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Research Paper

Correlation and heritability estimation for agronomic traits in rice (*Oryza sativa* L.) genotypes

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Abstract

The current study was conducted at the Botanical Garden, Department of Plant Breeding and Genetics, SAU, Tandojam during the Kharif season 2023. The experiment was laid out in a randomized complete block design with three replications. The ten genotypes Shandar, NIA Mehran, Sarshar, Shua-92, Shabab, NIA-19/A, Shandar-100-1, Shandar-200-1, Shandar-200-2, and NIA-Mehran-100-1 were evaluated for these traits i.e. days to heading, days to flowering, plant height, tillers hill^{-1}, panicle length, fertility %, no. Number of florets panicle^{-1}, grain yield hill^{-1}. The ANOVA revealed that all the traits were significant and showed great variation among the rice genotypes except fertility %. The relationship of days to heading with DTF (0.987**), TPH (0.564**), and GYPH (0.363*) was positive and significant. The relationship of days to flowering with TPH (0.630**), and GYPH (0.455*) was positive and significant. The association of tillers hill^{-1} with PL (-0.513**) was negative but significant. While the relationship with FPP (-0.289^{NS}) and FPCNT (-0.090^{NS}) was negative and non-significant. However, its relationship with GYPH (0.704**) was positive and highly significant. All the traits showed high heritability showing minimal environmental effect, however, panicle length and fertility% showed medium heritability showing some environmental effect on them.

Introduction

With 430 million metric tons produced annually, one of the crops with the greatest value in the world and the second most significant cereal crop after wheat is rice (*Oryza sativa* L.) (IRRI 2009). For half the world's population, it represents a significant part of their diet (Nascente et al., 2013; Prasad, 2011). Furthermore, compared to global rice production in 2010, it is anticipated that more than 116 million extra metric tons of rice will be needed in 2035 due to rising demand (GRiSP, 2013). Pakistan ranks fourth in terms of rice exports and eleventh in terms of production. In Pakistan, rice accounts for 3.2% (Space) of the agricultural sector's value-added and 0.7% of GDP. Since rice is the second main grain in Pakistan and is consumed domestically in amounts of over 2.8 million tons, the average Pakistani household spends more than 3.8 percent of its total food budget on rice and rice flour. Pakistan exports high-quality Basmati rice, which fetches a substantial premium in high-income markets, as well as moderate and low-quality non-aromatic long grain milled rice to developing countries, mostly in East Africa, where it is competed with by China and Vietnam. In general, Pakistani basmati rice costs cheaper than Indian basmati rice. According to Shahzadi et al. (2018), Pakistan's top export destinations for all types of rice are Sub-Saharan Africa, Afghanistan, Bangladesh, Indonesia, the Middle East, and the European Union. Due to its widespread adoption, rice is farmed in every province. Pakistan's rice-growing regions are dispersed from sea level in the south to elevations of up to 2500 meters in the northern highlands, valleys, and terraces; from arid hot plains to coastal tropical damp lowlands in southern Sindh; and from latitudes 24° to 36°. Gujranwala, Sheikhupura, Sialkot, Narowal, Hafizabad, Nankana Sahib, Chiniot, Gujrat, MandiBahaudin, and Kasure Districts are among the Punjabi locations where it is grown. The districts of Jacobabad, Larkana, Badin, Thatta, Shikarpur, and Dadu are where it is grown in Sindh. In addition, Baluchistan's Jaffarabad and Nasirabad districts are classified as rice-producing regions (Bhattacharjee et al., 2002).

Particularly in complex and economic features like yield, the degree of correlation between the characters is a significant aspect. According to Steel & Torrie (1984), correlations are indicators of how strongly the two attributes are related. When a single trait is chosen, all positively correlated characters advance, and all negatively correlated characters regress. As a quantitative characteristic, grain yield is a complicated aspect of each crop. A variety of physiological and morphological traits of plants influence yield. According to Prasad et al. (2001), these yield-contributing elements are intricately linked to one another and are also greatly impacted by the surrounding environment.

Chandrabhan Solanke et al. (2023) claim that the estimate of heritability is a helpful tool for plant breeders. The amount of variability that is caused by genotypic or additive effects can be appreciated by the breeder; in the former case, this is the heritable portion of the variation, and in the later, it is the portion of genetic variation that can be fixed in pure lines. A character with a high heritability should be relatively easy to select because the environment's contribution to phenotype would be relatively limited, resulting in a close connection between genotype and phenotype. However, because the environment tends to obscure genotypic effects, selection may be extremely challenging or practically impossible for a character with low heritability. Therefore, heritability estimates help forecast how traits will be passed down from parents to their children (replace it with from one generation to other). This study's primary goals were to assess the mean performance of agronomic characteristics among rice genotypes and to ascertain the general correlation and heredity of these traits.

Materials and Methods

The current research was conducted at the Botanical Garden, Department of Plant Breeding and Genetics, SAU, Tandojam during the Kharif season 2023. RCBD design with three replications were used in this experiment. The date of sowing was May 13, 2023. The ten genotypes Shandar, NIA Mehran, Sarshar, Shua-92, Shabab, NIA-19/A, Shandar-100-1, Shandar-200-1, Shandar-200-2, and NIA-Mehran-100-1 were evaluated for these traits i.e. days to heading, days to flowering, plant height (cm), tillers hill^{-1}, panicle length (cm), fertility %, no. of florets panicle^{-1}, grain yield hill^{-1} (g).

Statistical analysis

The Statistix 8.1 computer software was used for ANOVA and LSD tests. Whereas correlation was calculated by methods of Snedecor & Cochran (1980). Heritability was estimated as suggested by Falconer (1989).

Results and Discussion

Analysis of variance

The results from the ANOVA revealed that all the genotypes were significant at ($p<0.05$) and ($p<0.01$) levels of probability. However, the fertility % was non-significant. This shows that all the traits except fertility % showed significant differences among all the genotypes. Researchers like Poudel et.al. (2014) and Gyawali et al. (2018) also support our findings.

Table 1: Mean squares from the various traits of rice genotypes

SOV	D.F	DTH	DTF	PH	TPH	PL	FPP	FPCT	GYPH
Replications	2	0.24	0.14	46.81	0.03	0.03	14.70	0.34	2.09
Genotypes	9	115.36**	111.46**	137.15**	61.26**	4.76*	2592.53**	0.64^{NS}	729.55**
Error	18	0.05	0.08	7.66	2.77	1.63	7.92	0.24	4.98

Note: *, ** = Significant at 5% & 1% probability levels respectively. NS = Non-significant

SOV= Source of variation, D.F= Degrees of freedom, DTH= Days to heading, DTF= Days to flowering, PH= Plant height, TPH= Tillers per hill, PL=Panicle length, FPP= No. of florets per plant, FPCT= Fertility%, GYPH= Grain yield per hill.

Table 2: Mean performance from the various traits of rice genotypes

Genotypes	DTH	DTF	PH (cm)	TPH	PL (cm)	FPP	FPCT %	GYPH (g)
Shandar	116.36 a	120.60 b	94.07 f	41.80 a	30.34 ab	189.00 g	95.10 a-c	152.13 a
NIA Mehran	115.50 b	119.67 c	102.93 de	30.33 c	28.33 b-d	232.33 d	94.73 c	104.80 g
Sarshar	115.56 b	121.48 a	107.03 cd	41.67 a	30.33 ab	212.67 e	95.03 bc	145.33 b
Shua-92	108.62 d	113.73 e	98.80 ef	29.33 c	28.67 a-d	192.67 fg	95.17 a-c	114.50 f
Shabab	110.54 c	114.41 d	108.00 c	31.67 bc	30.00 cd	230.67 d	95.37 a-c	115.30 f
NIA-19/A	99.54 h	105.66 j	115.03 a	29.00 c	30.67 a	272.67 a	96.03 a	140.73 c
Shandar-100-1	101.79 g	106.70 i	112.93 ab	31.00 c	26.67 d	196.33 f	95.73 ab	128.27 d
Shandar-200-1	103.47 f	107.52 h	97.17 f	29.30 c	28.00 cd	247.67 c	94.80 bc	114.20 f
Shandar-200-2	103.48 f	108.28 g	104.73 cd	34.33 b	30.00 a-c	256.33 b	94.77 bc	117.67 f
NIA-Mehran-100-1	105.75 e	109.48 f	108.33 bc	29.33 c	30.00 a-c	251.67 bc	95.27 a-c	123.53 e
LSD 5%	0.39	0.49	4.75	2.86	2.19	4.82	0.99	3.83

Correlation coefficient:

The correlations of days to heading with DTF (0.987**), TPH (0.564**), and GYPH (0.363*) were positive and significant. However, the relationship with PH (-0.445*), PL (-0.601**), and FPP (-

0.406*) was also significant but negative. The relationship with FPCNT was negative and non-significant (-0.185^{NS}). The relationship of days to flowering with TPH (0.630**), and GYPH (0.455*) was positive and significant. However, the relation with PH (-0.417*), PL (-0.610**), and FPP (-0.488**) was significant but negative. The relationship with FPCNT was negative and non-significant (-0.182^{NS}). The association of plant height with PL (0.522**), and FPP (0.370*) was noted as positive and significant. However, the relationship with TPH (-0.313^{NS}), FPCNT (-0.007^{NS}), and GYPH (-0.13^{NS}) showed negative and non-significant. The relation of tillers hill^{-1} with PL (-0.513**) was negative but significant. While the relationship with FPP (-0.289^{NS}) and FPCNT (-0.090^{NS}) was negative and non-significant. However, its relationship with GYPH (0.704**) was positive and highly significant. The relationship of panicle length with FPP (0.360*) was positive and significant. While its relationship with FPNT (0.190^{NS}) was positive but non-significant. Its relationship with GYPH (-0.413*) was also significant but negative. The association of florets plant^{-1} with fertility% (r = 0.013^{NS}) and GYPH (r = -0.316^{NS}) was positive non-significant and negative non-significant respectively. However, the relationship between FPCNT and GYPH was (r = -0.033^{NS}) negative and non-significant. Our results are strongly supported by Mohammed, et al. (2007) and Ramakrishman, et al. (2006).

Table 3: Correlation coefficient among the various traits of rice genotypes

Traits	DTH	DTF	PH	TPH	PL	FPP	FPCNT
DTF	0.987**	-					
PH	-0.445*	-0.417*	-				
TPH	0.564**	0.630**	-0.313^{NS}	-			
PL	-0.601**	-0.610**	0.522**	-0.513**	-		
FPP	-0.406*	-0.488**	0.370*	-0.289^{NS}	0.360*	-	
FPCNT	-0.185^{NS}	-0.182^{NS}	0.007^{NS}	-0.090^{NS}	0.190^{NS}	0.013^{NS}	-
GYPH	0.363*	0.455*	-0.013^{NS}	0.704**	-0.413*	-0.316^{NS}	-0.033^{NS}

Note: *, ** = Significant at 5% & 1% probability levels respectively. NS = Non-significant

Table 4: Estimation of heritability for different agronomic traits in rice genotypes

Characters	Genotypic variance	Phenotypic variance	Heritability % (Broad sense)
Days to heading	115.31	115.38	99.9
Days to flowering	111.38	111.49	99.9
Plant height	129.49	139.70	92.7
Tillers hill^{-1}	58.49	62.18	94.1
Panicle length	3.13	5.30	59.1
Florets panicle^{-1}	2584.61	2595.17	99.6
Fertility %	0.40	0.72	55.5
Grain yield hill^{-1}	724.57	731.21	99.1

Heritability estimates:

Heritability estimates are an important technique to check how much the environment affects a character. For days to heading, there was less genotypic variance (115.31) than phenotypic variance (115.38) that caused high heritability. High heritability (99.9%) shows no environmental influence on days to heading. For days to flowering, there was less genotypic variance (111.38) than phenotypic variance (111.49) causing high heritability. High heritability (99.9%) shows no environmental influence on days to flowering. For plant height, there was less genotypic variance (129.49) than phenotypic variance (139.70) which caused high heritability. High heritability (92.7%) shows no environmental influence on plant height. For tillers hill^{-1}, there was less genotypic variance (58.49) than phenotypic variance (62.18) that caused high heritability. High heritability (94.1%) shows no environmental influence on tillers hill^{-1}. For panicle length, there was less genotypic variance (3.13) than phenotypic variance (5.30) causing high heritability. Moderate heritability (59.1%) shows there is some environmental influence on panicle length. For florets panicle^{-1}, there was less genotypic variance (2584.61) than phenotypic variance (2595.17) that caused high heritability. High heritability (99.6%) shows no environmental influence on florets panicle^{-1}. For fertility %, there was less genotypic variance (0.4) than phenotypic variance (0.72) that caused high heritability. Moderate heritability (55.5%) shows some environmental influence on fertility %. For grain yield hill^{-1}, there was less genotypic variance (724.57) than phenotypic variance (731.21) that caused high heritability. High heritability (99.1%) shows no environmental influence on grain yield hill^{-1}. In their study of aromatic and fine rice genotypes, Islam et al. (2016) and Bekele et al. (2013) found similar results for high heritability and genetic advancement in grain yield and days to heading and flowering, demonstrating the presence of additive genetic control. High heritability for the number of spikelets/florets per panicle was also reported by Bhatti et al. (1998).

Conclusions

It is concluded from the above study that all the traits including DTH, DTF, PH, TPP, PL, FPP, and GYPH were significant hence, showed great variation among the rice genotypes except fertility%. From the mean performance, it is concluded that among the ten genotypes Shandar and NIA Mehran took a maximum of days to heading and flowering. It also had maximum tillers plant^{-1} and panicle length that leads to maximum grain yield hill^{-1} as compared to other genotypes. For shortest days to heading and flowering and tallest height the genotypes NIA-19/A and Shandar-100-1 were noted, they also had maximum fertility% among the rest of the genotypes and also had a comparable grain yield hill^{-1}.

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