

Genetic Variability and Diversity Analysis in Traditional Rice (*Oryza sativa* L.) Varieties of Tamil Nadu

S. R. Sruthi, J. Johnny Subakar Ivin, Greetty Williams,
Y. Anbuselvam

Received 27 October 2022, Accepted 8 February 2023, Published on 24 April 2023

ABSTRACT

Traditional rice varieties have a substantial genetic diversity that can be utilized as potential genetic resources to promote yield and agronomic performance. Rice yield must be boosted to meet the requirements of a constantly increasing population, which can be addressed by developing high-yielding cultivars. Traits such as seed yield per plant, number of productive tillers per plant, number of tillers per plant, and 1000 seed weight indicated high PCV and GCV. Heritability and genetic advance as a percentage of mean were high for all of the traits studied, demonstrating the existence of an additive gene impact and accordingly, direct selection might be desirable for the desired genetic improvement. The current study demonstrated a positive and highly significant positive phenotypic and genotypic correlation between seed yield per plant and the following traits: Plant height, panicle length, number of tillers per plant,

number of productive tillers per plant, number of grains per panicle, 1000 seed weight, seed yield per plant and a significant positive correlation with days to fifty per cent flowering. Thus, yield intensification in rice may be realized by identifying parents with these characteristics. Tocher's approach was adopted to partition the genotypes into six groups. Cluster I has 18 genotypes, whereas clusters VI and VII only had one genotype each. The greatest inter-cluster D^2 values were found in Cluster VII and III, followed by Cluster VI and III. The genotypes in clusters VI and II with high mean values for various traits can be employed directly for adaptation or as parents in future hybridization program, as genetically varied parents for obtaining desired recombinants in a breeding program. In PCA, out of eight principal components, the first three PC's showed maximum cumulative variability. The characteristics, number of tillers per plant, number of productive tillers per plant, and plant height plant contributed the most to variation in PCA. The current study may indeed be applied to determine the traits that contribute to variability and choose genotypes to be used as donors for character development in future breeding program.

Keywords Rice, Variability, Genetic diversity, Seed yield per plant.

S. R. Sruthi¹, J. Johnny Subakar Ivin², Greetty Williams³, Y. Anbuselvam^{*4}

^{1,2,3}PhD Scholar, ⁴Professor

Department of Genetics and Plant Breeding, Faculty of Agriculture, Annamalai Nagar 608002, Tamil Nadu, India

Email: yanbuselvam@gmail.com

*Corresponding author

INTRODUCTION

Rice is the most important dietary staple for about 3.5 billion people, accounting for at least 35-75% of total calories (Rudresh *et al.* 2021). India has a diverse and

extensive genetic wealth of rice. According to several assessments, around 50,000 of rice varieties are still cultivated in the country (Patra 2000). Tamil Nadu in India, one of the historic rice growing locations, houses a diverse range of cultivars, wild and weedy relatives. Rice has been cultivated since ancient agriculture by art of selection and is still followed by the farmers across the Southern transitional zone, where farmers nurture and conserve indigenous rice types carried through several generations. The Green Revolution brought hybrid rice varieties, which contributed to the elimination of many traditional rice varieties that were insect resistant, salt tolerant, and could grow in both deep waters and inland locations. They possess medicinal, nutritional, and aromatic characteristics and are high in antioxidants and polyphenols. The traditional crop varieties contain a high degree of genetic variety and can serve as potential genetic resources for improving yield and agronomic performance (Hosington *et al.* 1999).

Rice area and production in India were around 45.8 million hectares and 124.37 million tons in 2020-21, respectively. The acreage and production of rice in Tamil Nadu were around 2.04 million hectares and 6.9 million tonnes, respectively (Annual report 2021). The ever-growing population necessitates boosting rice crop productivity, which may be accomplished by developing high-yielding cultivars.

The comprehensive assessment of genetic variability and genetic diversity present in the germplasm is the cornerstone for genetic improvement in any crop. Correlation analysis assists in extracting the strength of estimating the critical components of a complex trait like yield. The Mahalanobis D^2 analysis and Principal Component Analysis (PCA), which are robust and illustrious multivariate statistical approaches in data analysis for yield and its contributing variables, were applied to establish a quantitative gauging of genetic divergence. Exploration of genetic variability, genetic diversity and correlation studies between yield and its components on rice may complement the potential to escalate its prospective, allowing for trait selection which will facilitate in addressing the need for higher grain yield and nutrition supply.

MATERIALS AND METHODS

During *kharif* 2022, all the 40 genotypes collected from various Agro-climate Zones of Tamil Nadu were raised on nursery beds at the Department of Genetics and Plant Breeding farm, Annamalai University, Tamil Nadu located at latitude 11° 24'N, longitude 79.4'E, and height + 5.79 m. Table 1 lists the 40 traditional rice genotypes obtained from different sources. Twenty-five-day-old seedlings were transplanted in the main field, which was set out in a Randomized Block Design (RBD) with three replications. For parameters such as days to fifty percent flowering, plant height, panicle length, number of tillers per panicle, number of productive tillers per plant, number of grains per panicle, 1000 seed weight and seed yield per plant, the observations were recorded on five randomly selected plants of each genotype in every replication.

Genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were enumerated employing the method in accordance with Burton (1952). A pattern of variations were classified accordingly in the range; low (< 10 %), moderate (10 - 20%), high (> 20%) (Sivasubramanian and Madhavamenon 1973). Broad sense heritability was calculated applying the formula stated by Lush (1940)

Table 1. List of 40 traditional rice genotypes used in this study.

Code	Genotypes	Code	Genotypes
G1	Kottara Samba	G21	Kalurundai
G2	Kuruvai Kalangium	G22	KarunkKuruvai
G3	Cochin Samba	G23	Seru Milagu
G4	Kattu Ponni	G24	Karutha Kar
G5	Kulie Vedichan	G25	Milagu Samba
G6	Kulla Kar	G26	Katti Samba
G7	Kudai Vazhai	G27	Salem Sanna
G8	Sanna Samba	G28	Poongkarr
G9	Tulasi Vasana Seraga Samba	G29	Tenkai Poo Samba
G10	Kalarpalai	G30	Ilupai Poo Samba
G11	Kala jeera	G31	Rasakadam
G12	Kandasali	G32	Adukkunel
G13	Sivappu Kowni	G33	SeeragaSanna
G14	Pal Kodai Valai	G34	Sembuli Samba
G15	Neelan Samba	G35	Thanga Samba
G16	Ottatam	G36	KaruppuKavuni
G17	AnandanoorSanna	G37	Thooyamalli
G18	Kala namak	G38	Mapillai Sampa
G19	Navara	G39	Arupatham Kuruvai
G20	Athur Kitchili Samba	G40	Kothamalli Sampa

Table 2. Analysis of variance for yield and its attributing traits in 40 traditional rice varieties.

Source	df	Days to fifty percent flowering	Plant height	Panicle length	No. of tillers per plant	No. of productive tillers per plant	No. of grains per panicle	1000 seed weight	Grain yield
Mean sum of squares									
Replication	2	10.65	1.23	2.59	0.26	0.38	34.16	0.34	5.21
Genotypes	39	661.84**	865.94**	22.81**	41.76**	33.20**	2095.39**	56.32**	211.06**
Error	78	4.97	0.47	0.86	0.11	0.08	13.26	0.95	2.87

Where, df – Degrees of freedom, ** Significant at 1% level.

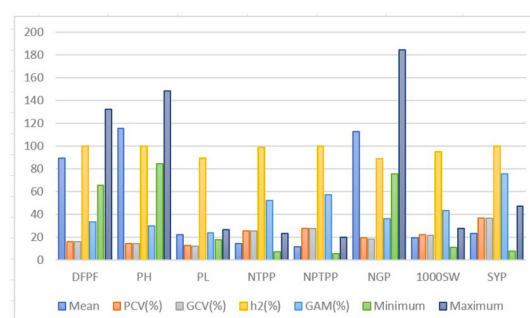
and graded as high (> 60%), moderate (30-60%) and low (0-30%). The genetic advance in mean per cent was assessed by adopting the technique by Johnson *et al.* (1955) wherein classification was marked to the extent of low (< 10%), moderate (10-20%), high (> 20%). The estimates of Analysis of variance (ANOVA), correlation coefficient (Weber and Moorthy 1952), multivariate cluster analysis (Mahalanobis D² statistics and Tocher's method of clustering) and Principal Component Analysis (PCA) were calculated by examining the data using R studio software version 5594.2.3.0.

RESULTS AND DISCUSSION

The analysis of variance (ANOVA) demonstrated that for all of the characteristics tested, the mean sum of squares attributable to genotypes was highly significant (Table 2). The highest mean value was recorded for the traits plant height (115.50 cm) followed by number of grains per panicle (112.72) while the lowest mean was established by number of productive tillers per plant (11.92). G15 determined highest mean for days to fifty per cent flowering (132.47) and plant height (148.50 cm). G21 revealed highest mean for traits such as panicle length (26.94), number of tillers per plant (23.66) and seed yield per plant (47.30). G1 expressed highest mean for number of productive tillers per plant (20.14) and number of grains per plant (184.42) while G38 exhibited highest mean for 1000 seed weight (27.91). G39 and G22 denoted lowest mean for days to fifty per cent flowering (65.14) and plant height (84.46) respectively. G40 and G13 signified lowest mean for panicle length (17.82) and number of productive tillers per plant (5.5) respec-

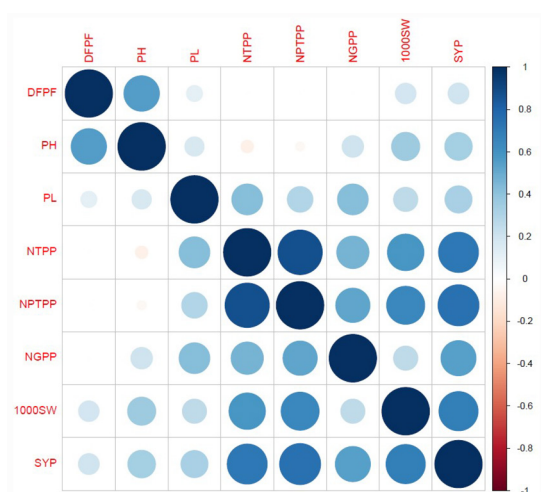
tively. G4 showed lowest mean for number of grains per panicle (75.38) and G9 estimated lowest mean for seed yield per plant (7.80). G12 indicated minimum range for number of tillers per panicle (7.13) and 1000 seed weight (11.26) (Fig. 1).

In this study, PCV was evinced to be greater than GCV for all traits examined, however the difference was negligible (Fig. 1). This unveiled that environmental influences had less of an effect on all of the characters. High PCV and GCV were affirmed by traits such as the seed yield per plant (36.70 and 36.60), number of productive tillers per plant (27.99 and 27.97), number of tillers per plant (26.62 and 25.52) and 1000 seed weight (22.2 and 21.74). Similar results were observed by Rao *et al.* (2020) and Mounika *et al.* (2022) in rice. A moderate PCV and



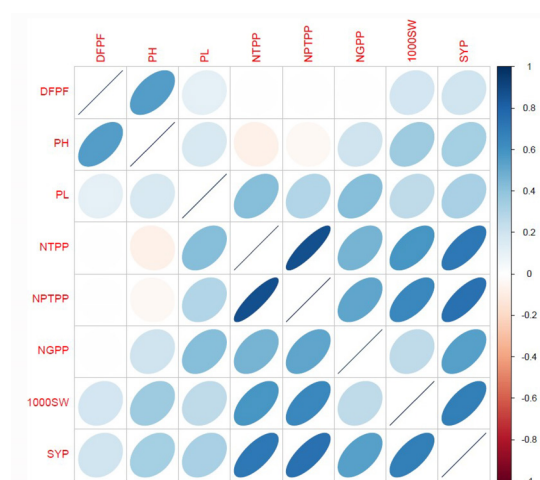
Where, DFPF – Days to fifty percent flowering; PH – plant height; PL – panicle length; NTPP- number of tillers per plant; NPTPP – Number of productive tillers per plant; NGPP – Number of grains per panicle; 1000 SW – thousand seed weight; SYP – Seed yield per plant.

Fig. 1. Genetic variability parameters of different biometrical traits in traditional rice genotypes used in this study.



Where, DFPF – Days to fifty percent flowering; PH – plant height; PL – panicle length; NTPP- number of tillers per plant; NPTPP – Number of productive tillers per plant; NGPP – Number of grains per panicle; 1000 SW – thousand seed weight; SYP – Seed yield per plant.

Fig. 2a. Heat map depicting genotypic correlation among the biometrical traits in traditional rice genotypes used in this study.



Where, DFPF – Days to fifty percent flowering; PH – plant height; PL – panicle length; NTPP- number of tillers per plant; NPTPP – Number of productive tillers per plant; NGPP – Number of grains per panicle; 1000 SW – thousand seed weight; SYP – Seed yield per plant.

Fig. 2b. Heat map depicting phenotypic correlation among the biometrical traits in traditional rice genotypes used in this study.

GCV were expressed by traits like days to fifty percent flowering (16.34 and 16.32), plant height (14.76 and 14.75), panicle length (12.92 and 12.22), and number of grains per panicle (19.68 and 18.56) which was in accordance with the findings of Bagudam *et al.* (2018) in NPT core set of rice.

Heritability percent should be assessed with genetic advance as a percentage of mean, although it is not obligatory that a trait exhibits high heritability will also show high genetic advance (Johnson *et al.* 1955). Days to fifty percent flowering (99.99) and seed yield per plant (99.98) expressed the highest heritability value, followed by plant height (99.87), number of productive tillers per plant (99.77), number of tillers per plant (99.20), 1000 seed weight (95.11), panicle length (89.48), and number of grains per panicle (88.86). Seed yield per plant (75.61) recorded the highest genetic advance as a mean percentage, followed by number of productive tillers per plant (57.54), number of tillers per plant (52.36), 1000 seed weight (43.67), number of grains per panicle (36.04), days to fifty percent flowering (33.67), plant height (30.37), and panicle length (23.81), respectively. For

all of the traits investigated, heritability and genetic advance as a percentage of mean were high, demonstrating the presence of additive gene effect and hence direct selection could be productive for the intended genetic improvement. Comparable interpretation was established by Allam *et al.* (2015) in some indigenous genotypes of basmati rice (Fig. 1).

To measure the strength and direction of the association between yield and yield contributing variables, correlation coefficients were computed (Figs 2a–2b). The current study demonstrated a positive and highly significant ($p > 0.01$) phenotypic and genotypic correlation between seed yield per plant and the following traits: Plant height, panicle length, number of tillers per plant, number of productive tillers per plant, number of grains per panicle, 1000 seed weight, and seed yield per plant. It also had a significant positive correlation ($p > 0.05$) with days to fifty percent flowering. Thus, yield intensification in rice may be realized by identifying parents with these characteristics. An indistinguishable correlation of seed yield per plant was reported for plant height and test weight (Tiwari *et al.* 2019), the number of grains

Table 3. Cluster composition of 40 traditional rice varieties (Tocher's method).

Cluster	Number of genotypes	Genotypes
1	18	G11, G14, G10, G40, G25, G7, G6, G27, G37, G36, G34, G4, G22, G8, G24, G13, G33, G3
2	3	G20, G23, G12
3	8	G30, G31, G19, G29, G39, G28, G17, G9
4	7	G2, G16, G26, G32, G1, G35, G38
5	2	G5, G18
6	1	G21
7	1	G15

per panicle (Devi *et al.* 2017), number of productive tillers per plant, number of grains per panicle, days to fifty percent flowering (Dhanuja *et al.* 2021) and panicle length (Sudeepthi *et al.* 2020). Taking into consideration the inter-association between traits, the current investigation revealed that almost all the independent attributes exhibited a positive and high significance. However, no significant inter-correlation was found between panicle length, number of tillers per plant, number of productive tillers per plant, and number of grains per panicle, days to fifty percent flowering, plant height. The genotypic correlations in the present investigation were found to be higher than the phenotypic correlations, illustrating that while there is a strong internal relationship between the characteristics tested, their expression is impeded by environmental parameters. Most quantitative features, such as yield and yield contributing traits, are heavily impacted by the association between genotype and environment, emphasizing that the correlation coefficient might enable breeders in determining key traits (Ahmadikhah *et al.* 2008).

Multivariate statistical approaches, such as

cluster analysis and PCA, are frequently employed in genetic diversity analysis as they assess numerous features for each genotype under investigation to categorize the available germplasm into discrete groups based on genetic diversity (Ranjith *et al.* 2019). Tocher's method was used to classify 40 genotypes into six clusters (Table 3) with the maximum number of 18 genotypes in cluster I followed by 8 genotypes in cluster III while the clusters VI and VII were found to be solitary clusters. Similar results were obtained by Lakshmi *et al.* (2022). The Mahalanobis D^2 analysis for yield and its contributing traits was applied to generate a quantitative assessment of genetic divergence (Table 4). The analysis revealed a substantial degree of diversity in the material. The genotypes were divided into six clusters. Cluster I had the greatest number of genotypes (18) and the cluster VI and VII housed the least number of genotypes (1). The genotypes of Cluster III exhibited the least deviation (14454.15) while the genotypes of the cluster I (27125.37) and III (20086.55) revealed maximum divergence. Germplasm that pertain to the same cluster have a strong alliance with one another opposed to the other clusters. Cluster VII and III had the highest inter-cluster D^2 values (639709.39), followed by Cluster VI and III (355550.51). The cluster mean values for different traits exhibited the differences between the clusters for all the traits. The cluster mean values for all eight traits were presented in Table 5. The cluster mean value for days to 50% flowering ranged from 68.30 (cluster V) to 132.47 (cluster VII). For plant height, cluster mean ranged from 103.22 (cluster II) to 148.5 cm (cluster VII). The panicle length ranged from 21.10 (cluster VII) to 26.94 (cluster V). Similarly, number of tillers per plant ranged from 11.99 cm (cluster III) to 23.66 cm (cluster VI), whereas number of productive tillers per plant ranged from 8.92 (cluster II) to 20.06 (cluster

Table 4. Inter-cluster and intra-cluster (diagonal) average of D^2 of 40 traditional rice varieties.

	Cluster 1	Cluster 2	Cluster 3	Cluster 4	Cluster 5	Cluster 6	Cluster 7
Cluster 1	27125.37	43254.58	110190.55	85892.27	47887.30	154873.91	269502.19
Cluster 2		19521.11	98653.94	129485.24	116838.12	285450.23	288870.39
Cluster 3			20086.55	322683.30	138204.74	355550.51	639709.39
Cluster 4				17471.88	103252.51	114393.98	83987.26
Cluster 5					14454.15	60147.15	339789.35
Cluster 6						0	314439.36
Cluster 7							0

Table 5. Cluster means for eight characters in 40 traditional rice varieties.

Cluster	DFPF	PH	PL	NTPP	NPTPP	NGPP	1000SW	SYP
1	89.86	115.20	21.81	14.28	11.95	108.55	19.83	23.35
2	101.04	103.22	22.52	12.35	8.92	109.41	14.29	14.23
3	73.69	106.28	21.25	11.99	9.38	105.07	16.53	13.71
4	103.70	130.29	23.33	17.25	14.25	128.92	24.00	31.67
5	72.78	103.23	21.84	17.44	13.78	110.59	21.36	32.91
6	68.30	119.63	26.94	23.66	20.06	152.27	27.64	47.30
7	132.47	148.50	21.10	14.64	12.80	110.22	20.11	29.80

Where, DFPF – Days to fifty percent flowering, PH – Plant height, PL – Panicle length, NTPP- Number of tillers per plant, NPTPP – Number of productive tillers per plant, NGPP – Number of grains per panicle, 1000 SW – Thousand seed weight, SYP – Seed yield per plant.

VI) and number of grains per panicle from 105.07 (cluster III) to 152.27 (cluster VI). The cluster mean for the 1000 seed weight ranged from 13.71 (cluster III) to 47.30 (cluster VI). The genotypes in the cluster VI exhibited superior performance for all the traits, while the genotypes in cluster II for reduced plant height. Similar results were recorded by Lakshmi *et al.* (2022) and Vennela *et al.* (2017). The genotypes in clusters VI and II with high mean values for various traits may be employed directly for adaptation or as parents in future hybridization program, as genetically varied parents for obtaining desired recombinants in a breeding program.

By focusing on the interconnectedness of the characteristics, principal component analysis (PCA) was used to reduce large data sets into smaller principle components without any loss of details. Table 6 illustrates the Eigenvector value, percentage of variation, and cumulative percentage. In the present investigation, two of the eight components assessed had Eigenvalues larger than one, indicating increased variation across rice genotypes for the selection of diverse parents. The percentage of variability for three components (PC1, PC2, PC3) accounted for 72.9% of the diversity across the genotypes analyzed, whereas the remaining five components accounted

for just 27%. Table 7 shows the contribution of eight quantitative features to the main components. In PC1, the seed yield per plant and the number of productive tillers per plant showed higher positive loading. PC1 increases when the aforementioned attributes increase, implying that these two features may vary concurrently. Furthermore, the PC 1 substantially corresponds with the number of productive tillers per plant and the seed yield per plant and serves as a measure of the same. PC 2 was comprised of negative loadings of two traits, plant height and days to 50% flowering, and is thus negatively associated with other traits. The PC3 increases as panicle length and grain number per panicle increase. Plant height, days to fifty percent flowering, panicle length, number of productive tillers per plant and seed yield per plant were ascertained to be the major yield contributing characters, and thus weightage should be given to these characters during selection for the development of high yielding rice cultivars. These parameters play a significant role in the divergence and account for the majority of the variability. Scree plot explained the percentage of variation by a graph between Eigen values and principal components (Fig. 3). It was clearly depicted in the graph that the maximum variation was observed in PC1, PC2, PC3. The traits, number of tillers per plant, number of productive tillers per

Table 6. Eigen values, percentage of variation and cumulative percentage for principal components.

	PC1	PC2	PC3	PC4	PC5	PC6	PC7	PC8
Eigen values	3.756	1.641	0.939	0.649	0.518	0.231	0.166	0.100
Proportion	0.470	0.205	0.117	0.081	0.065	0.029	0.021	0.012
Cumulative proportion	0.470	0.675	0.792	0.873	0.938	0.967	0.988	1.000

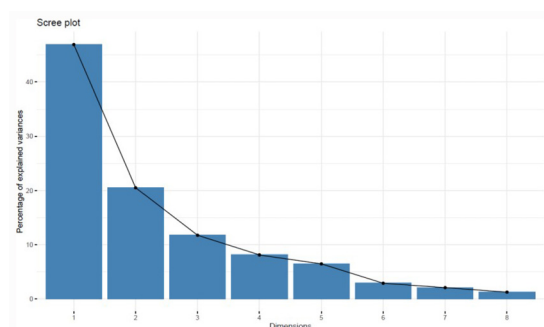
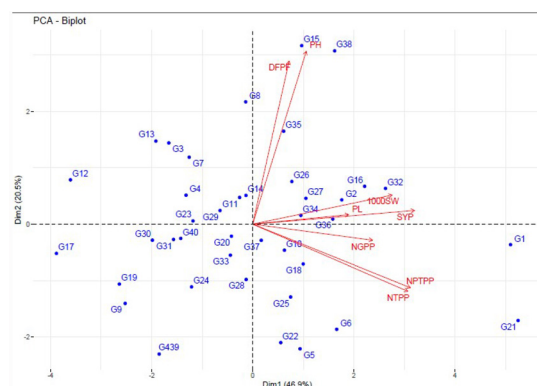


Fig. 3. Scree plot diagram using principal components of 40 traditional rice genotypes used in this study.

plant and plant height showed maximum vector length indicating its contribution to the total divergence. The angle between the trait vectors indicates the direction of association between the traits. All the seven traits showed a positive correlation with seed yield per plant. The genotypes viz., G34, G36 and others in the particular quadrant perform better for the traits like 1000 seed weight, panicle length and seed yield per plant while G9, G19 and others are some of the poor performing genotypes for the traits under consideration as they are present in the opposite direction to the trait vector (Fig. 4). Similar results were reported by Lakshmi *et al.* (2022) and Christina *et al.* (2021).

CONCLUSION

According to the findings of this study, the number of tillers per plant, number of productive tillers per plant, 1000 seed weight, and seed yield per plant demonstrated high GCV, PCV, heritability, and GAM. As a



Where, DFPF – Days to fifty percent flowering; PH – plant height; PL – panicle length; NTPP- number of tillers per plant; NPTPP – Number of productive tillers per plant; NGPP – Number of grains per panicle; 1000 SW – thousand seed weight; SYP – Seed yield per plant.

Fig. 4. Biplot diagram of principal components 1 and 2.

consequence, while choosing genotypes to improve yield, these traits should be accounted for. In accordance with the Mahalanobis D^2 analysis, genotypes with high mean values in clusters VI and II could be employed directly for adaptation or as parents in future hybridization programs, as genetically diverse parents for generating desirable recombinants in a breeding program. The characteristic seed yield per plant and days to fifty percent flowering might be deemed significant traits that contributed the most divergence to the genotypes based on the diversity analysis. The characteristics, number of tillers per plant, number of productive tillers per plant, and plant height plant contributed the most to variation in PCA. G34, G36, and other genotypes perform better for parameters such as 1000 seed weight, panicle length,

Table 7. Contribution of first three principal components to variation in 40 traditional rice varieties.

Characters	PC1	PC2	PC3	PC4	PC5	PC6	PC7	PC8
DFPF	0.104	-0.633	-0.091	-0.327	-0.639	0.195	0.161	-0.036
PH	0.153	-0.671	0.058	0.301	0.326	-0.215	-0.524	0.078
PL	0.274	-0.037	0.705	-0.566	0.267	-0.056	0.092	0.153
NTPP	0.444	0.260	-0.102	-0.243	-0.190	-0.176	-0.489	-0.600
NPTPP	0.451	0.246	-0.208	-0.012	-0.215	0.106	-0.280	0.746
NGP	0.343	0.063	0.507	0.611	-0.238	0.395	0.090	-0.167
1000SW	0.399	-0.113	-0.400	-0.109	0.524	0.550	0.231	-0.158
SYP	0.462	-0.053	-0.146	0.196	-0.006	-0.641	0.559	-0.001

Where, DFPF – Days to fifty percent flowering, PH – Plant height, PL – Panicle length, NTPP- Number of tillers per plant, NPTPP – Number of productive tillers per plant, NGPP – Number of grains per panicle, 1000 SW – Thousand seed weight, SYP – Seed yield per plant.

and seed yield per plant. As a consequence, the current study may indeed be applied to determine the traits that contribute to variability and choose genotypes to be used as donors for character development in future breeding program.

ACKNOWLEDGMENT

The authors are grateful to the Department of Genetics and Plant Breeding, Faculty of Agriculture, Annamalai University, Tamil Nadu for supporting and providing all the necessary facilities to conduct this research.

REFERENCES

- Ahmadikhah A, Nasrollanejad S, Alishah O (2008) Quantitative studies for investigating variation and its effect on heterosis of rice. *Int J Pl Prod* 2(4): 297-308.
- Allam CR, Jaiswal HK, Qamar A, Venkateshwarlu C, Reddy YS (2015) Variability, heritability and genetic advance studies in some indigenous genotypes of basmati rice (*Oryza sativa* L.). *Elect J Pl Breed* 6(2): 506-511.
- Annual report (2021) Ministry of Agriculture and Farmers Welfare: Government of India.
- Bagudam R, Eswari KB, Badri J, Rao PR (2018) Variability, heritability and genetic advance for yield and its component traits in NPT core set of rice (*Oryza sativa* L.). *Elect J Pl Breed* 9(4):1545-1551.
- Burton GW (1952) Quantitative inheritance in grasses. In: *Proc 6th Int Grassland Congr* 1: 356-363.
- Christina GR, Thirumurugan T, Jeyaprakash P, Rajanbabu V (2021) Principal component analysis of yield and yield related traits in rice (*Oryza sativa* L.) landraces. *Elect J Pl Breed* 12(3) : 907-911.
- Devi K, Rukmini, Chandra B, Satish, Lingaiah N, Hari Y, Venkana V (2017) Analysis of variability, correlation and path coefficient studies for yield and quality traits in rice (*Oryza sativa* L.). *Agric Sci Dig* 37(1): 1-9.
- Dhanuja N, Ganesamurthy K, Pushpam R, Amudha K, Uma D (2021) Studies on genetic diversity in selected rice (*Oryza sativa* L.) landraces of Tamil Nadu. *Elect J Pl Breed* 12(3): 990-997.
- Hosington D, Khairallah M, Reeves T, Ribaut JM, Skovmand B, Taba S, Warburton M (1999) Plant genetic resources: What can they contribute towards increased crop productivity? *Proc Nat Acad Sci* 96 (11): 5937-5943.
- Johnson HW, Robinson HF, Comstock RE (1955) Estimates of genetic and environmental variability in soybeans 1. *Agron J* 47(7):314-318.
- Lakshmi M, Shanmuganathan M, Jeyaprakash P, Ramesh T (2022) Genetic variability and diversity analysis in selected rice (*Oryza sativa* L.) varieties. *Elect J Pl Breed* 13(3): 959-966.
- Lush JL (1940) Intra - sire correlation and regression of offspring on dams as a method of estimating heritability of characters. *Proc Am Soc Anim Prod* 33: 293-301.
- Mounika K, Shivani D, Jabeen F, Chaitanya K, Chiranjeevi M, Sundaram RM, Fiyaz A (2022) Multivariate analysis and character association for agro-morphological traits in elite rice germplasm. *J Cereal Res* 13(3) : In press
- Patra BC (2000) Collection and characterization of rice genetic resources from Keonjhar district of Orissa. *Oryza* 34:324-326.
- Ranjith P, Sahu S, Dash SK, Bastia DN, Pradhan BD (2019) Principal component analysis of rice varieties under bacterial leaf blight incidence. *Int J Chem Stud* 7(3): 4184-4187.
- Rao NND, Roja V, Rao VS, Rao VS (2020) Assessment of genetic parameters for Yield and nutritional traits in rice (*Oryza sativa* L.). *J Pharmacog Phytochem* 9(6): 1641-1646.
- Rudresh NS, Jayamani P, Vijayakumar E, Manonmani S, Gangashetti M, Jeyakumar P, Latha KR (2021) Genetic analysis of rice germplasm suitable for direct and transplanted establishments. *Electro J Pl Breed* 12(4):1148-1156.
- Sivasubramanian J, Madhavamenon (1973) Genotypic and phenotypic variability in rice. *Madras Agric J* 12: 15-16.
- Sudeepthi K, Srinivas TVSR, Ravi Kumar BNVS, Jyothula DPB, Nafeez Umar SK (2020) Assessment of genetic variability, character association and path analysis for yield and yield component traits in rice (*Oryza sativa* L.). *Elect J Pl Breed* 11(01) : 144-148.
- Tiwari DN, Tripathi SR, Tripathi MP, Khatri N, Bastola BR (2019) Genetic variability and correlation coefficients of major traits in early maturing rice under rainfed lowland environments of Nepal. *Adv Agric* 1 :1-9.
- Vennela PR, Singh SK, Singh R, Gayatonde V, Singh DK (2017) Genetic divergence studies in rice (*Oryza sativa* L.) for yield and yield related traits. *Vegetos -An Int J Pl Res* 30:191-195.
- Weber CR, Moorthy BR (1952) Heritable and non-heritable relationships and variability of oil content and agronomic characters in the F² generation of soybean crosses 1. *Agron J* 44(4): 202-209.