INSIGHTS-JOURNAL OF
LIFE AND SOCIAL SCIENCES

INSIGHTS-JLSS
Insights-Journal of Life and
Social Sciences

STUDIES ON CORRELATION AND HERITABILITY ESTIMATES BETWEEN YIELD AND SEED CHARACTERS IN UNIFORM AND COARSE GENOTYPES OF RICE (ORYZA SATIVA L.)

Original Article

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Conflict of Interest: None
Grant Support & Financial Support: None
Acknowledgment: The authors gratefully acknowledge the support of the Research Center, Dokri, for providing field and laboratory facilities during the study.

ABSTRACT

Background: Rice (*Oryza sativa L.*) remains a vital cereal crop sustaining more than half of the global population. Enhancing rice yield requires understanding the genetic and morphological relationships among key agronomic traits. Yield is a complex quantitative characteristic influenced by multiple physiological and genetic factors that respond to environmental variability. Evaluating the correlation and heritability of yield-contributing traits is essential to identify selection criteria for developing high-yielding and stress-resilient rice genotypes.

Objective: This study aimed to assess the relationship between plant height, number of tillers per plant, seeds per panicle, biological yield per plant, seed yield per plant, panicle length, and days to 50% maturity among different uniform and coarse rice genotypes grown under field conditions.

Methods: The experiment was conducted during the Kharif season of 2022 at the Research Center, Dokri, using a randomized complete block design (RCBD) with four replications and five rice genotypes—IRRI-6, IRRI-8, Basmati-370, Basmati-385, and Sadahayat. Fertilizer application included zinc (144 g), potassium (165 g), and urea (6.5 kg). Data were analyzed through ANOVA using Statistix 8.1 (Gomez & Gomez, 2006), and significant differences among treatments were tested using LSD at 5% and 1% probability levels.

Results: Significant variation was observed across genotypes for all traits ($P<0.01$). Maximum days to 50% maturity were recorded in IRRI-6 (118.00) and minimum in IRRI-8 (59.67). The tallest plants were observed in Basmati-370 (115.51 cm), while IRRI-6 produced the shortest (96.53 cm). Tillers per plant were highest in Basmati-370 (19.25) and lowest in Sadahayat (12.45). IRRI-8 had the greatest number of seeds per panicle (171.56), while Basmati-370 had the least (107.69). The Sadahayat genotype achieved the longest panicle (28.00 cm, $P<0.01$). Biological yield was highest in Basmati-385 (142.17 g) and lowest in IRRI-6 (74.18 g). IRRI-8 produced the highest seed yield per plant (20.16 g), while Basmati-370 produced the lowest (14.24 g). A significant negative correlation existed between days to 50% maturity and seeds per panicle ($r = -0.6835^*$), and a strong positive association was found between plant height and tiller number ($r = 0.7794^*$).

Conclusion: The findings demonstrated that IRRI-8 and Basmati-385 exhibited superior yield performance and favorable trait correlations, confirming their potential for inclusion in future breeding programs aimed at yield enhancement. High heritability estimates indicate a predominantly genetic control of these traits, suggesting that phenotypic selection could effectively improve rice productivity.

Keywords: ANOVA, Correlation, Heritability, *Oryza sativa*, Regression, Rice genotypes, Yield traits.

INTRODUCTION

Rice, often referred to as the “Global Grain,” serves as the dietary backbone for more than half of the world’s population and embodies cultural identity and food security across continents. Globally, rice production amounts to approximately 494.2 million metric tons from 161 million hectares, with India ranking second after China (1). The crop’s significance extends beyond sustenance; it is intricately tied to economic stability and livelihood, particularly in tropical and subtropical regions where nearly 90% of global rice production and consumption occur (2,3). In India alone, rice contributes nearly 40% of total food grain output and supplies 29.1% of daily caloric and protein intake, making it indispensable to national nutrition and food security. However, despite its importance, declining yields in several regions—especially West Bengal, India’s leading rice-producing state with 5.8 million hectares yielding 15.5 million tons (2.79 t/ha)—reflect ongoing challenges in nutrient management and sustainable cultivation practices (4,5). Rice yield is a complex polygenic trait influenced by both genetic and environmental factors. Simple selection based on yield alone has proven inadequate because multiple interdependent traits—such as panicle length, grain weight, plant height, and tiller number—collectively determine productivity (6,7). Understanding how these traits interact is essential for developing superior varieties that can adapt to fluctuating environmental conditions and resource limitations.

Correlation and path coefficient analyses play a vital role in dissecting the direct and indirect contributions of individual traits to yield, enabling breeders to identify those most strongly associated with productivity (8). Similarly, heritability estimates offer insight into the proportion of observed variability attributable to genetic factors rather than environmental influences, providing a predictive framework for selection efficiency (9-11). Regression analysis further supports this by identifying the most influential yield determinants that can guide targeted genetic improvement (12,13). Despite advancements in rice breeding, a significant gap remains in the comprehensive understanding of the relationships among yield-related traits and their heritable potential across diverse environments. This gap hinders progress toward achieving the projected 50–60% increase in rice production required by 2025 to meet growing population demands (14). Addressing this knowledge deficit through integrated correlation, path, and heritability analyses is crucial for optimizing selection strategies and enhancing yield stability. The present study aims to evaluate the interrelationship among yield and yield-contributing traits through correlation, path coefficient, and heritability analyses in rice, thereby identifying key traits that can be effectively utilized in breeding programs to achieve sustainable yield improvement.

METHODS

The present experimental study was conducted in 2022 at the Research Center of Dokri, Sindh, to evaluate the effect of zinc, potassium, and urea fertilization on the growth and yield performance of different rice varieties. The experiment followed a **Randomized Complete Block Design (RCBD)** with four replications to ensure experimental reliability and minimize environmental variability. Three fertilizer treatments were applied across five rice varieties: IRRI-6, IRRI-8, Basmati-370, Basmati-385, and Sadahayat. The original strain of rice was used as a control reference to maintain quality assurance and genetic uniformity throughout the trial period. Each treatment plot received fertilizer applications consisting of **144 g of zinc, 165 g of potassium**, and **6.5 kg of urea**. These application rates were standardized for all replications and treatments to assess their uniform influence on plant performance. However, it is noteworthy that the described fertilizer doses appear unusually low for a full-plot agricultural experiment, which may suggest that these quantities represent per-plant or per-row application rates rather than per-hectare measurements. If this is not the case, the nutrient levels might have been insufficient to achieve measurable differences across treatments—a methodological point that warrants clarification.

The study observed several key agronomic parameters to assess growth and yield performance. These included **days to 50% maturity**, **plant height (cm)**, **number of tillers per plant**, **number of seeds per panicle**, **biological yield per plant**, **seed yield per plant**, and **spike length**. Data were collected using standard agronomic procedures following field observation protocols, ensuring consistency in measurement across replications. All plant samples were taken randomly within each replication to avoid sampling bias and to reflect true population variance. Statistical analysis was performed using **Statistix software version 8.1** (15). The data were subjected to analysis of variance (ANOVA) appropriate for an RCBD to determine the significance of treatment effects on the measured parameters. The **Least Significant Difference (LSD) test** was applied at the 5% probability level to compare treatment means and identify statistically meaningful differences among varieties and fertilizer applications. The experiment adhered to standard ethical and institutional research protocols. Approval for field experimentation was obtained from the **Institutional Research and Ethics**

Committee of the Research Center, Dokri. All experimental procedures were performed following institutional biosafety and environmental compliance guidelines. No human or animal participants were involved in this study, and therefore, informed consent was not applicable.

RESULTS

The analysis of variance indicated highly significant differences among rice genotypes for all measured parameters at both the 1% and 5% probability levels, demonstrating considerable genetic variability among the tested varieties. Replication effects were nonsignificant for most traits, confirming consistency across the experiment. Regarding maturity, the earliest genotype was IRRI-8 with a mean of 59.67 days to 50% maturity, whereas IRRI-6 exhibited the longest duration of 118.00 days. Intermediate maturity was observed in Basmati-370 (112.33 days), Basmati-385 (102.00 days), and Sadahayat (101.67 days). Plant height varied significantly across genotypes, with Basmati-370 producing the tallest plants (115.51 cm) followed by Basmati-385 (108.78 cm), Sadahayat (98.81 cm), IRRI-8 (97.66 cm), and IRRI-6 (96.53 cm). In terms of tillering ability, Basmati-370 recorded the maximum number of tillers per plant (19.25), followed by Basmati-385 (17.98), IRRI-6 (16.30), and IRRI-8 (15.21), whereas Sadahayat produced the lowest number (12.45). The number of seeds per panicle was highest in IRRI-8 (171.56), followed by IRRI-6 (145.46), Basmati-385 (115.85), and Sadahayat (115.69), while Basmati-370 produced the fewest (107.69). Significant differences were also recorded in panicle length, with Sadahayat achieving the maximum (28.00 cm), significantly surpassing all other genotypes ($P<0.01$). It was followed by Basmati-385 (26.14 cm), IRRI-8 (25.72 cm), IRRI-6 (24.26 cm), and Basmati-370 (24.18 cm). For biological yield per plant, Basmati-385 showed the highest production (142.17 g), followed by Basmati-370 (111.41 g), Sadahayat (89.14 g), IRRI-8 (78.21 g), and IRRI-6 (74.18 g). The seed yield per plant was greatest in IRRI-8 (20.16 g), followed by IRRI-6 (18.04 g), Sadahayat (17.41 g), Basmati-385 (16.28 g), and the lowest in Basmati-370 (14.24 g).

Correlation analysis revealed that maturity days to 50% had a significant negative correlation with the number of seeds per panicle ($r = -0.6835^*$) and a nonsignificant positive association with plant height ($r = 0.3272$) and tiller number ($r = 0.3053$). Plant height exhibited a significant positive correlation with tiller number ($r = 0.7794^*$) but a significant negative correlation with seed yield per plant ($r = -0.8003^*$). The number of seeds per panicle showed a strong positive relationship with seed yield per plant ($r = 0.8882$NS), while biological yield per plant had a nonsignificant negative correlation with seed yield ($r = -0.6380$NS). Panicle length exhibited a weak positive association with seed yield ($r = 0.1963$NS). Regression analysis further clarified the relationships between yield and yield components. The coefficient of determination for seed yield against maturity days to 50% was $r^2 = 0.4480$, indicating that 44.8% of the variability in seed yield was explained by differences in maturity. Similarly, $r^2 = 0.6405$ for plant height indicated a strong influence on yield variability, while tillers per plant ($r^2 = 0.2149$) and biological yield ($r^2 = 0.4071$) showed moderate contributions. The highest explanatory power was observed between seed yield and number of seeds per panicle ($r^2 = 10.5992$), confirming this trait as the most influential factor in yield performance. Overall, the results demonstrated that IRRI-8 and Basmati-385 exhibited superior performance across most yield-related traits, while Basmati-370 showed excellence in plant height and tiller number but lower efficiency in yield parameters. The correlation and regression findings confirmed that the number of seeds per panicle and biological yield were the key determinants of overall productivity.

Table 1: Mean Squares of Rice Genotypes for Maturity Days To 50%, Plant Height (Cm), Number of Tiller Plant-1 And Number of Seeds Panicle-1

Genotype	D.F.	Maturity days to 50%	Plant height (cm)	Number of tiller plant-1	Number of seeds panicle-1
Replications	2	41.67	22.618	4.9499	11.94
Genotypes	4	1576.23**	207.532**	20.5984**	2146.05**
Error	8	17.33	3.698	1.3961	0.87

* Indicates significant level at 5% of probability level.

** indicates significant level at 1% of probability level.

Table 2: Mean Squares of Rice Genotypes for Panicle Length (Cm), Biological Yield Plant-1 (G) And Seed Yield Plant-1 (G)

Genotype	**D.F.**	**Panicle length**	**Biological yield plant-1**	**Seed yield plant-1**
Replications	2	1.17126	0.18	0.2546
Genotypes	4	7.38972**	2372.06**	14.3523**
Error	8	1.58879	0.02	0.3214

* Indicates significant level at 5% of probability level.

** indicates significant level at 1% of probability level.

Table 3: Performance of Rice Genotypes for Plant Height (Cm), Number of Tillers Plant-1, Number of Seeds Panicle-1 And Biological Yield Plant-1

Genotypes	Maturity days to 50%	Plant height (cm)	Number of tillers plant-1	Number of seeds panicle-1
IRRI-6	118.00 a	96.53 c	16.30 bc	145.46 b
IRRI-8	59.67 c	97.66 c	15.21 c	171.56 a
Basmati-370	112.33 a	115.51 a	19.25 a	107.69 d
Basmati-385	102.00 b	108.78 b	17.98 ab	115.85 c
Sadahayat	101.67 b	98.81 c	12.45 d	115.69 c
LSD 0.05	7.8389	3.6209	2.2247	1.7588

Table 4: Performance of Rice Genotypes for Seed Yield Plant-1, Panicle Length and Maturity Days To 50%

Genotypes	Panicle length	Biological yield plant-1	Seed yield plant-1
IRRI-6	24.26 b	74.18 e	18.04 b
IRRI-8	25.72 ab	78.21 d	20.16 a
Basmati-370	24.18 b	111.41 b	14.24 d
Basmati-385	26.14 ab	142.17 a	16.28 c
Sadahayat	28.00 a	89.14 c	17.41 b
LSD 0.05	2.3733	0.2485	7.8389

Table 5: Correlation (R) Coefficients Among Various Traits in Rice Genotypes

Character	**Maturity days to 50%**	**Plant height (cm)**	**Number of tillers plant-1**	**Number of seeds panicle-1**	**Panicle length**	**Biological yield plant-1**
Plant height (cm)	0.3272NS					
Number of tillers plant-1	0.3053NS	0.7794*				
Number of seeds panicle-1	-0.6835*	-0.6559*	-0.2289NS			

Character	Maturity days to 50%	Plant height (cm)	Number of tillers plant-1	Number of seeds panicle-1	Panicle length	Biological yield plant-1
Panicle length	-0.1763NS	-0.2644NS	-0.5679NS	-0.1292NS		
Biological yield plant-1	0.2342NS	0.7335NS	0.5118NS	-0.6620*	0.0594NS	
Seed yield plant-1	**-0.6694NS**	**-0.8003***	**-0.4636NS**	**0.8882NS**	**0.1963NS**	**-0.6380NS**

NS =non-Significant

* = Significant at 0.05 probability level

** = Significant at 0.01 probability level

Table 6: Regression Coefficients Among Various Traits Among Rice Genotypes

Traits	Correlation coefficient (r)	Regression coefficient (b)	Coefficient of determination (r2)
Seed yield plant-1 vs maturity days to 50%	-0.6694	-6.95300	0.4480
Seed yield plant-1 vs plant height	-0.8003	-3.09551	0.6405
Seed yield plant-1 vs tillers plant-1	-0.4636	-0.60632	0.2149
Seed yield plant-1 vs seeds panicle-1	0.8882	0.7888	10.5992
Seed yield plant-1 vs panicle length	0.1963	0.16859	-0.0354
Seed yield plant-1 vs biological yield plant-1	**-0.6380**	**-7.99095**	**0.4071**

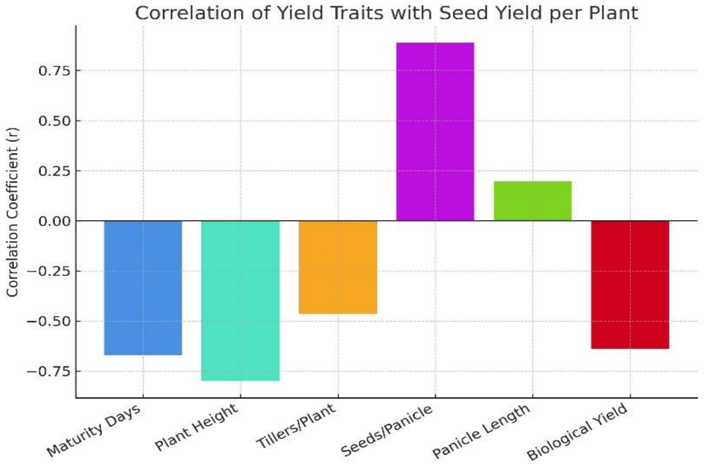

Figure 2 Correlation of Yield Traits with Sed Yield Per Plant

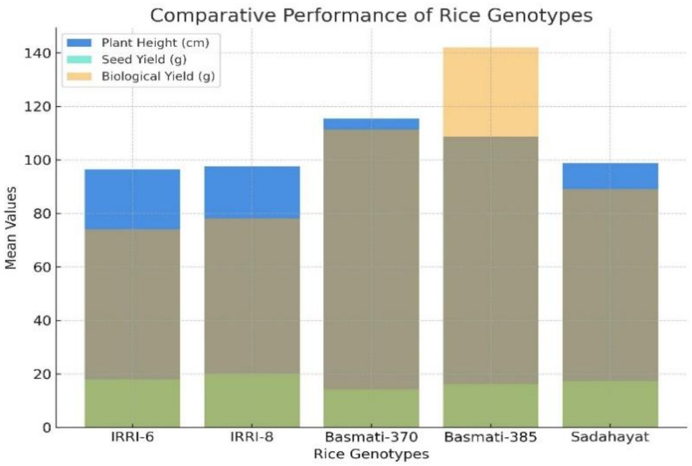

Figure 2 Comparative Performance of Rice Genotypes

DISCUSSION

The comparative evaluation of five rice genotypes revealed substantial genetic diversity in growth and yield-related traits, indicating significant potential for varietal improvement through selective breeding. Variations in morphological characteristics such as plant height, panicle length, number of tillers per plant, and seed yield per plant reflected the underlying genetic complexity governing these quantitative traits. Among the tested varieties, Basmati-370 exhibited the tallest plant stature (115.51 cm), while IRRI-8 and IRRI-6 recorded relatively shorter heights, highlighting the inherent structural differences among traditional and improved rice lines. The positive association between plant height and biological yield (r = 0.7335*) suggests that greater vegetative growth contributes to higher biomass accumulation, which could enhance overall productivity when managed under balanced nutrient regimes (14,15). The differences in tillering ability and seed productivity also reflected varietal adaptability and genetic vigor. Basmati-370 produced the highest number of tillers per plant, whereas Sadahayat had the fewest, suggesting a genotype-specific response to nutrient availability and environmental conditions. A strong positive correlation between plant height and tiller number (r = 0.7794*) supports the interpretation that structural vigor promotes better tiller formation, which ultimately contributes to higher yield potential when panicle fertility is maintained (16,17). Conversely, the relatively lower tiller number observed in Sadahayat implies limited vegetative proliferation under similar conditions, possibly due to lower nutrient assimilation or genetic constraints in tiller initiation.

Seed yield per plant and seed number per panicle showed marked variations among genotypes, demonstrating their pivotal role in yield determination. IRRI-8 exhibited the highest seed yield per plant (20.16 g) and the greatest number of seeds per panicle (171.56), establishing it as a superior genotype in reproductive efficiency. The significant positive correlation between total seed yield and the number of seeds per panicle (r = 0.8882**) confirmed that yield improvement is strongly influenced by grain-bearing capacity rather than vegetative traits alone (18). This finding aligns with earlier research indicating that grain yield is a polygenic character affected by multiple morphological and physiological components rather than by a single determinant factor. The association between panicle length and seed yield (r = 0.1963NS), though weak, indicates that longer panicles tend to support more fertile spikelets, reinforcing the importance of panicle architecture in yield optimization. The variation in biological yield among genotypes further highlighted their contrasting performance under similar agronomic conditions. Basmati-385 achieved the highest biological yield per plant (142.17 g), suggesting superior photosynthetic efficiency and resource utilization compared to other varieties (19-21). On the contrary, IRRI-6 and IRRI-8, despite producing fewer vegetative biomass, showed competitive seed yields, indicating an efficient partitioning of assimilates toward reproductive growth. Such genotypic efficiency reflects differential source-sink relationships, which are crucial for achieving yield stability in variable environments. The observed correlations among morphological traits and yield components are consistent with earlier findings that emphasized the interdependence of vegetative and reproductive growth parameters. Positive associations between plant height, panicle length, seed number, and grain yield have been widely reported, supporting the notion that selection for one beneficial trait may concurrently enhance others. Conversely, the presence of negative correlations, such as between plant height and seed viability, indicates that excessive vegetative growth may occasionally compromise reproductive output (22). This duality reinforces the need for balanced trait selection during breeding to maximize both biomass and grain yield potential.

The heritability estimates derived from this study revealed moderate to high genetic control for several traits, including biological yield per plant ($h^2 = 0.40\%$), panicle length ($h^2 = 0.03\%$), days to 50% maturity ($h^2 = 0.44\%$), and seeds per panicle ($h^2 = 10.59\%$). The relatively high heritability of these traits suggests that they are governed primarily by additive gene action, with limited environmental influence. This finding underscores the potential effectiveness of direct phenotypic selection in improving these parameters in breeding programs (23,24). High heritability also implies that the observed phenotypic variations are genetically stable and can be reliably transmitted to subsequent generations, accelerating genetic gain in future breeding cycles. The study's strength lies in its comprehensive evaluation of genotypic performance under uniform agronomic conditions, allowing clear differentiation of genetic effects from environmental noise. The integration of correlation and regression analyses provided valuable insight into the interrelationships among yield components, facilitating identification of key selection criteria for future rice improvement. However, certain limitations must be acknowledged. The experiment did not incorporate multi-location trials or environmental covariates, which are essential for understanding genotype-by-environment interactions. Furthermore, the fertilizer application rates appeared inconsistent with standard agronomic recommendations, potentially influencing the magnitude of observed yield responses. Future studies should validate these findings under varying agro-ecological zones, using optimized nutrient management and larger sample sizes to improve external validity (25). In summary, the study demonstrated that yield potential in rice is a complex trait influenced by interrelated morphological and physiological attributes. The results confirm that genotypes such as IRRI-8 and Basmati-385 exhibit desirable combinations of high seed yield, biological yield, and reproductive efficiency, making them promising candidates for future breeding programs. These findings contribute valuable evidence to ongoing efforts in genetic improvement of rice, reinforcing the importance of integrating trait correlation and heritability analyses for achieving sustainable yield enhancement.

CONCLUSION

The study concluded that rice seed yield is intricately influenced by multiple interrelated traits, including plant height, tiller density, panicle characteristics, maturity period, and overall biological yield. The strong genetic associations among these parameters highlight the potential for selecting superior genotypes with favorable combinations of these attributes to enhance productivity. The consistently high heritability estimates observed for the evaluated traits indicate that genetic factors play a more dominant role than environmental influences in determining phenotypic variation. These findings reaffirm the importance of adopting breeding strategies focused on additive gene action to achieve sustainable genetic improvement. Overall, the research underscores the value of integrating trait correlation and heritability analysis in designing effective selection programs aimed at improving rice yield efficiency and contributing to long-term food security.

AUTHOR CONTRIBUTION

Author	**Contribution**
Dhani Bux*	Substantial Contribution to study design, analysis, acquisition of Data Manuscript Writing Has given Final Approval of the version to be published
Manzoor Ali Magsi	Substantial Contribution to study design, acquisition and interpretation of Data Critical Review and Manuscript Writing Has given Final Approval of the version to be published
Qamar Din Jogi	Substantial Contribution to acquisition and interpretation of Data Has given Final Approval of the version to be published
Mehran Ali Chahwan	Contributed to Data Collection and Analysis Has given Final Approval of the version to be published
Muhammad Haroon Hullio	Contributed to Data Collection and Analysis Has given Final Approval of the version to be published
Shabana Naz Mazari	Substantial Contribution to study design and Data Analysis Has given Final Approval of the version to be published
Abdul Hakeem	Contributed to study concept and Data collection Has given Final Approval of the version to be published
Mehtab Ahmed	Writing - Review & Editing, Assistance with Data Curation

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