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ASSESSMENT OF GENETIC VARIABILITY AND DIVERSITY IN RICE (*ORYZA SATIVA* L.) UNDER PHOSPHORUS DEFICIENT CONDITIONS USING WILD DERIVED GERMPLASM

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ABSTRACT

Reduction in soil fertility is the major problem faced by farmers, especially in case of major crops like rice. Excessive usage of fertilizers not only cause the pollution of water bodies and environment but increase the farmer's investment to rice production. Development of nutrient use efficient rice varieties are most cost effective and environment friendly solution for the same. The present study was conducted using 41 breeding lines derived from wild accessions in low phosphorous soil screening facility available at ICAR-IIRR, Hyderabad, to estimate variability and diversity for low phosphorus tolerance. Diversity analysis through D^2 Mahalanobi's studies revealed the diversified lines as parents for hybridization to develop low phosphorous tolerant varieties. The present investigation on analysis of variance has shown significant difference between genotypes for all the traits. Mean performance of the 4 quantitative traits revealed that NSR-5 (17.56 g), C1-151 (16.61 g), C1-99 (16.43 g), NSR-13 (14.87 g), and C3-305 (13.90 g) have recorded highest single plant yield under low phosphorous soil conditions. Highest GCV and PCV has shown by single plant yield with variance of 38.29 and 54.63 respectively. However, high heritability and high genetic advance was detected for plant height (67.88% and 24.21). Non-hierarchical clustering by Tocher's method clustered 41 lines into 8 clusters, where cluster 1 has 22 lines followed by cluster 2. Cluster mean results revealed that, cluster 4, cluster 1, cluster 3 have scored highest mean values of 16.43, 16.22 and 8.63 for yield, indicating that the lines grouped in this clusters are having greater genetic divergence. The highest intra cluster distance of 48.56 is recorded between cluster 3 and cluster 8, followed by 46.82 of inter cluster distance between cluster 2 and cluster 5 indicating that the clusters contain the greater genetic divergence. UPGMA clustering method revealed the genetic divergence between the lines used in the study, that maximum genetic divergence is observed between C1-99 and C3-206 (70.11) and minimum genetic divergence is between C10-21 and NPS-110 (0.38). Out of all the 4 traits, plant height (43.71%) has showed highest contribution for genetic divergence. The elite lines detected in this study which are high in yield and greater in genetic divergence *viz.*, NSR-5, C1-151, C1-99, NSR-13, C3-305, C3-206 are useful as donors in hybridization programme for the development of low phosphorous tolerant varieties.

***Keywords* :** Low Phosphorus, D^2 Mahalanobi's, Variability, Tocher's method, UPGMA clustering.

Introduction

Rice, along with wheat and maize, is one of the most important staple crops globally, accounting for the highest levels of consumption and serving as a primary source of calories for a large proportion of the world's population. *Oryza sativa* L., the cultivated rice species, is a short-day, self-pollinating, annual monocotyledonous grass belonging to the Poaceae family with chromosome number 2n=2x=24 (Singh *et al.*, 2020). Rice requires application of a recommended dose of 60:30:30 kg/ha of NPK for better yield in irrigated fields (TNAU, 2022). Over 90% of Indian soils are deficient in available Phosphorus (P) (Behera *et al*., 2025). To meet the consumer demands and improve the production, excessive usage of fertilizers and fertilizer responsive varieties were employed during green revolution. Further mono-cropping and intensive agricultural practices to maximize crop productivity caused the depletion of available soil nutrients without adequate replenishment. Dependency on chemical fertilizers, excessive irrigation, and intensive tillage collectively accelerated soil degradation and declining soil fertility in major agricultural regions of India (Maheswarappa *et al*., 2015).

Phosphorus (P) is a major macronutrient essential for plant growth and development, as it plays a crucial role in the synthesis of DNA, RNA, proteins, and phospholipids and participates directly in several metabolic and physiological processes (Lu *et al*., 2023). Deficiency of phosphorus in soil leads to characteristic symptoms such as stunted growth, dark green plants with erect leaves, reduced tillering, thin and weak stems, delayed maturity, and in severe cases absence of flowering. It also results in poor grain filling and a high proportion of unfilled grains, ultimately causing significant yield losses (IRRI). Although yield losses can be mitigated through the application of phosphorus fertilizers, their use efficiency in soils is generally low. Only about 10–25% of the applied phosphorus fertilizer is absorbed by plants, while the remaining fraction becomes fixed in the soil or is lost to the environment, contributing to soil degradation and eutrophication of water bodies (Conley *et al*., 2009; Johnston *et al*., 2014). Furthermore, the long-term sustainability of phosphorus fertilization is threatened by the potential depletion of global rock phosphate reserves, since most phosphorus fertilizers are produced from finite, non-renewable resources (Kunhikrishnan *et al*., 2022). Therefore, both insufficient and excessive application of phosphorus fertilizers pose challenges: the former reduces crop productivity, whereas the latter leads to environmental problems.

Developing rice varieties tolerant to low phosphorus (P) conditions is an important strategy to address phosphorus deficiency in soils and improve crop productivity under nutrient-limited environments. To achieve this, several studies have focused on identifying and developing low-P tolerant rice genotypes (Magudeeswari *et al*., 2024; Sunandha *et al*., 2023). However, evaluating the genetic diversity among rice lines derived from different genetic backgrounds is equally important for effective breeding. Under phosphorus stress conditions, rice lines with diverse genetic backgrounds may exhibit considerable variation in yield and related traits, reflecting their differential capacity for adaptation and recombination potential.

Selection of suitable parents for hybridization is a crucial step in the success of rice improvement programs. Genetically diverse parents are more likely to generate greater recombination and variability in the segregating populations, which ultimately facilitates the selection of superior or elite lines. Diversity analysis methods, such as the Mahalanobis D^2 analysis, are widely used to assess genetic divergence based on yield and other quantitative traits and to predict the potential of parental combinations for heterosis and recombination (Sandhya *et al.,* 2014). Therefore, the present study aims to evaluate the genetic diversity of rice breeding lines with different genetic backgrounds under low-phosphorus conditions, in order to identify genetically diverse and high-yielding lines that can be used as potential parents in breeding programs to obtain desirable recombinants.

Materials and Methods

Experimental Site

The present study was conducted at ICAR-Indian Institute of Rice Research, Rajendra Nagar, Hyderabad, located at 17°19' North latitude and 78°23' East longitude, approximately 542 meters above mean sea level, during *Kharif*' 2023. The lines are raised in nursery and transplanted to the low phosphorus soil screening facility (with zero phosphorous) at the institute. Low P plot with available P < 2 kg/ha was supplied with NK at 100:60 kg ha-1, respectively. The entire K, 50% N, and 12.5 kg ha^{-1} zinc (Zinc sulphate) was applied as a basal dose in both (normal, low P) plots, and the remaining 50% N was applied as two splits, 25% N at tillering stage and 25% at the booting stage. Entire phosphorous was applied as a basal dose before transplanting.

Low Phosphorus condition

Low soil P plot has been maintained at IIRR, Hyderabad for the past 35 years without an external application of P fertilizers (Sunandha *et al*., 2023). The available P content is very low (Olsen P 1.8 kg ha^{-1}) in this soil. The water level and other crop management practices were maintained as similar to normal plot.

Plant Material

A set of forty-one pre-breeding lines from different genotypic backgrounds is used for the study (Table1). All the rice lines are obtained from the

Department of Plant Breeding, Crop Improvement Section, ICAR–Indian Institute of Rice Research, Rajendra Nagar, Hyderabad, India.

Field Experiment

The genotypes were sown in a raised bed of wet nursery during *Kharif 2023.* After 25 days in nursery, the lines were transplanted to the main field (P_0 plot). Randomised Complete Block Design (RCBD) was followed in the study to raise the material and evaluate the traits, the experimental area was divided into 3 blocks, treated as three replications. Spacing of 20×25 cm is followed during planting. In each replication, five randomly chosen plants were observed for the following characteristics: plant height (cm) (PH), number of tillers (NT), number of productive tillers (NPT) and seed yield per plant (g) (SPY). The experimental plot was supplemented with recommended dosages of nitrogen and potassium, and all required nutrients for rice cultivation except phosphorus. All the standard inter cultivation operations like weeding, plant protection activities of rice cultivation, are followed in the study.

Statistical Analysis

Analysis of Variance (Fisher, 1925), broad sense heritability (h^2) was computed using the formula provided by Allard (1960). To quantify the genetic progress as a percentage, mean, GCV, PCV, h^2 and GA, Burton (1952) was followed. D^2 Mahalanobis (1936), UPGMA (Unweighted Pair Group Method with Arithmetic Mean) dendrogram, Tocher's method (Rao (1952) were analysed through R software.

Results and Discussion

Descriptive Statistics

The descriptive statistics indicate considerable variability among the 41 genotypes for all four traits studied (Table 2; Fig. 1). Mean plant height was 82.02 cm with a moderate standard deviation (15.77), indicating substantial variation in plant stature, while the positive skewness suggests a slight tendency toward taller plants. The average number of tillers (6.96) and productive tillers (6.40) showed relatively low dispersion, as reflected by smaller standard deviations (~2.08), and near-symmetrical distributions, indicating uniformity among genotypes for these traits. Single plant yield recorded a mean of 8.82 g with a variability of SD = 3.88, highlighting wide differences in yield potential. Negative kurtosis values for all traits indicate a relatively flat distribution, suggesting the absence of extreme outliers. Overall, the wide range and significant variability observed, particularly for plant height and yield, provide good scope for selection in breeding programmes.

Genetic Variability Studies

Analysis of variance (ANOVA) revealed significant differences among the genotypes for all the traits studied, indicating the presence of substantial variability among the rice lines under low phosphorus conditions (Table 3). The mean performance of the four quantitative traits showed that several lines performed better than the majority of genotypes included in the study. In terms of single plant yield under low phosphorus soil conditions, the lines NSR-5 (17.56 g), C1-151 (16.61 g), C1-99 (16.43 g), NSR-13 (14.87 g), and C3-305 (13.90 g) recorded the highest values. Among the lines evaluated, C1-99 (58.67 cm), R-86 (59 cm), C1-11 (63.67 cm), NPS-110 (64 cm), and NPV-37 (65 cm) exhibited comparatively lower plant height which is more preferable. A higher number of tillers was recorded in NSR-86 (11), NSR-96 (10.33), C1-11 (10.33), R-198 (9.67), 175-24K (9.67), and R-67 (9.33). Similarly, a greater number of productive tillers was observed in NSR-86 (11), NSR-96 (10.33), C1-11 (9.67), 175-24K (9.33), and NSR-32 (9) (Table 4).

Among the variability parameters, the highest genotypic coefficient of variation (GCV) was observed for single plant yield (38.29), followed by number of productive tillers (27.34) and number of tillers (25.45), indicating considerable genetic variability for these traits (Table 5). Similarly, the highest phenotypic coefficient of variation (PCV) was recorded for single plant yield (54.63), followed by number of productive tillers (46.30), number of tillers (40.29), and plant height (21.45). High heritability was observed for plant height (67.88%), suggesting that this trait is largely governed by additive genetic factors. High genetic advance was also recorded for plant height (24.21). Moreover, genetic advance as percent of mean was highest for single plant yield (55.30), followed by number of productive tillers (33.27), number of tillers (33.12), and plant height (29.99), indicating the effectiveness of selection for these traits. Similar findings have been reported in previous studies by Faysal *et al*. (2022), Lakshmi *et al*. (2022), Awad-Allah *et al*. (2022), Kulsum *et al*. (2022), Debsharma *et al*. (2022), Umadevi *et al*. (2023), Akshay *et al*. (2022), Khan *et al*. (2023), Demeke *et al*. (2023), Pradhan *et al*. (2023), and Soundharya *et al.* (2024).

D^2 Diversity Studies

The 41 rice genotypes were grouped into eight clusters based on D² statistics. Cluster I was the largest, comprising 22 genotypes, whereas Cluster II contained eight genotypes and Cluster III contained five genotypes. Cluster IV included two genotypes and Clusters V, VI, VII, and VIII were solitary clusters, each containing a single genotype, indicating their distinct genetic divergence from the remaining lines. D² values are calculated between all possible pairs of genotypes to estimate the degree of genetic divergence.

The Mahalanobis D² analysis revealed considerable genetic divergence among the rice lines studied. The genotype C1-99 exhibited the highest genetic distance with C3-206(70.11), followed by NSR-86 (57.53), NSR-23 (56.24), NSR-96 (54.43), NSR-105 (43.5), NSR-32 (42.23) and NSR-86-11 (41.19). C1-151 showed greater genetic distance with C3-206 (45.45) followed by NSR-96 (42.73), NPS-40 (41.30) and NSR-23 (40.71). The genotype R-67 showed higher divergence with C3-226 (59.59) followed by NSR-96 (44.75), NSR-13 (42.05), NPS-40 (43.29). R-198 & C3-206 (50.72), R-86 & C3-241 (48.79), C1-11 & C3-220 (47.86), C1-99 & NPS-58-1 (43.29), NPS-110 & C3-206 (41.41), C10-21 & C2-243 (41.28) also shown greater genetic divergence. These results indicate substantial genetic divergence among the lines originating from different genetic backgrounds. Higher D² values indicated greater genetic diversity, which is useful for selecting diverse parents for hybridisation to maximise recombination.

Cluster mean analysis revealed substantial variation among clusters for the traits studied. The highest mean plant height was recorded in Cluster VIII (117.33 cm), while the lowest mean (58.67 cm) was observed in Cluster IV. The highest mean number of tillers was observed in Cluster VII (8.87), whereas the lowest mean (3.67) occurred in Cluster II. For the number of productive tillers, Cluster III recorded the highest mean (10.47), while Cluster II showed the lowest mean (2.33). With respect to single plant yield, Cluster I exhibited the highest mean (16.22 g), whereas the lowest mean yield was recorded in Cluster II (2.70 g). Inter-cluster distances were generally higher than intra-cluster distances, indicating greater genetic divergence between clusters than within clusters. Since Clusters V, VI, VII, and VIII consisted of single genotypes, no intra-cluster distance was observed for these clusters. The highest inter-cluster distance (48.56) was recorded between Cluster III and Cluster VIII, followed by Cluster II and Cluster V (46.82) and Cluster VI and Cluster VIII (45.46). The inter-cluster distance between Cluster III and Cluster IV was 33.01, suggesting moderate genetic divergence between these clusters. Among the four traits studied, plant height contributed the highest proportion (43.71%) to the total genetic divergence, followed by number of productive tillers (21.10%), single plant yield (20.67%), and number of tillers (14.52%). The results obtained in the present study are in agreement with earlier reports on genetic diversity and variability in rice by Sandhya *et al*. (2014), Singh *et al*. (2020), Vanisri *et al*. (2020), Mohamud *et al*. (2022), Jangala *et al*. (2022), Aruna *et al*. (2024), Dutta *et al*. (2024), Jha *et al*. (2024), and Takare *et al*. (2024).

Grouping by Tocher's method:

Based on the Mahalanobis D^2 statistics, Fig. 2 shows that the non-hierarchical clustering of 41 genotypes was grouped into 8 distinct clusters using Tocher's method. Cluster 1 was the largest, comprising 22 genotypes, while Clusters 5, 6, 7, and Cluster 8 were solitary. Higher cluster mean values were observed in Clusters 3, 4, 6, and 7, indicating greater divergence among these groups. The average intra-cluster distance ranged from 0.98 to 5.33, with the maximum distance observed in Cluster 1, indicating higher internal genetic diversity within that group. The inter-cluster distances varied between 8.36 and 70.12, reaching a maximum between Cluster 5 and Cluster 8. These high inter-cluster values suggest significant genetic divergence, identifying these clusters as ideal candidates for hybridisation programmes to achieve maximum heterosis.

Dendrogram Analysis Based on UPGMA Clustering

The UPGMA (Unweighted Pair Group Method with Arithmetic Mean) dendrogram successfully partitioned the 41 genotypes into a clear hierarchical structure based on Euclidean distance. The tree structure confirmed that genotypes within the same cluster share a high degree of genetic similarity, while the distinct branching patterns highlight the significant divergence. The UPGMA dendrogram Fig. 3 constructed using Euclidean distance grouped the rice genotypes into distinct clusters, revealing substantial genetic diversity among the studied material. Euclidean distance grouped the genotypes into three major clusters at a similarity threshold of 80, with further subdivision into seven subclusters at an Euclidean distance of 40, indicating substantial genetic diversity among the studied lines. Cluster I comprised a relatively less number of genotypes with higher Euclidean distances (120–130) to rest of the genotypes, indicating their pronounced genetic divergence. Cluster II included a moderate number of genotypes with clustering occurring at intermediate distances (60–80), reflecting moderate genetic variability. In contrast, Cluster III was the largest group, where most genotypes clustered at lower distances (20–50), suggesting close genetic similarity and a comparatively narrow genetic base. Further subdivision within each major cluster into several sub-clusters at lower distance levels (10–40) highlighted the presence of closely related genotypes. Overall, the clustering pattern indicates the existence of both divergent and closely related genotypes, providing valuable opportunities for the selection of genetically diverse parents in rice breeding programs. Maximum genetic divergence is observed between C1-99 and C3-206 (70.11) and minimum genetic divergence is between C10-21 and NPS-110 (0.38).

Conclusion

The present investigation revealed significant differences among rice genotypes across all traits studied, indicating substantial genetic variability among pre-breeding lines under low-phosphorus conditions. Mean performance analysis identified NSR-5, C1-151, C1-99, NSR-13, and C3-305 as superior lines, with higher single-plant yields indicating wild species as potential donors for nutrient-use efficiency. Among the variability parameters, single-plant yield exhibited the highest genotypic and phenotypic coefficients of variation, along with high genetic advance as a percentage of the mean, indicating considerable scope for selection under nutrient-stress conditions. Among the traits studied, plant height contributed the most to total genetic divergence, suggesting its major role in survival under nutrient stress conditions, differentiating genotypes and highlighting the potential of divergent parents for developing improved low-phosphorus-tolerant rice varieties. Various clustering methods, such as Mahalanobis D² analysis, Tocher's method, and UPGMA dendrogram, revealed substantial genetic divergence among the genotypes used in the study. Maximum genetic divergence was observed between C1-99 and C3-206. These diverse genotypes are useful in further breeding programmes to develop novel recombinants with nutrient stress tolerance.

Table 1 : List of 41 Rice (*Oryza sativa* L.) lines used in the study

S No.	Genotype	IET No	Parentage
1	C1-99	32740	RP6458 Swarna//166S (Swarna/ *Oryza nivara*)
2	C1-151	31939	RP6458 Swarna //166S (Swarna/ *Oryza nivara*)
3	NSR 5	30252	KMR3/*Oryza rufipogon* WR120
4	NSR 61	32295	KMR3/*Oryza rufipogon* WR120
5	NPS 40	33191	Swarna /*Oryza nivara* IRGC81848
6	NSR 86	27641	KMR3/*Oryza rufipogon* WR120
7	NSR40	31330	KMR3/*Oryza rufipogon* WR120
8	NSR52	-	KMR3/*Oryza rufipogon* WR120
9	NSR32	-	KMR3/*Oryza rufipogon* WR120
10	NSR96	31737	KMR3/*Oryza rufipogon* WR120
11	NSR105	31974	KMR3/*Oryza rufipogon* WR120
12	NSR 23	31855	KMR3/*Oryza rufipogon* WR120
13	NSR 13	31861	KMR3/*Oryza rufipogon* WR120
14	C3-305	-	RP6460 166S/148S(Swarna/ *Oryza nivara*)
15	C1-200	32277	RP6458 Swarna //166S(Swarna/ *Oryza nivara*)
16	C1 SEL-7	-	RP6458 Swarna//166S(Swarna/ *Oryza nivara*)
17	C1-227	-	RP6458 Swarna//166S(Swarna/ *Oryza nivara*)
18	C1-11	-	RP6458 Swarna ///166S(Swarna/ *Oryza nivara*)
19	MTU47	28776	MTU1010/ *Oryza rufipogon* IC309814
20	NPS41	-	Swarna /*Oryza nivara* IRGC81848
21	NPK 24	30180	Swarna/*Oryza nivara* IRGC81832
22	NPS 56-2	30061	Swarna/*Oryza nivara* IRGC81848
23	R-198	-	Swarna/*Oryza rufipogon* IRGC309814
24	R-67	32150	Swarna/*Oryza rufipogon* IRGC309814
25	NPS 38	-	Swarna/*Oryza nivara* IRGC81848
26	C3-206	31989	RP6460 166S/148S
27	C2 SEL-12	31607	RP6459 166S/14S
28	175-24K	31101	Swarna/*Oryza nivara* IRGC81832
29	C10-183	31524	RP6420 MTU1010/Tulasi
30	C3-312	31647	RP6460 166S/148S
31	NPV 37	31141	MTU1010/*Oryza rufipogon* IC309814
32	NPS 44	-	Swarna/*Oryza nivara* IRGC81848
33	RN116	31957	Swarna/SM363
34	NSR 86-11	-	KMR3/*Oryza rufipogon* WR120
35	NSR 53-1	-	KMR3/*Oryza rufipogon* WR120
36	NSR 86 (5205)	-	KMR3/*Oryza rufipogon* WR120
37	NPS 110	31325	Swarna/*Oryza nivara* IRGC81848
38	NPS 58-1	31002	Swarna/*Oryza nivara* IRGC81848
39	R- 86	-	Swarna/*Oryza rufipogon* IRGC309814
40	NPS 21	31926	Swarna/*Oryza nivara* IRGC81848
41	C10-21	31118	RP6420 MTU1010/ Tulasi

Table 2 : Descriptive Statistics for all the quantitative traits studied for 41 rice lines

Statistical Parameter	Plant Height	Number of Tillers	Number of Productive Tillers	Single Plant Yield
Mean	82.03	6.99	6.40	8.82
Standard Error	2.5	0.32	0.32	0.61
Median	79	7	6.33	8.03
Mode	102.67	5.67	5.67	5.59
Standard Deviation	15.77	2.08	2.05	3.87
Sample Variance	7.45	31.49	36.51	36.39
Kurtosis	-0.73	-0.82	-0.54	-0.62
Skewness	0.56	-0.04	0.20	0.58
Range	58.67	8	8.5	14.33
Minimum	58.67	3.00	2.50	2.70
Maximum	117.33	11.00	11.00	17.57
Sum	3363	285.33	262.5	361.47
Count	41	41	41	41
Largest (1)	117.3	11	11	17.57
Smallest (1)	58.67	3	2.5	3.23
Confidence Level (95.0%)	4.98	0.66	0.65	1.22

Table 3 : ANOVA Summary for traits for 41 rice lines under low phosphorous soil condition

S No.	Source of Variation	Mean Sum of Squares		
		Replication	**Genotypes**	**Error**
	Degree of freedom	**2**	**40**	**80**
1	Plant Height	453.0976**	753.4093**	37.3142
2	Number of Tillers	7.3415	12.6565**	4.8248
3	Number of productive tillers	1.3984	12.8037**	5.4567
4	Single Plant Yield	5.5533	42.9763**	9.5207

Table 4 : Mean Performance of traits for 41 rice lines under low phosphorus soil condition

S No.	Genotypes	PH	NT	NPT	SPY
1	C1-99	58.67	5.67	4.33	16.43
2	C1-151	67.00	3.00	2.50	16.61
3	NSR-61	93.00	7.33	7.33	12.73
4	NPS-40	79.67	4.00	4.00	13.57
5	NSR-5	102.67	9.00	8.67	17.57
6	NSR-86	101.00	11.00	11.00	6.87
7	NSR40	108.00	7.00	6.67	12.03
8	NSR-52	84.33	3.00	3.00	8.03
9	NSR-32	88.33	9.00	9.00	4.73
10	NSR-96	108.00	10.33	10.33	11.27
11	NPS-105	105.33	8.33	8.33	12.43
12	NSR-23	110.67	8.33	8.33	10.17
13	NSR-13	102.67	7.67	7.67	14.87
14	C3-305	79.00	6.33	6.33	13.90
15	C1-200	83.67	7.67	7.67	9.57
16	C1-SEL-7	81.33	4.67	4.67	9.87
17	C1-277	78.00	7.33	6.33	5.59
18	C1-11	63.67	10.33	9.67	9.67
19	MTU-47	73.00	7.00	5.67	11.73
20	NPS-41	85.67	7.67	7.67	4.83
21	NPK-24	71.67	9.00	8.00	11.53
22	NPS-56-2	72.67	8.33	6.67	4.10
23	R-198	76.67	9.67	5.33	6.23
24	R-67	68.67	9.33	5.33	5.60
25	NPS-38	90.33	6.00	6.00	6.90
26	C3-206	117.33	5.67	5.67	7.63
27	C2-SEL-12	73.67	4.33	4.00	3.97
28	175-24K	79.33	9.67	9.33	8.26
29	C10-183	73.00	5.67	5.67	11.90
30	C3-312	72.00	5.67	5.33	8.60
31	NPV-37	65.00	8.33	8.33	5.93
32	NPS-44	73.33	7.00	7.00	4.59
33	RN-116	65.33	4.67	4.00	3.23
34	NSR-86-11	99.33	9.00	8.00	7.93
35	NSR-53-1	84.00	7.00	6.33	6.27
36	NSR-86(5205)	74.33	5.00	5.00	10.10
37	NPS-110	64.00	4.00	3.33	4.90
38	NPS-58-1	98.00	6.00	5.67	5.79
39	R-86	59.00	6.67	6.00	5.59
40	NPS-21	65.33	4.67	4.67	4.83
41	C10-21	66.33	5.00	3.67	5.10
Overall Mean		81.95	6.97	1.34	8.47
Range	**Min**	58.67	3.00	2.50	2.70
	Max	117.33	11.00	11.00	17.57
SEm		3.5268	1.2682	1.3487	1.7814
Sed		4.9876	0.7935	1.9073	2.5193
CD at 5%		9.9256	3.5691	3.7957	5.0137
CD at 1%		13.1607	4.7324	5.0328	6.6478
CV		7.4539	31.4889	36.5086	36.3982

PH: Plant Height, NT: Number of Tillers, NPT: Number of Productive Tillers, SPY: Single Plant Yield

Table 5 : Genetic Parameters for the 4 quantitative traits

S No.	TRAIT	GCV	PCV	h^2 (Broad Sense)	GA 5%	GA as % of Mean 5%
1	Plant Height	17.67	21.45	67.88	24.21	29.99
2	Number of Tillers	25.45	40.30	39.90	2.28	33.12
3	Number of Productive Tillers	27.35	46.30	34.88	2.12	33.27
4	Single Plant Yield	38.30	54.63	49.14	4.58	55.30

GCV: Genotypic Coefficient of Variation, PCV: Phenotypic Coefficient of Variation, h^2: Heritability, GA: Genetic Advancement

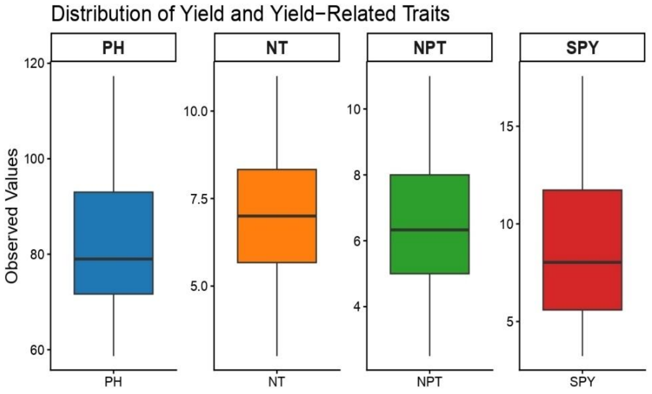

Fig. 1 : Box plots illustrating the distribution and variability of plant height, number of tillers, number of productive tillers and single plant yield among rice (*Oryza sativa L.*) genotypes

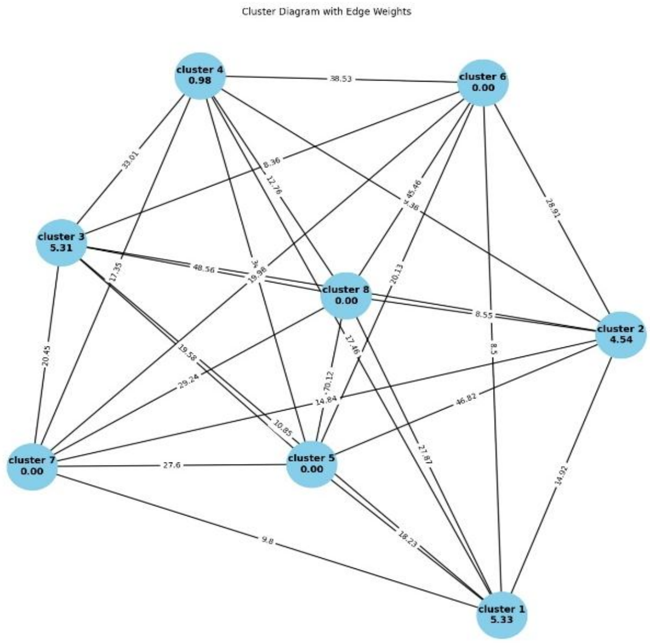

Fig. 2 : Inter-cluster distance network depicting genetic divergence among rice genotypes by Tocher’s method

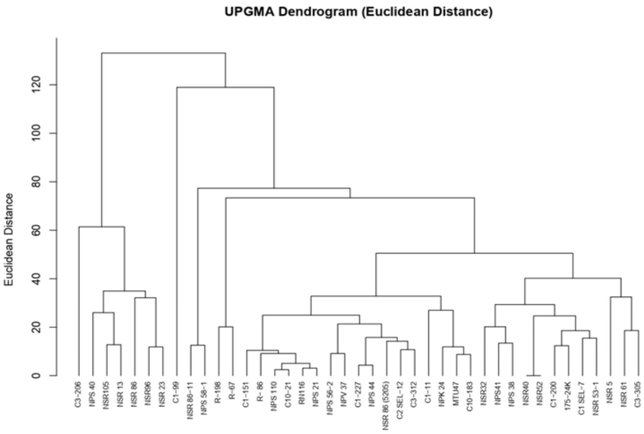

Fig. 3 : UPGMA-based phylogenetic dendrogram illustrating genetic relationships among 41 genetic materials using Euclidean distance

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