyanarayana, P.V., Madhukumar, K., Udayababu, P., Srinivas, T. and Manojkumar, D. (2023). Association studies for identifying the selection criteria among early varieties of rice in north coastal zone of Andhra Pradesh. *Biological Forum-An International Journal*. **15(11):** 329-335.

Sheela, V., Robin, S. and Manonmani, S. (2020). Multivariate analysis of rice genotypes for yield and physiological traits. *Plant Archives.* **20:** 3981-3986.

Shoba, D., Manivannan, N. and Senthil, N. (2021). Nutritional and medicinal significance of traditional rice landraces of India. *Journal of Ethnic Foods.* **8:** 1-10.

Singh, A.K., Dwivedi, D.K., Kumar, D. *et al.* (2023). Genetic variability and path coefficient analysis in rice. *Indian Journal of Agricultural Sciences*. **93:** 10 V0-108.

Singh, S.K., Gour, L., Mishra, D.K. and Koutu, G.K. (2020). Genetic divergence analysis in rice germplasm using D^2 statistics. *Journal of Experimental Biology and Agricultural Sciences.* **8:** 512-519.

Singh, S.K., Singh, P., Korada, M. *et al.* (2020). Character association and path analysis for yield traits in rice. *Current Journal of Applied Science and Technology.* **39:** 545-556.

Sinha, D., Maurya, A.K., Abdi, G., Majeed, M., Agarwal, R., Mukherjee, R. *et al.* (2023). Integrated genomic selection for accelerating breeding programs of climate-smart cereals. *Genes.* **14(7):** 1484.

Sudeepthi, K., Jyothula, D.P.B., Suneetha, Y. and Rao, V.S. (2017). Character association and path coefficient analysis in rice. *International Journal of Current Microbiology and Applied Sciences.* **6:** 2360-2367.

Swarup, S., Cargill, E.J., Crosby, K., Flagel, L., Kniskern, J. and Glenn, K.C. (2021). Genetic diversity is indispensable for plant breeding to improve crops. *Crop Science*. **61(2):** 839-852.

Thakur, P. and Sarma, D. (2023). Genetic approaches for enhancing early maturity and yield potential in field crops: Recent perspectives. *Plant Breeding Research.* **29(2):** 145-158.