



Analysis of Genetic Variability and Association for Yield Traits in Rice (*Oryza sativa* L.) Germplasm Lines

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ABSTRACT

Background: To analyze the genetic variability and association among 130 rice germplasm lines for yield and yield attributing traits.

Methods: An experiment was done to study 11 quantitative traits in 130 rice genotypes for yield and yield components. Data analyze for variability and correlation were done using R studio version 4.4.2 software.

Result: The traits of yield per plant, weight of thousand grain, productive tillers per plant, grains per panicle, length of flag leaf, weight of the leaf and length of the panicle had high PCV and GCV. Yield per plant had significant and positive correlation with weight of thousand grain and grains per panicle. Hence, these traits may be utilized as selection indices to improve yield in the rice breeding program.

Key words: Correlation analysis, Genetic variability, Germplasm lines, Rice.

INTRODUCTION

As an essential staple crop, rice (*Oryza sativa* L.) contributes >50% of total food production worldwide. It is classified as part of the Poaceae family and is cultivated effectively in diverse environments, including lowland flooded fields, rainfed uplands and coastal areas, in a wide range of agroclimatic zones. Besides its economic and nutritional importance, rice also has considerable cultural, religious and heritage significance, for instance in Asia, where it is omnipresent in the life of people. Rice is a major source of carbohydrates and is essential to the world's dietary needs and food safety. (Yu *et al.*, 2024). But global rice production is not without challenges: climate change, soil erosion, water scarcity and shifting weather patterns. The food and agriculture organization (FAO) has information indicating rice production around the world increased from about 509 million tonnes in 2020 to almost 520 million tonnes in 2023. Asia continues to be the epicenter for rice production, with both China and India among its top contributors. Rice production in India registered an increase, from 118.87 million tonnes in 2019-20 to 130.29 million tonnes in 2022-23, according to the Department of Agriculture and Farmers Welfare. Tamil Nadu in particular is one of India's major rice-growing states, producing between 8 to 10 million tonnes every year. The yield of rice varies considerably depending on the variety and agro-climatic conditions, ranging from 3.5 to 4.2 tonnes per hectare (Naik *et al.*, 2021).

Rice production productivity has also improved significantly through rice mechanization, high-yielding varieties and advanced irrigation systems. But now, sustainable rice production is increasingly threatened by unpredictable monsoon patterns, increased insect pest invasions and deteriorating soil health. As such, it will

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require innovative practices and policies that address these issues for the future of rice agriculture. India serves as a significant reservoir of rice diversity, with several traditional rice landraces with unique adaptability to local climate and resistance to various stresses, besides being highly nutritious (Shoba *et al.*, 2021; Naik *et al.*, 2021). Recent studies highlight the need to safeguard these landraces for future breeding programs to create nutrient-enriched and climate-resilient rice (Shoba *et al.*, 2019; Ramesh *et al.*, 2024). Karuppu Kavuni (Rajan *et al.*, 2019) reacts to a rich source of antioxidant anthocyanins and Mappillai Samba (Selvi *et al.*, 2023) is rich in iron and zinc and promotes strength and endurance are examples of such rice

varieties. Kumar *et al.* (2024) recommended consumption of Poongar, a drought resistant medicinal rice, especially for expectant mothers because of its excellent nutritional profile. Kattuyanam is an important flood-resistant race; Seeraga Samba is well known for its unique flavor and pest resilience to reduce chemical input (Arunkumar *et al.*, 2020).

To protect genetic diversity and enhance future food security, it is crucial to implement comprehensive conservation and documentation strategies for traditional rice. Advances in genetic research methods, such as genetic variability and correlation analysis, can significantly enhance our understanding of the breeding potential of these landraces. With increasing demands for climate adaptation and improved nutrition, interest in traditional rice continues to grow. Therefore, integrating traditional rice varieties into mainstream breeding efforts will be essential for fostering sustainable rice farming and ensuring global food security. A collaborative approach that emphasizes expanded research, supportive policies and dedicated conservation initiatives will be pivotal in maintaining biodiversity and securing the future of rice agriculture.

MATERIALS AND METHODS

The yield and yield components of 130 lines (Table 1) of genetic material were observed in a field. These rice genotypes were sown in an augmented design at SRM College of Agricultural Sciences during Kharif 2024. Each rice genotype was sown in three rows with a 30 cm × 30 cm spacing. Yield and yield component data at maturity were recorded from five randomly tagged plants per genotype for each replication. Data on eleven agronomic characteristics were: plant height (PH), length of flag leaf (LFL), weight of the leaf (WL), length of the panicle (LP), internode length (INL), productive tillers per plant (PTP), grains per panicle (GP), weight of thousand grain (WTG), yield per plant (YP) and for every genotype in every replication, morphological data for days to maturity (DM) and days to fifty per cent flowering (DFF) were observed on plot basis.

RESULTS AND DISCUSSION

The evaluation of the genetic variability parameters of association, mean, range, genetic variability, heritability, genetic advance for the 130 rice genotypes in each of the 11 yield attributing traits is required (Singh *et al.*, 2024 and Sheshnath *et al.*, 2017) for the selection of successful breeding programme (Table 2).

Plant height, days to 50% flowering and days to maturity was not suitable for selection, since it is indicating moderate GCV and PCV which is influenced by the environment on these traits (Upadhyaya *et al.*, 2010). For days to 50% flowering, Rajkumar and Ibrahim (2025) obtained similar results. It is possible that the environment influences these traits because internode length has a

Table 1: List of 130 rice genotypes used for the variability and correlation studies.

Genotype number	Rice genotypes
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	Sempalai
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 vasana 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

Table 1: Continue....

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G50	Raja mudi
G51	Kuruvai kalanjiyam
G52	Karunjeeraga samba
G53	Payan kundathan
G54	Vaikunda
G55	Selam sanna
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	Sempalai
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

Table 1: Continue....

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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	Mutrana sannam
G124	Kallu valai
G125	NLR3354
G126	Guna parva
G127	Sinigar
G128	Sabari
G129	Jaya
G130	TPS-5

little genotypic coefficient of variation (GCV) and a high phenotypic coefficient of variation (PCV).

The traits of length of flag leaf, weight of the leaf, productive tillers per plant, length of the panicle, weight of thousand grain, grains per panicle, yield per plant had high PCV and GCV. This suggests significant variations for these traits (Maurya *et al.*, 2022; Divya *et al.*, 2018 Ranjani *et al.*, 2018).

Heritability and genetic advance as per cent of mean

Heritability estimates demonstrate the patterns of trait inheritance. The advancement of genetics facilitates the development of selection strategies (Kaushik *et al.*, 2007). Genetic advancement and heritability in leaf weight and internode length are minimal. This trait indicated non-additive gene action. Nath and Alam (2002) asserted that phenotypic selection for these traits was not likely to yield improvement.

Several traits showed high genetic advance and high heritability such as plant height, days to fifty percent flowering, days to maturity, length of the panicle, productive tillers per plant, length of the flag leaf, weight of thousand

grain, grains per panicle and yield per plant. Hence, the aforementioned traits may be under the control of additive gene action. So, selection for these traits would be rewarding, immediately. This implied that additive gene activity primarily governs these traits, enabling improvement by direct selection. Divya *et al.* (2018) reported comparable findings regarding the weight of thousand grain, productive tillers per plant and number of grains per panicle while Shaili *et al.* (2022) observed the positive correlation between the number of grains per panicle and plant height.

Correlation among yield components

The data illustrated the relationships for correlation among yield components. This understanding will contribute towards improving yield traits and overall productivity in breeding programs (Table 3).

Days to 50% flowering exhibited positive correlation with days to maturity (DM), plant height (PH) and negative correlation with flag leaf length (FLL), leaf weight (LW), internode length (INL), number of productive tillers (NPT) and number of grains per panicle (NGP). According to Kamana *et al.* (2019), plant height and the number of days till 50% flowering were positively correlated.

Days to maturity had positive correlation with plant height and had negative correlation with flag leaf length (FLL), leaf weight (LW), internode length (INL), number of productive tillers (NPT) and number of grains per panicle (NGP). Plant height is significantly correlated with the flag leaf length (FLL), leaf weight (LW), panicle length (PL), internode length (INL). Flag leaf length had positive correlation with leaf weight (LW) and internode length (INL). Leaf weight had negative correlation with panicle length (PL) and internode length (INL). Panicle length was significantly positively correlated with internode length (INL) and negatively correlated with number of grains per panicle (NGP). These results were agreement with Iqbal *et al.*, (2018).

Thousand grain weight is significantly negatively correlated with days to fifty percent flowering (DFF), plant height (PH), flag leaf length (FLL), panicle length (PL), internode length (INL), number of productive tillers (NPT), number of grains per panicle (NGP) and thousand grain weight (TGW). This result was in conformity with the earlier findings of Ramanjaneyulu *et al.*, (2014).

Single plant yield (SPY) was positively correlated with number of productive tillers (NPT), number of grains per panicle (NGP) and thousand grain weight (TGW) and negatively correlated with days to fifty percent flowering

Table 2: Estimate of the mean, range and genetic variability for 11 quantitative traits in 130 rice genotypes.

Characters	Max	Min	Mean	GCV	PCV	H ²	GA	GAM
DFF	91.00	3.00	62.29	14.77	16.17	83.42	17.31	27.78
DM	178.00	54.00	1.26	14.17	14.24	98.96	35.68	29.03
PH	176.25	48.00	126.97	19.40	19.72	96.72	49.91	39.31
LFL	72.60	3.40	36.54	28.56	30.39	88.27	20.19	55.27
WL	11.96	0.30	1.06	59.21	124.59	22.59	0.61	57.97
LP	57.8	10.60	29.86	25.41	25.57	98.76	15.53	52.02
INL	54.00	11.40	24.74	12.37	25.71	23.13	3.03	12.25
PTP	42.20	8.40	21.49	28.52	30.09	89.84	11.97	55.69
GP	211.00	28.00	98.93	37.78	38.34	97.09	75.86	76.68
WTG	42.00	6.50	19.74	20.74	24.68	70.57	7.08	35.88
YP	214.45	4.68	43.06	52.97	60.12	77.62	41.40	96.14

Table 3: Phenotypic correlation coefficients between 11 rice characteristics among 130 rice genotypes.

Characters	DM	PH	LFL	WL	LP	INL	PTP	GP	WTG	YP
DFF	0.39**	0.13*	-0.45**	-0.24**	-0.09	-0.38**	-0.35**	-0.34**	-0.16**	-0.30**
DM		0.13*	-0.51**	-0.29**	-0.10	-0.47**	-0.42**	-0.39**	-0.11	-0.41**
PH			0.57**	0.28**	-0.09	0.16**	0.04	0.08	-0.20**	-0.35**
LFL				0.82**	-0.01	0.24**	0.11	0.10	-0.18**	-0.14*
WL					-0.28**	-0.20**	-0.11	-0.02	0.08 NS	-0.01
LP						0.42**	0.01	-0.25**	-0.18**	0.01
INL							0.02	-0.11	-0.18**	0.06
PTP								-0.06	-0.23**	0.45**
GP									-0.15*	0.57**
WTG										0.34**

Significance of correlation at the 0.05 level is (*) and 0.01 level is (**).

Days to fifty per cent flowering (DFF); days to maturity (DM); plant height (PH); length of flag leaf (LFL); weight of the leaf (WL); length of the panicle (LP); productive tillers per plant (PTP); grains per panicle (GP); weight of thousand grain (WTG); yield per plant (YP).

(DFF), days to maturity (DM), plant height (PH) and flag leaf length (FLL). In selecting traits to enhance yield, it is suggested to prioritize these characteristics. Similar associations were previously reported by Pachauri *et al.* (2017).

The traits flag leaf length (FLL), leaf weight (LW), panicle length (PL), number of productive tillers (NPT), number of grains per panicle (NGP), thousand grain weight (TGW), single plant yield (SPY) exhibited a high magnitude of genetic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV), indicating potential for improvement through selection. A significant heritability was observed along with a substantial genetic advance as a percentage of the mean for the traits days to fifty percent flowering (DFF), days to maturity (DM), plant height (PH), flag leaf length (FLL), panicle length (PL), number of productive tillers (NPT), number of grains per panicle (NGP), thousand grain weight (TGW), single plant yield (SPY) suggests that these traits were predominantly controlled by additive gene action, indicating that selection for these characteristics would be more effective for achieving the desired genetic improvement.

CONCLUSION

The evaluation of 130 rice genotypes across 11 yield-attributing traits revealed significant genetic variability for several key characteristics, including flag leaf length, leaf weight, productive tillers per plant, panicle length, thousand grain weight, grains per panicle and yield per plant. These traits exhibited high PCV and GCV, suggesting substantial scope for genetic improvement through selection. Furthermore, traits like days to 50% flowering, days to maturity, plant height, flag leaf length, panicle length, productive tillers per plant, grains per panicle, thousand grain weight and single plant yield demonstrated high heritability coupled with high genetic advance as a percentage of the mean, indicating the predominance of additive gene action and the potential for effective improvement through direct selection. Conversely, plant height, days to 50% flowering and days to maturity showed moderate GCV and PCV, suggesting a greater environmental influence, while leaf weight and internode length displayed minimal heritability and genetic advance, implying non-additive gene action and limited improvement through phenotypic selection. Correlation analysis further highlighted significant relationships among yield components, providing valuable insights for developing effective breeding strategies aimed at enhancing yield and overall productivity in rice. Prioritizing traits such as productive tillers per plant, number of grains per panicle and thousand grain weight, which showed positive correlations with single plant yield, is recommended for achieving yield enhancement in breeding programs.

Conflict of interest

All authors declared that there is no conflict of interest.

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