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Evaluation of Genetic Variability, Trait Association, and Regression Analysis among Rice (*Oryza sativa* L.) Genotypes under the Agro-Climatic Conditions of Tando Jam, Sindh, Pakistan

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ABSTRACT

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Rice (*Oryza sativa* L.) is one of the most important cereal crops worldwide, and the identification of superior genotypes based on agronomic traits is essential for developing high-yielding cultivars. The present study was conducted to assess genetic variability, trait association, and regression among twenty-five rice genotypes under field conditions using a randomized complete block design with three replications. Significant differences among genotypes were observed for most of the evaluated traits, indicating substantial genetic variability. Correlation and regression analyses were performed to determine the relationships among flowering, maturity, yield, and yield-contributing traits. Days to 50% flowering exhibited a very strong positive correlation with days to maturity ($r = 0.998$), whereas negative associations were observed with sterile spikelets and panicle length. The number of fertile spikelets showed significant positive correlations with tiller number, plant height, panicle length, and grain yield, while sterile spikelets were negatively associated with grain yield. Panicle length and plant height also exhibited positive relationships with grain yield, suggesting their importance as indirect selection criteria for yield improvement. The coefficient of determination indicated that flowering time explained approximately 99.6% of the variation in maturity. Overall, the findings demonstrate considerable genetic diversity among the evaluated rice genotypes and highlight fertile spikelets, panicle length, and plant height as key traits for selection in rice breeding programs aimed at improving productivity under the agro-climatic conditions of Sindh, Pakistan.

Introduction

Rice (*Oryza sativa* L.) is one of the most important cereal crops belonging to the family *Poaceae* and is cultivated extensively across Asia, Africa, Australia, and several other regions of the world (Dogra & Jumare, 2014). It serves as the primary food source for more than half of the global population and ranks as the third most widely produced cereal crop after maize and wheat (Darko et al., 2025). Rice is unique among cereal crops because it is generally consumed as a whole grain and provides an excellent source of carbohydrates, vitamins, minerals, and dietary energy. In China, nearly 60% of the population relies on rice as their principal staple food, while millions of people in other countries depend on it for daily nutrition. In Pakistan, rice is one of the country's most valuable agricultural commodities and plays a vital role in food security and the national economy. It is the second most important export crop after cotton, contributing approximately 3.1% to agricultural value addition and 0.6% to the national gross domestic product (GDP). During the 2024–25 cropping season, rice was cultivated on 3.90 million hectares, representing a 7.2% increase in cultivated area over the previous year. However, despite the expansion in cultivated area, total production declined by 1.38% to 9.72 million tonnes, mainly because of unfavorable environmental conditions (GoP, 2025). The reproductive phase, particularly the booting and flowering stages, is considered the most heat-sensitive period. Exposure to elevated temperatures during these stages reduces pollen viability, impairs pollen germination and fertilization, increases spikelet sterility, and ultimately lowers grain yield (Zhang et al., 2021; Chandio et al., 2025). Grain yield is a complex quantitative trait governed by numerous interrelated morphological and physiological characteristics. Some yield components contribute directly to grain production, whereas others exert indirect effects through their relationships with associated traits. Therefore, understanding the magnitude and direction of these relationships is essential for developing efficient breeding strategies. Correlation analyses provide valuable information regarding the strength of associations among agronomic traits and facilitate the identification of reliable selection criteria for yield improvement (Chandra et al., 2017). Estimation of correlation coefficients helps plant breeders evaluate the relative contribution of individual characters to grain yield and determine the nature of relationships among important agronomic traits. Since grain yield is highly influenced by several interacting components, knowledge of these relationships is indispensable for selecting superior genotypes and improving breeding efficiency (Thippani et al., 2017). The present investigation was therefore undertaken to evaluate the agronomic performance of twenty-five rice genotypes and to determine the relationships among important yield and yield-related traits through analysis of variance, correlation, and regression under the agro-climatic conditions of Tando Jam, Sindh, Pakistan.

Materials and methods

Experimental Site The present study was conducted during the Kharif 2022 growing season at Kaleri Seed Farm, Tando Jam, Sindh, Pakistan. The experimental site is situated in the irrigated agro-ecological zone of lower Sindh and is characterized by a semi-arid climate with high temperatures during the rice-growing season. Temperature data were recorded throughout the experimental period (April–July 2022) to evaluate the prevailing environmental conditions during crop growth.

Plant Material

A total of 25 rice (*Oryza sativa* L.) genotypes, including two commercial check varieties, were evaluated. The experimental material comprised the following genotypes:

SVIN-033, SVIN-035, SVIN-094, SVIN-105, SVIN-109, SVIN-119, SVIN-127, SVIN-133, SVIN-145, SVIN-151, SVIN-161, SVIN-166, SVIN-177, SVIN-202, SVIN-193, SVIN-207, SVIN-285, SVIN-292, SVIN-264, SVIN-291, SVIN-346, SVIN-465, SVIN-636, IR-6, and SS-22 (Sindh Sudhar).

Experimental Design and Crop Management

Seeds of all genotypes were sown in a nursery during the first week of April 2022. Healthy seedlings were transplanted approximately 30 days after sowing into the main field following a Randomized Complete Block Design (RCBD) with three replications.

Each experimental plot consisted of four rows, each 4.0 m long. Plant-to-plant and row-to-row spacing were maintained at 20 cm and 25 cm, respectively. All recommended agronomic practices, including irrigation, fertilizer application, weed management, and plant protection measures, were uniformly applied throughout the crop-growing period to minimize environmental variation among treatments.

Data Collection

Observations were recorded from ten randomly selected plants from the two central rows of each experimental plot. The following agronomic and yield-related traits were measured according to standard rice evaluation procedures:

Days to 50% flowering

Days to 90% maturity

Number of tillers per plant

Plant height (cm)

Panicle length (cm)

Number of grains per panicle

Number of fertile spikelets per panicle

Number of sterile spikelets per panicle

Grain yield (kg ha^{-1})

Grain yield was recorded after harvesting and threshing each plot and was converted to kilograms per hectare (kg ha^{-1}).

Meteorological Observations

Daily maximum and minimum temperatures were recorded throughout the experimental period from April to July 2022 using the nearby meteorological station. These data were utilized to characterize the thermal environment experienced by the crop during vegetative and reproductive growth stages.

Statistical Analysis

The collected data were subjected to analysis of variance (ANOVA) following the procedures described by Gomez and Gomez (1984) for a Randomized Complete Block Design. The significance of treatment means was determined at the 5% and 1% probability levels.

Mean comparisons among genotypes were performed using the Least Significant Difference (LSD) test at the 5% probability level.

To determine the relationships among agronomic and yield-related traits, Pearson's correlation coefficients (r) were estimated according to Snedecor and Cochran (1980). Simple linear regression analysis was performed to estimate regression coefficients (b) and coefficients of determination (R^2), thereby quantifying the contribution of individual traits toward grain yield and other associated characteristics. All statistical analyses were performed using Statistix 8.1 (Analytical Software, Tallahassee, FL, USA), while graphs and figures were prepared using Microsoft Excel 2021.

Results

The analysis of variance (ANOVA) revealed significant genetic variability among the 25 rice genotypes for the majority of the studied traits (Table 1). Highly significant ($P \leq 0.01$) differences were observed for days to 50% flowering, days to 90% maturity, plant height, number of fertile spikelets per panicle, number of sterile spikelets per panicle, and grain yield, indicating the presence of substantial genetic variation among the evaluated genotypes. This variability suggests that these traits can be effectively utilized in selection and breeding programs aimed at improving rice productivity. The mean square due to genotypes was highest for grain yield (1,489,362), followed by number of grains per panicle (7,286.91), reflecting considerable variation among the rice genotypes for these economically important traits. Significant differences in plant height (37.85) and days to 50% flowering (31.26) also indicate diverse growth habits and maturity periods, which provide opportunities for developing varieties suitable for different agro-climatic conditions. In contrast, number of tillers per plant (9.34), panicle length (4.28),

and number of grains per panicle (7,286.91) showed non-significant differences among genotypes, suggesting relatively limited genetic variability for these characters under the experimental conditions. The relatively low error mean squares for most traits indicate good experimental precision and reliable estimates of treatment effects. Overall, the ANOVA results demonstrate that sufficient genetic diversity exists among the evaluated rice genotypes, particularly for flowering time, maturity, plant height, spikelet fertility, and grain yield. These traits may therefore serve as important selection criteria in future rice improvement programs aimed at developing high-yielding and well-adapted cultivars.

Table 1. Mean squares (ANOVA) of various characters of rice (*Oryza sativa* L.)

Traits	Replications (DF = 2)	Genotypes (DF = 24)	Error (DF = 48)
Days to 50% flowering	22.18	31.26**	5.41
Days to 90% maturity	20.74	30.87**	5.06
Number of tillers plant ⁻¹	0.52	9.34NS	6.72
Plant height (cm)	19.68	37.85**	3.89
Panicle length (cm)	15.94	4.28NS	2.12
Number of grains panicle ⁻¹	4385.24	7286.91NS	4926.48
Number of fertile spikelets panicle ⁻¹	692.51	1036.74**	118.43
Number of sterile spikelets panicle ⁻¹	1043.26	701.18**	181.92
Grain yield (kg ha ⁻¹)	768,915	1,489,362**	481,624
Note: ** = Highly significant at P ≤ 0.01; NS = Non-significant.			

The mean performance of the 25 rice genotypes exhibited considerable variation for all agronomic traits evaluated (Table 2). Days to 50% flowering ranged from 53.8 days (SS-22) to 65.8 days (SVIN-202), whereas days to 90% maturity varied between 83.7 days (SS-22) and 95.8 days (SVIN-202), indicating the presence of both early- and late-maturing genotypes. The number of tillers per plant ranged from 14.2 (SVIN-465) to 20.8 (SS-22). The highest tillering ability observed in SS-22 suggests its potential for producing greater panicle numbers, while genotypes such as SVIN-291 (19.4 tillers plant⁻¹) and IR-6 (18.8 tillers plant⁻¹) also demonstrated superior performance. Plant height varied from 100.5 cm (SVIN-109) to 112.8 cm (SS-22). Taller genotypes included SS-22, SVIN-166, SVIN-207, and IR-6, whereas SVIN-094 and SVIN-109 were comparatively shorter. Panicle length ranged from 22.2 cm (SVIN-127) to 26.8 cm (SS-22). Longer panicles were also recorded for SVIN-285 (25.8 cm), SVIN-292 (25.4 cm), SVIN-264 (25.4 cm), and IR-6 (25.2 cm). Overall, SS-22 emerged as the most promising genotype, combining early flowering and maturity with the highest tiller number, tallest plant stature, and longest panicles. In contrast, SVIN-202 was the latest maturing genotype, while several genotypes, including IR-6, SVIN-285, SVIN-292, SVIN-264, and SVIN-291, showed desirable agronomic performance and may be considered valuable candidates for future rice breeding programs.

Table 2: Mean performance of (25) genotype for days to 50% flowering, days to 90%, maturity number of tillers plant⁻¹, plant height (cm) and panicle length (cm).

Genotype	Days to 50% flowering	Days to 90% maturity	Tillers plant ⁻¹	Plant height (cm)	Panicle length (cm)
SVIN-033	62.3	92.4	15.8	104.8	22.8
SVIN-035	59.4	89.5	15.2	108.4	23.5
SVIN-094	60.0	90.0	14.5	100.8	23.2
SVIN-105	58.9	88.9	14.4	103.1	23.4
SVIN-109	57.3	87.2	16.8	100.5	22.5
SVIN-119	62.9	92.9	14.8	104.7	24.5
SVIN-127	56.9	86.9	14.8	101.5	22.2
SVIN-133	59.2	89.3	16.2	103.5	22.8
SVIN-145	63.2	93.2	18.2	104.8	22.5
SVIN-151	61.2	91.3	15.9	108.0	22.9
SVIN-161	56.4	86.3	15.8	102.0	22.8
SVIN-166	61.9	91.8	15.5	111.0	23.2
SVIN-177	61.5	91.5	17.2	107.4	23.8
SVIN-202	65.8	95.8	16.8	103.8	23.3
SVIN-193	59.3	89.2	15.2	104.7	23.2
SVIN-207	55.7	85.6	16.8	110.8	24.8
SVIN-285	61.5	91.5	17.5	102.5	25.8
SVIN-292	64.4	94.4	17.8	106.6	25.4
SVIN-264	59.5	89.5	17.8	107.7	25.4
SVIN-291	60.0	90.0	19.4	105.7	23.2
SVIN-346	57.9	87.8	15.8	101.0	23.8
SVIN-465	61.5	91.5	14.2	101.7	23.5
SVIN-636	63.5	93.5	16.5	105.4	22.9
IR-6	65.2	95.5	18.8	109.8	25.2

SS-22	53.8	83.7	20.8	112.8	26.8
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The performance of the 25 rice genotypes showed substantial variation for reproductive traits and grain yield (Table 3). The number of sterile spikelets per panicle ranged from 11.2 in SVIN-292 to 70.4 in SS-22, indicating considerable genetic diversity in spikelet sterility. Genotypes such as SVIN-285 (15.8), IR-6 (22.8), SVIN-465 (28.4), and SVIN-193 (31.0) exhibited relatively lower sterility, which is generally associated with improved grain filling and higher yield potential. The number of grains per panicle varied from 247.6 in SVIN-465 to 347.8 in SS-22. High grain numbers were also recorded for SVIN-291 (306.2), IR-6 (300.5), SVIN-151 (296.5), and SVIN-161 (295.8), reflecting their superior sink capacity. Similarly, the number of fertile spikelets per panicle ranged from 213.2 (SVIN-094) to 278.2 (IR-6). Other genotypes, including SS-22 (275.8), SVIN-285 (263.1), SVIN-292 (260.4), SVIN-346 (253.1), SVIN-291 (251.6), and SVIN-264 (251.3), also produced a high number of fertile spikelets. Grain yield exhibited wide variation among the evaluated genotypes, ranging from 3,125 kg ha⁻¹ (SVIN-161) to 5,825 kg ha⁻¹ (SVIN-285). The highest yielding genotypes were SVIN-285 (5,825 kg ha⁻¹), followed by SVIN-207 (5,560 kg ha⁻¹) and IR-6 (5,480 kg ha⁻¹). These genotypes combined relatively high grain number and fertile spikelet production with comparatively low spikelet sterility, contributing to their superior yield performance. Overall, SVIN-285, IR-6, and SVIN-207 emerged as the most promising genotypes because of their favorable reproductive characteristics and high grain yield. These genotypes may serve as valuable parental material for future rice breeding programs aimed at improving grain productivity and yield stability under diverse environmental conditions.

Table 3: Mean performance of 25 genotype for number of grain panicle-1, number of fertile spikelets panicle-1, number of sterile spikelets panicle-1 and yield kg ha⁻¹.

Genotype	Sterile spikelets panicle ⁻¹	Grains panicle ⁻¹	Fertile spikelets panicle ⁻¹	Grain yield (kg ha ⁻¹)
SVIN-033	42.0	268.4	226.4	4050
SVIN-035	41.2	262.5	221.3	3550
SVIN-094	44.1	262.1	213.2	3710
SVIN-105	50.6	279.5	228.9	4210
SVIN-109	54.8	281.2	226.4	3320
SVIN-119	53.5	274.8	221.3	3725
SVIN-127	68.9	283.6	214.7	3210
SVIN-133	47.2	270.4	213.8	4205
SVIN-145	38.5	270.8	232.3	4040
SVIN-151	56.1	296.5	231.0	3335
SVIN-161	60.2	295.8	235.6	3125
SVIN-166	45.8	277.6	230.5	4120
SVIN-177	34.1	278.5	2	

Correlation and regression analysis demonstrated significant associations among the evaluated agronomic traits (Table 4). Days to 50% flowering exhibited a very strong positive correlation with days to maturity ($r = 0.998$), indicating that late-flowering genotypes generally required more time to reach physiological maturity. Conversely, days to 50% flowering showed significant negative correlations with both the number of sterile spikelets ($r = -0.578$) and panicle length ($r = -0.267$), suggesting that earlier flowering genotypes tended to produce longer panicles with fewer sterile spikelets. Days to maturity was also negatively associated with sterile spikelets ($r = -0.586$) and panicle length ($r = -0.256$). The number of fertile spikelets exhibited positive and highly significant relationships with the number of tillers ($r = 0.521$), plant height ($r = 0.362$), panicle length ($r = 0.448$), and grain yield ($r = 0.317$), whereas it showed a negative association with sterile spikelets ($r = -0.328$). Grain yield displayed

significant positive correlations with plant height ($r = 0.394$) and panicle length ($r = 0.472$), while a significant negative association was observed between sterile spikelets and grain yield ($r = -0.294$). The highest coefficient of determination (99.6%) was recorded between flowering and maturity, indicating that flowering time explained nearly all of the variation in maturity. Overall, the results suggest that panicle length, fertile spikelets, and plant height are valuable selection criteria for improving grain yield in rice breeding programs.

Table 4. Correlation coefficient (r), regression coefficient (b), and coefficient of determination (R^2) among important agronomic traits of rice genotypes

Character association	Correlation coefficient (r)	Regression coefficient (b)	Coefficient of determination (R^2)
Days to 50% flowering vs. days to maturity	0.998	0.992	] 99.6%
Days to 50% flowering vs. number of sterile spikelets	- 0.578	-0.108	33.4%
Days to 50% flowering vs. panicle length	-0.267	-0.071	7.1%
Days to maturity vs. number of sterile spikelets	-0.586	-0.105	34.3%
Days to maturity vs. panicle length	-0.256	-0.281	6.6%
Number of fertile spikelets vs. number of sterile spikelets	-0.328	-0.301	10.8%
Number of fertile spikelets vs. number of tillers plant ⁻¹	0.521	3.245	27.1%
Number of fertile spikelets vs. plant height	0.362	0.067	13.1%
Number of fertile spikelets vs. panicle length	0.448	5.18	20.1%
Number of fertile spikelets vs. grain yield (kg ha ⁻¹)	0.317	0.0054	10.0%
Number of sterile spikelets vs. grain yield (kg ha ⁻¹)	-0.294	-0.0062	8.6%
Number of tillers plant ⁻¹ vs. plant height	0.391	0.417	15.3%
Number of tillers plant ⁻¹ vs. panicle length	0.347	0.118	12.0%
Plant height vs. panicle length	0.446	0.171	19.9%
Plant height vs. grain yield (kg ha ⁻¹)	0.394	0.338	15.5%
Panicle length vs. grain yield (kg ha ⁻¹)	0.472	0.089	22.3%

Note: ** = Significant at $P \leq 0.01$; * = Significant at $P \leq 0.05$.

Discussion

The present study demonstrated significant genetic variability among the evaluated rice genotypes for most agronomic and yield-related traits, indicating the availability of sufficient genetic diversity for crop improvement. Significant differences among genotypes for flowering time, maturity, plant height, fertile and sterile spikelets, and grain yield suggest that these traits are primarily controlled by genetic factors and can be effectively exploited through selection. Similar findings have been reported by (Bano et al., 2017; Chandra et al., 2017; and Darko et al., 2025), who emphasized that genetic variability forms the basis of successful rice breeding programs.

Flowering and maturity exhibited a very strong positive correlation, indicating that genotypes requiring more days to reach 50% flowering also tended to mature later. This relationship is expected because flowering duration largely determines crop maturity in rice. Similar observations have been reported by (Baloch et al., 2017; Thippiani et al., 2017; and Zhang et al., 2021), who found that flowering time is one of the strongest predictors of maturity and adaptation under different environmental conditions.

The significant negative association between flowering time and sterile spikelets indicates that earlier flowering genotypes generally produced fewer sterile spikelets under the prevailing environmental conditions. High temperature during reproductive development has been widely recognized as one of the principal causes of spikelet sterility in rice. Elevated temperatures reduce pollen viability, pollen germination, and fertilization success, resulting in poor grain set and lower productivity (Baloch et al., 2018; Tayade et al., 2018; Wu et al., 2021; Chandio et al., 2025). The relatively lower sterility observed in several genotypes evaluated in the present study may therefore indicate greater adaptation to local climatic conditions.

Positive correlations observed between fertile spikelets, tiller number, panicle length, plant height, and grain yield demonstrate that improvement in these traits is likely to enhance productivity. The number of fertile spikelets directly contributes to sink size and grain production, while longer panicles generally accommodate a greater number of spikelets, ultimately increasing grain yield. Similar positive relationships among these yield components have been reported by (Junejo et al., 2019; Chandra et al., 2017; Darko et al., 2025, and Thippiani et al., 2017), who identified panicle length and fertile spikelets as reliable indirect selection criteria for yield improvement.

The negative relationship between sterile spikelets and grain yield further confirms that spikelet sterility remains one of the major constraints limiting rice productivity under warm environments. Heat stress during panicle initiation and flowering has been reported to decrease pollen fertility, shorten grain filling duration, reduce assimilate translocation, and ultimately lower grain yield (Aghamolki et al., 2014; Henry et al., 2020; Wu et al., 2021 and Rajper et al., 2018). These observations are consistent with the present findings, where genotypes exhibiting lower sterility generally produced comparatively higher grain yields.

Correlation and regression analyses proved useful in identifying important yield-contributing traits. Although grain yield is a complex quantitative trait influenced by multiple genes and environmental factors, positive associations with fertile spikelets, panicle length, and plant height suggest that simultaneous selection for these traits may improve breeding efficiency. Similar conclusions have been reported by Chandra et al. (2017) and Thippiani et al. (2017), who recommended the use of correlation and regression analyses to identify indirect selection criteria in rice breeding programs.

Overall, the present findings indicate that considerable genetic variability exists among the evaluated rice genotypes. Genotypes exhibiting superior performance for fertile spikelets, panicle length, plant height, and grain yield together with lower spikelet sterility may serve as valuable parental materials for developing high-yielding and heat-tolerant rice cultivars suitable for the agro-climatic conditions of Sindh, Pakistan.

Conclusion

The evaluated rice genotypes exhibited substantial genetic variability for most agronomic and yield-related traits. Significant positive relationships between fertile spikelets, panicle length, plant height, and grain yield indicate that these characters can be effectively utilized as indirect selection criteria for yield improvement. Conversely, spikelet sterility showed a negative association with grain yield, highlighting the adverse effects of high temperature during reproductive development. Among the evaluated genotypes, SVIN-285, IR-6, and SVIN-207 consistently demonstrated superior yield performance and desirable agronomic characteristics. These genotypes may therefore be recommended as promising breeding materials for developing high-yielding rice cultivars adapted to the climatic conditions of Sindh, Pakistan.

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